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# Anaconda Documentation

**Anaconda Inc.**

**Sep 18, 2020**



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## Anaconda Enterprise

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Anaconda Enterprise is an enterprise-ready, secure, and scalable data science platform that empowers teams to govern data science assets, collaborate, and deploy data science projects.

Enterprise 5 includes these capabilities:

- Easily deploy your projects into interactive data applications, live notebooks, and machine learning models with APIs.
- Share those applications with colleagues and collaborators.
- Manage your data science assets: notebooks, packages, environments, and projects in an integrated data science experience.

View [Anaconda Enterprise 5 documentation](#).



## CHAPTER 2

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### Anaconda Team Edition

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Anaconda Team Edition is our latest generation repository for all things Anaconda. With support for all major operating systems, the repository serves as your central conda, PyPI, and CRAN packaging resource for desktop users, development clusters, CI/CD systems, and production containers.



## CHAPTER 3

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### Anaconda Individual Edition

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Anaconda Individual Edition is a free, easy-to-install package manager, environment manager, and Python distribution with a collection of 1,500+ open source packages with [free community support](#). Anaconda is platform-agnostic, so you can use it whether you are on Windows, macOS, or Linux.

View [Anaconda Individual Edition documentation](#).



Anaconda Cloud is a package management service that makes it easy to find, access, store, and share public notebooks and environments, as well as conda and PyPI packages.

View [Anaconda Cloud documentation](#).

### 4.1 Anaconda Enterprise 4

Anaconda Enterprise 4 includes [Anaconda Distribution](#), Anaconda Enterprise 4 Repository and Anaconda Enterprise 4 Notebooks. This is our previous-generation product, and documentation is provided for our current customers.

[Anaconda Enterprise 4 Repository](#) is an enterprise server on your network or your private cloud where open source and proprietary packages may be stored, retrieved and shared.

[Anaconda Enterprise 4 Notebooks](#) is a browser-based Python data analysis environment and visualization tool in a secure, governed environment.

Please refer to [Anaconda Enterprise 5](#) documentation for our current-generation product.

#### 4.1.1 Anaconda Enterprise 4 Repository

##### *Open Data Science Hub*

Anaconda Repository is an enterprise server on your network or your private cloud where open source and proprietary packages may be stored, retrieved and shared. It is used to govern access to data science assets including packages, environments and notebooks.

Anaconda Repository has a self-contained internal mirror of packages and can install securely behind an enterprise firewall or in an air gapped environment. It supports many repositories including PyPI, conda and the Anaconda Repository.

Many enterprises have customized local instances of Repository. Anaconda also makes an instance of Repository available for public use at [Anaconda Cloud](#).

## User guide

### Getting started

- *Finding, downloading and installing packages*
- *Building and uploading new packages*
- *Sharing notebooks*
- *Viewing notebooks*
- *Sharing environments*

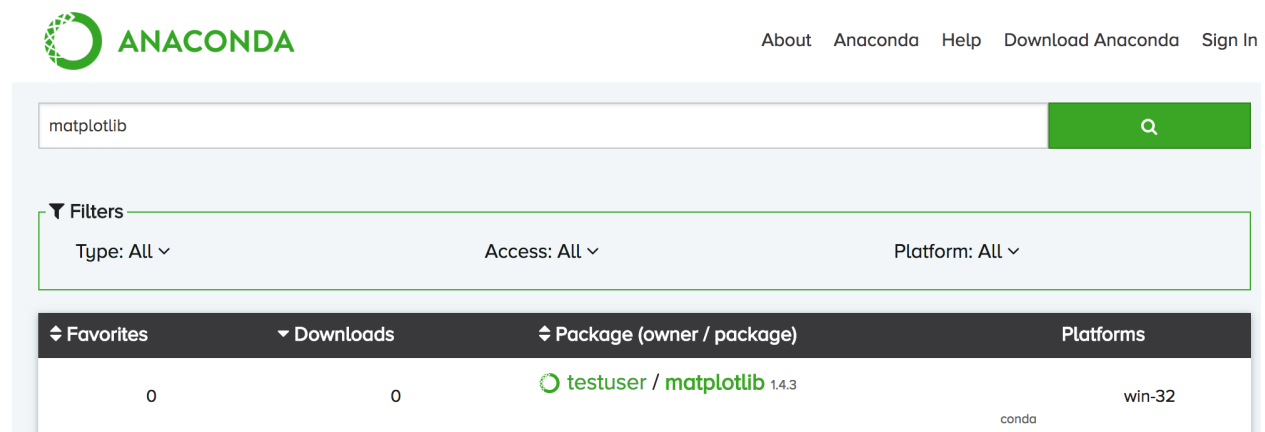
### Finding, downloading and installing packages

You do not need to have an Anaconda Repository account or be logged in to search for, download, or install packages, notebooks, environments or installers.


You do need an account to access *private packages* without an *access token* and to upload and share your own packages, notebooks, environments and installers with others.

### Searching for packages

1. In the top Search box, type part or all of the name of a file you are searching for, and then press Enter.
2. Packages that match your search string are displayed. To see more information, click the package name.



The screenshot shows the Anaconda Cloud search interface. At the top is the Anaconda logo and navigation links: About, Anaconda, Help, Download Anaconda, and Sign In. Below the logo is a search bar containing the text 'matplotlib' and a green search button. Under the search bar is a 'Filters' section with three dropdown menus: 'Type: All', 'Access: All', and 'Platform: All'. Below the filters is a table with the following columns: 'Favorites', 'Downloads', 'Package (owner / package)', and 'Platforms'. The table contains one row of results for 'matplotlib' by 'testuser', version '1.4.3', available on 'conda' for 'win-32' platform. The 'Favorites' and 'Downloads' columns show a count of 0.

⬆ Favorites	⬇ Downloads	⬆ Package (owner / package)	Platforms
0	0	 testuser / matplotlib 1.4.3	conda win-32

### Refining your search results

You can filter search results using 3 filter controls:

- Type: All, conda only or PyPI only.



- Access: All, Public and/or Private—available only if you are logged in.
- Platform: All, Source, Linux-32, Linux-64, Noarch, OSX-64, Win-32 and Win-64.

NOTE: Source packages are source code only, not yet built for any specific platform. Noarch packages are built to work on all platforms.

## Downloading and installing packages from Anaconda Repository

You can download and install packages using *Anaconda Navigator*, the graphical user interface for Anaconda®. Advanced users may prefer a Terminal window or an Anaconda Prompt.

### Using Navigator

Navigator is automatically installed when you install Anaconda.

To download and install a package into its own environment:

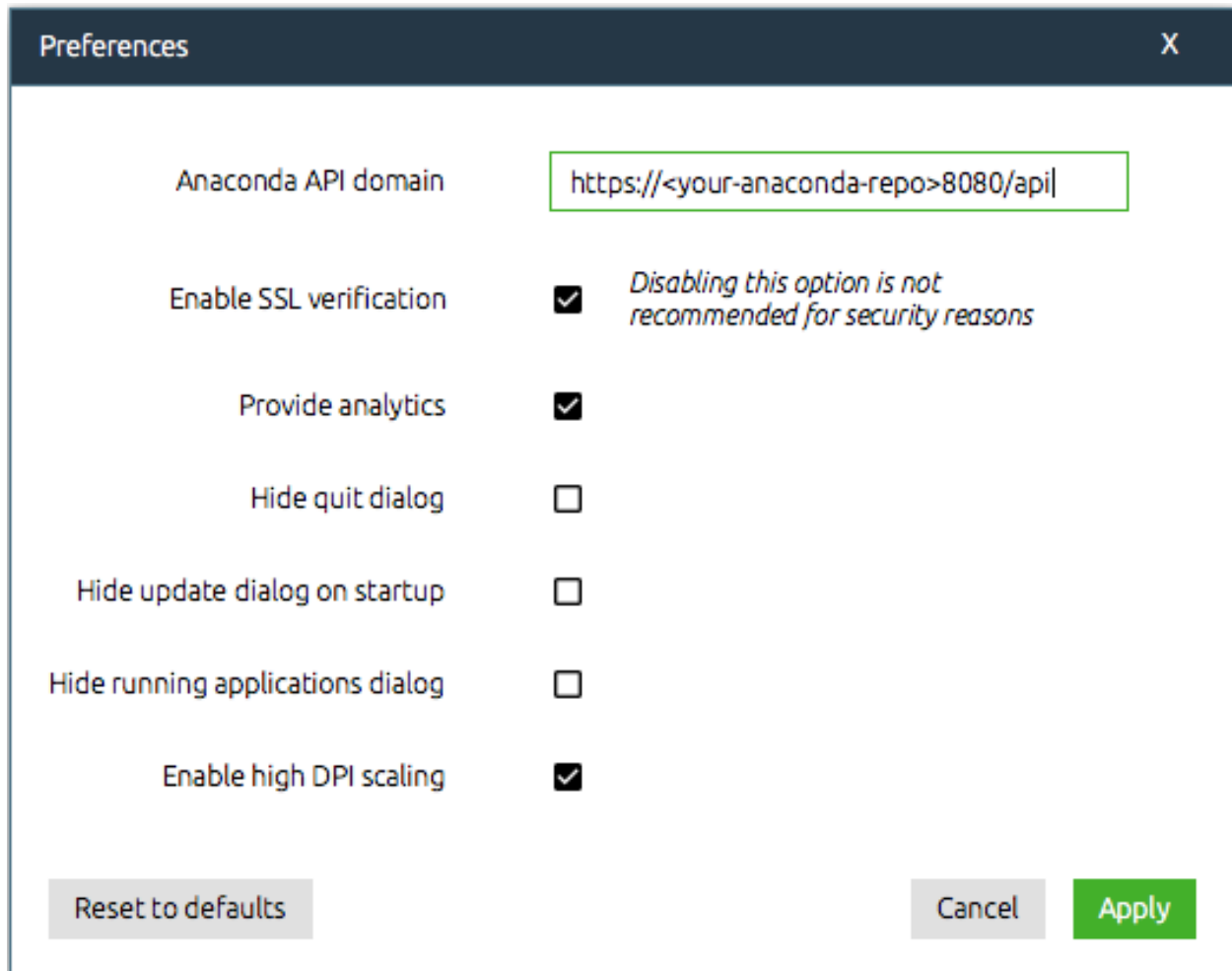
1. Start Navigator by clicking its program icon on your desktop or in your programs menu.
2. Set up Navigator to search your local Repository:
  1. From the top menu bar, select Preferences.
  2. In the Anaconda API domain box, type the address of your local Repository:

NOTE: If your organization does not use HTTPS, use `http` in the domain box and clear the Enable SSL verification checkbox.

NOTE: If your organization uses subdomains, enter the address as `https://api.<your-anaconda-repo>:8080`. Replace `<your-anaconda-repo>` with the name of your local Repository. If that does not work, contact your system administrator.

3. Click the Apply button.
3. Sign Navigator into your local Anaconda Cloud—Repository— so you can search for packages marked as private:
  1. Click the top right Sign in to Anaconda Cloud button.
  2. Type your Repository username and password:
3. Click the Login button.
4. On the **Environments** tab, in the far-right Search packages box, type the name of the desired package.
5. In the list to the left of Channels, select either Not installed or All, then click the Search button.
6. Select the checkbox of the package you want to install, then click the Apply button.

For more information, see the full Navigator documentation *Anaconda Navigator*.



Sign in

X

**Anaconda Cloud** is where packages, notebooks, and environments are shared. It provides powerful collaboration and package management for open source and private projects.

You can register by visiting the [Anaconda Cloud](#) website.

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**Already a member? Sign in!**

Username:

Password:

[I forgot my username](#)  
[I forgot my password](#)

### Using conda in a Terminal window or an Anaconda Prompt

Conda is automatically installed when you install Anaconda.

To download and install a package into its own environment:

1. Locate a package on Anaconda Repository that you want to download, then click the package name.  
A detail page displays specific installation instructions for the current operating system.
2. Enter the command into your Terminal window or Anaconda Prompt.

EXAMPLE: To download and install a package with conda:

```
conda install -c USERNAME PACKAGE
```

TIP: Conda expands USERNAME to a URL such as `https://<your-anaconda-repo>/USERNAME`, based on the settings in the `.condarc` file.

### Building and uploading new packages

Building and uploading new packages is optional, and best suited for advanced users who are comfortable using a Terminal application. It requires the `anaconda-client`, which is easy to get if you have installed Anaconda.

Use Terminal window or Anaconda Prompt to run the following command line commands.

1. To build and upload packages, first install the Anaconda Client CLI:

```
conda install anaconda-client
```

2. Log into your Repository account:

```
anaconda login
```

At the prompt, enter your Repository username and password.

3. Choose the package you would like to build. For this example, you can download our public test package:

```
git clone https://github.com/anaconda-platform/anaconda-client
cd anaconda-client/example-packages/conda/
```

4. To build your test package, first install `conda-build` and turn off automatic Client uploading, then run the `conda build` command:

```
conda install conda-build
conda config --set anaconda_upload no
conda build .
```

5. Find the path where the newly-built package was placed, so that you can use it in the next step:

```
conda build . --output
```

6. Upload your test package to your Repository account:

```
anaconda login
anaconda upload /your/path/conda-package.tar.bz2
```

NOTE: Replace `/your/path/` with the path you found in the previous step.

For more information, see [Working with conda packages](#).

## Sharing notebooks

To upload a notebook to Anaconda Repository with `anaconda-client`, open Anaconda Prompt or Terminal and then enter:

```
anaconda upload my-notebook.ipynb
```

NOTE: Replace `my-notebook` with the name of your notebook.

## Viewing notebooks

You can view an HTML version of your notebook in Anaconda Repository. Log into your account, then from the drop-down menu of the view button, select Notebooks. Click the name of the notebook you want to view.

You can also view an HTML version of your notebook directly from:

```
http://<your-anaconda-repo>/USERNAME/my-notebook
```

NOTE: Replace `<your-anaconda-repo>` with your Repository name, `USERNAME` with your username and `my-notebook` with the name of your notebook.

Anyone who has `anaconda-client` and access to Repository can download your notebook. To download the notebook, open Anaconda Prompt or Terminal and enter:

```
anaconda download USERNAME/my-notebook
```

## Sharing environments

A **saved conda environment** can be uploaded to Anaconda Repository with the web interface or the `anaconda upload` command.

To save the environment, run this command in an Anaconda Prompt or Terminal window:

```
conda env export -n my-environment -f my-environment.yml
```

To upload it with the web interface go to:

```
https://<your-anaconda-repo>/<USERNAME>/environments
```

Then use the Upload button in the top right corner.

To upload it with the `anaconda upload` command:

```
anaconda upload my-environment.yml
```

NOTE: Replace `my-environment` with the name of your environment.

You can view a list of your uploaded environments at:

```
http://envs.<your-anaconda-repo>/USERNAME
```

NOTE: Replace `<your-anaconda-repo>` with the name of your local Repository and `USERNAME` with your username.

Anyone who has access can download and install your environment. Open Anaconda Prompt or Terminal and then enter:

```
conda env create user/my-environment
source activate my-environment
```

NOTE: Replace `user` with your username and `my-environment` with the name of your environment.

### How to...

- *Use packages*
- *Use the Anaconda Client CLI*
- *Build packages*

## Use packages

### Find a package

From Anaconda Repository, you can search for packages by package name. From the top navigation bar of any page, in the search box enter the package name. You can filter your searches using type of the packages, access or labels and you can sort results by number of favorites or number of downloads by clicking the search results column heading.

### Download and install a conda package from Repository

To install a conda package, in a Terminal window or an Anaconda Prompt run:

```
conda install -c USERNAME PACKAGE
```

NOTE: Conda expands `USERNAME` to a URL such as `https://<your-anaconda-repo>/username` based on the settings in the `.condarc` file.

NOTE: Replace `USERNAME` with your username and `PACKAGE` with the name of the desired package.

### Download and install a PyPI package from Repository

To install a PyPI package, in a Terminal window or an Anaconda Prompt run:

```
pip install --index-url pypi.anaconda.org/USERNAME/PACKAGE
```

NOTE: Replace `USERNAME` with your username and `PACKAGE` with the name of the desired package.

## Use the Anaconda Client CLI

### Install Client

See *Installing the Anaconda Client CLI*.

## Find my Client login credentials

Your credentials for Client are those that you used to create an account on Repository.

To get help:

1. In a browser, navigate to your Repository.
2. Select the **Sign In** tab.
3. Click either the I forgot my password link or the I forgot my username link.

## Log into Client

After you have downloaded and configured Client, in a Terminal window or an Anaconda Prompt, run:

```
anaconda login
```

## Display a list of Client commands

In a Terminal window or Anaconda Prompt, run:

```
anaconda --help
```

## Find out more about a Client command

In a Terminal window or Anaconda Prompt, run:

```
anaconda COMMANDNAME -h
```

NOTE: Replace `COMMANDNAME` with the name of the command about which you want more information.

## List all available Client configuration files

In a Terminal window or Anaconda Prompt, run:

```
anaconda config --files
```

## List all of your Client configuration variables

In a Terminal window or Anaconda Prompt, run:

```
anaconda config --show
```

## Find out more about Client

If you have a question that you cannot answer using the help command or documentation, contact your system administrator who has access to Anaconda Enterprise Support.

### Build packages

#### Build and upload a package

For a quick example, see *Building and uploading new packages*.

#### Test a built package

In a Terminal window or Anaconda Prompt, specify the `--use-local` option:

```
conda create --use-local -n test PACKAGE
```

NOTE: Replace `PACKAGE` with the name of your package.

#### Upload a package to Repository

In a Terminal window or Anaconda Prompt, run:

```
anaconda upload PACKAGE
```

NOTE: Replace `PACKAGE` with the name of your package.

#### Find help for uploading packages

You can obtain a complete list of upload options, including:

- Package channel.
- Label.
- Availability to other users.
- Metadata.

In a Terminal window or Anaconda Prompt, run:

```
anaconda upload -h
```

### Tutorials

- *Using labels in the development cycle*
- *Working with other file types*

#### Using labels in the development cycle

Anaconda Repository *labels* can be used to facilitate a development cycle and organize the code that is in development, in testing and in production, without affecting non-development users.



In this tutorial, we show how to use a “test” label, so that you can upload files without affecting your production-quality packages. Without a `--label` argument the default label is “main.”

1. You need to begin with a conda package. If you do not have one, use our example conda package. Before you build the package, edit the version in the `meta.yaml` file in `anaconda-client/example-packages/conda/` to be 2.0:

```
git clone https://github.com/anaconda-platform/anaconda-client
cd anaconda-client/example-packages/conda/
nano meta.yaml # Bump version to 2.0
conda config --set anaconda_upload no
conda build .
```

2. Upload your test package to Repository using the Client `upload` command. Adding the `--label` option tells Repository to make the upload visible only to users who specify that label:

```
anaconda upload /path/to/conda-package-2.0.tar.bz2 --label test
```

NOTE: Replace `/path/to/` with the path to where you stored the package.

3. You now can see that even when you search conda “main,” you do not see the 2.0 version of the test package. This is because you need to tell conda to look for your new “test” label.
4. The `--override` argument tells conda not to use any channels in your `~/.condarc` file.

The following command produces no 2.0 results:

```
conda search --override -c USERNAME conda-package
```

NOTE: Replace `USERNAME` with your username.

Your 2.0 package is here:

```
conda search --override -c USERNAME/label/test conda-package
```

NOTE: Replace `USERNAME` with your username.

5. You can give the label `USERNAME/label/test` to your testers.

NOTE: Replace `USERNAME` with your username.

6. Once they finish testing, you may then want to copy the test packages back to your “main” label:

```
anaconda label --copy test main
```

Your version 2.0 is now in main:

```
conda search --override -c USERNAME conda-package
```

NOTE: Replace `USERNAME` with your username.

You can also manage your package labels from your dashboard: <https://<your-anaconda-repo>/USERNAME/conda-package>.

NOTE: Replace `<your-anaconda-repo>` with the name of your local Repository, and `USERNAME` with your username.

If you use `anaconda-client` 1.7 or higher, you can use `anaconda move` to move packages from one label to another:

```
anaconda move --from-label OLD --to-label NEW SPEC
```

Replace OLD with the old label, NEW with the new label, and SPEC with the package to move. SPEC can be either “user/package/version/file”, or “user/package/version” in which case it moves all files in that version.

### Working with other file types

In addition to uploading or downloading *packages*, you can also upload or download other file types to/from Anaconda Repository.

### Uploading other file types

You can upload any type of file with *Anaconda Client command line interface* (CLI) by using the steps below.

PyPI package files, conda package files and notebook files are automatically detected. There is no auto-detect for other types of files, so you must explicitly specify the `package`, `package-type` and `version` fields.

In the following example, we upload a spreadsheet named `baby-names` in comma separated value (CSV) format.

1. Create a new package, which creates a *namespace* that can hold multiple files:

```
anaconda login
anaconda package --create jsmith/baby-names
```

2. Upload the file to the new namespace:

```
anaconda upload --user jsmith --package baby-names --package-type file --version_
↪1 baby-names1.csv
```

NOTE: In this example:

- The user or organization name is “jsmith.”
- The package name is “baby-names.”
- The package type is “file.”
- The version is “1.”
- The full filename is `baby-names1.csv`.

### Downloading other file types

Files, such as the one created above, are available at:

```
https://<your-anaconda-repo>/USERNAME/PACKAGE
```

Anyone can download these files using Client:

```
anaconda download USERNAME/PACKAGE
```

NOTE: Replace `<your-anaconda-repo>` with the name of your local Repository, `USERNAME` with the desired username and `PACKAGE` with the desired package name.

If the repository has multiple files with the same name and different extensions, `anaconda download` will download all of them by default. If you use `anaconda-client` 1.7 or higher, you can use `anaconda download` with the option `--package-type` or `-t` to specify only one of these files. This option can work with the values `pypi`, `conda`, `ipynb`, and `env`.

## Tasks

This guide covers all the everyday tasks for a user of Anaconda Repository.

### Creating an account

The information below applies to personal Anaconda Repository accounts. For information on organization accounts, see [Working with organizations](#).

You do not need an Anaconda Repository account to find, download and use packages.

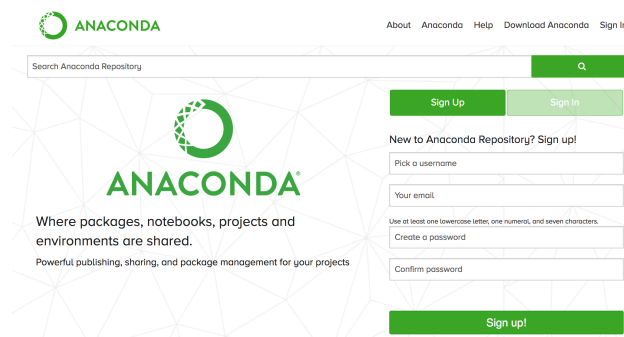
However, you do need a Repository account to:

- Author packages.
- Upload packages, notebooks and environments.
- Access private packages that are shared with you.
- Create organizations.

If your administrator sent you an email with a login address, username and password, use them.

Otherwise, to sign up for an Anaconda Repository account:

1. In a browser, go to the address your administrator gave you.



1. Make sure the **Sign Up** tab is active.  
NOTE: There is also a **Sign In** tab for existing users.
2. Select a username.
3. Enter your email address.
4. Create a password that is at least 7 characters long.
5. Enter the password again to confirm it.
6. Read and accept the Terms and Conditions.
7. Click the Sign up button.

The system creates your user account, logs you in and displays your *personal dashboard*.

## Using your Repository dashboard

When you log in to Repository, your personal dashboard is displayed.

The screenshot shows the Anaconda Repository dashboard. At the top, there is a navigation bar with the Anaconda logo, a search bar labeled "Search Anaconda Repository", and user controls including "View", "Help", and a user profile icon labeled "testuser1". Below the navigation bar is the "My Anaconda Landscape" section. This section contains five cards: "Packages", "Notebooks", "Environments", "Installers", and "Favorites". Each card has a "View all" link and a green box with instructions on how to upload or create items. At the bottom of the landscape section is an "Activity Feed" card showing a welcome message and links for getting started.

In the top navigation bar, the currently active user or organization is shown at the far right.

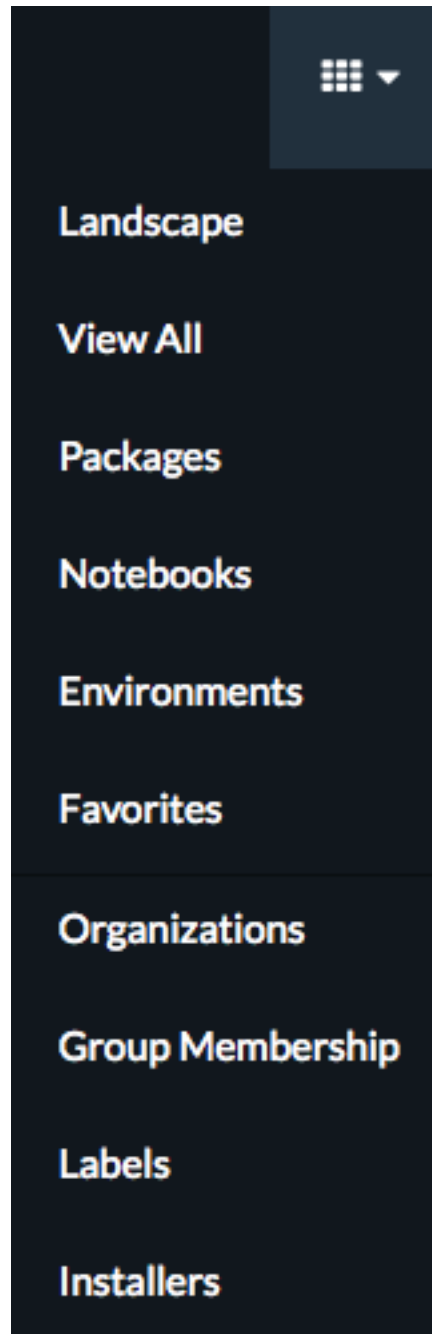
**TIP:** If the email address on your account is associated with a Gravatar account, Repository displays your profile photo. To associate your email address with Gravatar or to change your Gravatar profile photo, see [gravatar.com](https://gravatar.com).

Packages, notebooks, environments, projects and installers that you have created with this account appear on your Landscape.

Click the view button to see the following options:

- Landscape: Your home page.
- Favorites: Other users' packages that you have starred.
- Packages: Only packages you have created.
- Notebooks: Only notebooks you have created.

- Environments: Only environments you have created.
- Installers: If you have created and uploaded installers using *Cloudera*, they are displayed here.
- Projects: If you have created and uploaded *projects*, they are displayed here.



### Installing the Anaconda Client CLI

You can use the Anaconda Client command line interface (CLI) in an Anaconda Prompt or Terminal window to:

- Connect to and manage your Anaconda Repository account.
- Upload *packages* you have created.
- Generate access *tokens* to allow access to private packages.

NOTE: Anaconda Client is not necessary to search for and download packages.

Anaconda Client requires conda to be installed. If you have Anaconda, conda is already installed.

To install with conda, open Anaconda Prompt or Terminal window and enter:

```
conda install anaconda-client
```

After installing, view the complete list of Client tasks with this command from Anaconda Prompt or Terminal window:

```
anaconda -h
```

### Working with organizations

- *Creating an organization*
- *Uploading packages to an organization*
- *Transferring packages to an organization*
- *Customizing users and groups*
- *Creating groups for differing access levels*
- *Deleting an organization*

### Creating an organization

1. Log in to your Anaconda Repository.
2. From the far-right drop-down menu next to your username, select New Organization.
3. Scroll to the “Create Organization” box and enter a name for your organization.

NOTE: Organization names can include dashes, but not spaces or special characters.

4. Supply an email address for the organization, then click the Create Organization button.

The system displays the dashboard for the new organization.

As the creator and owner of an organization, you have automatic administrative access to this organization and any packages associated with the organization.

From the far-right drop-down menu, Profile option shows a list of all organizations to which you belong.

## Uploading packages to an organization

Only the co-owners of an organization may upload packages to the organization.

To upload a package to an organization, in a Terminal or Anaconda Prompt use the `-u/--user` option:

```
anaconda upload --user ORGANIZATION package.tar.bz2
```

NOTE: Replace `ORGANIZATION` with the name of the organization, and `package.tar.bz2` with the name of the package.

## Transferring packages to an organization

See *Transferring a package to a new owner*.

## Customizing users and groups

Only the co-owners of an organization may customize users and groups of the organization.

To add, remove, or edit group and user access for an organization you administer:

From the top right drop-down menu, select Groups, then click the name of the group you want to edit.

In the Members box, type the username of the user you want to add as a member, then click the Add button.

To remove a member, in the list on the Members page, click the delete icon (trash can).

Users receive a dashboard notification when you add them to an organization.

## Creating groups for differing access levels

Within an organization, you can create a group to customize access for a group of users:

1. From the top right drop-down menu, select Groups, then click the + New Group button.
2. Give the group a name and click the Create group button.
3. In the Members box, add the desired members by username.
4. Add installers, packages, notebooks, projects or environments that this group can access.
5. Click the Save Group button.

## Deleting an organization

To delete an organization you administer and erase all data associated with it:

1. At the top right of the Repository interface, in the Profile list, select Switch To.
2. Select the organization you want to delete.
3. In the Profile list, select Settings.
4. Select the Account option. You may be asked to verify your password.
5. In the Delete Account section, click the Delete button.

A confirmation page requests that you provide the full name of the organization.

### Working with packages

All files uploaded to Anaconda Repository are stored in *packages*. Each Repository package is visible at its own unique URL based on the name of the user who owns the package and the name of the package. You can create a Repository package and then upload files into it.

Each user and organization has their own location called a *namespace* where they may host packages.

A *label* is part of the URLs for Repository where conda looks for packages. Each file within a package may be tagged with one or more labels, or not tagged at all to accept the default label of `main`. Labels are searched only if you specify a label.

### Using package managers

- *Working with conda packages*
- *Working with PyPI packages*

Repository supports two package managers, `conda` and `PyPI`. To work with conda or PyPI packages, you must use their corresponding subdomains.

EXAMPLE: To install conda packages from the user “travis,” use the Repository URL:

```
https://conda.<your-anaconda-repo>/travis
```

EXAMPLE: To install PyPI packages from the user “travis,” use the Repository URL:

```
https://pypi.<your-anaconda-repo>/travis
```

### Working with conda packages

#### Building a conda package

To build a package using `conda build`:

1. Install Anaconda Client and conda build:

```
conda install anaconda-client conda-build
```

2. Choose the repository for which you would like to build the package. In this example, we use a simple, public `conda test` package:

```
git clone https://github.com/anaconda-platform/anaconda-client
cd anaconda-client/example-packages/conda/
```

In this directory, there are two required files, `build.sh`, and `meta.yaml`.

NOTE: Linux and macOS systems are Unix systems. Packages built for Unix systems require a `build.sh` file, packages built for Windows require a `bld.bat` file, and packages built for both Unix and Windows systems require both a `build.sh` file and a `bld.bat` file. All packages require a `meta.yaml` file.

3. To build the package, turn off automatic Client uploading and then run the `conda build` command:



```
conda config --set anaconda_upload no
conda build .
```

All packages built in this way are placed in a subdirectory of *Anaconda's* `conda-bld` directory.

4. You can check where the resulting file was placed with the `--output` option:

```
conda build . --output
```

For more information on conda's overall build framework, you may also want to read the articles [Building conda packages](#) and [Tutorials on conda build](#).

## Uploading a conda package

Upload the test package to Repository with the *anaconda upload* command:

```
anaconda login
anaconda upload /path/to/conda-package.tar.bz2
```

NOTE: Replace `/path/to/` with the path to where you stored the package.

## Installing conda packages

You can install conda packages from Repository by adding channels to your conda configuration.

1. Because conda knows how to interact with Repository, specifying the channel "sean" translates to `https://<your-anaconda-repo>/sean`:

```
conda config --add channels sean
```

2. You can now install public conda packages from Sean's Repository account. Try installing the `testci` package at `https://<your-anaconda-repo>/sean/testci`:

```
conda install testci
```

You can also install a package from a channel with a token and a label:

```
conda install -c https://conda.anaconda.org/t/<token>/<channel>/label/<labelname>
↪<package>
```

NOTE: Replace `<token>` with the provided token, "`<channel>`" with the user channel, `<labelname>` with the label name and `<package>` with the package name you want to install.

## Working with PyPI packages

### Uploading PyPI packages

You can test PyPI package uploading with a small, public example package saved in the *anaconda-client* repository:

1. Begin by cloning the repository from the command line:

```
git clone git@github.com:anaconda-platform/anaconda-client.git
cd anaconda-client/example-packages/pypi/
```

2. You can now create your PyPI package with the `setup.py` script:

```
python setup.py sdist
```

3. Your package now is built as a source “tarball” and is ready to be uploaded with:

```
anaconda upload dist/*.tar.gz
```

Your package is now available at:

```
http://<your-anaconda-repo>/USERNAME/PACKAGE
```

NOTE: Replace `<your-anaconda-repo>` with the name of your local Repository, `USERNAME` with your user-name and `PACKAGE` with the package name.

### Installing PyPI packages

The best way to install a PyPI package is using `pip`. For the following command, you can use the package you authored in the above steps:

```
pip install --extra-index-url https://pypi.<your-anaconda-repo>/USERNAME/PACKAGE
```

NOTE: Replace `<your-anaconda-repo>` with the name of your local Repository, `USERNAME` with your user-name and `PACKAGE` with the test-package name.

### Using cross-platform “noarch” packages

As of Anaconda Repository version 2.6.0, your Repository supports conda “noarch” packages that contain no operating system-specific files.

The conda build system allows you to specify “no architecture” when building a package, so it is compatible with all platforms and architectures. Noarch packages from your Repository instance can be downloaded and installed on any platform.

NOTE: Noarch packages are not compatible with Anaconda constructor. If you intend to use the packages with Anaconda constructor, build the packages for specific operating systems.

### Building noarch packages

To specify a noarch build, use the `noarch` key in the `build` section of your conda recipe’s `meta.yaml` file:

```
build:
  noarch: generic
```

See the conda documentation for full information on [noarch packages](#).

Additional examples can be found in the [conda-recipes](#) repository on github.





### Uploading noarch packages

You can upload noarch packages to Repository in the same manner as any other package:

```
anaconda upload babel
```

Noarch packages are identified on Repository by a cross-platform icon:

**msarahan / Packages / noarch\_test\_package 1.0**

Conda	Files	Labels	Badges
<p>Unspecified</p> <p>0 total downloads</p>			
<h3>Installers</h3> <p>conda install ?</p> <div>     </div> <p>To install this package with conda run:</p> <pre>conda install -c msarahan noarch_test_package=1.0</pre>			

## Uploading a package

To upload a package to Repository, using the Client CLI, run the *upload* command:

```
anaconda login
anaconda upload PACKAGE
```

NOTE: Replace PACKAGE with the name of the desired package.

Repository automatically detects packages and notebooks, package or notebook types, and their versions.

Your package is now available at:

```
https://<your-anaconda-repo>/USERNAME/PACKAGE
```

NOTE: <your-anaconda-repo> is the name of your local Repository, USERNAME is your username and PACKAGE is the package name.

Anyone can download your package by using Client:

```
anaconda download USERNAME/PACKAGE
```

NOTE: USERNAME is their username, and PACKAGE is your package name.

If you want to restrict access to your package, see *Controlling access to packages*.

### Controlling access to packages

- *Making a package private*
- *Using groups to allow access to private packages*
- *Creating a token to allow access to a private package or channel*
- *Using a token*
- *Revoking a token*

By default, all packages, notebooks and environments uploaded to Repository are public, meaning they are accessible to anyone who has access to Repository.

When you *make a package private*, only you and the users you authorize can access it.

You can authorize users to access your private package in two ways:

- *Use a group* inside an organization account—only group members who are logged in can access the package. This is the best way to control access to your private packages because it allows you to set separate permissions for each package, notebook or environment.
- *Use a token control system*—only users who have the appropriate *token* can access the private package or channel.

After you grant other users access, they can *download and install* your package using the Web UI or Client.

### Making a package private

1. In the Web UI, in the **Tools** menu, select Packages.
2. OPTIONAL: If the packages you are looking for are not visible, under Filters, in the Type list, select All.
3. Select the checkbox next to each package you want to make private.
4. Click the **Settings** tab, and then click the **Admin** tab in the sidebar.

NOTE: You can also reach this page at the following URL:

```
https://<your-anaconda-repo>/USERNAME/PACKAGE/settings/admin
```

Replace <your-anaconda-repo> with the name of your local Repository, USERNAME with your username and PACKAGE with the name of the package.

5. Click Set access, then select Private.

NOTE: You can use the same procedure and URL to make Jupyter Notebooks and conda environments private.

### Using groups to allow access to private packages

1. *Create an organization.*
2. *Upload or transfer* the package to the organization.

3. Within the organization, *create a group* with the appropriate users, permissions, and packages.

## Creating a token to allow access to a private package or channel

You can control access to private packages and channels with the *token* system. All Repository URLs can be prefixed with `/t/<token>` to allow access.

The degree of access a token grants is completely configurable when you generate it. You can generate multiple tokens to control which groups of users have access to certain features if they have the appropriate token.

Tokens provide access to all packages in a specified channel. Separate permissions per package, notebook or environment may be better handled with *organizations and groups*.

You can generate tokens using the Web UI or Anaconda Client.

NOTE: By default, tokens expire after one year.

## Generating a token in the Web UI

1. Navigate to:

```
https://<your-anaconda-repo>/<channel>/settings/access
```

NOTE: Replace `<your-anaconda-repo>` with the name of your local Repository, and `<channel>` with the name of the desired channel.

2. In the Token Name box, type a name for the token:

3. Select the appropriate checkboxes for the type of access you want to allow for users of this token.

EXAMPLE: To allow users to download private packages or packages from private channels, select Allow private downloads from Conda repositories.

4. Click the Create button.

## Generating a token with Client

1. In a Client Terminal window or Anaconda Prompt, run:

```
anaconda auth --create --name YOUR-TOKEN-NAME --scopes repos conda:download'
```

NOTE: Replace `YOUR-TOKEN-NAME` with a name for the new token.

Provide scopes as a space-separated, quoted list. The token produced by the above command provides access to download any of your private conda repositories. The available scopes are:

- `all`: Allow all operations.
- `api`: Allow all API operations.
- `api:modify-group`: Allow addition and modification of groups.
- `api:read`: Allow read access to the API site.

[Public Profile](#)  
[My Account](#)  
**[Access](#)**  
[Security Log](#)  
[Storage](#)

## API Tokens ?

Create access token for: newuser

Token Name

Strength

Strong (longer token) ▾

Scopes

☐ Allow all operations

☐ Allow all API operations

☐ Allow addition and modification of groups

☐ Allow read access to the API site

☐ Allow write access to the API site

☐ Allow all operations on Conda repositories

☐ Allow private downloads from Conda repositories

☐ Allow all operations on PyPI repositories

☐ Allow private downloads from PyPI repositories

☐ Allow uploads to PyPI repositories

☐ Allow access to all package repositories

Expiration date (YYYY/MM/DD)

2017/11/17

Create

- `api:write`: Allow write access to the API site.
- `conda`: Allow all operations on conda repositories.
- `conda:download`: Allow private downloads from conda repositories.
- `pypi`: Allow all operations on PyPI repositories.
- `pypi:download`: Allow private downloads from PyPI repositories.
- `pypi:upload`: Allow uploads to PyPI repositories.
- `repos`: Allow access to all package repositories.

2. You can enable the token with the `conda config` command:

```
conda config --add channels https://conda.anaconda.org/t/<token>/<channel>
```

Or to add a channel with a token and label:

```
conda config --add channels https://conda.anaconda.org/t/<token>/<channel>/label/
↪<labelname>
```

NOTE: Replace `<token>` with your token string, “`<channel>`” with the desired channel name, and `<labelname>` with the label name.

NOTE: If you lose the token’s random alphanumeric string, you must *revoke the token* and create a new one.

## Using a token

The token can be used to:

- Add a channel from which to install private packages:

```
conda config --add channels https://conda.<your-anaconda-repo>/t/<token>/<channel>
```

NOTE: Replace `<your-anaconda-repo>` with the name of your local Repository, `<token>` with the provided token and `<channel>` with a user channel.

- Install a private package without first adding a channel:

```
conda install -c https://conda.<your-anaconda-repo>/t/<token>/<channel> <package>
```

To install a package from a channel using a token and a label name:

```
conda install -c https://conda.<your-anaconda-repo>/t/<token>/<channel>/label/
↪<labelname> <package>
```

NOTE: Replace `<your-anaconda-repo>` with the name of your local Repository, `<token>` with the provided token, `<channel>` with a user channel, `<labelname>` with the label name and `<package>` with the name of the package to install.

- Install a private PyPI package:

```
pip install --index-url https://pypi.<your-anaconda-repo>/t/<token>/<channel>/
↪PACKAGE
```

NOTE: Replace `<your-anaconda-repo>` with the name of your local Repository, `<token>` with the provided token, `<channel>` with a user channel and `PACKAGE` with the name of the desired package.

NOTE: Private PyPI packages can also be installed using:

```
https://pypi.<your-anaconda-repo>/t/<token>/<channel>
```

### Revoking a token

You can revoke tokens using the Web UI or Client.

To revoke a token using the Web UI, from the far-right drop-down menu, select My Settings, then from the left navigation select Access.

At the bottom of the page, you will see a list of all tokens you have generated. Click the name of the token you want to revoke, then in the dialog box that appears, click the Revoke Token button.

Or to revoke a token using Client, run:

```
anaconda auth -r YOUR-TOKEN-NAME
```

NOTE: Replace YOUR-TOKEN-NAME with the name of the token you want to revoke.

### Downloading and installing a package

To download a package using the Web UI, in a web browser, navigate to the organization's or user's channel.

To download a package using Client:

- Run:

```
conda install anaconda-client
anaconda login
conda install -c OrgName PACKAGE
```

NOTE: Replace OrgName with the organization or username and PACKAGE with the package name.

- Or run:

```
conda install anaconda-client
anaconda login
conda install -c https://conda.<your-anaconda-repo>/OrgName PACKAGE
```

NOTE: Replace <your-anaconda-repo> with the name of your local Repository, OrgName with the organization name or username and PACKAGE with the package name.

### Transferring a package to a new owner

When you create or add a package, by default it is attached to your individual profile. You can transfer ownership to another owner account you control, such as an organization profile you manage.

To transfer a package to a new owner:

1. On your dashboard—or the dashboard of an organization you administer—select the package for which you want to transfer ownership.  
The system displays options for that package.
2. To display the package settings, select the Settings option.
3. Select the Admin option.



4. Under Transfer this package to a new owner, click the Transfer button.
5. Select the organization name for the new owner.
6. Click the Transfer Ownership button.

### Adding and removing collaborators

You can add other users that are not part of an organization to collaborate on your packages. You need the usernames of the other users. You can also remove collaborators at any time.

All collaborators have full read/write permissions to the package, even if the package is private.

1. On your dashboard, click the package name.
2. Select the Settings option.
3. In the package settings, select the Collaborators option.
4. To add a collaborator, in the current collaborators, type the username of the person you want to add, then click the Add button.
5. To remove a collaborator, click the red X button next to the collaborator name.

### Removing a previous version of a package

To remove a previous version of one of your packages from Repository:

1. On your dashboard, click the package name.
2. Select the **Files** tab.
3. Select the checkbox to the left of the version you want to remove.
4. In the **Actions** menu, select Remove.

You can also use the Client CLI to remove a previous version of a package:

```
anaconda remove jsmith/testpack/0.2
```

NOTE: Replace `jsmith` with your username, `testpack` with the package name and `0.2` with the desired version.

You can now see the change on your profile page:

```
https://<your-anaconda-repo>/USERNAME/PACKAGE
```

NOTE: Replace `<your-anaconda-repo>` with the name of your local Repository, `USERNAME` with your username and `PACKAGE` with the package name.

### Copying a package

To copy a package from the channel `conda-forge` to a personal channel such as `jsmith`:

```
anaconda copy conda-forge/glueviz/0.10.4 --to-owner jsmith
```

`conda-forge/glueviz/0.10.4` is a “spec” and can match either of two formats: `user/package/version` or `user/package/version/filename`.

## Deprecated options

Previously labels were called “channels”, and the `anaconda copy` command has deprecated options `from-channel` and `to-channel` that expect to operate on labels.

These deprecated options should not be used.

If you attempt to use them in a command such as `anaconda copy --from-channel conda-forge --to-channel jsmith glueviz`, you will get an error that Label `conda-forge` does not exist.

## Deleting files from a package

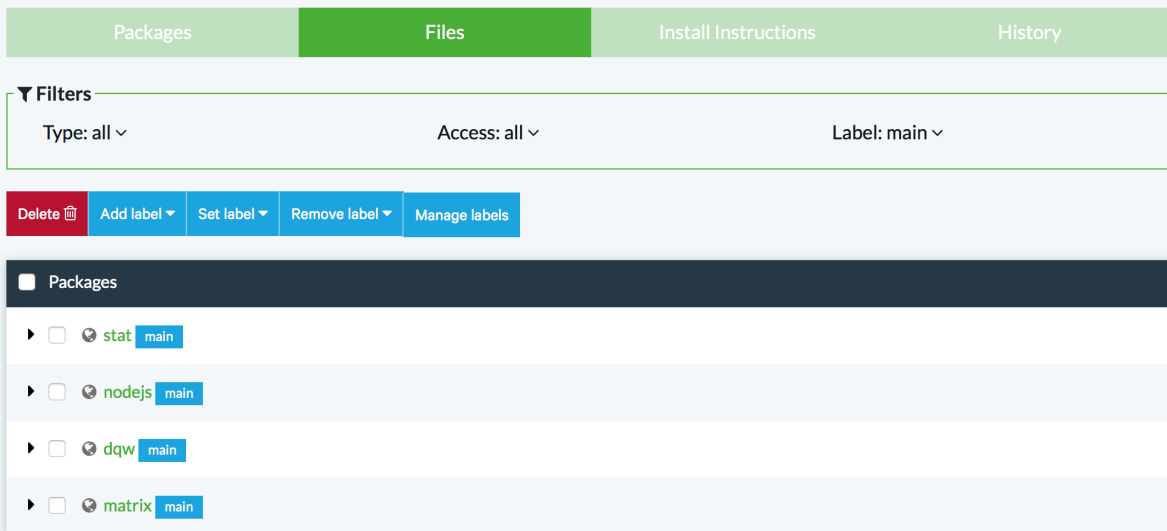
You can delete individual files from a package in Repository, without deleting the entire package.

CAUTION: There is no undo for deleting a file.

To delete individual files from a package in Repository:

1. Access Repository using the Web UI.
2. In the **Tools** menu, select Packages.
3. Click the **Files** tab.
4. OPTIONAL: If the files you want to delete are not visible, under Filters, in the Type list, select All.

## Package Repository for superuser



5. To select individual files, expand the package in which the files are located.
6. Select the checkboxes next to the files you want to delete.
7. Click the Delete button.
8. Enter your account name in the confirmation window.

- Click Delete to permanently delete the selected files.

## Deleting a package

You can delete an entire package from Repository, including all of its versions.

CAUTION: There is no undo for deleting a package.

To delete a package from Repository:

- Access Repository using the Web UI.
- In the **Tools** menu, select Packages.
- OPTIONAL: If the packages that you want to delete are not visible, under Filters, in the Type list, select All.

## Package Repository for superuser

Package Name	Access	Summary	Updated
<input type="checkbox"/> test	public	No Summary	2017-04-24
<input type="checkbox"/> stat	public	No Summary	2017-04-21
<input type="checkbox"/> nodejs	public	No Summary	2017-04-21
<input type="checkbox"/> dqw	public	No Summary	2017-04-21
<input type="checkbox"/> matrix	public	No Summary	2017-04-20
<input type="checkbox"/> waqas	public	No Summary	2017-04-20

- Select the checkbox next to the packages you want to delete.
- Click the Delete button.
- Enter the account name in the confirmation window.
- Click Delete to permanently delete the selected package(s).

You can also use the Client CLI to delete a package:

```
anaconda remove jsmith/testpak
```

NOTE: Replace `jsmith` with your user name, and `testpak` with the package name.

You can now see the change on your profile page:

```
https://<your-anaconda-repo>/USERNAME
```

NOTE: Replace `<your-anaconda-repo>` with the name of your local Repository and `USERNAME` with your username.

Also see the tutorial *Using labels in the development cycle*.

### Working with Jupyter notebooks

As of Anaconda Repository version 2.3.0, you can upload and download [Jupyter notebooks](#) like other files.

You can also view a static copy of notebooks in Repository. The ability to run notebooks inside Repository will become available in a future release.

To run notebooks, use Anaconda Navigator or AE Notebooks server.

### Uploading a notebook

The default maximum allowed size for notebooks is 25 MB. This limit can be changed by setting the `MAX_IPYNB_SIZE` variable in the `config.yaml` file.

To upload a notebook to your user account, at the Anaconda Prompt or in a Terminal window, run:

```
anaconda upload -p my-notebook my-notebook.ipynb
```

NOTE: Replace `my-notebook` with the name of the notebook you want to upload.

To upload a new version of your notebook, while retaining the original version, upload it with the version switch from a Terminal window or an Anaconda Prompt:

```
anaconda upload -p my-notebook -v 1.1 my-notebook.ipynb
```

NOTE: Replace `my-notebook` with the name of the notebook you want to upload.

### Finding a notebook

You can view an HTML version of your notebook at:

```
http://notebooks.<your-anaconda-repo>/USERNAME/my-notebook
```

NOTE: Replace `<your-anaconda-repo>` with the name of your local Repository, `USERNAME` with your username and `my-notebook` with the name of your notebook.

To see another user's notebook, browse to the associated user account on your Repository installation.

### Downloading a notebook

Anyone with access to Repository can download your notebook using the Anaconda Prompt or Terminal window:

```
anaconda download USERNAME/my-notebook
```

NOTE: Replace `USERNAME` with your username, and `my-notebook` with the name of your notebook.

## Working with environments

A `saved conda environment` can be uploaded to Anaconda Repository with the web interface or the `anaconda upload` command.

**# To save the environment, run this command in an Anaconda Prompt or Terminal window:**

```
conda env export -n my-environment -f my-environment.yml
```

To upload it with the web interface go to:

```
https://<your-anaconda-repo>/<USERNAME>/environments
```

Then use the Upload button in the top right corner.

To upload it with the `anaconda upload` command:

```
anaconda upload -f my-environment.yml
```

NOTE: Replace `my-environment` with the name of your environment.

1. You can view a list of your uploaded environments in the web interface at:

```
http://envs.anaconda.org/USERNAME
```

NOTE: Replace `USERNAME` with your username.

2. Anyone who has access can download and install your environment. Open a Terminal window or an Anaconda Prompt and then enter:

```
conda env create user/my-environment
source activate my-environment
```

NOTE: Replace `my-environment` with the actual name of your environment.

## Working with projects

You can add Anaconda Projects to Anaconda Repository. Projects can be any directory of code and assets. For example, projects often contain notebooks or Bokeh apps.

### Adding a project

Use the Anaconda Client to add a project to Repository.

### Accessing and managing a project

1. Access Repository using the Web UI.
2. From the drop-down menu of the view button, select Projects.  
The Projects page shows your existing projects.
3. Click on a project to display the Details page for that project, including the files, revisions, history and settings for the project.

- Under Settings for an individual project, you can change options, set groups and collaborations, and manage administration of the project, including making it public, private or authenticated, transferring membership, or deleting it.

### Working with Cloudera Manager parcels

Anaconda Repository provides a way to integrate with Cloudera Manager to distribute your Anaconda data science artifacts to your Hadoop cluster.

### Creating parcels, management packs and installers

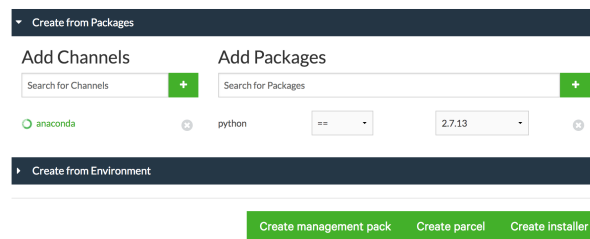
You can create custom Cloudera Manager parcels with the packages you want, including your own packages.

NOTE: Creating custom parcels requires a local mirror of the Anaconda packages.

When creating a parcel, Repository generates a 64-bit Linux installer including the specified packages and a file named `construct.yaml`, which can be used with [conda constructor](#).

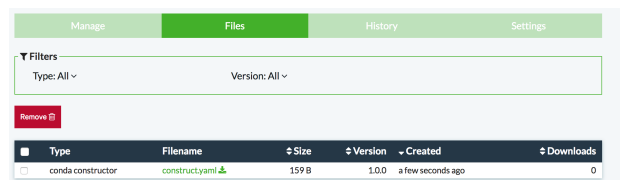
To create a custom parcel, management pack or installer:

- From the view button, select Installers.
- Click the Create new installer button.



NOTE: Use only letters, numbers, dashes and underscores in the installer name.

When creating a parcel, Anaconda Repository generates a 64-bit Linux installer with the specified packages, and a file named `construct.yaml` which can be used with [conda constructor](#).



To create just the installer script, click **Create installer**; to create a parcel, click **Create parcel**.

## Creating a parcel by selecting packages

The screenshot shows the 'Create from Packages' tab in the Anaconda Enterprise interface. At the top, there are input fields for 'Name' (containing 'InstallerFromPackage') and 'Version' (containing '1'). Below these is a dark blue header bar with 'Create from Packages' selected. Under this header, there are two main sections: 'Add Channels' and 'Add Packages'. The 'Add Channels' section has a search box with a green '+' button; below it, 'anaconda' is listed with a green checkmark. The 'Add Packages' section has a search box with a green '+' button; below it, 'python' and 'zlib' are listed. Each package has a version requirement dropdown (currently showing '>='), a version selection dropdown (showing '2.7.13' for python and '1.2.8' for zlib), and a green '+' button. At the bottom of the main content area is a dark blue header bar with 'Create from Environment' selected. At the very bottom, there are three green buttons: 'Create management pack', 'Create parcel', and 'Create installer'.

1. Click the **Create from Packages** tab.
2. Add channels from which to fetch packages into the Search for Channels box. Add each channel by clicking the green + (plus) button next to the Search for Channels box.  
NOTE: The `anaconda` user is added by default.
3. Add package names into the Search for Packages box. Add each package by clicking the green + (plus) button next to the Search for Packages box.
4. Set version requirements for each package using the list next to the package name.

## Creating a parcel by selecting an environment

The screenshot shows the 'Create from Environment' tab in the Anaconda Enterprise interface. At the top, there are input fields for 'Name' (containing 'InstallerFromEnvironment') and 'Version' (containing '1'). Below these is a dark blue header bar with 'Create from Environment' selected. Under this header, there is a 'Select Environment' section. It contains a search box with a green checkmark button. Below the search box, 'snowflakes' is listed with a version dropdown showing '2017.05.10.1314' and a green '+' button. At the bottom of the main content area, there are three green buttons: 'Create management pack', 'Create parcel', and 'Create installer'.

1. Click the **Create from Environment** tab.
2. Type the environment name and click the green checkbox button.
3. Select the environment version from the list next to the environment name.

4. Click the Create management pack button, Create parcel button or Create installer button.

NOTE: By default, conda is not included in a custom parcel. To add additional packages to your environment, you can add them using the Repository Web UI.

A parcel is generated with the prefix of `/opt/cloudera/parcels/PARCEL_NAME`. This is the default location where activated parcels are loaded. If you are deploying parcels in a different directory, you can change this prefix with the `PARCELS_ROOT` [configuration setting](#).

### Viewing a list of packages in a custom parcel

To see a list of packages included in your custom parcel, see:

```
/opt/cloudera/parcels/PARCEL_NAME/meta/parcel.json
```

NOTE: Replace `PARCEL_NAME` with the name of the desired parcel.

### Distributing custom parcels

After you have created a custom parcel, you can distribute it to your cluster by adding `http://<repository ip>:<port>/USERNAME/installers/parcels/` as a [Remote Parcel Repository URL](#).

NOTE: Replace `<repository ip>` with the Repository IP address, `<port>` with the port address and `USERNAME` with your user name.

Cloudera Manager detects the parcels hosted on Repository and provides the option to download and distribute the parcels.

By default, Repository generates a parcel file for every [compatible distribution](#).

You can customize which parcel distributions are created by configuring the `PARCEL_DISTRO_SUFFIXES` [configuration setting](#).

NOTE: If you have configured conda via `~/ .condarc` on your server for use of a proxy—for example, to mirror behind a proxy—you must disable proxying for Repository. For more information, see the [conda documentation](#).

EXAMPLE:

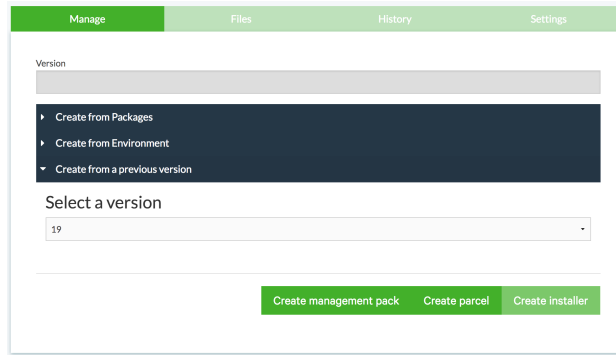
```
proxy_servers:
  https: http://proxy.corp.example.com
  http: http://proxy.corp.example.com
  'http://<repository ip>': false
```

### Creating from a previous version

Once you have an installer created, you can return to this page and create a management pack or a parcel from a specific version. Use the **Create from a previous version** option to choose which version you want to use. The **Create Installer** button will be disabled since you have already created an installer. The other buttons will be disabled if you have already created management packs or parcels for those versions.

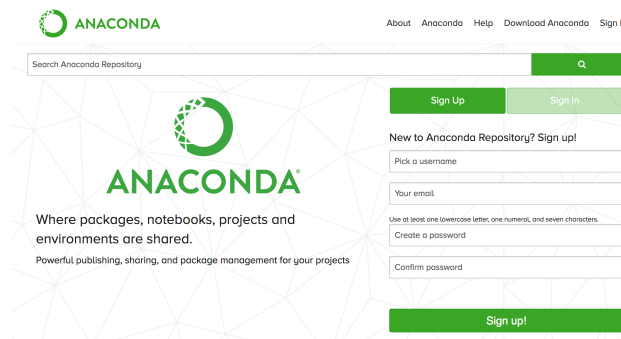
The versions listed on the drop-down list are the versions that successfully created an installer. An installer is needed to create a management pack or a parcel, so versions which failed won't be listed.





## Resetting your password

Open the Anaconda Repository login page:



The **Sign In** tab provides two links to help regain access to your account:

- I forgot my username. Click this link to have the username emailed to the email address of record.
- I forgot my password. Click this link to have a reset password link sent to the email address of record.

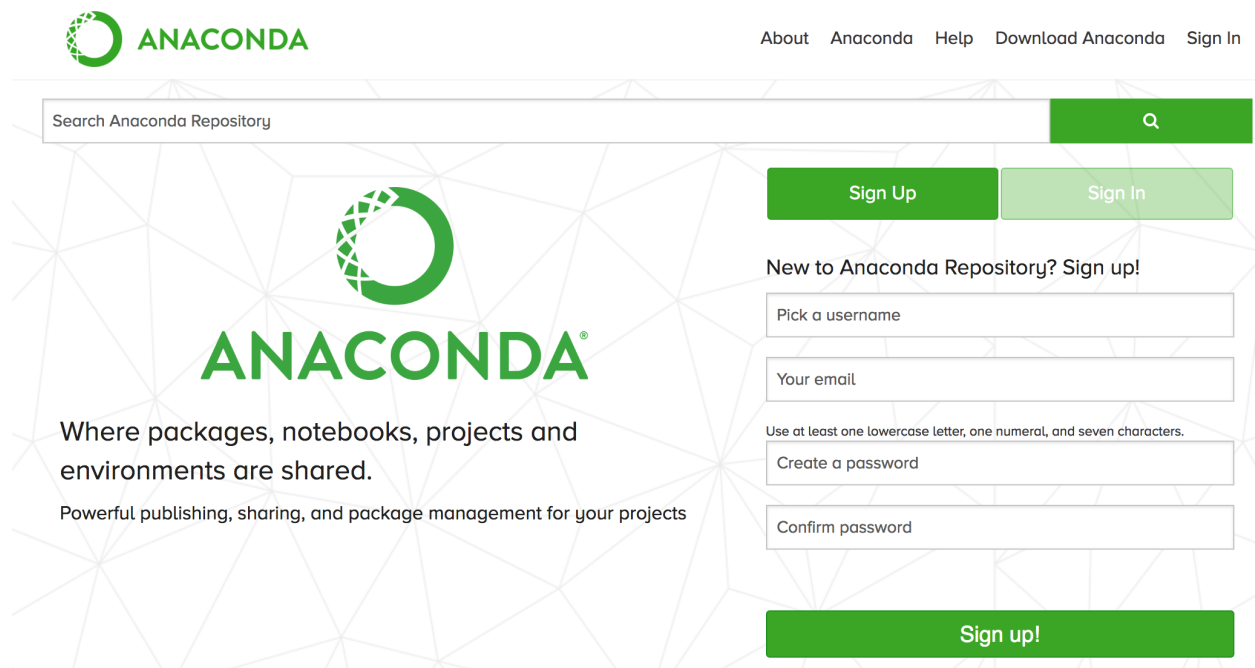
NOTE: The reset password link expires within 24 hours. If you no longer have access to the email account, you can create a new account or email your administrator for assistance.

Also see [Tutorials](#).

Anaconda Repository is package management server software that makes it easy to find, access, store and share public and private notebooks, projects, installers, environments, and conda and PyPI packages. Repository also makes it easy to stay current with updates made to the packages and environments you are using.

Anaconda also makes an instance of Anaconda Repository for private enterprises at Anaconda Cloud.

To begin using Repository, read [Getting started](#), then the remaining sections of the user guide.



### Administration guide

This Anaconda Repository Administration guide is intended for installers and administrators of Anaconda Repository version 2.33.

### Installation

This guide provides instructions for installing and configuring Anaconda Repository.

### System requirements

Your server must meet the requirements for hardware, software, security and network. Please review and verify that you have met all system requirements before beginning your installation.

- *Hardware requirements*
- *Software requirements*
- *Security requirements*
- *Network requirements*
- *Hardware verification*
- *Software verification*
- *Security verification*

See also the system requirements for all of Anaconda Enterprise.

## Hardware requirements

- Physical server or virtual machine.
- CPU: 2 x 64-bit, 2.8 GHz, 8.00 GT/s CPUs or better. *Verify machine architecture.*
- Memory: minimum RAM size of 32 GB, or 16 GB RAM with 1600 MHz DDR3 installed, for a typical installation with 50 regular users. *Verify memory requirements.*
- Storage: Recommended minimum of 100 GB, or 300 GB if you are planning to mirror both Anaconda Repository, which is approximately 90 GB, and the PyPI repository, which is approximately 100 GB, or at least 1 TB for an air gapped environment. Additional space is recommended if Repository is used to store packages built by your organization. *Verify storage requirements.*
- Internet access to download the files from Anaconda Cloud, or a USB drive containing all of the files you need with alternate instructions for air gapped installations.

## Software requirements

- Linux environment: Installations have been tested on Red Hat Enterprise Linux/CentOS 6.7, 7.3, 7.4, and 7.5, and Ubuntu 12.04+. *Verify Linux version.*
- Client environment may be Windows, macOS or Linux.
- Ubuntu users may need to install cURL. *Verify cURL access.*
- MongoDB version 2.6+ installed as root and running. Versions through 3.6 are supported. *Verify MongoDB installation.*
- bzip2. *Verify bzip2 installation.*

## Security requirements

- Root access or sudo capabilities. *Verify root access and sudo privileges.*
- OPTIONAL: Ability to make IPTables modifications.
- SELinux policy edit privileges.

NOTE: SELinux does not have to be disabled for Repository operation.

## Network requirements

TCP ports are used as follows:

- Inbound TCP 8080, 8443: Anaconda Repository.
- Inbound TCP 22: SSH.
- Outbound TCP 443: Anaconda Cloud.
- Outbound TCP 25: SMTP.
- Outbound TCP 389/636: LDAP(s).

You need your [Anaconda.org](https://anaconda.org)—Repository in the cloud—account username and password and the installation token provided to you by Anaconda at the time of purchase. If you did not receive your token, please contact your sales representative or our [Professional Support Team](#).

### Hardware verification

#### Machine architecture

Repository is built to operate only on 64-bit computers.

To verify that you have a 64-bit or x86\_64 computer, in a terminal window, run:

```
arch
```

This command displays what your system is: 32-bit “i686” or 64-bit “x86\_64.”

#### Memory requirements

You need a minimum RAM size of 32 GB, or 16 GB RAM with 1600 MHz DDR3.

In a terminal window, run:

```
free -m
```

This command returns the free memory size in MB.

#### Storage requirements

To check your available disk space—hard drive or virtual environment size—use the built-in Linux `df` utility with the `-h` parameter for human readable format:

```
df -h
```

### Software verification

#### Other versions of the Linux environment

Please contact us by filing a [GitHub issue](#) if you have problems with a version other than Redhat, CentOS or Ubuntu. Prompts may vary slightly depending on your version.

#### cURL access for Ubuntu users

RedHat and CentOS Linux distributions have cURL pre-installed, but Ubuntu does not.

To verify cURL access, in a terminal window, run:

```
curl --version
```

If cURL is not found, Ubuntu users can use the Advanced Packaging Tool (APT) to get and install cURL:

```
sudo apt-get install curl
```

**TIP:** If you already have Miniconda or Anaconda installed, in all versions of Linux you can use the `conda` command:

```
conda install curl
```

## MongoDB version 2.4+ installed

MongoDB version 2.4 or higher must be installed as root and running. Versions through 3.4 are supported. To check for the existence of MongoDB and its version number, in a terminal window, run:

```
mongod --version
```

If you get a “not found” message or if the MongoDB version is 2.3 or earlier, then install MongoDB 2.4 or higher using the [official installation instructions](#). Remember to install as root with the sudo command.

MongoDB must always be running before Repository can be started.

To start MongoDB:

```
sudo service mongod start
```

To verify that MongoDB is running:

```
mongo --eval 'db.serverStatus().ok'
```

## bzip2 is installed

To check for the existence of bzip2 and its version number, in a terminal window, run:

```
bzip2 --version
```

## Security verification

### Root access and sudo privileges

The Repository installation process cannot be completed without root access.

To verify that you have sudo privileges, in a terminal window, run:

```
sudo -v
```

Enter your root password when prompted and press Enter.

If you receive a message like the following, contact your system administrator for root access:

```
Sorry, user [username] may not run sudo on [hostname].
```

## Installing on an online system

These instructions are for normal Linux installations on machines that have access to the internet.

NOTE: If the destination server is an air gapped system or otherwise does not have access to the internet, see [Installing on an air gapped system](#).

- *Before you start*
- *1. Install MongoDB 2.6*
- *2. Create the Repository administrator account*
- *3. Install Repository*
- *4. Configure Repository*
- *5. Set up automatic restart on reboot, fail or error*
- *6. Start and log in to Repository*
- *7. Client configuration*
- *8. Install the Repository license*
- *9. OPTIONAL: Mirror installers for Anaconda and Miniconda*
- *10. Mirror Anaconda Cloud*

### Before you start

Your server must meet the requirements for hardware, software, security and network. Please review and verify that you have met all *system requirements* before beginning your installation.

Your support representative provides you with a download URL for the Anaconda Repository installer. Make sure you have the download URL.

### 1. Install MongoDB 2.6

In a terminal window, create the yum repo file as the root user:

```
RPM_CDN="https://820451f3d8380952ce65-4cc6343b423784e82fd202bb87cf87cf.ssl.cf1.
↪rackcdn.com"
curl -O $RPM_CDN/mongodb-org-tools-2.6.8-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-shell-2.6.8-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-server-2.6.8-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-mongos-2.6.8-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-2.6.8-1.x86_64.rpm
```

NOTE: Ubuntu users use apt-get instead of yum.

### MongoDB for Redhat and CentOS 7

1. Install MongoDB:

```
sudo yum install -y mongodb-org*
```

2. Start MongoDB:

```
sudo systemctl start mongod
```

3. Verify that MongoDB is running:

```
$ sudo systemctl status mongod
mongodb (pid 17258) is running...
```

## MongoDB for Redhat and CentOS 6.7+

### 1. Install MongoDB:

```
sudo yum install -y mongodb-org*
```

### 2. Start MongoDB:

```
sudo /etc/init.d/mongod start
```

### 3. Verify that MongoDB is running:

```
$ sudo /etc/init.d/mongod status
mongodb (pid 17258) is running...
```

## MongoDB for Ubuntu 12.04+

### 1. Install MongoDB:

```
sudo apt-key adv --keyserver hkp://keyserver.ubuntu.com:80 --recv 7F0CEB10

echo 'deb http://downloads-distrow.mongodb.org/repo/ubuntu-upstart dist 10gen' | \
↪ sudo tee /etc/apt/sources.list.d/mongodb.list

sudo apt-get update

sudo apt-get install -y mongodb-org=2.6.9 mongodb-org-server=2.6.9 mongodb-org-
↪ shell=2.6.9 mongodb-org-mongos=2.6.9 mongodb-org-tools=2.6.9
```

NOTE: If you do not specify a version, such as 2.6.9, `apt-get` installs the latest stable version, which is 3.x.

### 2. Start MongoDB:

```
sudo /etc/init.d/mongod start
```

Verify that MongoDB is running:

```
$ sudo /etc/init.d/mongod status
mongodb (pid 17258) is running...
```

You receive verification that MongoDB is running:

```
start: Job is already running: mongod
```

## Additional MongoDB resources

For additional MongoDB installation information see <https://docs.mongodb.org/manual/>.

### 2. Create the Repository administrator account

1. In a Terminal window, create a new user account for Anaconda Repository named “anaconda-server,” and switch to this new account:

```
sudo useradd -m anaconda-server
```

NOTE: The anaconda-server user is the default for installing Repository. Any username can be used, but using the root user is discouraged.

2. Create a Repository package storage directory:

```
sudo mkdir -m 0770 -p /opt/anaconda-server/package-storage
```

3. Assign ownership of this directory to the anaconda-server user:

```
sudo chown -R anaconda-server:anaconda-server /opt/anaconda-server
```

4. Switch to the Repository administrator account:

```
sudo su - anaconda-server
```

### 3. Install Repository

#### Download the installer

Download the Repository installer from the download URL provided by your support representative:

```
curl "$INSTALLER_URL" > anaconda_repository.sh
```

Install Repository, following the prompts in the installation routine:

```
bash anaconda_repository.sh
```

1. Review and accept the license terms:

```
Welcome to Anaconda Repository 2.33 (by Anaconda, Inc.)
In order to continue the installation process, please review the license
->agreement.
Please, press ENTER to continue.
```

2. Once you have reviewed the license terms, approve them by typing yes:

```
Do you approve the license terms? [yes|no] yes
```

3. Accept the default location or specify an alternative:

```
anaconda_repository will now be installed into this location:
/home/anaconda-server/repo -Press ENTER to confirm the location
-PRESS CTRL-C to abort the installation
-Or specify a different location below
[/home/anaconda-server/repo] >>> /home/anaconda-server/repo" [Press ENTER]
PREFIX=/home/anaconda-server/repo
installing: python-2.7.11-0
...
```

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```
Python 2.7.11 :: Anaconda, Inc.
creating default environment... installation finished.
```

4. At the end of the installation routine, update the `anaconda-server` user's path—prepending `/home/anaconda-server/repo`—by answering “yes” at the prompt to add the install location to your path:

```
Do you wish the installer to prepend the anaconda_repository install location to
↳PATH in your /home/anaconda-server/.bashrc ? [yes|no]
```

5. Type `yes` and press ENTER.
6. For the new path changes to take effect, source your `.bashrc`:

```
source ~/.bashrc
```

## 4. Configure Repository

1. Initialize the web server and indicate the filepath for the package storage location:

```
anaconda-server-config --init
anaconda-server-config --set fs_storage_root /opt/anaconda-server/package-storage
```

NOTE: The location for file storage can be any location owned by the `anaconda-server` user that you created in section 2 above.

NOTE: As of Repository 2.33.8, the `fs_storage_root` configuration setting is mandatory for local filesystem storage and the Repository server will not run without it.

2. Configure the connection to your MongoDB database:

```
anaconda-server-config --set MONGO_URL mongodb://localhost
```

NOTE: You may also *configure an external MongoDB database*.

3. If you are not using LDAP or Kerberos authentication, create an initial superuser account for Repository. Set the environment variable `USER_PASSWORD` with the desired password for the initial user. Then run:

```
anaconda-server-create-user --username "superuser" --email "your@email.com" --
↳superuser
```

NOTE: Replace `superuser` with a username of your choice and `your@email.com` with an email address where you wish to receive system email notifications.

NOTE: To ensure the bash shell does not process any of the characters in this password, limit the password to letters and numbers, with no punctuation. After setup, you can change the password in the web UI.

4. Initialize the Repository database:

```
anaconda-server-db-setup --execute
```

NOTE: The above command is also run when upgrading Repository. Upgrade and then run:

```
anaconda-server-db-setup --execute
```

5. Restart the server.

NOTE: More configuration options can be controlled with one or more `.yaml` configuration files. Repository reads configuration files in this order:

1. From `/etc/anaconda-server/*.yaml`.
2. From `$PREFIX/etc/anaconda-server/*.yaml`.
3. From the path specified in the environment variable `ANACONDA_SERVER_CONFIG`, if it is set and the command line argument `--config-file` was not used.
4. From the path specified in the command line argument `--config-file`, if it was used.

All configuration is merged, and options from files read earlier are overwritten by files read later. If there are multiple files in the same directory, they are read in alphabetical order.

### 5. Set up automatic restart on reboot, fail or error

1. Run the `anaconda-server-install-supervisord-config.sh` script to configure supervisord management of the Anaconda server and worker processes:

```
anaconda-server-install-supervisord-config.sh
```

This will generate the `/home/anaconda-server/repo/etc/supervisord.conf` file and add a crontab rule to restart supervisor after each reboot.

It will also create the folder `/home/anaconda-server/repo/etc/supervisord/conf.d/` where you can add `.conf` files with custom configuration.

NOTE: If you don't want to include the crontab rule, use the `--no-crontab` option when running the script.

If an error message says that the user is disallowed from using cron and could not add the crontab rule, you can add it manually with `sudo`. Edit the crontab file:

```
sudo crontab -e -u anaconda-server
```

When the file is open for editing, add this entry:

```
@reboot /home/anaconda-server/repo/bin/supervisord
```

2. Verify that the server is running:

```
supervisorctl status
```

If installed correctly, you see:

```
anaconda-server RUNNING    pid 10831, uptime 0:00:05
```

3. View the log file at:

```
$PREFIX/var/log/anaconda-server/application.log
```

### 6. Start and log in to Repository

1. Open your browser and log into Repository by visiting `http://your.anaconda.repository:8080/` using the superuser account you created in section 4 above.

NOTE: Replace `your.anaconda.repository` with the IP address or domain name of your repository.

2. If you are using LDAP or Kerberos authentication, modify your user account to be a superuser.

EXAMPLE: If your user account is “jsmith”:

```
anaconda-server-admin set-superuser "jsmith"
```

NOTE: See *Troubleshooting* if you have issues starting the repo server.

## 7. Client configuration

Follow the *Configuring Anaconda Client* instructions so you can use one or more clients to communicate with the server.

## 8. Install the Repository license

1. In your browser, go to `http://your.anaconda.repository:8080`. Follow the onscreen instructions to upload the license file that you received in an email from your sales representative.

NOTE: Replace `your.anaconda.repository` with the IP address or domain name of your repository.

Contact your sales representative or support representative if you cannot find or have any questions about your license.

2. After uploading the license file, you will see the login page. Log in using the superuser user and password that you created in section 4 above.

TIP: You can view the current license information and upload a new license file by visiting the URL `http://your.anaconda.repository:8080/admin/license`.

NOTE: Replace `your.anaconda.repository` with the IP address or domain name of your repository.

Alternatively, you can install the license by copying the license file directly into the `/home/anaconda-server/.continuum` directory.

## 9. OPTIONAL: Mirror installers for Anaconda and Miniconda

Miniconda and Anaconda installers can be served by Repository via the static directory located at `/home/anaconda-server/repo/opt/anaconda-server/installers`. To serve up the latest installers for each platform, download them to this directory.

Define the URL for miniconda installers:

```
URL="https://repo.anaconda.com/miniconda/"
```

The `Miniconda*latest*.sh` always point to the latest Miniconda installers. Either these can be mirrored or the ones with the latest version number can be mirrored. Define the list of installers to mirror:

```
versions="Miniconda2-4.5.4-Linux-ppc64le.sh
Miniconda2-4.5.4-Linux-x86.sh
Miniconda2-4.5.4-Linux-x86_64.sh
Miniconda2-4.5.4-MacOSX-x86_64.pkg
Miniconda2-4.5.4-MacOSX-x86_64.sh
Miniconda2-4.5.4-Windows-x86.exe
Miniconda2-4.5.4-Windows-x86_64.exe
Miniconda3-4.5.4-Linux-ppc64le.sh
Miniconda3-4.5.4-Linux-x86.sh"
```

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```
Miniconda3-4.5.4-Linux-x86_64.sh
Miniconda3-4.5.4-MacOSX-x86_64.pkg
Miniconda3-4.5.4-MacOSX-x86_64.sh
Miniconda3-4.5.4-Windows-x86.exe
Miniconda3-4.5.4-Windows-x86_64.exe"

# miniconda installers
pushd /home/anaconda-server/repo/opt/anaconda-server/installers

for installer in $versions
do
    curl -O $URL$installer
done
```

Define the URL for Anaconda installers:

```
URL="https://repo.anaconda.com/archive/"
```

Define the anaconda version to mirror.

EXAMPLE: To mirror version 5.2.0:

```
versions="Anaconda3-5.2.0-Linux-ppc64le.sh
Anaconda3-5.2.0-Linux-x86.sh
Anaconda3-5.2.0-Linux-x86_64.sh
Anaconda3-5.2.0-MacOSX-x86_64.pkg
Anaconda3-5.2.0-MacOSX-x86_64.sh
Anaconda3-5.2.0-Windows-x86.exe
Anaconda3-5.2.0-Windows-x86_64.exe
Anaconda2-5.2.0-Linux-ppc64le.sh
Anaconda2-5.2.0-Linux-x86.sh
Anaconda2-5.2.0-Linux-x86_64.sh
Anaconda2-5.2.0-MacOSX-x86_64.pkg
Anaconda2-5.2.0-MacOSX-x86_64.sh
Anaconda2-5.2.0-Windows-x86.exe
Anaconda2-5.2.0-Windows-x86_64.exe"

# miniconda installers
pushd /home/anaconda-server/repo/opt/anaconda-server/installers

for installer in $versions
do
    curl -O $URL$installer
done

popd
```

Users can download the installers using curl from the following URL:

```
# Fill in server name, port, and specific installer for your platform
curl -s -O http://your.anaconda.repository:8080/downloads/Miniconda-latest-Linux-x86_
↪64.sh
```

NOTE: Replace your.anaconda.repository with the IP address or domain name of your repository.

## 10. Mirror Anaconda Cloud

The final step is to mirror the packages from a subset of channels on Anaconda Cloud to the local Repository. The channels to mirror are as follows:

Channel	Description
anaconda	Default anaconda channel containing all packages built and supported by Anaconda, Inc. Also contains custom packages.
r	If you would like conda packages for <i>r</i> , mirror this channel. It is typically done under an <i>r</i> account.
wakari anaconda-nb-extensions	If the local Repository will be used by Anaconda Enterprise Notebooks the recommended method is to mirror these channels under the <i>wakari</i> account.
anaconda-adam	Anaconda-adam is used to manage the environments on a cluster. If you plan to use anaconda-scale for cluster management, mirror the anaconda-adam packages.
msys2	msys2 is required by quite a few windows packages. See <a href="http://www.msys2.org/">http://www.msys2.org/</a>

The packages will be mirrored to the package store defined by the `fs_storage_root` key as described in section 4 above.

### Mirror Anaconda

Mirror the Anaconda channel from Anaconda Cloud:

```
anaconda-server-sync-conda
```

NOTE: Due to the size of the Cloud repository and depending on the available internet bandwidth, the mirroring process can take hours.

*Mirroring an Anaconda repository* contains documentation and advanced `yaml` configuration for mirroring other channels.

### Installing on an air gapped system

These instructions are for installation on air gapped systems or other machines that do not have access to the internet. The air gap archives contain installers, dependencies and packages to mirror.

- *Before you start*
- *1. Install MongoDB 2.6*
- *2. Create the Repository administrator account*
- *3. Install Repository*
- *4. Configure Repository*
- *5. Set up automatic restart on reboot, fail or error*

- 6. *Start and log in to Repository*
- 7. *Client configuration*
- 8. *Install the Repository license*
- 9. *OPTIONAL: Mirror installers for Anaconda and Miniconda*
- 10. *Mirror Anaconda Cloud*

### Before you start

Your server must meet the requirements for hardware, software, security and network. Please review and verify that you have met all *system requirements* before beginning your installation.

Download the installers archive and the appropriate mirrors archive for your needs. The *Air gap archives* page lists the archives and their contents.

NOTE: These installation instructions assume the air gap media is available on the target server at \$INSTALLER\_PATH.

EXAMPLE:

```
tar xf <installer-archive> -C /installer/  
export INSTALLER_PATH=/installer/anaconda-enterprise-`date +%Y-%m-%d`
```

Also download and expand the archive of conda packages you plan to mirror. These instructions assume packages are expanded to \$INSTALLER\_PATH:

```
tar xf <archive-of-pkgs-to-mirror> -C /installer/  
export MIRRORS_ARCHIVE=/installer/repo-mirrors-`date +%Y-%m-%d`
```

### Air gap archives

This section provides information about where to get the air gap archives and their contents.

The air gap archives are generated monthly, generally on the 1st of each month. Monthly archives are hosted at <http://airgap.demo.continuum.io/> organized in folders by date.

### Installers Archive

All the installers and the latest Miniconda and Anaconda installers for all platforms are in the archive titled:

```
anaconda-enterprise-`date +%Y-%m-%d`.tar
```

The archive size is about 14 GB. It contains everything to install Anaconda Repository, Anaconda Enterprise Notebooks, Anaconda Adam and Anaconda Scale.

The archive contains:

Contents	Description
aen-*.sh	anaconda-enterprise-notebooks server, gateway, compute installers
anaconda_repository*.sh	anaconda-repository installer
adam-installer*.sh	adam installer
conda/	latest version of Miniconda and Anaconda for all platforms
rpms6x/	dependencies for installing on RHEL-6x/CentOS-6x
rpms7x/	dependencies for installing on RHEL-7x/CentOS-7x

## Mirror archives

In addition, the `anaconda-server-sync-conda` subdirectory contains mirror archives. These are platform-specific conda packages that must be mirrored after AE-Repo is installed. If you only need packages for a subset of platforms, download the platform-based installers as they will be much smaller in size.

Each component has an md5 file and a list file which are both small and included for convenience.

Tarball	Contents	Size
repo-mirrors- <i>date</i> +%Y-%m-%d.tar	All AE-channels for all platforms	160 GB
x64-repo-mirrors- +%Y-%m-%d.tar	x64 conda packages for all AE-channels	100 GB
linux-64-pkgs.tar	conda packages for linux-64 for all AE-channels	45 GB
win-64-pkgs.tar	conda packages for win-64	30 GB
osx-64-pkgs.tar	conda packages for osx-64	30 GB

NOTE: The archives contain packages for channels: Anaconda, R, Adam, Wakari. The `anaconda-nb-extensions` packages are in the [anaconda-nb-extensions channel](#).

## 1. Install MongoDB 2.6

Change the directory to the appropriate `rpms*` directory to find dependencies:

```
cd $INSTALLER_PATH/rpms*x/
```

## MongoDB for Redhat and CentOS 7

### 1. Install MongoDB:

```
sudo yum install -y mongodb-org*
```

### 2. Start MongoDB:

```
sudo systemctl start mongod
```

### 3. Verify that MongoDB is running:

```
$ sudo systemctl status mongod
mongodb (pid 17258) is running...
```

### MongoDB for Redhat and CentOS 6.7+

1. Install MongoDB:

```
sudo yum install -y mongodb-org*
```

2. Start MongoDB:

```
sudo /etc/init.d/mongod start
```

3. Verify that MongoDB is running:

```
$ sudo /etc/init.d/mongod status
mongodb (pid 17258) is running...
```

### MongoDB for Ubuntu 12.04+

1. Install MongoDB:

```
sudo apt-key adv --keyserver hkp://keyserver.ubuntu.com:80 --recv 7F0CEB10

echo 'deb http://downloads-distro.mongodb.org/repo/ubuntu-upstart dist 10gen' | \
↪ sudo tee /etc/apt/sources.list.d/mongodb.list

sudo apt-get update

sudo apt-get install -y mongodb-org=2.6.9 mongodb-org-server=2.6.9 mongodb-org-
↪ shell=2.6.9 mongodb-org-mongos=2.6.9 mongodb-org-tools=2.6.9
```

NOTE: If you do not specify a version, such as 2.6.9, apt-get installs the latest stable version, which is 3.x.

2. Start MongoDB:

```
sudo /etc/init.d/mongod start
```

Verify that MongoDB is running:

```
$ sudo /etc/init.d/mongod status
mongodb (pid 17258) is running...
```

You receive verification that MongoDB is running:

```
start: Job is already running: mongod
```

### Additional MongoDB resources

For additional MongoDB installation information see <https://docs.mongodb.org/manual/>.

### 2. Create the Repository administrator account

1. In a Terminal window, create a new user account for Anaconda Repository named “anaconda-server,” and switch to this new account:



```
sudo useradd -m anaconda-server
```

NOTE: The anaconda-server user is the default for installing Repository. Any username can be used, but using the root user is discouraged.

2. Create a Repository package storage directory:

```
sudo mkdir -m 0770 -p /opt/anaconda-server/package-storage
```

3. Assign ownership of this directory to the anaconda-server user:

```
sudo chown -R anaconda-server:anaconda-server /opt/anaconda-server
```

4. Switch to the Repository administrator account:

```
sudo su - anaconda-server
```

### 3. Install Repository

Install Repository, following the prompts in the installation routine:

```
bash $INSTALLER_PATH/anaconda_repository-*-linux-64.sh
```

NOTE: Path should have only one installer that is for the latest stable version of Repository.

1. Review and accept the license terms:

```
Welcome to Anaconda Repository 2.33 (by Anaconda, Inc.)
In order to continue the installation process, please review the license
↵agreement.
Please, press ENTER to continue.
```

2. Once you have reviewed the license terms, approve them by typing yes:

```
Do you approve the license terms? [yes|no] yes
```

3. Accept the default location or specify an alternative:

```
anaconda_repository will now be installed into this location:
/home/anaconda-server/repo -Press ENTER to confirm the location
-PRESS CTRL-C to abort the installation
-Or specify a different location below
[/home/anaconda-server/repo] >>> /home/anaconda-server/repo" [Press ENTER]
PREFIX=/home/anaconda-server/repo
installing: python-2.7.11-0
...
Python 2.7.11 :: Anaconda, Inc.
creating default environment... installation finished.
```

4. At the end of the installation routine, update the anaconda-server user's path—prepending /home/anaconda-server/repo—by answering “yes” at the prompt to add the install location to your path:

```
Do you wish the installer to prepend the anaconda_repository install location to
↵PATH in your /home/anaconda-server/.bashrc ? [yes|no]
```

5. Type yes and press ENTER.

6. For the new path changes to take effect, source your `.bashrc`:

```
source ~/.bashrc
```

## 4. Configure Repository

1. Initialize the web server and indicate the filepath for the package storage location:

```
anaconda-server-config --init  
anaconda-server-config --set fs_storage_root /opt/anaconda-server/package-storage
```

NOTE: The location for file storage can be any location owned by the `anaconda-server` user that you created in section 2 above.

NOTE: As of Repository 2.33.8, the `fs_storage_root` configuration setting is mandatory for local filesystem storage and the Repository server will not run without it.

2. Configure the connection to your MongoDB database:

```
anaconda-server-config --set MONGO_URL mongodb://localhost
```

NOTE: You may also *configure an external MongoDB database*.

3. If you are not using LDAP or Kerberos authentication, create an initial superuser account for Repository. Set the environment variable `USER_PASSWORD` with the desired password for the initial user. Then run:

```
anaconda-server-create-user --username "superuser" --email "your@email.com" --  
↪superuser
```

NOTE: Replace `superuser` with a username of your choice and `your@email.com` with an email address where you wish to receive system email notifications.

NOTE: To ensure the bash shell does not process any of the characters in this password, limit the password to letters and numbers, with no punctuation. After setup, you can change the password in the web UI.

4. Initialize the Repository database:

```
anaconda-server-db-setup --execute
```

NOTE: The above command is also run when upgrading Repository. Upgrade and then run:

```
anaconda-server-db-setup --execute
```

5. Restart the server.

NOTE: More configuration options can be controlled with one or more `.yaml` configuration files. Repository reads configuration files in this order:

1. From `/etc/anaconda-server/*.yaml`.
2. From `$PREFIX/etc/anaconda-server/*.yaml`.
3. From the path specified in the environment variable `ANACONDA_SERVER_CONFIG`, if it is set and the command line argument `--config-file` was not used.
4. From the path specified in the command line argument `--config-file`, if it was used.

All configuration is merged, and options from files read earlier are overwritten by files read later. If there are multiple files in the same directory, they are read in alphabetical order.

## 5. Set up automatic restart on reboot, fail or error

1. Run the `anaconda-server-install-supervisord-config.sh` script to configure supervisord management of the Anaconda server and worker processes:

```
anaconda-server-install-supervisord-config.sh
```

This will generate the `/home/anaconda-server/repo/etc/supervisord.conf` file and add a crontab rule to restart supervisor after each reboot.

It will also create the folder `/home/anaconda-server/repo/etc/supervisord/conf.d/` where you can add `.conf` files with custom configuration.

NOTE: If you don't want to include the crontab rule, use the `--no-crontab` option when running the script.

If an error message says that the user is disallowed from using cron and could not add the crontab rule, you can add it manually with `sudo`. Edit the crontab file:

```
sudo crontab -e -u anaconda-server
```

When the file is open for editing, add this entry:

```
@reboot /home/anaconda-server/repo/bin/supervisord
```

2. Verify that the server is running:

```
supervisorctl status
```

If installed correctly, you see:

```
anaconda-server RUNNING    pid 10831, uptime 0:00:05
```

3. View the log file at:

```
$PREFIX/var/log/anaconda-server/application.log
```

## 6. Start and log in to Repository

1. Open your browser and log into Repository by visiting `http://your.anaconda.repository:8080/` using the superuser account you created in section 4 above.

NOTE: Replace `your.anaconda.repository` with the IP address or domain name of your repository.

2. If you are using LDAP or Kerberos authentication, modify your user account to be a superuser.

EXAMPLE: If your user account is "jsmith":

```
anaconda-server-admin set-superuser "jsmith"
```

NOTE: See [Troubleshooting](#) if you have issues starting the repo server.

## 7. Client configuration

Follow the [Configuring Anaconda Client](#) instructions so you can use one or more clients to communicate with the server.

## 8. Install the Repository license

1. In your browser, go to `http://your.anaconda.repository:8080`. Follow the onscreen instructions to upload the license file that you received in an email from your sales representative.

NOTE: Replace `your.anaconda.repository` with the IP address or domain name of your repository.

Contact your sales representative or support representative if you cannot find or have any questions about your license.

2. After uploading the license file, you will see the login page. Log in using the superuser user and password that you created in section 4 above.

TIP: You can view the current license information and upload a new license file by visiting the URL `http://your.anaconda.repository:8080/admin/license`.

NOTE: Replace `your.anaconda.repository` with the IP address or domain name of your repository.

Alternatively, you can install the license by copying the license file directly into the `/home/anaconda-server/.continuum` directory.

## 9. OPTIONAL: Mirror installers for Anaconda and Miniconda

Miniconda and Anaconda installers can be served by Repository via the static directory located at `/home/anaconda-server/repo/opt/anaconda-server/installers`. To serve up the latest installers for each platform, copy them from your *air gap archive* to this directory.:

```
cp Miniconda-latest-Linux-x86_64.sh /home/anaconda-server/repo/opt/anaconda-server/  
↪ installers
```

Replace `Miniconda-latest-Linux-x86_64.sh` with your Anaconda or Miniconda installer name.

NOTE: Air gap archive only contains the latest version of both Miniconda and Anaconda installers.

Users can download the installers using curl from the following URL:

```
# Fill in server name, port, and specific installer for your platform  
curl -s -O http://your.anaconda.repository:8080/downloads/Miniconda-latest-Linux-x86_  
↪ 64.sh
```

NOTE: Replace `your.anaconda.repository` with the IP address or domain name of your repository.

## 10. Mirror Anaconda Cloud

The final step is to mirror the packages from a subset of channels on Anaconda Cloud to the local Repository. The channels to mirror are as follows:

Channel	Description
anaconda	Default anaconda channel containing all packages built and supported by Anaconda, Inc. Also contains custom packages.
r	If you would like conda packages for <i>r</i> , mirror this channel. It is typically done under an <i>r</i> account.
wakari anaconda-nb-extensions	If the local Repository will be used by Anaconda Enterprise Notebooks the recommended method is to mirror these channels under the <i>wakari</i> account.
anaconda-adam	Anaconda-adam is used to manage the environments on a cluster. If you plan to use anaconda-scale for cluster management, mirror the anaconda-adam packages.
msys2	msys2 is required by quite a few windows packages. See <a href="http://www.msys2.org/">http://www.msys2.org/</a>

The packages will be mirrored to the package store defined by the `fs_storage_root` key as described in section 4 above.

## Mirror Anaconda

Since we are mirroring from a local file system, some additional configuration is necessary. The steps are the same for each channel:

1. Create a mirror configuration `yml` typically stored in `$PREFIX/etc/anaconda-server/mirror/`.
2. *Customize your mirror*. An example is if you only need to mirror packages for a subset of platforms. By default, it mirrors all packages found in the channels `linux-64`, `osx-64`, `win-64`, `win-32` and `linux-32`.
3. Invoke the mirror command by pointing it to the config file:

```
echo "channels:" > ~/repo/etc/anaconda-server/mirror/conda.yml
echo " - file://$MIRRORS_ARCHIVE/anaconda-suite/pkg" >> \
~/repo/etc/anaconda-server/mirror/conda.yml
```

4. Mirror the default Anaconda packages:

```
anaconda-server-sync-conda --mirror-config ~/repo/etc/anaconda-server/mirror/
↳ conda.yml
```

*Mirroring an Anaconda repository* contains documentation and advanced `yml` config for mirroring other channels.

## Configuration

### Enabling HTTPS

Before you begin, purchase an SSL certificate and download the `SSL *.cert` file and `SSL *.key` file.

NOTE: If security is not an issue, for testing, you may set up a self-signed SSL certificate. For more information, see <http://www.selfsignedcertificate.com/>.

1. Save the `SSL *.cert` file and an `SSL *.key` file in your home directory.
2. Configure the server to use those keys and the correct ports:

```
anaconda-server-config --set ssl_options.keyfile ~/localhost.key
anaconda-server-config --set ssl_options.certfile ~/localhost.cert
anaconda-server-config --set port 8443
```

3. Restart your server for the changes to take effect:

```
supervisorctl restart all
```

4. To test, navigate to the site using `https` in the address bar.

NOTE: If you use a self-signed SSL certificate, your web browser issues a warning that the website certificate cannot be verified.

Next, configure your client side tools `conda` and `anaconda-client` to pull packages from the local repo by setting the `ssl_verify` flags.

### Configure conda

If your `conda` client is configured to point to this local repo, update the configuration file `.condarc` to contain the `ssl_verify` flag. If you're using a self-signed certificate, configure the `ssl_verify` flag in `.condarc` to point to the root CA used to sign the Anaconda Enterprise Repository server certificate.

### Configure anaconda-client

If you're using `anaconda-client` to connect to Anaconda Enterprise Repository with the command line, set the `ssl_verify` flag.

Use `anaconda config --files` to find the `anaconda-client` configuration files.

SEE the [command reference](#) for updating the client sites configuration for `anaconda-client`.

### Enabling email and SMTP

To send emails such as password reset emails, Repository must have the [email settings](#) configured.

### Configuring a standard or alternate port

The easiest way to enable clients to access a Repository server on standard ports is to configure the server to redirect traffic received on standard HTTP port 80 to the standard Repository HTTP port 8080:

```
sudo iptables -t nat -F
sudo iptables -t nat -A OUTPUT -d localhost -p tcp --dport 80 -j REDIRECT --to-ports 8080
sudo iptables -t nat -I PREROUTING -p tcp --dport 80 -j REDIRECT --to-port 8080
```

### HTTPS

To use HTTPS, redirect traffic from standard HTTPS port 443 to standard Repository HTTPS port 8443:

```
sudo iptables -t nat -A OUTPUT -d localhost -p tcp --dport 443 -j REDIRECT --to-ports 8443
sudo iptables -t nat -I PREROUTING -p tcp --dport 443 -j REDIRECT --to-port 8443
```

NOTE: See also *Enabling HTTPS*.

## Alternate port

To run Repository on a port other than the standard port 8080:

1. Modify the usual instructions by adjusting the port numbers in your *iptables configuration*.
2. Specify the correct port in your `supervisord.conf` file.

## Adjusting IPTables to accept requests on port 80

Enable clients to access a Repository on standard ports by configuring the server to redirect traffic received on standard HTTP port 80 to the standard Repository HTTP port 8080.

NOTE: These commands assume the default state of IPTables, which is on and allowing inbound SSH access on port 22. This is the factory default state for CentOS 6.7. If this default has been changed, you can reset it:

```
sudo iptables -L
```

CAUTION: Mistakes with IPTables rules can render a remote machine inaccessible.

1. Allow inbound access to tcp port 80:

```
sudo iptables -I INPUT -i eth0 -p tcp --dport 80 -m comment --comment "# Anaconda Repo #" -j ACCEPT
```

2. Allow inbound access to tcp port 8080:

```
sudo iptables -I INPUT -i eth0 -p tcp --dport 8080 -m comment --comment "# Anaconda Repo #" -j ACCEPT
```

3. Redirect inbound requests to port 80 to port 8080:

```
sudo iptables -A PREROUTING -t nat -i eth0 -p tcp --dport 80 -m comment --comment "# Anaconda Repo #" -j REDIRECT --to-port 8080
```

4. Display the current IPTables rules:

```
iptables -L -n
Chain INPUT (policy ACCEPT)
target     prot opt source                destination            tcp dpt:8080 /* # Anaconda Repo # */
ACCEPT     tcp  --  0.0.0.0/0              0.0.0.0/0              tcp dpt:80 /* # Anaconda Repo # */
ACCEPT     all  --  0.0.0.0/0              0.0.0.0/0              state RELATED,ESTABLISHED
ACCEPT     icmp --  0.0.0.0/0              0.0.0.0/0
ACCEPT     all  --  0.0.0.0/0              0.0.0.0/0
ACCEPT     tcp  --  0.0.0.0/0              0.0.0.0/0              state NEW tcp dpt:22
```

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```

REJECT    all  --  0.0.0.0/0          0.0.0.0/0          reject-with icmp-
↪host-prohibited

Chain FORWARD (policy ACCEPT)
target     prot opt source                destination
REJECT    all  --  0.0.0.0/0          0.0.0.0/0          reject-with icmp-
↪host-prohibited

Chain OUTPUT (policy ACCEPT)
target     prot opt source                destination

```

NOTE: The PREROUTING (nat) IPTables chain is not displayed by default. To display the chain:

```

iptables -L -n -t nat
Chain PREROUTING (policy ACCEPT)
target     prot opt source                destination
REDIRECT   tcp  --  0.0.0.0/0          0.0.0.0/0          tcp dpt:80 /* # ↵
↪Anaconda Repo # */ redir ports 8080

Chain POSTROUTING (policy ACCEPT)
target     prot opt source                destination

Chain OUTPUT (policy ACCEPT)
target     prot opt source                destination

```

5. Save the running IPTables configuration to `/etc/sysconfig/iptables`:

```
sudo service iptables save
```

## Connecting to an existing MongoDB database

If you already have a MongoDB server running, you can connect to it by setting the `MONGO_URL` configuration variable:

```
anaconda-server-config --set MONGO_URL 'mongodb://<hostname>'
```

For more information, see the [MongoDB Connection String URI Format](#) manual.

See also *Configuring MongoDB authentication*.

## Configuring MongoDB authentication

By default, MongoDB does not require a username or password to access or modify the database. We recommend enabling and configuring mandatory authentication.

1. Open a MongoDB shell:

```
mongo
```

2. Repository requires read/write access to the database `binstar`. Enter the following commands into the MongoDB shell to create an administrative user and a service user:

```
use admin
```



## 3. Create an administrative user to manage database users:

```
db.createUser({user:'siteUserAdmin', pwd: '<secure password #1>', roles:[
  ↳ 'userAdminAnyDatabase']})
```

## 4. Authorize as that user to verify the password:

```
db.auth('siteUserAdmin', '<secure password #1>')
```

## 5. Create a service user for Repository:

```
db.createUser({user:'anaconda', pwd: '<secure password #2>', roles:[{db:'binstar',
  ↳ role:'readWrite'}]})
```

## 6. Enable mandatory authentication in MongoDB:

- If you are using the legacy MongoDB configuration format, add the `auth` key to `/etc/mongod.conf`:

```
auth=true
```

- If you are using the current MongoDB configuration format, add the `security.authorization` key to `/etc/mongod.conf`:

```
security:
  authorization: enabled
```

## 7. Restart MongoDB to reload the configuration:

```
sudo service mongod restart
```

8. Edit the Repository configuration file and set the `MONGO_URL` parameter to `mongodb://<username>:<password>@<hostname>`.

After editing the configuration file, restart Repository for the changes to take effect.

9. Edit the Repository configuration file and set the `MONGO_URL` parameter to `mongodb://<username>:<password>@<hostname>`.

After editing the configuration file, restart Repository for the changes to take effect.

NOTE: For more information about MongoDB authentication and authorization, see <https://docs.mongodb.com/v2.6/core/authentication/> and <https://docs.mongodb.com/v2.6/core/authorization/>.

## Whitelisting or blacklisting packages

Sometimes you do not want to replicate all the packages from Repository into your mirror. The `anaconda-server-sync-conda` tool includes whitelist/blacklist functionality to manipulate your list of mirrored packages in a variety of ways.

A mirror config file can be specified when you run `anaconda-server-sync-conda` with the flag `--mirror-config=FILEPATH` and replace `FILEPATH` with the path to your config file.

NOTE: Configuration files are `yaml` files.

To customize your distribution, you have the following options:

- `remote_url`: Repository mirrors packages from this source URL.
- `mirror_dir`: Repository stores packages in this directory on the machine where the script is executed.

- `platforms`: Repository mirrors packages for these platforms.
- `license_blacklist`: Repository omits packages with these licenses.
- `blacklist`: Repository omits these packages.
- `whitelist`: Repository always mirrors these packages.

**TIP:** You do not need to set up every option manually. If you only want to adjust one or two options, that is allowed. Untouched options remain defined by the default setting.

**EXAMPLE:** The following example only selects packages that are available for `linux-32` and `linux-64` platforms. Win-32 or win-64 packages are not mirrored at all:

```
mirror_dir: /opt/anaconda-server/package-storage
platforms:
  - linux-32
  - linux-64
license_blacklist: GPL
whitelist:
  - distribute
  - conda
blacklist:
  - flask
  - readline
```

The step-by-step algorithm that is used by `cas-mirror` to create the ultimate list of packages to mirror follows this order:

1. Get a full list of packages from `default_url`.
2. If the `platforms` option is present, only those packages available to the platforms listed here are left on the list.
3. If `license_blacklist` is present, then all the packages subject to any of the licenses mentioned here are removed from the list. See the [list of license families that can be blacklisted](#).
4. If `blacklist` is present, then all member packages explicitly mentioned here are removed from the list.
5. If `whitelist` is present, then those assigned member packages are added to the list. The `whitelist` option overrides `license_blacklist` and `blacklist`, so that a package listed here is mirrored even when under a GPL license or if it appears in the `blacklist` option.

After performing all of the above actions sequentially, the script produces the ultimate list of packages that are mirrored.

### Securing user-created content

To prevent cross-site scripting attacks (XSS), user content—such as Jupyter Notebooks—can be served from a separate domain.

To enable this:

1. Configure the project to use a separate content domain:

```
anaconda-server-config --set SERVER_NAME your.anaconda.repository
anaconda-server-config --set USER_CONTENT_DOMAIN your.usercontent.server
```

**NOTE:** Replace `your.anaconda.repository` and `usercontent.your.anaconda.repository` with the respective server IP address or domain name.

1. If your user content domain is a subdomain of your Repository domain, you must also configure the session cookie to only send to the root domain:

```
anaconda-server-config --set SERVER_NAME your.anaconda.repository
anaconda-server-config --set USER_CONTENT_DOMAIN usercontent.your.anaconda.
↪ repository
anaconda-server-config --set SESSION_COOKIE_DOMAIN your.anaconda.repository
```

NOTE: Replace `your.anaconda.repository` and `usercontent.your.anaconda.repository` with the respective server IP address or domain name.

## Configuring Repository to use LDAP

To enable Lightweight Directory Access Protocol (LDAP) support:

1. Open the Repository configuration file `$PREFIX/etc/anaconda-server/config.yaml` and add the following configuration:

```
account_names_filter: false
USER_REGEX: ^[a-z0-9_][a-z0-9_-.]+$
LDAP:
  # Replace with company LDAP server
  URI: 'ldap://<ldap.company.com>'

  # Replace <uid=%(username)s,ou=People,dc=company,dc=com> with your company_
↪ specific LDAP Bind/Base DN
  # Bind directly to this Base DN.
  BIND_DN: '<uid=%(username)s,ou=People,dc=company,dc=com>'

  # Map LDAP keys into application specific keys
  KEY_MAP:
    name: 'cn'
    company: 'o'
    location: 'l'
    email: 'mail'
```

2. When switching authentication to LDAP, the admin account is lost, so you need to add your admin account again:

```
anaconda-server-admin set-superuser "jsmith"
```

3. Run the `flask-ldap-login-check` command to verify LDAP connectivity:

```
flask-ldap-login-check binstar.wsgi:app --username 'jsmith' --password 'abc123DEF'
```

NOTE: Replace `jsmith` and `abc123DEF` with your LDAP username and password.

4. To apply the changes, restart the Repository server:

```
supervisorctl restart all
```

5. Open a new browser window and navigate to your local Repository installation:

```
http://your.anaconda.repository
```

NOTE: Replace `your.anaconda.repository` with your Repository server IP address or domain name.

6. Log in using your LDAP credentials.

7. Optional. You may set an LDAP network timeout in seconds with the options `OPT_NETWORK_TIMEOUT` and `OPT_TIMEOUT`. The default value is 0, meaning no timeout.

For example, to set the timeout to 60 seconds, add this block to the LDAP settings in your configuration file:

```
OPTIONS:
  OPT_NETWORK_TIMEOUT: 60
  OPT_TIMEOUT: 60
```

## Configuring Repository to use Active Directory

Microsoft Active Directory is a server program that provides directory services and uses the open industry standard Lightweight Directory Access Protocol (LDAP).

To enable Active Directory support:

1. Open the Repository configuration file `$PREFIX/etc/anaconda-server/config.yaml` and add the following configuration:

```
account_names_filter: false
USER_REGEX: ^[a-z0-9_][a-z0-9_-.]+$
LDAP:
  # Replace with company LDAP server
  'URI': 'ldap://<ldap.server.url>'

  # This BIND_DN/BIND_PASSWORD default to '', this is shown here for
  # demonstrative purposes. To enable Authorized Bind, insert the AD
  # BIND_DN and BIND_AUTH password for an authorized AD user.
  #
  #e.g. 'BIND_DN': '<cn=Authorized User,cn=users,dc=company,dc=local>'
  #e.g. 'BIND_AUTH': '<AuthUsrPassword>'

  # The values '' perform an anonymous bind so we may use search/bind method
  BIND_DN: ''
  BIND_AUTH: ''

  # Adding the USER_SEARCH field tells the flask-ldap-login that we
  # are using the search/bind method
  USER_SEARCH:
    base: <cn=users,dc=company,dc=local>
    filter: sAMAccountName=%(username)s

  # Map ldap keys into application specific keys
  KEY_MAP:
    name: 'cn'
    company: 'o'
    location: 'l'
    email: 'userPrincipalName'
```

2. To apply the changes, restart the Repository server:

```
supervisorctl restart all
```

3. Run the `flask-ldap-login-check` command to verify Active Directory connectivity:

```
flask-ldap-login-check binstar.wsgi:app --username 'jsmith' --password 'abc123DEF'
```

NOTE: Replace `jsmith` and `abc123DEF` with your Active Directory username and password.

You see a response similar to the following:

```
[anaconda.server] Started Site
Got userdata for jsmith
{'company': None, 'email': None, 'location': None, 'name': 'Jane Smith'}
```

4. Open your browser and navigate to your local Repository installation:

```
http://your.anaconda.repository
```

NOTE: Replace `your.anaconda.repository` with your Repository IP address or domain name.

5. Log in with Active Directory.

## Configuring Repository to use LDAP groups

Repository can be configured to allow synchronizing the membership of organization groups with groups in an LDAP directory. Owners of an organization can select a specific LDAP group as the source of group members.

Once this is enabled, users who sign in to Repository who are members of the LDAP group automatically are granted the permissions of the organization group.

To enable LDAP groups, configure the following:

- Authenticated bind to LDAP. Repository needs to perform searches against the directory to determine the available groups and the membership of those groups.
- A query for Repository to identify the groups in your LDAP directory. For more information, see [GROUP\\_SEARCH](#).

If LDAP synchronization is disabled or the LDAP server is unreachable, the member list at the time is used for the group.

To administer and debug LDAP synchronization, a superuser can visit:

```
http://your.anaconda.repository/admin/ldap
```

NOTE: Replace `your.anaconda.repository` with your Repository IP address or domain name.

## Enabling TLS on LDAP/Active Directory

To enable a secure Transport Layer Security (TLS) connection on LDAP/Active Directory, add the following to the LDAP configuration section of the file `$PREFIX/etc/anaconda-server/config.yaml`, replacing `/path/to/certfile` with the actual path to the certfile.:

```
LDAP:
... # Rest of the LDAP config
START_TLS: true,
OPTIONS:
  OPT_PROTOCOL_VERSION: 3
  OPT_X_TLS_DEMAND: true
  OPT_X_TLS_REQUIRE_CERT: 'OPT_X_TLS_NEVER'
  OPT_X_TLS_CACERTFILE: '/path/to/certfile'
```

**NOTE:** `START_TLS` is not compatible with LDAPS. When using `START_TLS`, the `URI` value in the LDAP configuration section must start with `ldap://`. When using `START_TLS`, the connection starts as a regular connection, and is upgraded to use TLS after connection has been established.

If you're using self-signed certificates, you'll need to add `OPT_X_TLS_NEWCTX` as the **last entry** of the `OPTIONS` field of the LDAP options:

```
LDAP:
... # Rest of the LDAP config
START_TLS: true,
OPTIONS:
  OPT_PROTOCOL_VERSION: 3
  OPT_X_TLS_DEMAND: true
  OPT_X_TLS_REQUIRE_CERT: 'OPT_X_TLS_NEVER'
  OPT_X_TLS_CACERTFILE: '/path/to/certfile'
  OPT_X_TLS_NEWCTX: 0
```

## Using LDAP and TLS configuration options

### URI

Start by setting `URI` to point to your server. The value of this setting can be anything that your LDAP library supports. For instance, `openldap` may allow you to give a comma- or space-separated list of `URI` values to try in sequence.

### BIND\_DN

The distinguished name to use when binding to the LDAP server with `BIND_AUTH`. Use the empty string—the default—for an anonymous bind.

### BIND\_AUTH

The password to use with `BIND_DN`.

### USER\_SEARCH

A dictionary that locates a user in the directory. The dict object must contain the required entries `base` and `filter` and may contain the optional entry `scope`.

- `base`: The base DN to search.
- `filter`: Should contain the placeholder `%(username)s` for the username.
- `scope`: One of `LDAP_SCOPE_BASE`, `LDAP_SCOPE_ONELEVEL` or `LDAP_SCOPE_SUBTREE`.

EXAMPLE:

```
{ 'base': 'dc=example,dc=com', 'filter': 'uid=%(username)s' }
```

## SUPERUSER\_SEARCH

A dict that will determine whether a valid user is a superuser. The dict object must contain the required entries `base` and `filter` and may contain the optional entry `scope`. If the search is successful, then something is returned by the LDAP server, and the user is given superuser permissions.

- `base`: The base DN to search.
- `filter`: Should contain the placeholder `%(username)s` for the username.
- `scope`: One of `LDAP_SCOPE_BASE`, `LDAP_SCOPE_ONELEVEL`, or `LDAP_SCOPE_SUBTREE`.

For example:

```
{ 'base': 'cn=admin,ou=Groups,dc=example,dc=com', 'filter': 'memberUid=%(username)s' }
```

Notice that this check is done during the login procedure, so even though privileges might have been removed from (or added to) the LDAP server, the user will have to authenticate again to see the changes.

## ENABLE\_GROUPS

This attribute enables LDAP group synchronization, allowing users to synchronize group membership with an LDAP directory. Defaults to `false`.

EXAMPLE:

```
ENABLE_GROUPS: true
```

## GROUP\_SEARCH

A dictionary that locates a group in the directory. An LDAP search is performed using the `base` distinguished name and `filter`.

**NOTE:** Unlike `USER_SEARCH`, **you must put parenthesis around the `GROUP_SEARCH` filter**. It may appear to work without parenthesis, when it's actually failing or behaving unpredictably.

EXAMPLE:

```
GROUP_SEARCH:
  base: dc=example,dc=com
  filter: (objectClass=group)
```

**NOTE:** Anaconda Repository assumes that the groups' `objectClass` is `groupOfNames` (or a compatible schema). The following **LDIF** snippet shows an example group instance:

```
dn: cn=Analysts,ou=Anaconda Groups,dc=example,dc=com
cn: Analysts
member: cn=John Doe,ou=Users,dc=example,dc=com
member: cn=Jane Doe,ou=Users,dc=example,dc=com
member: cn=John Q. Public,ou=Users,dc=example,dc=com
member: cn=Guy Incognito,ou=Users,dc=example,dc=com
objectclass: groupOfNames
objectclass: top
```

### GROUP\_MEMBERS\_ATTR

The LDAP attribute on a group object that indicates the users that are members of the group. Defaults to `member`.

EXAMPLE:

```
GROUP_MEMBERS_ATTR: 'member'
```

NOTE: Anaconda Repository assumes that the groups' *objectClass* is *groupOfNames* (or a compatible schema).

### REFRESH\_INTERVAL

The number of seconds that group membership information from LDAP is used before being fetched from the directory server again. Defaults to 3600, which is 1 hour.

EXAMPLE:

```
REFRESH_INTERVAL: 600
```

### KEY\_MAP

This is a dict mapping application context to LDAP. An application may expect user data to be consistent, and not all LDAP setups use the same configuration:

```
'application_key': 'ldap_key'
```

EXAMPLE:

```
KEY_MAP={'name': 'cn', 'company': 'o', 'email': 'mail'}
```

### START\_TLS

If `true`, each connection to the LDAP server calls `start_tls_s()` to enable TLS encryption over the standard LDAP port. There are a number of configuration options that can be given to `OPTIONS` that affect the TLS connection. For example, `OPT_X_TLS_REQUIRE_CERT` can be set to `OPT_X_TLS_NEVER` to disable certificate verification, perhaps to allow self-signed certificates.

### OPTIONS

This stores LDAP specific options.

EXAMPLE:

```
LDAP:
  OPTIONS:
    OPT_PROTOCOL_VERSION: 3
    OPT_X_TLS_REQUIRE_CERT: 'OPT_X_TLS_NEVER'
```



## TLS—secure LDAP

To enable a secure TLS connection you must set `START_TLS` to `true`. There are a number of configuration options for `OPTIONS` that affect the TLS connection.

EXAMPLE: `OPT_X_TLS_REQUIRE_CERT` set to `OPT_X_TLS_NEVER` disables certificate verification, perhaps to allow self-signed certificates:

```
LDAP :
  START_TLS: true
  OPTIONS:
    OPT_PROTOCOL_VERSION: 3
    OPT_X_TLS_DEMAND: true
    OPT_X_TLS_REQUIRE_CERT: 'OPT_X_TLS_NEVER'
    OPT_X_TLS_CACERTFILE: '/path/to/certfile'
```

## Configuring Repository to use Kerberos

Kerberos is an authentication protocol designed to allow nodes communicating over an insecure network to verify identity. Repository can use Kerberos to authenticate users.

The Kerberos protocol uses timestamps to prevent replay attacks on expired credentials, so the Network Time Protocol (NTP) service must be set up and working correctly.

Several aspects of Kerberos rely on name service. Your domain name system (DNS) entries and your hosts must have the correct information. The `hostname` command and the configuration file `/etc/hostname` must reflect the fully-qualified domain name (FQDN) of the machine. The configuration file `/etc/hosts` must include an entry with the FQDN, to allow reverse-DNS lookups to be performed.

To allow clients to authenticate against Anaconda Repository, create a principal for the service with a private key that identifies the service. Create a service principal `HTTP/your.anaconda.repository`, and create the keytab containing this principal to `$PREFIX/etc/anaconda-server/http.keytab`:

```
SERVER_NAME=your.anaconda.repository
```

NOTE: Replace `your.anaconda.repository` with your server IP address or domain name.

If you are using MIT Kerberos:

```
kadmin -q "addprinc HTTP/${SERVER_NAME}"
kadmin -q "ktadd -k $PREFIX/etc/anaconda-server/http.keytab HTTP/${SERVER_NAME}"
chown anaconda-server:anaconda-server $PREFIX/etc/anaconda-server/http.keytab
chmod 600 $PREFIX/etc/anaconda-server/http.keytab
```

If you are using Active Directory:

1. Open Active Directory Users and Computers.
2. Select the Users container.
3. In the **Action** menu, select New, then select User.
4. In the New Object - User dialog, type the user information. In this example, we use `your-anaconda-repository` as the login.
5. In the next dialog, select the options Password never expires and User cannot change password.
6. Right-click on the newly created user, and select Properties.

7. In the Properties dialog, select the **Account** tab, and ensure the Do not require Kerberos preauthentication option is selected.
8. Open an Administrative prompt and run:

```

ktpass -princ HTTP/your.anaconda.repository@YOUR.DOMAIN -out http.keytab -pass "*"
↪ " -mapUser your-anaconda-user@your-anaconda-server -ptype KRB5_NT_PRINCIPAL

```

9. Copy the newly created file http.keytab to \$PREFIX/etc/anaconda-server/http.keytab on your Repository server.

To enable Kerberos authentication on Repository, add the configuration options to \$PREFIX/etc/anaconda-server/config.yaml:

```

AUTH_TYPE: KERBEROS
KRB5_KTNAME: /home/anaconda-server/repo/etc/anaconda-server/http.keytab

```

For a minimal configuration example see [Kerberos-Anaconda Repository setup example](#).

## Kerberos configuration options

AUTH_TYPE	string	Configures the authentication scheme used for Repository. Set to KERBEROS to enable Kerberos authentication. Default: NATIVE.
KRB5_KTNAME	string	The file path of the keytab containing the service principal for Repository. Default: /etc/krb5.keytab.
KRB5_SERVICE_NAME	string	The service type used to identify the service principal for Repository. HTTP in HTTP/your.anaconda.repository@YOUR.REALM. Default: HTTP.
KRB5_HOSTNAME	string	The hostname used to identify the service principal for Repository. your.anaconda.repository in HTTP/your.anaconda.repository@YOUR.REALM. Default: the hostname of the machine on which Repository is running.

## Kerberos-Anaconda Repository setup example

Kerberos authentication adds a layer of security to Anaconda Repository. The following example show how to set up a minimal working installation with three machines: One running anaconda server, one running the MIT Kerberos Key Distribution Center (KDC), and a client from where we are going to connect to both services.

For this example we assume that both the KDC and Anaconda Repository are already configured and the 3 systems have the Network Time Protocol (NTP) service working.

### Initial Setup

All 3 machines are running CentOS 7 but the configurations mentioned here apply for many other Linux distributions. We are going to use the following domain names:

- Anaconda Repository: anaconda.kerberos.local
- Kerberos KDC: kdc.kerberos.local
- Client: client.kerberos.local

Make sure that the information is correct in the configuration files `/etc/hostname` and `/etc/hosts` to allow reverse-DNS lookups.

The name of the Kerberos realm is `KERBEROS.LOCAL`. The 3 machines have the same configuration file `/etc/krb5.conf`:

```
[logging]
    kdc = FILE:/var/log/krb5kdc.log
    admin_server = FILE:/var/log/kadmind.log
    default = SYSLOG:NOTICE:DAEMON

[libdefaults]
    dns_lookup_realm = true
    dns_lookup_kdc = true
    ticket_lifetime = 24h
    renew_lifetime = 7d
    forwardable = true
    rdns = false
    default_realm = KERBEROS.LOCAL
    default_ccache_name = KEYRING:persistent:%{uid}

[realms]
    KERBEROS.LOCAL = {
        kdc = kdc.kerberos.local
        admin_server = kdc.kerberos.local
    }

[domain_realm]
    .kerberos.local = KERBEROS.LOCAL
    kerberos.local = KERBEROS.LOCAL
```

On `kdc.kerberos.local` the files `/var/kerberos/krb5kdc/kdc.conf` and `/var/kerberos/krb5kdc/kadm5.acl` should be configured accordingly.

## Configure Anaconda Repository

At this point Anaconda Repository is up and running, it's installed on `/home/anaconda-server/repo`, the administrator account in this example is `superuser`. To allow authentication we first create a service principal and the keytab containing this principal. This is accomplished running the following commands as root from a terminal on `anaconda.kerberos.local`.

```
kadmin -q "addprinc HTTP/anaconda.kerberos.local"
kadmin -q "ktadd -k /home/anaconda-server/repo/etc/anaconda-server/http.keytab HTTP/
↪anaconda.kerberos.local"
chown anaconda-server:anaconda-server \
    /home/anaconda-server/repo/etc/anaconda-server/http.keytab
chmod 600 /home/anaconda-server/repo/etc/anaconda-server/http.keytab
```

Now edit the configuration file `/home/anaconda-server/repo/etc/anaconda-server/config.yaml` and add the following lines:

```
AUTH_TYPE: KERBEROS
KRB5_KTNAME: /home/anaconda-server/repo/etc/anaconda-server/http.keytab
```

Finally, add the principal for the admin account on the kerberos realm:

```
kadmin -q "addprinc superuser@KERBEROS.LOCAL"
```

Reboot the server for the changes to take effect.

### Client Configuration

To log in to Anaconda Repository with Kerberos Authentication, a browser that supports said authentication protocol is necessary. In this example we are using Firefox. Some extra tweaking is required.

- Open Firefox and type **about:config** in the navigation bar, click the confirmation button if necessary to proceed to the configuration page.
- Type **negotiate** in the Search field to filter out the options, double click **network.negotiate-auth.trusted-uris** and enter `.kerberos.local` in the text box.
- Do the same for **network.negotiate-auth.delegation-uris**.

Finally a ticket for the `superuser` should be stored on the local machine. The following command will request it:

```
kinit superuser@KERBEROS.LOCAL
```

Now it is possible to open anaconda server on firefox, in this case the URL is `anaconda.kerberos.local:8080`, after clicking **Sign In**, the user should be able to log in immediately without having to enter any credentials.

### Configure Anaconda Repository to use PAM

Open the Anaconda Repository configuration file `$PREFIX/etc/anaconda-server/config.yaml` and add the following configuration to enable Pluggable Authentication Module (PAM) support:

```
AUTH_TYPE: PAM
```

When switching authentication to PAM the admin account is lost, so you need to add your admin account again:

```
anaconda-server-admin set-superuser "jsmith"
```

To apply the changes, restart the Anaconda Repository server:

```
supervisorctl restart all
```

Open a new browser window and navigate to your local Anaconda Repository installation:

```
http://your.anaconda.server
```

NOTE: Replace “your.anaconda.server” with your actual Anaconda Repository server IP address or domain name.

You can now log in using your PAM credentials.

NOTE: To use the “shadow” PAM backend, add the user under which Anaconda Repository is running (usually “anaconda-server”) to the “shadow” group:

```
sudo usermod -a -G shadow anaconda-server
```

## Read only mode

The site can be put into **read only** mode to disable any action that modifies the database.

This may be useful when mirroring from the site.

NOTE: Logging in modifies the database, so in **read only** mode users and admins may not log in.

To enable **read only** mode use the setting:

```
READ_ONLY: true
```

## Configuring Anaconda Client

- *Client configuration*
- *Conda configuration*
- *Pip configuration*
- *Kerberos configuration*

Anaconda Client gives you the ability to upload packages to your on-site Anaconda Repository and provides highly granular access control capabilities. The instructions below describe how to configure Client to use your local Repository instead of Anaconda Cloud.

### Client configuration

On each machine that accesses your on-site Repository, run this command as the machine's local user:

```
anaconda config --set url http://your.server.name:<port>/api
```

Or, to set the default repo on a system-wide basis, run this command:

```
anaconda config --set url http://your.server.name:<port>/api --site
```

NOTE: Replace `your.server.name` with the name of your local Repository and `<port>` with the name of the port used by Repository.

The system level `config` file is used only if no user-level `config` file is present.

To show the system and user `config` file locations and configuration settings:

```
anaconda config --show
```

### Conda configuration

When the above `anaconda config` steps are completed, you can access all packages and channels from the local on-site Repository instead of the public Anaconda.org.

Users can then add individual accounts to their `.condarc` file by running the following command:

```
conda config --add channels USERNAME
```

If you still want to access certain channels from the public Anaconda.org, run:

```
conda config --add channels http://conda.anaconda.org/USERNAME
```

NOTE: Replace USERNAME with your username.

### Conda channel priority

To set a preferred priority for the channels conda searches for package installs, edit your `~/.condarc` file and change the order. Channels at the top are searched first.

For example:

```
channels:
- channel
- https://conda.anaconda.org/t/<token>/<channel2>
- http://conda.anaconda.org/<channel1>
- defaults
```

The order of search is:

1. Private on-site Repository channel.
2. Private Anaconda.org channel2.
3. Public Anaconda.org channel1.
4. Default channel on the on-site Repository.

### Pip configuration

To install PyPI packages from your Repository, add your channel to your `~/.pip/pip.conf` configuration file.

Edit the file and add an extra-index-url entry to the global config section:

```
[global]
extra-index-url = http://your.server.name:<port>/pypi/USERNAME/simple
```

NOTE: Replace `your.server.name` with the name of your local Repository, `<port>` with the name of the port used by Repository and USERNAME with your username.

### Kerberos configuration

If you have enabled Kerberos authentication as described in *Configuring Repository to use Kerberos*, your browser and Client should be able to authenticate to Repository using Kerberos.

In macOS/Unix, configure the file `/etc/krb5.conf`:

```
[libdefaults]
default_realm = YOUR.DOMAIN

[realms]
YOUR.DOMAIN = {
```

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```
kdc = your.kdc.server
}

[domain_realm]
your.anaconda.repository = YOUR.DOMAIN
```

**NOTE:** Replace `YOUR.DOMAIN` with your domain, `your.kdc.server` with your Kerberos key distribution center (KDC) and `your.anaconda.repository` with your local Repository server.

If your configuration is correct, you should be able to authenticate using the command line tool `kinit`:

```
kinit jsmith
anaconda login
```

**NOTE:** Replace `jsmith` with your username.

## Browser Setup

Many browsers do not present your Kerberos credentials by default, to prevent leaking credentials to untrusted parties. In order to use Kerberos authentication, you must whitelist Repository as a trusted party to receive credentials.

You must restart your browser after configuring the whitelist in order for changes to be reflected.

### Safari

Safari requires no configuration—it automatically presents your credentials without whitelisting.

### Chrome

The `AuthServerWhitelist` policy must be set to `your.anaconda.repository` to allow Chrome to present credentials to Repository with the hostname `your.anaconda.repository`. Depending on your DNS configuration, `DisableAuthNegotiateCNameLookup` may also be required to prevent Chrome from canonicalizing the hostname before generating a service name.

**NOTE:** Replace `your.anaconda.repository` with your local Repository server.

To configure on macOS:

```
defaults write com.google.Chrome AuthServerWhitelist "your.anaconda.repository"
```

On Linux:

```
mkdir -p /etc/opt/chrome/policies/managed
mkdir -p /etc/opt/chrome/policies/recommended
chmod -w /etc/opt/chrome/policies/managed
echo '{"AuthServerWhitelist": "your.anaconda.repository"}' > /etc/opt/chrome/policies/
↳ managed/anaconda_repo_policy.json
```

On Windows, use Group Policy objects to set the Authentication server whitelist setting to `your.anaconda.repository`.

For more information, see Chrome's [SPNEGO authentication](#) and [administration](#) documentation.

### Firefox

1. Navigate to the configuration page `about:config`.
2. Search for `negotiate`.
3. Set the configuration item `network.negotiate-auth.trusted-uris` to `your.anaconda.repository`

NOTE: Replace `your.anaconda.repository` with your local Repository server.

### Internet Explorer

1. In the **Tools** menu, select Internet Options.
2. On the **Advanced** tab, in the Security section, select Enable Integrated Windows Authentication.

### Configuring local mirrors

You can add a local copy—mirror—of Anaconda or PyPI repositories to your Anaconda Repository installation. This section explains how to use Repository’s convenient syncing tools to create and configure local mirrors:

#### Mirroring an Anaconda repository

- *Before you start*
- *Mirroring all packages*
- *Mirroring some packages*
- *Offline mirroring*
- *Mirroring with the deprecated `anaconda-mirror` command*
- *Mirroring additional channels*
- *Configuring conda*

NOTE: This documentation is for versions of Anaconda Repository 2.26 and newer. For versions from 2.23 through 2.25, see [2.23 documentation](#). For versions before 2.23, see [2.20 documentation](#).

#### Before you start

You need to have already installed and configured your Repository instance. Due to the size of Repository, it is important that you have configured a file storage location with sufficient disk space. If necessary, see the [requirements for the file storage location](#).

A full Anaconda mirror requires approximately 90 GB.

You will also need to install `cas-mirror` as it is the recommended mirroring tool.

NOTE: The `anaconda-mirror` tool has been deprecated and will not be updated any further.



## Mirroring all packages

You can mirror some or all of the contents of the [Anaconda repository](#) using the `cas-sync-api-v4` command:

```
$ cas-sync-api-v4 --help
usage: cas-sync-api-v4 [-h] [-f FILENAME] [--config] [--version]
                      [-l LOG_LEVEL] [-v]

Updates an Anaconda repository instance

optional arguments:
  -h, --help            show this help message and exit
  -f FILENAME, --file FILENAME
                        Configuration file location (Defaults to:
                        /home/abarto/.cas-mirror or /etc/cas-mirror)
  --config, --show-config
                        Show running configuration and exit
  --version             Print version and exit
  -l LOG_LEVEL, --log-level LOG_LEVEL
                        Set the log level (CRITICAL, ERROR, WARNING, INFO,
                        DEBUG)Default: INFO.
  -v, --verbose         Shorthand for --log-level DEBUG
```

This tool mirrors all of the packages from the Anaconda repository default channels into the `anaconda` user account. It leverages the functionality exposed by the `anaconda-client` package to import the remote packages into an existing site.

1. Associate the URL of your Anaconda repository with a site using the `anaconda` command:

```
anaconda config --set sites.myrepo.url "http://your-anaconda-repo/"
```

NOTE: Replace `your-anaconda-repo` with the URL to your installation of Repository.

2. Create a configuration file `sync.yaml` that tells `cas-sync-api-v4` which site to use:

```
dest_site: myrepo
```

3. Check that the configuration is valid with the `--config` parameter:

```
$ cas-sync-api-v4 -f sync.yaml --config
path: /home/ec2-user/sync.yaml
remote_url: https://repo.anaconda.com/
mirror_dir: /opt/cas-mirror
platforms: ['osx-32', 'osx-64', 'win-32', 'win-64', 'linux-32', 'linux-64',
↳ 'linux-armv6l', 'linux-armv7l', 'linux-ppc64le']
fetch_installers: True
repodata_source: False
dir_names: ['archive']
server_log_dir: None
server_port: None
dest_site: myrepo
dest_channel: anaconda
verify_checksum: False
delta: False
delta_dir: None
log_dir: None
log_level: 20
python_versions: []
```

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```
pkg_list: []
license_blacklist: []
blacklist: []
whitelist: []
channels:
  - https://repo.anaconda.com/pkgs/main/
  - https://repo.anaconda.com/pkgs/free/
  - https://repo.anaconda.com/pkgs/pro/
```

With this configuration, `cas-sync-api-v4` mirrors the contents of all the default channels into the anaconda account of the myrepo site.

#### 4. Run `cas-sync-api-v4`:

```
cas-sync-api-v4 -f sync.yaml
```

#### 5. Verify the mirroring by opening a browser and loading this URL:

```
http://your-anaconda-repo/anaconda/
```

NOTE: Replace `your-anaconda-repo` with the URL to your installation of Repository.

## Mirroring some packages

Alternately, you may not want to mirror all packages. To mirror a subset of the total repository, specify which platforms you want to include, or use the `whitelist`, `blacklist` or `license_blacklist` functionality to control which packages are mirrored, by copying the default configuration file `$PREFIX/etc/anaconda-server/mirror/anaconda.yaml` to `$PREFIX/etc/anaconda-server/mirror/anaconda-custom.yaml`.

For Repository 2.27 or newer, there are sample `yaml` config files located at: `$PREFIX/etc/anaconda-server/mirror`. `PREFIX` is the install location of Repository, which by default is `~anaconda-server/repo/etc/anaconda-server/mirror`.

This command mirrors the repository according to the settings in the configuration file `anaconda-custom.yaml`:

```
cas-sync-api-v4 -f anaconda-custom.yaml
```

For more information, see [Customizing mirrors](#).

## Offline mirroring

Offline mirroring is done by using both `cas-sync` and `cas-sync-api-v4`. First download all the packages onto a host with Internet access.

### EXAMPLE:

To download the packages, create a configuration file named `export.yaml`:

```
mirror_dir: /opt/mirror/export/
platforms:
  - linux-64
  - win-64
python_versions:
  - 2.7
  - 3.6
```

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```

fetch_installers: false
pkg_list:
  - ca-certificates
  - certifi
  - libedit
  - libffi
  - libgcc-ng
  - libstdcxx-ng
  - ncurses
  - openssl
  - pip
  - python
  - readline
  - setuptools
  - sqlite
  - tk
  - wheel
  - xz
  - zlib

```

This example downloads only a subset of the default channels.

Run `cas-sync`:

```
cas-sync -f export.yaml
```

After it finishes, a conda repository for each platform is created in the directory `/opt/mirror/export/pkgs`. We can now take the contents of the directory `/opt/mirror/export/` to the air-gapped environment.

To import the packages, create a config file named `import.yaml`:

```

dest_site: mysite
dest_channel: anaconda
channels:
  - file:///opt/mirror/export/pkgs/
platforms:
  - linux-64
  - win-64
python_versions:
  - 2.7
  - 3.6

```

Make sure these requirements are true:

- The files mirrored onto the connected box have been put in the `/opt/mirror/export` directory.
- An anaconda site named `mysite` is properly configured and the user has logged into it using the `anaconda` command.
- An “anaconda” account exists in the “mysite” site and the logged in user has access to it.

After these requirements are true, run `cas-sync-api-v4`:

```
cas-sync-api-v4 -f import.yaml
```

## Mirroring with the deprecated `anaconda-mirror` command

The `anaconda-mirror` command is deprecated but still in use at some installations.

It is used with the command `anaconda-mirror sync`, or with a configuration file such as `anaconda-custom.yaml` with the command `anaconda-mirror --config-file anaconda-custom sync`.

### Resetting packages

Use the `--reset` option to reset the previously mirrored packages:

```
anaconda-mirror --config-file anaconda-custom sync --reset
```

This resets the “last sync” time for the repository, so `anaconda-mirror` requests all packages, not just those changed or added since the last sync. As the requests are processed, `anaconda-mirror` still automatically downloads only those files that differ from the files currently in the repository.

### Exporting a mirror

To generate a mirror archive:

```
anaconda-mirror export mirror.tar
```

This command dumps the packages, according to the *configured settings*, into the file `mirror.tar`.

This mirror can be used in an air gapped environment.

### Importing a mirror

To mirror the Anaconda repository in an air gapped environment, point `anaconda-mirror` to the exported mirror archive.

Mount the USB drive and then run:

```
anaconda-mirror import $USB/mirror.tar
```

This command mirrors the contents of the local Anaconda repository to your Repository installation under the user-name “anaconda.”

### Filtering

If you want to update the filters on your mirror—for example, to exclude additional licenses—running `anaconda-mirror sync` again retrieves new packages that match this filter, but it does not remove existing packages that no longer match the filter.

To see which packages no longer match your filter:

```
anaconda-mirror clean --dry-run
```

To remove these packages from your mirror:

```
anaconda-mirror clean
```

## Mirroring additional channels

If mirroring from an air gap archive, the channel in the following configuration points to a local directory to which the archive is expanded.

In addition, if a platform-specific archive is downloaded, then the config file needs the platforms section. The examples in the following sections assume `x64-repo-mirrors-*.tar` <airgap-archive-mirrors> is expanded to `$MIRRORS_ARCHIVE`.

Similarly, for an online system, the channel points to Anaconda Cloud. The platforms are optional and limit the mirrored conda packages to the specified platforms.

## Mirroring R channel

1. Create the `yaml` config file.

EXAMPLE: The following is a config to mirror from an air gap archive containing only x64 packages:

```
cat $PREFIX/etc/anaconda-server/mirror/r.yaml

channels:
  - file://$MIRRORS_ARCHIVE/r/pkgs

# The platforms should correspond to the platforms contained in
# the archive. Omit if the archive contains conda packages for all platforms.
platforms:
  - linux-64
  - osx-64
  - win-64
```

EXAMPLE: The following is for an online system:

```
cat $PREFIX/etc/anaconda-server/mirror/r.yaml

channels:
  - https://conda.anaconda.org/r
```

2. Mirror the packages to r-channel:

```
anaconda-server-sync-conda --mirror-config \
  $PREFIX/etc/anaconda-server/mirror/r.yaml --account=r-channel
```

## Mirroring Wakari channel for AEN

1. Create the `yaml` config file.

EXAMPLE: The following is a config to mirror from an air gap archive containing only x64 packages:

```
cat $PREFIX/etc/anaconda-server/mirror/wakari.yaml

channels:
  - file://$MIRRORS_ARCHIVE/wakari/pkgs

# The platforms should correspond with the platforms contained in
# the archive. Omit if the archive contains conda packages for all platforms.
```

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```
platforms:
- linux-64
- osx-64
- win-64
```

EXAMPLE: The following is for an online system:

```
cat $PREFIX/etc/anaconda-server/mirror/wakari.yaml

channels:
- https://conda.anaconda.org/t/<TOKEN>/anaconda-nb-extensions
- https://conda.anaconda.org/wakari
```

NOTE: Replace <TOKEN> with the token for the anaconda-nb-extensions channel that you should have received along with your Repository license.

2. Mirror the packages to the Wakari channel:

```
anaconda-server-sync-conda --mirror-config \
    $PREFIX/etc/anaconda-server/mirror/wakari.yaml --account=wakari
```

## Mirroring anaconda-adam channel for cluster management

1. Create the yaml config file.

EXAMPLE: The following is a config to mirror from an air gap archive containing only x64 packages:

```
cat $PREFIX/etc/anaconda-server/mirror/anaconda-adam.yaml

channels:
- file://$MIRRORS_ARCHIVE/anaconda-adam/pkgs

# The platforms should correspond with the platforms contained in
# the archive. Omit if the archive contains conda packages for all
# platforms.
platforms:
  * linux-64
  * osx-64
  * win-64
```

EXAMPLE: The following is for an online system:

```
cat $PREFIX/etc/anaconda-server/mirror/anaconda-adam.yaml

channels:
- https://conda.anaconda.org/anaconda-adam
```

2. Mirror the packages to anaconda-adam channel:

```
anaconda-server-sync-conda --mirror-config \
    $PREFIX/etc/anaconda-server/mirror/anaconda-adam.yaml --account=anaconda-adam
```

## Configuring conda

Having created the mirror, you still need to configure conda to search for packages here rather than on the default Anaconda repository. You can do that by editing your `~/.condarc` file to add the appropriate channel:

```
channels:
  - http://<anaconda.repo.ipaddress>:<port>/conda/anaconda/
```

NOTE: Replace `<anaconda.repo.ipaddress>` with the URL to your installation of Repository.

NOTE: This configuration change can be made at the user level or via an [administrative](#) conda file, to force all internal users to use your local Anaconda mirror rather than querying the Anaconda repository.

NOTE: Users can download Anaconda installers that are pre-configured to search your Repository from `http://<anaconda.repository.addr>/downloads`. To learn how to generate these installers, see [Customizing installers](#).

## Mirroring a PyPI repository

- *Before you start*
- *Running the PyPI mirror command*
- *Customizing the mirror*
- *Configuring pip*

### Before you start

You need to have already installed and configured your Repository instance. Due to the size of Repository, it is important that you have configured a file storage location with sufficient disk space. If necessary, see the [requirements for the file storage location](#).

The full PyPI mirror requires approximately 120 GB.

### Running the PyPI mirror command

To create a PyPI mirror:

```
anaconda-server-sync-pypi
```

This command loads all of the packages on `pypi.python.org` into the `~pypi` binstar user account.

Verify that the command ran successfully by opening your browser to `http://your-anaconda-repo/pypi/~pypi`.

NOTE: Replace `your-anaconda-repo` with the URL to your installation of Repository.

### Customizing the mirror

It is possible to customize the mirror behavior by creating a configuration file such as `$PREFIX/etc/anaconda-server/mirror/pypi.yaml` and using the `--mirror-config` option:

```
anaconda-server-sync-pypi --mirror-config /etc/binstar/mirrors/pypi.yaml
```

The following configuration options are available:

Name	Description
user	The local user under which the PyPI packages are imported. Default: <code>pypi</code> .
pkg_list	A list of packages to mirror. Only packages listed are mirrored. If this is set, blacklist and whitelist settings are ignored. <b>Default:</b> <code>[]</code> .
whitelist	A list of packages to mirror. Only packages listed are mirrored. If the list is empty, all packages are checked. <b>Default:</b> <code>[]</code> .
blacklist	A list of packages to skip. The packages listed are ignored. <b>Default:</b> <code>[]</code> .
latest_only	Only download the latest versions of the packages. <b>Default:</b> <code>false</code> .
remote_url	The URL of the PyPI mirror. <code>/pypi</code> is appended to build the XML RPC API URL, <code>/simple</code> for the simple index and <code>/pypi/{package}/{version}/json</code> for the JSON API. <b>Default:</b> <code>https://pypi.python.org/</code> .
xml_rpc_url	A custom value for XML RPC URL. If this value is present, it takes precedence over the URL built using <code>remote_url</code> . <b>Default:</b> <code>null</code> .
simple_index_url	A custom value for the simple index URL. If this value is present, it takes precedence over the URL built using <code>remote_url</code> . <b>Default:</b> <code>null</code> .
use_xml_rpc	Whether to use the XML RPC API as specified by <a href="#">PEP381</a> . If this is set to <code>true</code> , the XML RPC API is used to determine which packages to check. Otherwise the scripts falls back to the simple index. If the XML RPC fails, the simple index is used. <b>Default:</b> <code>true</code> .
use_serial	Whether to use the serial number provided by the XML RPC API. Only packages updated since the last serial saved are checked. If this is set to <code>false</code> , all PyPI packages are checked for updates. <b>Default:</b> <code>true</code> .
create_org	Create the mirror user as an organization instead of a regular user account. All superusers are added to the “Owners” group of the organization. <b>Default:</b> <code>false</code> .
private	Save the mirrored packages as private. <b>Default:</b> <code>false</code> .

EXAMPLE:

```
whitelist:
  - requests
  - six
  - numpy
  - simplejson
latest_only: true
remote_url: http://pypimirror.local/
use_xml_rpc: true
```

## Configuring pip

To configure pip to use this new mirror, edit `/etc/pip.conf` as follows:

```
[global]
index-url=https://pypi.anaconda.org/pypi/simple
```

## Customizing mirrors



- *Before you start*
- *Customizing your mirror*
- *Mirroring a platform-specific list*
- *Mirroring a package-specific list*
- *Mirroring Python version-specific packages*
- *Mirroring with a license blacklist*
- *Mirroring with a blacklist*
- *Mirroring with a whitelist*
- *Combining multiple mirror configurations*

This section explains how you can customize your PyPI or Anaconda repository mirror.

NOTE: This documentation applies to versions of Repository 2.26 and newer. For versions between 2.23 and 2.26, see [2.23 documentation](#). For older versions, see [2.20 documentation](#).

## Before you start

Your Anaconda Repository should already be installed and configured, as well as the mirroring tool `cas-mirror`. See [mirroring an Anaconda repository](#).

## Customizing your mirror

The following commands can be used with the `cas-mirror` tool:

- `cas-sync`: Creates or updates an existing local Anaconda package repository. The packages are saved into a local directory. This directory is defined by the `mirror_dir` configuration setting.
- `cas-sync-api-v4`: Creates or updates an existing remote Anaconda package repository. The packages are uploaded into an account of an existing Anaconda repository instance. The account and instance are controlled by the `dest_channel` and `dest_site` configuration settings.
- `cas-merge`: Combines delta repositories into an existing Anaconda package repository. A delta repository contains the changes between the local and remote Anaconda package repositories. Delta repositories are generated by `cas-sync` using the `delta` configuration setting.

All the commands can read a YAML configuration file specified by the `--file` (or `-f`) command line option. The YAML file can contain any of the following valid keys:

### remote\_url

Conda packages, Anaconda installers and Miniconda installers are fetched from this remote URL.

DEFAULT: `https://repo.anaconda.com/`

### channels

Conda packages are fetched from these remote channels.

DEFAULT: A list of these channels:

- `<remote_url>/pkgs/main/`
- `<remote_url>/pkgs/free/`
- `<remote_url>/pkgs/pro/`

### **mirror\_dir**

The mirror is saved in this local directory.

NOTE: A full mirror of the Anaconda repository uses about 100 GB of disk space. Make sure the mirror directory has enough space.

DEFAULT: `/opt/cas-mirror`

### **platforms**

Conda packages and installers for this list of platforms are mirrored.

DEFAULT: A list of all platforms. This is:

```
['osx-32', 'osx-64', 'win-32', 'win-64', 'linux-32', 'linux-64',  
'linux-armv6l', 'linux-armv7l', 'linux-ppc64le']
```

### **fetch\_installers**

Whether to fetch all Anaconda and Miniconda installers from `remote_url`.

If `fetch_installers` is set to `false` then installers are not fetched.

DEFAULT: `true`

### **python\_versions**

Python versions to mirror.

DEFAULT: All versions.

EXAMPLE: `['2.7', '3.6']`

### **pkg\_list**

An explicit list of package names to be mirrored.

When this list is provided, the `license_blacklist`, `blacklist` and `whitelist` keys are not allowed to be set.

### **license\_blacklist**

A list of licenses to be excluded from the mirror.

The license families that can be blacklisted are:

- AGPL
- APACHE
- BSD
- GPL2
- GPL3
- LGPL
- MIT
- PROPRIETARY
- PUBLICDOMAIN
- PSF
- OTHER
- NONE

### **blacklist**

A list of package names to be excluded from the mirror.

### **whitelist**

A list of package names to be included in the mirror.

The whitelist overrides the blacklists. If a package is both blacklisted and whitelisted, then it is included and mirrored.

EXAMPLE: The package `numpy` has a license in the license family `BSD`.

If `license_blacklist` contains `BSD` and `whitelist` is empty, then `numpy` and all other `BSD` licensed packages are excluded and not mirrored.

If `license_blacklist` contains `BSD` and `whitelist` contains `numpy`, then the `numpy` package is included and mirrored and other `BSD` licensed packages are excluded and not mirrored.

### **dest\_channel**

Optional channel to use when synchronizing with a local Repository instance.

DEFAULT: “anaconda”

### **dest\_site**

Optional site to use when synchronizing with a local Repository instance.

DEFAULT: None

### **delta**

If `delta` is `true`, then a delta is generated from `mirror_dir`.

If `delta` is `false`, then the changes are applied directly.

### **delta\_dir**

The delta is generated (or merged) onto this directory.

If this is not specified, the generated delta directory is named `delta-<timestamp>-pkgs`. `<timestamp>` is replaced with a timestamp.

### **max\_retries**

The number of retries to allow before failing.

When it is set to 0, `cas-mirror` fails at the first error. Default is 0.

This is supported only for the `cas-sync` and `cas-sync-api-v4` commands.

DEFAULT: 0

### **safe**

If `safe` is `true`, synchronizing repositories or merging delta directories never delete anything.

DEFAULT: `false`

### **repodata\_source**

Uses a `repodata.json` (or `repodata.json.bz2`) as the source of existing packages.

This file must be in the mirror directory for a specific platform.

EXAMPLE: `/mirror/linux-64/repodata.json`

## **Mirroring a platform-specific list**

By default, `cas-sync` and `cas-sync-api-v4` mirror all platforms. If you do not need all platforms, you can save time and disk space by editing the `yaml` file to specify which platform(s) you want to mirror.

EXAMPLE:

```
platforms:
  - linux-64
  - win-32
```

## Mirroring a package-specific list

You may want to mirror only a small subset of Repository. Rather than blacklisting a long list of packages you do not want to be mirrored, you can instead simply enumerate the list of packages you do want to mirror.

EXAMPLE: This example mirrors only the three packages Accelerate, PyQt and Zope. All other packages are ignored:

```
package_list:
- accelerate
- pyqt
- zope
```

## Mirroring Python version-specific packages

You may want to mirror only a subset of versions.

EXAMPLE: This example mirrors only Anaconda packages built for Python 3.3:

```
python_versions:
- 3.3
```

## Mirroring with a license blacklist

As of Repository 2.26.0, the Anaconda mirroring script supports license blacklisting for the following license families:

- AGPL
- APACHE
- BSD
- GPL2
- GPL3
- LGPL
- MIT
- PROPRIETARY
- PUBLICDOMAIN
- PSF
- OTHER
- NONE

EXAMPLE: This example mirrors all the packages in the repository except those that are GPL2-, GPL3- or BSD-licensed:

```
license_blacklist:
- GPL2
- GPL3
- BSD
```

NOTE: Older versions of Anaconda mirror support only license blacklisting for GPL. If you are using an older version of Repository, see the documentation for [customizing your PyPI or Anaconda Repository mirror](#).

### Mirroring with a blacklist

The `blacklist` allows access to all packages except those explicitly listed.

EXAMPLE: This example mirrors the entire Repository except the `bzip2`, `tk` and `openssl` packages:

```
blacklist:
- bzip2
- tk
- openssl
```

### Mirroring with a whitelist

The `whitelist` functions in combination with either the `license_blacklist` or `blacklist` arguments, and re-adds packages that were excluded by a previous argument.

EXAMPLE: This example mirrors the entire Repository except any GPL2- or GPL3-licensed packages, but including `readline`, despite the fact that it is GPL3-licensed:

```
license_blacklist:
- GPL2
- GPL3
whitelist:
- readline
```

### Combining multiple mirror configurations

You may find that combining two or more of the arguments above is the simplest way to get the exact combination of packages that you want.

The `platforms` argument is evaluated before any other argument.

EXAMPLE: This example mirrors only `linux-64` distributions of the `dnspython`, `shapely` and `gdal` packages:

```
platforms:
- linux-64
package_list:
- dnspython
- shapely
- gdal
```

If the `license_blacklist` and `blacklist` arguments are combined, the `license_blacklist` is evaluated first, and the `blacklist` is a supplemental modifier.

EXAMPLE: In this example, the mirror configuration does not mirror GPL2-licensed packages. It does not mirror the GPL3-licensed package `PyQt` because it has been blacklisted. It does mirror all other packages in Repository:

```
license_blacklist:
- GPL2
blacklist:
- pyqt
```

If the `blacklist` and `whitelist` arguments are both employed, the `blacklist` is evaluated first, with the `whitelist` functioning as a modifier.

EXAMPLE: This example mirrors all packages in the repository except `astropy` and `pygments`. Despite being listed on the blacklist, `Accelerate` is mirrored because it is listed on the whitelist:

```
blacklist:
- accelerate
- astropy
- pygments
whitelist:
- accelerate
```

## Verifying the checksum of a file

To help ensure that a file was correctly uploaded or synced you can use the checksum tool. This routine fetches a file from a database and verifies that the stored hash checksum and the calculated hash checksum of the file on disk are the same.

On a package's page, view the file list and click the Info button next to a file to see the file's keyname.

To check the file's hash checksum run:

```
anaconda-server-checksum keyname
```

NOTE: Replace "keyname" with the file's keyname.

The output will be either `Hashes are the same` or `Hashes differ`.

To overwrite the old hash checksum in the database with the new hash checksum you calculated, use the option `--fix`.

## Customizing installers

Anaconda Repository can distribute copies of the Anaconda distribution and the Miniconda installer that are pre-configured to use your installation of Repository.

This applies to Anaconda Distribution version 4.1 and higher, and Miniconda version 4.1.11 and higher.

By default the installers will be stored in `$PREFIX/opt/anaconda-server/installers`. If you prefer to store the installers in a different location, configure a new path:

```
anaconda-server-config --set INSTALLER_DIR /preferred/directory
```

NOTE: Replace `"/preferred/directory"` with the path to the directory where you prefer to store the installers.

If necessary, edit the script below and replace `"5.2.0"` with the current version number.

To download the installers:

```
mkdir -p /tmp/extras
pushd /tmp/extras

URL="https://repo.anaconda.com"

version="5.2.0"
miniconda="Miniconda3-latest-Linux-x86_64.sh \
  Miniconda3-latest-MacOSX-x86_64.sh \
  Miniconda3-latest-Windows-x86.exe \
  Miniconda3-latest-Windows-x86_64.exe \
  Miniconda-latest-Linux-x86_64.sh \
```

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```

Miniconda-latest-MacOSX-x86_64.sh \
Miniconda-latest-Windows-x86.exe \
Miniconda-latest-Windows-x86_64.exe"
anaconda="Anaconda2-$version-Linux-x86_64.sh \
Anaconda3-$version-Linux-x86_64.sh \
Anaconda2-$version-MacOSX-x86_64.sh \
Anaconda3-$version-MacOSX-x86_64.sh \
Anaconda2-$version-MacOSX-x86_64.pkg \
Anaconda3-$version-MacOSX-x86_64.pkg \
Anaconda2-$version-Windows-x86_64.exe \
Anaconda3-$version-Windows-x86_64.exe"

for installer in $miniconda; do
    curl -O $URL/miniconda/$installer
done
for installer in $anaconda; do
    curl -O $URL/archive/$installer
done

# Move the files into the installers directory
popd
cp -a /tmp/extras $PREFIX/opt/anaconda-server/installers

```

The installers will be available for download from `http://your.anaconda.server:port/downloads`.

NOTE: Replace “your.anaconda.server:port” with the name or IP address and port of your Anaconda server.

The downloadable file will be a zip file containing the Anaconda distribution and the configuration files specific to your Repository. These zip files are cached in the server’s configured storage for quick retrieval.

Check that the `SERVER_NAME` *setting* has been set so you generate the correct URLs in the next step.

To pre-generate these installer bundles based on the downloaded installers, or to re-generate after downloading new installers, execute the command:

```
anaconda-server-admin update-installers
```

This command requires that the `SERVER_NAME` *setting* be set in order to generate the correct URLs.

By default, the included `conda` installation will point to the default `anaconda` and `r-channel` accounts on your Anaconda Repository server, if those accounts exist.

You can change these default channels by setting the `DEFAULT_CHANNELS` *setting*, and then running the `anaconda-server-admin update-installers` command.

## Configuration reference

- *Files*
- *Logging*
- *Username*
  - *USER\_REGEX*
- *Database*



- *MONGO\_URL*
- *MONGO\_DBNAME*
- *MQ\_DBNAME*
- *MONGO\_REPLICA\_SET*
- *File storage*
  - *Storage\_type*
  - *keyname\_full\_path*
  - *Fs\_storage\_root*
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  - *S3\_SERVER\_SIDE\_ENCRYPTION*
- *Notebooks*
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- *Web server*
  - *SERVER\_NAME*
  - *port*
  - *subdomains*
  - *SESSION\_COOKIE\_DOMAIN*
  - *USER\_CONTENT\_DOMAIN*
  - *ssl\_options*
    - \* *certfile*
    - \* *keyfile*
    - \* *ssl\_version*
  - *PREFERRED\_URL\_SCHEME*
  - *gunicorn*
    - \* *timeout*
    - \* *workers*
- *Authentication*
  - *AUTH\_TYPE*
  - *KRB5\_HOSTNAME*
  - *KRB5\_SERVICE\_NAME*
  - *KRB5\_KTNAME*
  - *LDAP*
  - *LOCK\_DOWN*
- *Email*

- *SMTP\_HOST*
- *SMTP\_PORT*
- *SMTP\_TLS*
- *SMTP\_USERNAME*
- *SMTP\_PASSWORD*
- *USE\_SES*
- *RETURN\_ADDRESS*
- *ALLOW\_DUPLICATED\_EMAILS*
- *require\_email\_validation*
- *Advanced*
  - *AVATAR\_METHOD*
  - *AVATAR\_GRAVATAR\_URL*
  - *AVATAR\_STATIC\_URL*
  - *CONSTRUCTOR\_TIMEOUT*
  - *CONSTRUCTOR\_TOKEN\_TIMEOUT*
  - *CONSTRUCTOR\_ALLOWED\_OPTIONS*
  - *PARCELS\_ROOT*
  - *PARCEL\_DISTRO\_SUFFIXES*
  - *DEFAULT\_CHANNELS*
  - *CONSTRUCTOR\_TMPDIR*
  - *STANDARD\_LABELS*
  - *CONDA\_CACHE\_SIZE*
  - *CACHE\_METHOD*
- *REMEMBER\_COOKIE\_ENABLED*
- *PERMANENT\_SESSION\_LIFETIME*
- *REMEMBER\_COOKIE\_DURATION*
- *SUPERUSER\_ORG\_ADMIN*
- *NEXT\_URL\_WHITELIST*
- *NEXT\_URL\_WHITELIST\_REGEX*

## Files

Anaconda Repository loads configuration files with the extension `.yaml` from the following locations:

- `/etc/binstar/`
- `/etc/anaconda-server/`
- `$PREFIX/etc/anaconda-server`

NOTE: `$PREFIX` is the location where repository is installed.

Files are loaded from these directories in order, with later files overriding earlier files. Files are loaded from each directory in alphabetical order.

If an environment variable `ANACONDA_SERVER_CONFIG` is set with the path of a configuration file, this file is loaded after the three already listed. Its settings override any conflicting settings in the earlier files.

Each configuration setting variable can have its value set with the `anaconda-server-config --set` command, or by editing a configuration file.

EXAMPLE: To set a value named `VALUE_ONE` to 50, add this to a configuration file:

```
VALUE_ONE: 50
```

Or, you can set a value named `VALUE_ONE` to 50 with this command:

```
anaconda-server-config --set VALUE_ONE 50
```

## Logging

The location of the server's log file is defined in the supervisord configuration file `$PREFIX/etc/supervisord.conf` by the `stdout_logfile` config entry located in the `[program:anaconda-server]` section.

Advanced configuration of logging requires setting a `LOGGING` key on the server's `config.yaml`. It uses Python's logging module config structure.

## Username

### USER\_REGEX

A regular expression that defines the allowable user names.

For example, this setting specifies that user names contain only lowercase letters, periods, plus and minus characters (`.`, `+` and `-`):

```
USER_REGEX: '^[a-z.+-]+$'
```

NOTE: The default value for `USER_REGEX` is `^[a-z0-9_][a-z0-9_-]+$` which translates to: at least one alphanumeric character or underscore, followed by zero or more alphanumeric, dash or underscore characters.

NOTE: Escape any extra instances of the single quote character `'` as `\'`. Do not use the slash and ampersand characters `/` and `&`, which have special meanings in URLs.

NOTE: If `USER_REGEX` is changed and the server is restarted, existing usernames that do not match the new `USER_REGEX` do not cause errors.

## Database

Repository uses MongoDB as the database back end.

### MONGO\_URL

A [MongoDB connection URI](#) is used to connect to the MongoDB database server. It can be used to configure the hostname and port, as well as database authentication.

For example:

```
MONGO_URL: mongodb://anaconda-server:Pa55w0rd@mongodb.serv/
```

### MONGO\_DBNAME

The MongoDB database where Repository stores its data.

### MQ\_DBNAME

The MongoDB database where Repository stores data used for asynchronous processing.

### MONGO\_REPLICA\_SET

The name of a [MongoDB replica set](#) Repository connects to after establishing a connection to the database server.

### File storage

Repository can serve package contents from a local file-system, or from Amazon Web Services Simple Storage Service: AWS S3.

### Storage\_type

The storage mechanism to use. Valid choices are `fs`, for file-system storage, or `s3`, for AWS S3 storage.

### keyname\_full\_path

When this option is set, Repository stores the files by full paths and not just by hashes. This way a tensorflow file uploaded by the user *Bob* will be stored on `<fs_storage_root>/Bob/tensorflow/osx-64/tensorflow-1.1.0-np112py36_0.tar.bz2-594ac56e7e042600648defdb`.

NOTE: The storage path does not always contain the current file owner and their user name. This is because the file location on the storage does not change when you rename a user or transfer a file to a different user.

### Fs\_storage\_root

If configured to use file-system storage, the absolute path to a directory where Repository stores all uploaded packages.

## PACKAGE\_BUCKET\_ID

If configured to use AWS S3 storage, the name of an AWS S3 bucket where Repository stores uploaded packages.

You can identify the name of your bucket by using `<bucket>` in your `http://<bucket>.s3.amazonaws.com` URL.

## S3\_REGION\_NAME

The S3 region that the bucket is located in. The available regions can be found in the [Amazon AWS documentation](#).

## S3\_SERVER\_SIDE\_ENCRYPTION

This variable can be set to `AES256` to enable [server-side encryption](#) for packages stored in the S3 bucket.

## Notebooks

### MAX\_IPYNB\_SIZE

Specifies the maximum allowed size when uploading notebooks to the server. The default is 25 MB. This variable can be set in `config.yaml`.

## Web server

### SERVER\_NAME

The name and port number of the server. This option is required for subdomain support.

For example:

```
SERVER_NAME: anaconda.srv:8080
```

### port

The port number of the server. Defaults to 8080.

### subdomains

If set to `true`, Repository serves `conda` package from a separate subdomain. Defaults to `false`.

For example:

```
SERVER_NAME: anaconda.srv:8080
subdomains: true
```

Allows access to `conda` packages at `http://conda.anaconda.srv:8080/`.

### SESSION\_COOKIE\_DOMAIN

The domain that Repository sets on the session cookie. If this is not set, the cookie is valid for all subdomains of `SERVER_NAME`.

See *Securing user-created content*.

### USER\_CONTENT\_DOMAIN

As a cross-site scripting (XSS) protection, notebook content can be served from a separate domain name. If this option is configured, Repository only serves rendered notebooks from this domain.

See *Securing user-created content*.

### ssl\_options

Repository can serve content over HTTPS, using user-provided SSL certificates.

For example:

```
ssl_options:
  certfile: /etc/anaconda-server/server.crt
  keyfile: /etc/anaconda-server/server.key
PREFERRED_URL_SCHEME: https
```

### certfile

The absolute path to a PEM-formatted X.509 certificate file.

### keyfile

The absolute path to a PEM-formatted private key for the associated certificate.

### ssl\_version

An integer that specifies the SSL protocol version as defined by Python's `ssl` module:

```
PROTOCOL_SSLv2 = 0
PROTOCOL_SSLv23 = 2
PROTOCOL_SSLv3 = 1
PROTOCOL_TLS = 2
PROTOCOL_TLSv1 = 3

PROTOCOL_TLSv1_1 = 4
PROTOCOL_TLSv1_2 = 5
```

The default is 5 (TLS v1.2).

### PREFERRED\_URL\_SCHEME

The preferred scheme that is used to generate URLs. Set this to `https` if HTTPS is configured.

## gunicorn

Repository uses [Gunicorn](#). The most commonly used options are `timeout` and `workers`. A complete list of settings can be found in [Gunicorn's documentation](#).

For example:

```
gunicorn:
  timeout: 60
  workers: 5
```

## timeout

The number of seconds for which a worker is allowed to process a request, before being forcefully terminated.

Default: 120

## workers

The number of workers that Gunicorn spawns to serve Repository. Defaults to  $2 \times$  the number of CPUs + 1.

## Authentication

### AUTH\_TYPE

The method Repository uses to authenticate users. Valid choices are `NATIVE`, for built-in authentication, `KERBEROS`, for Kerberos, and `LDAP`.

### KRB5\_HOSTNAME

See *Kerberos configuration options*.

### KRB5\_SERVICE\_NAME

See *Kerberos configuration options*.

### KRB5\_KTNAME

See *Kerberos configuration options*.

## LDAP

Options for configuring LDAP authentication and group synchronization.

For example:

```
LDAP:
# Replace with company LDAP server
URI: 'ldap://<ldap.company.com>'
# Replace <uid=%(username)s,ou=People,dc=company,dc=com> with your company specific_
↳LDAP Bind/Base DN
# Bind directly to this Base DN.
BIND_DN: '<uid=%(username)s,ou=People,dc=company,dc=com>'
# password of the user specified in the BIND_DN
BIND_AUTH: abc123456

USER_SEARCH:
  base: cn=Users,dc=example,dc=com
  filter: sAMAccountName=%(username)s

# Map LDAP keys into application specific keys
KEY_MAP:
  name: 'cn'
  company: 'o'
  location: 'l'
  email: 'mail'

OPTIONS:
  OPT_NETWORK_TIMEOUT: 60
  OPT_TIMEOUT: 60
```

**NOTE:** To use LDAP with SSL, set the `USER_REGEX` and `account_names_filter` options:

```
account_names_filter: false
USER_REGEX: ^[a-z0-9_][a-z0-9_-.]+$
LDAP:
  [configuration continues as above with URI, BIND_DN, and so on]
```

See *Using LDAP and TLS configuration options*.

## LOCK\_DOWN

Makes all views with the exception of the login form and welcome page, inaccessible to anonymous users.

## Email

Repository can be configured to send email for various reasons, including to reset forgotten usernames and passwords. Email can be sent using SMTP protocol, or through Amazon Web Services Simple Email Service (AWS SES).

## SMTP\_HOST

The hostname of the SMTP server.

## SMTP\_PORT

The port of the SMTP server.



## SMTP\_TLS

If set to `true`, Repository attempts an SSL connection to the SMTP server.

## SMTP\_USERNAME

The username to authenticate against the SMTP server before attempting to send email.

## SMTP\_PASSWORD

The password to authenticate against the SMTP server before attempting to send email.

## USE\_SES

If set to `true`, Repository sends email with AWS SES. To authenticate to AWS, the server should be configured with an appropriate IAM role, or have credentials specified in a [Boto configuration file](#).

## RETURN\_ADDRESS

The `From:` email address that Repository uses as sender.

## ALLOW\_DUPLICATED\_EMAILS

If set to `true`, Repository allows different users to share the same email or secondary email. Defaults to `false`.

## require\_email\_validation

If set to `true`, Repository emails new users a unique token to validate their email address before permitting them to log in.

## Advanced

### AVATAR\_METHOD

The method to use to generate the user avatar URL. Valid choices are:

- ‘gravatar’ to use the gravatar.com service
- ‘default’ to show a predefined static icon
- ‘static’ to use a custom static URL

### AVATAR\_GRAVATAR\_URL

A URL for a Gravatar compatible service. Default: `https://www.gravatar.com/`. This URL is used as the prefix to build a valid gravatar URL.

### AVATAR\_STATIC\_URL

A static URL to use when `AVATAR_METHOD` is set to `static`. Defaults to an empty string.

### CONSTRUCTOR\_TIMEOUT

The timeout in seconds for the call to `constructor` while building installers, parcels and management packs. Defaults to 60 seconds.

### CONSTRUCTOR\_TOKEN\_TIMEOUT

To provide access to private packages while building an installer, a temporary token is created. It must be valid during the call to `constructor` and it should expire soon after the call completes. `CONSTRUCTOR_TOKEN_TIMEOUT` sets the token's valid lifetime in seconds. Defaults to 60 seconds. This value should be greater than or equal to `CONSTRUCTOR_TIMEOUT`.

### CONSTRUCTOR\_ALLOWED\_OPTIONS

A list of `constructor` option names that are allowed to be included in the installer construction form. The default is `[]` (no options are allowed).

### PARCELS\_ROOT

The prefix with which Cloudera parcels are generated. Defaults to `/opt/cloudera/parcels`.

### PARCEL\_DISTRO\_SUFFIXES

The distributions for which Cloudera parcels are generated. Defaults to `['el5', 'el6', 'el7', 'lucid', 'precise', 'trusty', 'wheezy', 'jessie', 'squeeze', 'sles11', 'sles12']`.

For example, if you want to support only Ubuntu:

```
PARCEL_DISTRO_SUFFIXES:
- lucid
- precise
- trusty
```

### DEFAULT\_CHANNELS

The Repository accounts that environments installed with the *bundled Anaconda distributions* pull packages from. Defaults to `['anaconda', 'r-channel']`.

For example, to add an additional `custom` account:

```
DEFAULT_CHANNELS:
- anaconda
- r-channel
- custom
```

## CONSTRUCTOR\_TMPDIR

When `constructor` builds an installer it stores the configuration in this temporary directory. The default is `None`, which tells `constructor` to create a temporary directory using Python's `tempfile.mkdtemp`.

## STANDARD\_LABELS

A list of standardized labels. If a user defines a label that is not listed as standard, a warning notice will be shown in the package's page. Defaults to `['main', 'dev', 'alpha', 'beta', 'broken']`.

## CONDA\_CACHE\_SIZE

The maximum size (in bytes) of the `repodata.json` requests cache. Set to 0 to disable `repodata.json` caching. Default: 1 Gb. When the maximum size is reached, the 10 least recently used entries of the cache are evicted.

## CACHE\_METHOD

The method used for caching `repodata` info. It can either be `tempfile` (the prior method of caching) or `diskcache`, which uses SQLite as a back-end. Default: `diskcache`.

## REMEMBER\_COOKIE\_ENABLED

Sets whether to use the *remember me* cookie to keep the session alive. If it's set to `true` the `REMEMBER_COOKIE_DURATION` setting is relevant, and if it's set to `false`, the `PERMANENT_SESSION_LIFETIME` is relevant. Defaults to `true`.

## PERMANENT\_SESSION\_LIFETIME

An integer that sets how many **minutes** the session will live. Only used when `REMEMBER_COOKIE_ENABLED` is `false`. Default is 44640 (31 days).

## REMEMBER\_COOKIE\_DURATION

An integer that sets how many **minutes** the session will live when using the *remember me* cookie. Only used when `REMEMBER_COOKIE_ENABLED` is `true`. Default is 525600 (365 days).

## SUPERUSER\_ORG\_ADMIN

Whether superusers should automatically be granted admin rights on organizations. Default is `false`.

## NEXT\_URL\_WHITELIST

List of hostnames that are marked as safe when redirecting requests due to the presence of a "next" request parameter. It is mainly used under an Anaconda Enterprise Notebooks Single Sign-on Set-up. The default is `[]` (no external redirects are safe).

### NEXT\_URL\_WHITELIST\_REGEX

A regular expression to match hostnames that are marked as safe when redirecting requests due to the presence of a “next” request parameter. It is mainly used under an Anaconda Enterprise Notebooks Single Sign-on Set-up. The default is ‘(!)’ which matches nothing, so only local redirects are allowed.

Repository has two installation options:

- *Online*: If you have internet access on the destination server, follow the online instructions.
- *Air gap*: If you have an air gapped system or the destination server does not have internet access, follow the air gap instructions.

Repository provides *advanced configuration options* that can be used to meet site-specific needs.

Repository includes a number of *optional components* that can be installed and used individually.

You may also want to see *Updating Repository* and *Uninstalling Repository*.

### User management

- *Adding a user*
- *Searching for users*
- *Promoting an existing user*
- *Resetting user passwords*
- *Resending welcome emails to new users*
- *Changing a user’s storage size or changing their plan to free unlimited*
- *Removing a user*

### Adding a user

New users can navigate in a browser to your local Repository web page and sign themselves up for an account, or you can add them using the command line:

1. Set the `USER_PASSWORD` environment variable (e.g., `export USER_PASSWORD=abc123DEF`).
2. Run the `anaconda-server-create-user` command, with the following syntax:

```
anaconda-server-create-user [-h] -u USERNAME [-e EMAIL] [--superuser]
```

EXAMPLE:

```
anaconda-server-create-user --username jsmith --email jsmith@your-domain.com  
--superuser
```

### Searching for users

As of Anaconda Repository version 2.33.5, you can search for users by username or email address. Open this URL in a browser:

`http://your.anaconda.server:port/admin/users`

NOTE: Replace “your.anaconda.server:port” with the name or IP address and port of your Anaconda server.

### Promoting an existing user

As of Anaconda Repository version 2.28, administrators can use the Administration Accounts page to promote users to staff or superuser status.

### Viewing rights of staff and superuser

The staff user and superuser can view the following sections of the Administration page:

- Reports.
- User administration.
- License downloads.
- Trial licenses.
- Current LDAP configuration.
- Current server configuration.
- Downloads summary.
- Downloads from a specific address.
- Security feed and security feed details.
- Storage administration.

### Privileges of staff and superuser

The staff user and superuser have the following privileges:

- Create licenses.
- Download a CSV of the user database.
- Search for a package in the Administration panel.
- Resend confirmation emails to users.
- Resend password reset emails to users.
- Download a CSV with the users emails.

### Additional rights of superuser

In addition to all of the above, a superuser can also view the following on the Administration page:

- Plans.
- User details.

To promote an existing user to a staff user or superuser:

1. On the Administration page, in the left navigation pane, select Accounts.
2. Select the username you want to promote.

Repository displays the user information page:

The screenshot shows the Anaconda Cloud interface. At the top, there's a navigation bar with the Anaconda logo, a search bar, and user information (View, Help, superuser). The left sidebar contains a navigation menu with options like Report, Security Feed, Accounts (highlighted), Password Reset, Downloads, Package Search, Deployment, Package Storage (56%), View License Downloads, View License, and Read Only. The main content area is titled 'Users / testuser'. It features an 'Actions' section with two boxes: 'Set access' containing 'Set Staff' and 'Set Superuser' buttons, and 'Account' containing 'View profile' and 'Delete user' buttons. Below this is a 'History' section with a table showing a single action.

Action	Timestamp	Actor(s)
user.create	Thu Mar 22 16:38:19 2018	testuser <a href="#">details</a>

Navigation links: « Previous    showing 1 of 1    Next »

3. Click the Set Staff button to give the user staff privileges or click the Set Superuser button to give the user superuser privileges.
4. In the dialog box that appears, retype the user's name.
5. Click the Set button.

## Resetting user passwords

If a user forgets their password, you can request a reset link to provide to the user.

To send emails, Repository must have the *email settings* configured.

1. Log into your Repository administrative account.
2. From the top **Tools** menu, select Admin.
3. From the left navigation pane, select Password Reset.
4. Enter the user's email address.

The Web UI generates a password reset link.

5. Email the link to the user.

You can also reset passwords without sending emails:

```
anaconda-server-admin reset-password jsmith
```

NOTE: Replace `jsmith` with the username whose password you want to reset.

### Resending welcome emails to new users

To send emails, Repository must have the *email settings* configured.

If a user reports that they did not receive their welcome email after registering on your local Repository web page, it may have been caught in a spam filter.

Follow the above instructions for resetting user passwords.

### Changing a user's storage size or changing their plan to free unlimited

To change a user's storage size or plan:

1. Log into your Repository administrative account.
2. From the top **Tools** menu, select Admin.
3. From the left navigation pane, select Accounts.
4. Select the username of the user whose account you want to change.
5. To update the storage limits click Update Storage.
6. To set the user's plan to free and unlimited, click Set free unlimited plan.

### Removing a user

1. Log into your Repository administrative account.
2. From the top **Tools** menu, select Admin.
3. From the left navigation pane, select Accounts.
4. Select the username of the user you want to remove.
5. Click the Delete user button.
6. Optional: Use `anaconda-server-admin clean-storage` to remove files from that user's account.

## System management

### Recommended workflow

One of the most useful features of Anaconda Repository is its ability to help manage package development and deployment in a seamless fashion. This page describes the development process and channel usage employed by one of our internal teams, to serve as an example of how you can leverage channels for workflow separation.

Multiple channels allow our team to maintain separate package states and easily earmark and control the versions and states of packages that users can install.

Our team created the following channels:

- Master.

- Staging.
- Release.

We have used this workflow through 4 release cycles and it has worked out well for us.

### Master

A master is created any time something is merged into our master branch. It is considered the development build of all of the components that make up the software. Code that makes it to this channel should be stable and should have been confirmed independently, but a full QA test has not been run on it yet.

### Staging

Once we are ready to start working on a release, we create a staging:X.Y.Z branch. This contains all code that is going to go into a release. No new features should be introduced at this point, just any last minute bug fixes to existing code.

### Release

The staging channel gets culled so that only the latest package is maintained in it. Any alpha, beta, or dev packages are removed. After all testing is complete, all issues are resolved, and the channel contains only one version of each package, we copy that package into a release:X.Y.Z channel, then lock that channel.

### Performing general maintenance

To maintain a Repository installation, perform all of these tasks regularly:

- Review the error logs at `/var/log/anaconda-server`
- *Back up* the file system and database.
- Update the anaconda-server package with the command:

```
conda update anaconda-server
```

### Anaconda repository backup and restore procedure

This guide is for backing up and restoring an Anaconda Repository instance that uses local file system storage. If your instance uses Amazon S3 or any other storage provider, please consult their specific documentation on backup and restore procedures.

### Before you start

These instructions are for a Repository that is:

- Installed in the directory `/home/anaconda-server/repo` as suggested by the installation guide.
- Owned by the `anaconda-server` user.
- Using the storage directory `/opt/anaconda-server/package-storage`.
- Storing the configuration file in `/etc/anaconda-server`.



If any of these items are different for your instance, modify these instructions accordingly.

- Unless noted, run all shell commands while logged in as the `anaconda-server` user. Using `sudo` privileges, log in as the `anaconda-server` user with this command:

```
sudo su - anaconda-server
```

- Execute all commands in the working directory `/home/anaconda-server`:

```
$ pwd
/home/anaconda-server
```

## Backup

Before starting the backup process, shut the service down using `supervisorctl`:

```
$ supervisorctl stop all
anaconda-server: stopped
$ supervisorctl status
anaconda-server                STOPPED      Jul  6 05:05 PM
```

Make a `$VERSION` environment variable and set it to the version of the currently installed Anaconda Repository:

```
$ VERSION=`conda list anaconda-server --json | python -c 'import sys, json; print_
↪ json.load(sys.stdin)[0]["version"]'`
$ echo $VERSION
2.33.27
```

This version string will be used in all backup file names.

It's also useful to add a timestamp to the files, so generate one now:

```
$ TIMESTAMP=`date +%Y-%m-%d`
$ echo $TIMESTAMP
2018-07-30
```

## Code/Binaries

Generate a tarfile archive with the installed code, binaries and any dependencies:

```
$ tar -cpsz anaconda-server-repo-$VERSION-$TIMESTAMP.tar --exclude var/run -C /home/
↪ anaconda-server repo/
$ shasum anaconda-server-repo-$VERSION-$TIMESTAMP.tar > anaconda-server-repo-
↪ $VERSION-$TIMESTAMP.tar.sha1
```

Notice that this also generated a SHA1 checksum. This checksum will be used to verify when you restore the archive.

## Configuration

This step is necessary only if you stored Anaconda Repository's configuration in a custom location outside of the instance installation folder (usually `/home/anaconda-server/etc/`).

These commands show how to generate the tarfile if the configuration is stored in `/etc/anaconda-server`.

Generate the tarfile with its SHA1 checksum:

```
$ tar -cpsz anaconda-server-etc-$VERSION-$TIMESTAMP.tar /etc/anaconda-server
$ shasum anaconda-server-etc-$VERSION-$TIMESTAMP.tar > anaconda-server-
↳$TIMESTAMP.tar.shal
```

### Storage

As before, create a tarfile archive and its checksum with the contents of the package storage location:

```
$ tar -cpsz anaconda-server-package-storage-$VERSION-$TIMESTAMP.tar -C /opt/anaconda-
↳server/ package-storage
$ shasum anaconda-server-package-storage-$VERSION-$TIMESTAMP.tar > anaconda-server-
↳package-storage-$VERSION-$TIMESTAMP.tar.shal
```

### Database

Generate a dump of Anaconda Repository's MongoDB database. We recommend you follow MongoDB's guidelines for [backup and restore](#). This guide uses [MongoDB tools](#):

```
$ mongodump --host=127.0.0.1 --port=27017 --archive=anaconda-server-mongodb-$VERSION-
↳$TIMESTAMP.archive
$ shasum anaconda-server-mongodb-$VERSION-$TIMESTAMP.archive > anaconda-server-
↳mongodb-$VERSION-$TIMESTAMP.archive.shal
```

### .bashrc

If you chose to let the Anaconda Repository installer update the `.bashrc` file of the user `anaconda-server`, back it up:

```
$ cp /home/anaconda-server/.bashrc anaconda-server-bashrc-$VERSION-$TIMESTAMP.sh
$ shasum anaconda-server-bashrc-$VERSION-$TIMESTAMP.sh > anaconda-server-bashrc-
↳$VERSION-$TIMESTAMP.sh.shal
```

### Restore

#### Before you start

- Verify that the restore environment meets the requirements listed in the [Installation Guide](#) for Anaconda Repository. You will need:
  - MongoDB (any supported version) installed
  - A user account (usually `anaconda-server`)
  - A storage directory (usually `/opt/anaconda-server/package-storage`) owned by the Anaconda Repository user account. This is only needed if you're using a local filesystem as a storage backend.
- Run all shell commands while logged in as the `anaconda-server` user, as you did when backing up Anaconda Repository. Using `sudo` privileges, log in as the `anaconda-server` user with this command:

```
sudo su - anaconda-server
```

- Execute all commands in the working directory `/home/anaconda-server`.

## Verify checksums

Verify the integrity of the backup files:

```
$ sha1sum --check *.sha1
anaconda-server-bashrc-2.33.27-2018-07-30.sh: OK
anaconda-server-mongodb-2.33.27-2018-07-30.archive: OK
anaconda-server-package-storage-2.33.27-2018-07-30.tar: OK
anaconda-server-repo-2.33.27-2018-07-30.tar: OK
```

## .bashrc

If you backed up the `.bashrc` file of the user `anaconda-server`, restore it:

```
cp anaconda-server-bashrc-$VERSION-$TIMESTAMP.sh /home/anaconda-server/.bashrc
```

After restoring this file, log out and log in as `anaconda-server` again for the changes to take effect.

## Database

If you followed the Anaconda Repository [Installation Guide](#), MongoDB is up and running and you can use `mongorestore` to restore the database archive:

```
mongorestore --host=127.0.0.1 --port=27017 --db=binstar --archive=anaconda-server-
↳mongodb-$VERSION-$TIMESTAMP.archive
```

## Storage

Assuming that the storage directory is `/opt/anaconda-server/package-storage`, restore it with:

```
tar -xpsf anaconda-server-package-storage-$VERSION-$TIMESTAMP.tar -C /opt/anaconda-
↳server/
```

## Code/Binaries

Restore the code and binaries:

```
tar -xpsf anaconda-server-repo-$VERSION-$TIMESTAMP.tar -C /home/anaconda-server
```

Restore the supervisord configuration:

```
repo/bin/anaconda-server-install-supervisord-config.sh
```

The server should now be up and running. Check the status with `supervisorctl`:

```
$ repo/bin/supervisorctl status
anaconda-server          RUNNING      pid 8446, uptime 0:03:18
```

### Checking for Orphan Files or Packages

You can use the “orphan-check” tool to resynchronize the filesystem and the database if the filesystem and the database get out of sync.

The system can get out of sync when files in the filesystem are not referenced from the database, or when packages in the database do not have a corresponding file in the filesystem.

The orphan-check tool prints on stdout a list of files on the filesystem that are not referenced from the database:

```
anaconda-server-orphan-check --dryrun
```

You can use the `-json` option if you want a JSON representation of the output:

```
anaconda-server-orphan-check --json
```

NOTE: Running `anaconda-server-orphan-check` without arguments is the same as running `anaconda-server-orphan-check --dryrun`.

After you’ve viewed the list of files without references, “orphan-check `--clean`” can delete them:

```
anaconda-server-orphan-check --clean
```

You can also check for packages that have missing files:

```
anaconda-server-orphan-check --reverse
```

Then you can delete those file objects from the database:

```
anaconda-server-orphan-check --reverse --clean
```

### Using optional components

Anaconda Repository includes a number of components that can be installed and used individually.

This section describes how to install and use two such tools:

- *cas-mirror*.
- *cas-installer*.

As a convention, all packages and commands that are part of the Repository product share the common `cas` prefix, which is short for Continuum Anaconda Server. (Anaconda, Inc. was formerly known as Continuum Analytics, Inc.)

All packages are installed using the `conda` command, which is part of the Miniconda installer. For Repository installation and configuration instructions, see [Installation](#).

#### Using cas-mirror

The `cas-mirror` tool is a component of the Anaconda Repository Enterprise product.

The `cas-mirror` tool makes an exact copy of Anaconda’s package Repository, or part of it, on a your local Repository server.

For more information about the `cas-mirror` tool’s functionality and configurable options, see [Configuring local mirrors](#).

## Installing cas-mirror

To install the mirror tool, run:

```
conda install cas-mirror
```

After cas-mirror has been installed, the following commands are available:

```
cas-sync --help
cas-merge --help
cas-sync-api-v4 --help
cas-server --help
```

## Using the cas-sync command

The `cas-sync` command brings the local mirror of Repository up-to-date with our remote servers.

To configure the location of the mirror on your file system, check the output of:

```
cas-sync --config
```

If necessary, create a configuration file, either `~/.cas-mirror` or system-wise `/etc/cas-mirror`, which contains the desired location of the local mirror on the file system, the platforms that should be mirrored and an optional blacklist of packages that which should not be mirrored.

EXAMPLE:

```
mirror_dir: /home/data/mirror
remote_url: "" # where to get miniconda and anaconda installers -- blank to skip
# possible platforms are: linux-64, linux-32, osx-64, win-32, win-64 platforms:
- linux-64
- win-32
blacklist:
- dnspython
- shapely
- gdal
```

Once you are satisfied with the mirror directory—which may be the default—run:

```
cas-sync
```

Running this command for the first time takes many hours, because the entire Repository is being downloaded. Subsequent runs take significantly less time.

## Using the cas-server command

You need to run `cas-server` as root when you intend to serve on port 80.

To serve repository over HTTP, run:

```
cas-server
```

If needed, use the `--port` option to change the port on which the repository is being served.

## Using the “delta” option

If you’ve already downloaded most of the anaconda repository, and you’re only interested in the changes since `cas-sync` was last run, you can use the `delta` configuration option:

```
mirror_dir: /home/data/mirror
remote_url: "" # where to get miniconda and anaconda installers -- blank to skip
# possible platforms are: linux-64, linux-32, osx-64, win-32, win-64
platforms:
  - linux-64
  - win-32
blacklist:
  - dnspython
  - shapely
  - gdal
delta: true
delta_dir: delta_pkgs
```

Instead of mirroring to the existing local repository, it will record the necessary changes to bring the mirror up to date in a separate directory (`delta_pkgs` in this case). You can then use this generated directory to update air-gapped mirrors using the `cas-merge` command.

The `cas-merge` command takes a delta directory and combines its contents with an existing mirror directory. New packages are added, missing packages are deleted, and the repodata is updated.

If instead of mirroring to a local directory, you want to make the changes directly into an existing Anaconda Repository instance, the `cas-sync-api-v4` can be used. You’ll need to use the `dest_site` config option:

```
mirror_dir: /home/data/mirror
remote_url: "" # where to get miniconda and anaconda installers -- blank to skip
# possible platforms are: linux-64, linux-32, osx-64, win-32, win-64
platforms:
  - linux-64
  - win-32
blacklist:
  - dnspython
  - shapely
  - gdal
dest_site: some_site
```

Make sure that the site is defined in the anaconda config and you’re properly logged into it before invoking `cas-sync-api-v4`.

More extensive information about the `cas-mirror` tool’s functionality and configurable options is available at [Customizing mirrors](#).

## Using cas-installer

The `cas-installer` tool makes an environment installer, which is a bash script or Windows executable file that can be run on any machine to install an exact copy of a conda environment and its packages on that machine.

## Installing cas-installer

A token from Anaconda is required to install `cas-installer`, and you should have received it when your organization purchased Repository, Workgroup or Enterprise. If you no longer have access to your token, submit a support ticket

or contact us at [Enterprise Support](#). You can also email support at the email address given to you by your sales representative.

When you have the token, run:

```
export TOKEN=<your_anaconda_cloud-token>
conda config --add channels https://conda.anaconda.org/t/$TOKEN/anaconda-server
```

Because this tool allows you to create an installer for a conda environment, it is important that the cas-installer package is installed into the root conda environment, not root user. The following command ensures that this happens:

```
conda install -n root cas-installer=1.3.2
```

## Using the cas-installer command

Once installed, the cas-installer command is available:

```
cas-installer -h
```

The command takes an installer specification file as its argument, which specifies the name of the installer, the conda channel to pull packages from, the conda packages included in the installer, and so on.

EXAMPLE:

```
# ----- required -----
# name
name: test

# channels to pull packages from
# The &channels creates a back reference so that it can be reused as
# *channels in the conda_default_channels section below.
channels: &channels
  - https://repo.anaconda.com/pkgs/free/

# specifications
specs:
  - python
  - grin

# ----- optional -----
# platform e.g. linux-32, osx-64, win-32 defaults to current platform
# platform: linux-64

# The conda default channels which are used when running a conda which
# was installed be the cas-installer created: requires conda--3.6.2 or
# greater--in the specifications. The *channels is a YAML reference to
# &channels above. It inserts all the channels from the channels key, so
# that they do not have to be typed twice.

conda_default_channels: *channels

# installer filename
# installer_filename: grin.sh

# default install prefix
default_prefix: /opt/anaconda
```

For Windows, the tool creates nsis-based .exe installers, which can only be created on a Windows platform, although the architecture may be different. For Unix, the tool creates bash-based .sh installer, which can only be created on Unix—Linux or macOS—systems.

### Updating Repository

**CAUTION:** You must have a tested backup of your installation before starting the update process. If updating more than one version, all updates must be performed in sequential order.

Your support representative can provide you with a download URL for an updated Repository installer.

To update to the latest Repository release:

```
curl '$INSTALLER_URL' > anaconda_repository.sh
bash anaconda_repository.sh -u
anaconda-server-db-setup --execute
supervisorctl stop all
supervisorctl reload
supervisorctl start all
```

**NOTE:** To use a Repository version from 2.33.3 through 2.33.10 and Anaconda Enterprise Notebooks with single sign-on (SSO), you must set `USE_SERVER_BASED_SESSIONS: false` in the Repository configuration. This setting affects the network security properties of AEN and Repository. Specifically, if `USE_SERVER_BASED_SESSIONS` is set to `false`, and if a new cross-site scripting (XSS) vulnerability is discovered, it could expose an additional server fixation vulnerability. Please discuss this with your Anaconda representative and be sure the feature is compatible with your network requirements before setting `USE_SERVER_BASED_SESSIONS: false`.

**NOTE:** As of Repository 2.33.8, the `fs_storage_root` configuration setting is mandatory for local filesystem storage and the Repository server will not run without it. You can set it with this command:

```
anaconda-server-config --set fs_storage_root /opt/anaconda-server/package-storage
```

You may replace `/opt/anaconda-server/package-storage` with any location owned by the `anaconda-server` user.

Please contact your Professional Support Team contact or sales person if you have any questions or problems regarding the update.

### Updating to current and previous versions

Updating to 2.33:

```
curl '$INSTALLER_URL' > anaconda_repository.sh
bash anaconda_repository.sh -u
anaconda-server-db-setup --execute
supervisorctl stop all
supervisorctl reload
supervisorctl start all
```

**NOTE:** To use a Repository version from 2.33.3 through 2.33.10 and Anaconda Enterprise Notebooks with single sign-on (SSO), you must set `USE_SERVER_BASED_SESSIONS: false` in the Repository configuration. This setting affects the network security properties of AEN and Repository. Specifically, if `USE_SERVER_BASED_SESSIONS` is set to `false`, and if a new cross-site scripting (XSS) vulnerability is discovered, it could expose an additional server fixation vulnerability. Please discuss this with your Anaconda representative and be sure the feature is compatible with your network requirements before setting `USE_SERVER_BASED_SESSIONS: false`.



NOTE: As of Repository 2.33.8, the `fs_storage_root` configuration setting is mandatory for local filesystem storage and the Repository server will not run without it. You can set it with this command:

```
anaconda-server-config --set fs_storage_root /opt/anaconda-server/package-storage
```

You may replace `/opt/anaconda-server/package-storage` with any location owned by the `anaconda-server` user.

Updating to 2.32:

```
curl '$INSTALLER_URL' > anaconda_repository.sh
bash anaconda_repository.sh -u
anaconda-server-db-setup --execute
supervisorctl stop all
supervisorctl reload
supervisorctl start all
```

Updating to 2.31:

```
curl '$INSTALLER_URL' > anaconda_repository.sh
bash anaconda_repository.sh -u
anaconda-server-db-setup --execute
supervisorctl stop all
supervisorctl reload
supervisorctl start all
```

Updating to 2.30:

```
curl '$INSTALLER_URL' > anaconda_repository.sh
bash anaconda_repository.sh -u
anaconda-server-db-setup --execute
supervisorctl stop all
supervisorctl reload
supervisorctl start all
```

Updating to 2.29:

```
curl '$INSTALLER_URL' > anaconda_repository.sh
bash anaconda_repository.sh -u
anaconda-server-db-setup --execute
supervisorctl stop all
supervisorctl reload
supervisorctl start all
```

Updating to 2.28:

```
curl '$INSTALLER_URL' > anaconda_repository.sh
bash anaconda_repository.sh -u
anaconda-server-db-setup --execute
supervisorctl stop all
supervisorctl reload
supervisorctl start all
```

Updating to 2.27:

```
curl '$INSTALLER_URL' > anaconda_repository.sh
bash anaconda_repository.sh -u
anaconda-server-db-setup --execute
```

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```
supervisorctl stop all
supervisorctl reload
supervisorctl start all
```

**Updating to 2.26.6:**

The logging configuration can be removed. Logs have been moved to `$PREFIX/var/log/anaconda-server/`:

```
curl '$INSTALLER_URL' > anaconda_repository.sh
bash anaconda_repository.sh -u
anaconda-server-db-setup --execute
anaconda-server-config --remove LOGGING
supervisorctl stop all
supervisorctl start all
```

**Updating to 2.26:**

```
curl '$INSTALLER_URL' > anaconda_repository.sh
bash anaconda_repository.sh -u
anaconda-server-db-setup --execute
supervisorctl stop all
supervisorctl reload
supervisorctl start all
```

**Updating to 2.25:**

```
curl '$INSTALLER_URL' > anaconda_repository.sh
bash anaconda_repository.sh -u
anaconda-server-db-setup --execute
supervisorctl stop all
supervisorctl reload
supervisorctl start all
```

**Updating to 2.24:**

```
conda update binstar-server binstar-static anaconda-client
anaconda-server-db-setup --execute
anaconda-server-install-supervisord-config.sh
supervisorctl stop all
supervisorctl reload
supervisorctl start all
```

**Updating to 2.23:**

```
conda update binstar-server binstar-static anaconda-client
anaconda-server-db-setup --execute
supervisorctl stop all
supervisorctl reload
supervisorctl start all
```

**Updating to 2.22:**

```
conda update binstar-server binstar-static anaconda-client
anaconda-server-db-setup --execute
supervisorctl stop all
supervisorctl reload
supervisorctl start all
```

**Updating to 2.21:**

```
conda update binstar-server binstar-static anaconda-client
anaconda-server-db-setup --execute
supervisorctl stop all
supervisorctl reload
supervisorctl start all
```

**Updating to 2.20:**

```
conda update binstar-server binstar-static anaconda-client
anaconda-server-db-setup --execute
supervisorctl stop all
supervisorctl reload
supervisorctl start all
```

**Updating to 2.19:**

```
conda update binstar-server anaconda-client anaconda-build
anaconda-server-db-setup --execute
supervisorctl stop all
supervisorctl reload
supervisorctl start all
```

**Updating to 2.18:**

```
conda update binstar-server anaconda-client anaconda-build
anaconda-server-db-setup --execute
supervisorctl stop
supervisorctl reload
supervisorctl start all
```

**Updating to 2.17:**

```
conda update binstar-server anaconda-client anaconda-build
anaconda-server-db-setup --execute
supervisorctl stop
supervisorctl reload
supervisorctl start all
```

**Updating to 2.16:**

```
conda update binstar-server anaconda-client anaconda-build
anaconda-server-db-setup --execute
supervisorctl restart all
```

**Updating to 2.15:**

```
conda update binstar-server anaconda-client anaconda-build
anaconda-server-db-setup --execute
supervisorctl restart all
```

**Updating to 2.14:**

```
conda update binstar-server anaconda-client anaconda-build
anaconda-server-db-setup --execute
supervisorctl restart all
```

**Updating to 2.13:**

```
conda update binstar-server anaconda-client anaconda-build
anaconda-server-db-setup --execute
anaconda-server-config --config-file /etc/binstar/config.yaml --set LABEL_NAME "
↪ 'channel'"
supervisorctl restart all
```

### Updating to 2.12:

```
conda update binstar-server anaconda-client anaconda-build
anaconda-server-db-setup --execute
supervisorctl restart all
```

### Updating to 2.9:

```
conda update binstar-static binstar-server cas-mirror
anaconda-server-db-setup --execute
supervisorctl restart all
```

### Updating to 2.8:

```
conda update binstar-static binstar-server cas-mirror
anaconda-server-db-setup --execute
supervisorctl restart all
```

### Updating to 2.6.0:

```
conda update binstar-server
conda install cas-mirror
```

### Updating to 2.5.1:

```
conda update binstar-server
```

### Updating to 2.3:

```
conda update binstar-server
conda install cas-mirror
```

### Updating to 2.2:

```
conda update binstar-server
```

## Uninstalling Repository

Before deleting Repository, you may want to make a backup for security reasons. For suggestions on mongo backups, see <https://docs.mongodb.org/manual/reference/program/mongodump/>.

To delete Repository:

1. Check the file storage path:

```
anaconda-server-config --get fs_storage_root
```

2. Delete the contents of `/home/anaconda-server/repo`:

```
rm -rf /home/anaconda-server/repo
```

3. Delete the appropriate MongoDB database, “binstar.”

4. Delete the contents of /etc/binstar:

```
rm -rf /etc/binstar
```

5. Delete the contents of the Repository file storage path.

## Troubleshooting

- *Cannot connect to the server on port x*
- *Error: “No environment named ‘search’ exists in...” on Windows*
- *Anaconda upload fails while behind a reverse proxy*
- *Start Repository application as a foreground process*

This page provides instructions for troubleshooting issues that may occur with your Anaconda Repository installation.

### Cannot connect to the server on port x

This could be because you are behind a firewall. Check if your IPTables rules are blocking your ports:

```
iptables -L -n
```

If a rule blocks a port you want to use, then you must allow the port:

```
sudo iptables -t nat -F
sudo iptables -A INPUT -p tcp -m tcp --dport <PORT> -j ACCEPT
sudo service iptables save
sudo service iptables restart
```

### Error: “No environment named ‘search’ exists in...” on Windows

If Anaconda Client is not yet installed and you try to search for a package on Anaconda.org using the `anaconda` command, you may receive the following error message:

```
C:\Users\USERNAME>anaconda search -t conda PACKAGE
No environment named "search" exists in C:\anaconda\envs
```

This error occurs because the Windows version of Anaconda contains an `anaconda.bat` file that is used for setting environment paths and switching environments. If Client is not installed, this batch file is called instead. Once you install Client, the Anaconda search command will work:

```
conda install anaconda-client
anaconda search -t conda PACKAGE
```

### Anaconda upload fails while behind a reverse proxy

When configuring Client to connect to a Repository behind a reverse proxy, the `anaconda upload` command may appear to try connecting to the internal hostname rather than the external configured one.

This can be corrected in the settings of the reverse proxy, such as NGINX or Apache.

In NGINX, add the setting `proxy_set_header Host $host;` to access the internal host with the external hostname.

In Apache, turn on the option `ProxyPreserveHost`.

Other reverse proxies each have their own settings to handle hostnames correctly.

EXAMPLE: Some other reverse proxies use a settings syntax such as `http_proxy=id:passwd@proxyhost:port`.

### Start Repository application as a foreground process

Repository should normally be started as a daemon. For troubleshooting, it can instead be started as a foreground process on a specified port:

```
anaconda-server --port 8080
```

Stop the application with Control-C.

### Administrative commands

Many of these actions can be done in the web interface. This command reference is for those administrators who prefer to use command line shortcuts.

In all examples below, replace “jsmith” with the name of the user whose settings you wish to change.

Reset a user’s password interactively:

```
anaconda-server-admin reset-password jsmith
```

The above command will prompt you to enter the new password twice. You may also reset the password directly:

```
anaconda-server-admin reset-password --password abcDEF123! jsmith
```

NOTE: Replace “abcDEF123!” with the new password.

Set a user’s plan to a free and unlimited plan:

```
anaconda-server-admin free-unlimited-plan jsmith
```

Set all users with a given email domain to a free and unlimited plan:

```
anaconda-server-admin free-unlimited-plan-for-domain yourdomain.com
```

You can do a “dry run” of the command to display what the command will do without changing anything:

```
anaconda-server-admin free-unlimited-plan-for-domain --dry-run yourdomain.com
```

NOTE: Replace “yourdomain.com” with the domain whose users you wish to upgrade.

Give the user the privileges of a superuser or remove them:

```
anaconda-server-admin set-superuser jsmith
anaconda-server-admin unset-superuser jsmith
```

Give the user the privileges of a staff user or remove them:

```
anaconda-server-admin set-staff jsmith
anaconda-server-admin unset-staff jsmith
```

Change a user's login name (username):

```
anaconda-server-admin move-user old_name new_name
```

NOTE: Replace “old\_name” with the current username, and “new\_name” with the new username.

Ensure the files recorded in the database exist.

```
anaconda-server-admin verify-storage
```

Ensure that files recorded in the database exist and have the correct checksum:

```
anaconda-server-admin verify-storage --md5
```

List the key names of files with problems:

```
anaconda-server-admin verify-storage --list-files
```

Scan the storage for unused files and delete them:

```
anaconda-server-admin clean-storage
```

Update the bundled installers:

```
anaconda-server-admin update-installers
```

Delete a user:

```
anaconda-server-admin delete-user jsmith
```

Set or unset “read only” mode:

```
anaconda-server-admin read-only --enable/--disable
```

Convert a regular user account to an organization and add another user to the owners group:

```
anaconda-server-convert-account to-organization --owner some_user regular_user
```

Convert an organization into a regular user account:

```
anaconda-server-convert-account to-user some_organization
```

## FAQs

- *What is Anaconda Repository?*
- *What kind of packages does Repository support?*

- *What is Anaconda?*
- *How do I get started with Repository?*
- *What is an organization account, and how is it different from an individual account?*
- *Who can upload packages to an organization?*

### What is Anaconda Repository?

Anaconda Repository is package management server software that makes it easy to find, access, store and share public and private notebooks, projects, installers, environments, and conda and PyPI packages. Repository also makes it easy to stay current with updates made to the packages and environments you are using.

Many enterprises have customized local instances of Repository. Anaconda also makes an instance of Repository available for public use at [Anaconda Cloud](#).

### What kind of packages does Repository support?

Repository supports any type of package. It is primarily used for conda, PyPI and R packages, as well as notebooks and environments.

### What is Anaconda?

Anaconda is a software development and consulting company of passionate, open source advocates based in Austin, Texas, USA. We are committed to the open source community. We created the Anaconda Python distribution and contribute to many other open source-based data analytics tools. You can find out more about us by reading [our story](#).

### How do I get started with Repository?

If you have access to Repository, you can search, download and install hundreds of public packages without having an account.

If you want to upload packages to Repository, you need to sign up for a Repository account, get Anaconda and the Anaconda Client. For more information, see [Creating an account](#) or ask your system administrator.

### What is an organization account, and how is it different from an individual account?

An organization account allows multiple individual users to administer packages and have more control over package access by other users. An individual account is for use by one person.

### Who can upload packages to an organization?

Only users who are co-owners of an organization may upload packages to that organization. Administrators who are not co-owners cannot upload packages to the organization. Users who are members of groups with read/write access but who are not co-owners, cannot upload packages to the organization.



## Help and support

Your organization receives [Professional Support](#) with your purchase of Anaconda Repository. Please contact your system administrator for help.

## Joining community support

You are also welcome to join our community support mailing lists for both [Anaconda](#) and [conda](#). On these lists you can ask questions, answer questions and discuss ways to use Anaconda. You can also submit requests for new features and make any other comments you may have.

Note that the community support forums cannot provide Anaconda Repository support.

## Reporting a bug

Issues with Repository are tracked on [GitHub](#). If you think you have found a bug, search to see if it has been reported, and report it if no one else has.

## Release notes

The Anaconda Repository 2.33 release is available to all Anaconda Repository customers as of September 19, 2017.

NOTE: If you have a subscription but do not have a license, contact [support](#) to receive that license. Otherwise contact [sales](#) to acquire it.

Administrators can update to the new Anaconda Repository release as described in [Updating Repository](#).

Please contact your enterprise support representative if you have any questions or problems regarding the release.

## Changelog

SEE ALSO: *[update instructions for current and past versions](#)*.

### 2.33.27 - 2018-07-30

User facing changes

- Remove /about/pricing
- Allow the disabling of new Personal and Organization private accounts via Stripe API

### 2.33.26 - 2018-07-19

User facing changes

- Captcha on organization creation

### 2.33.25 - 2018-07-19

User facing changes

- Captcha on account creation

### 2.33.24 - 2018-07-03

User facing changes

- Remove 'Pricing' links from header and footer
- Updated compatibility docs

Non visible changes

- Cloudflare cache invalidation
- Fixed pypi simple index mirroring
- Fixed installers and environments downloads on read-only mode
- Raise exception when an invalid USER\_REGEX value is used
- Fixed "All labels" file filter
- Fix broken session

### 2.33.23 - 2018-05-23

User facing changes

- Policy change notice

### 2.33.22 - 2018-05-21

User facing changes

- Support for ppc64le installers
- Constructor form advanced option validation
- Added explicit Redhat versions to requirements
- Improved API docs regarding the basename of files
- Search includes package summaries
- Bug fixes and broken link fixes
- Added note about compatibility between LDAPS and START\_TLS
- Fixed pypi mirror config example

### 2.33.21 - 2018-05-03

User facing changes

- Added advanced options on installer creation form

- Warn about label `main` when manually editing labels
- Package summary shows summary of latest `main` release

### 2.33.20 - 2018-04-24

#### Non visible changes

- Support for serving files from the origin

### 2.33.19 - 2018-04-19

#### User facing changes

- Flash warning when label doesn't exist
- Searching using unicode characters
- Notebooks without labels are rendered

#### Admin facing changes

- Added option to customize constructor temp dir
- Forbid supplying the same account as owner when converting account to org

#### Non visible changes

- Fix download stats link
- Avoid saving generated zip for installers
- Add quotes on paths in AIC templates
- Add support for unicode characters in version
- Removed server header from responses
- Fixed label validation

### 2.33.18 - 2018-04-03

#### User facing changes

- Added icons to the repo files page
- Changed package search placeholder
- Updated notebook upload icon
- Show warning when copying a label onto itself
- Fixed navbar spacing when logged out
- Fixed org feed links

#### Admin facing changes

- Re-use owners group when converting account to org

#### Non visible changes

- Fixed redirection after label operations

- Fixed transferring from org to superuser account
- Fixed update of installers and parcels
- Label filters are reset if the label set changes

### 2.33.17 - 2018-03-09

Non visible changes

- Next URL whitelist

### 2.33.16 - 2018-03-08

User facing changes

- Add warnings when removing main label
- Update last seen on account change
- Allow signing up with an orgs email
- Show favorites on dropdown menu for orgs
- Show settings tab for collaborators
- Fixed LDAP TLS docs

Admin facing changes

- Allow superusers to be organization admins
- Add billing history

Non visible changes

- Added validation of build number
- Add scheme to AIC templates
- Removed hotjar
- Remove marketo

### 2.33.15 - 2018-02-27

Non visible changes

- Standardize If-Modified-Since handling

### 2.33.14 - 2018-02-20

Non visible changes

- Fix HEAD support by stripping quotes from s3's object

### 2.33.13 - 2018-02-19

#### User facing changes

- Custom ordering of notebooks and environments
- Added tooltips showing the exact upload date and time of files on the repo page
- New command to convert regular user accounts to organizations and back
- Last upload date on package and installer info pages
- Fixed error message wording when deleting packages on groups
- Fixed error message when deleting packages, environments and notebooks
- Fixed the wording on the empty dashboard cards
- Fixed navbar fonts on IE11
- Fixed file management actions for package collaborators
- Fixed transferring of packages to and from the same user
- Show file actions for collaborating organizations
- Forbid downloads on read-only mode
- Allow collaborators with admin rights to delete ownables

#### Admin facing changes

- Mirror tools now create organization accounts by default

#### Non visible changes

- Add custom X-Anaconda-Lockdown and X-Anaconda-Read-Only response headers
- Use database info to construct filenames of conda downloads
- Fixed support for HEAD method on download endpoints
- Added extra validation of the basename on conda package uploads
- Use upserts instead of inserts to stage files

### 2.33.12 - 2018-02-07

#### User facing changes

- Updated terms of service

### 2.33.11 - 2018-02-06

#### User facing changes

- Added badge for the date of the latest release
- Added badge for platform support
- Show warning if no revision is selected when working with projects
- Updated terms of service
- Favorites are now shown on org dashboards

- A warning message is now shown when all packages are added to a given group

### Admin facing changes

- Disable password reset admin option while using LDAP

### Non visible changes

- Added proper HEAD support on download endpoints
- Disabled USE\_SERVER\_BASED\_SESSIONS by default
- Disabled database based settings
- Strengthened validation of labels
- Fixed popups for operations when no files or packages are selected
- Fixed deletion of files by collaborators
- Fixed access to static content while on LOCK\_DOWN
- Fixed transfer of ownership of items between orgs

## 2.33.10 - 2018-01-19

### User facing changes

- Added “noarch” to the platforms mirrored by anaconda-server-sync-conda

## 2.33.9 - 2018-01-16

### Admin facing changes

- Made fs\_storage\_root setting mandatory only for local filesystem storage

## 2.33.8 - 2018-01-15

### User facing changes

- Updated LDAP docs
- Hide actions on a user’s repo page when viewing it with an org

### Admin facing changes

- Made fs\_storage\_root setting mandatory
- Block uploading a new license when read-only mode is enabled

### Non visible changes

- Fixed exception logging on anaconda-server-sync-conda
- Remove debug code
- Better handling of next url redirect on login link
- Fixed response of repodata endpoint when an invalid If-Valid-Since header is given
- Remove install instructions from label table
- Fix orgs favorites

- Removed suggestions from confirmation dialogs

### 2.33.7 - 2017-12-11

#### User facing changes

- Updated support links
- Added activity feed item for installer upload
- Clarified pip install example command
- Added close icon for installer log popup
- Organizations are able to see their email on the profile page

#### Admin facing changes

- Removed READ\_ONLY config option. Added admin cli tool to change read only state

#### Non visible changes

- Added index in database for package ‘\_name’ attribute
- Several fixes on license creation page
- Added proper message to groups permission set
- Fixed actors for some feed items actions
- Validate that users exists when adding a group member
- E-mail confirmation error message for organizations
- Enable read-only option with repo page
- Fixed profile description not being wrapped

### 2.33.6 - 2017-11-27

#### Added

- Filter for authenticated packages in search/favorites view
- Updated message for input field when copying label
- Updated support links
- Added email notification when group member is added
- Installation info for R and pypi packages using labels
- Support for defining standard labels
- Added support to remove user using anaconda-server-admin
- Show licence url for packages, environments and notebooks
- Validation for empty fields in credit card info for plan upgrade

#### Fixed

- Updated instructions to create initial user
- Prevent organizations to have admin access for ownables of its original user

- Fixed package view when a release description is not a string
- Panels for ownables not showing in profile page if there are no packages
- Set limit to installers log height to prevent modal going below the footer
- Validation to prevent organization adding itself to one of his groups
- Set invalid license messages on mirroring script to debug instead of warning
- Generated tokens can be viewed without password prompt if kerberos authentication is used
- Fixed link on R package label page
- Remove password reset option if auth\_type is not native
- Replaced urls for R packages sources
- Fixed counts in billing overview page
- Added quotes to install instructions to avoid issues with spaces
- Documentation tooltip in conda packages
- Hide transfer modal if there are no accounts to transfer to
- Use dashboard used instead of current user as actor for feed items
- Fixed feed url links
- Redirection for labels on package files list
- Removed duplicated feed item on package transfer
- Fixed installer version validation message
- Fixed query to retrieve non-private packages
- Fixed dead links to deleted projects on the feed
- Expanded LDAP groups docs
- Handling of duplicate package exceptions on API
- Remove word kapsel from email when collaborator is added

### **2.33.5 - 2017-11-07**

#### Added

- Added a CLI tool to manage group membership
- Missing tooltips on header and admin section
- Added some missing feed items
- Account search now uses both names and emails
- Filter for authenticated packages

#### Fixed

- File info modal now works with list attributes that contain dicts
- Validate uploaded environment name
- Improved UX of installer creation form
- Updated feed icon for group collaboration removal



- Show all feed items related to a particular ownable in the History tab for that ownable
- Added main channel to default mirror config
- Generic exceptions during LDAP auth are now caught and logged
- Fixed supervisord script crontab option
- Updated read only rules on projects and installers
- Disable autocomplete suggestions for confirmation input fields
- Added authenticated packages to the billing package limit notice
- Add quotes around conda install help message if label has spaces
- Specify correct package type on tooltip text for label removal
- Updated flask-login-ldap dependency
- Validate name of copied label
- Removed validation of label name on deletion
- Removed duplicate HTTP headers on cached responses
- Do not allow pypi packages in installers
- Updated mirroring docs
- Make installers/projects summary optional
- Replaced some occurrences of word kapsel
- Align upvote icon
- Set package access from packages list
- Only owners can upload installers/environments to its own channel

#### 2.33.4 - 2017-10-24

##### Added

- Use environment variable to set initial user's password
- Usernames blacklist
- Show projects and installers summaries on header
- Added tooltips to package page buttons
- Instructions to generate tokens for organizations
- Feed items for projects and installers
- Settings for session timeout
- Supervisor script creates folder for extra config
- Updated EULA
- Set private packages and storage to unlimited individually
- Added progress indicator on installer upload
- Command to mirror only latest versions of conda packages

##### Fixed

- Fixed creation of private packages from the API
- Feed now uses the package database when it doesn't know the package type
- Hidden installers empty panel on profile page
- Infer access attribute from other attributes when adding package
- Incorrect logging of user downloads
- Show 'Set access' options for organizations in packages list
- Flash error messages when an errors occur on LDAP admin page
- Replaced word kapsel with project on flash messages
- Changed s3 content-disposition of anaconda server installers
- Date ranges for stats in admin page
- Transfer projects with the same name as a deleted project
- Remove package groups when package is archived
- No longer is possible to upload expired licenses
- Hide brand from delete user modal if user is an organization
- Package and environment file modal style issue
- Filter public packages from package search in admin
- Allow access to ownable settings to collaborators with 'write' permissions
- Fixed pypi installer tooltip
- In admin user account, prevent setting lower storage than the used storage
- Delete groups when the org is removed
- Removed add-ons page
- Handling missing package after deleting files
- Do not allow to create tokens expiring today
- Fixed redirections to packages on feed items
- Show installer and project feed items in history tab
- Show all collaborators of an organization's package
- Fix issues with package icons on dashboard
- Sorted tabs in group settings
- Always display collaborators tab as 'Collaborators'

### 2.33.3 - 2017-10-20

Added

- Added support for server based sessions

### 2.33.2 - 2017-10-10

#### Fixed

- Exception in admin after updating private packages for a user

### 2.33.1 - 2017-10-03

#### Added

- New feed items for group membership and groups collaborations
- Download stats for files API endpoint
- Option to set amount of private packages for a user from admin
- Improved license creation page
- Added distribution\_types to downloads feed
- Set packages access as authenticated from packages list
- Added option –authenticated to anaconda-server-sync-conda
- Added conda-build as dependency
- Relaxed expired tokens restrictions for public endpoints
- Add organizations as collaborators for packages, environments and notebooks
- Send email when adding collaborator to a project/installer

#### Fixed

- Link to docs in packages view
- Catch all exceptions raised when loading environment file
- Return json responses on api calls when an error is encountered
- Error message when uploading an invalid installer file
- Group permissions moved to the settings
- Fix wrong autocomplete using firefox
- Fix typeahead initial suggestions in installers form
- Updated callout in contact us form
- Hiding package access settings for collaborators
- Fixed refresh when closing user menu on the navbar
- Show info about installers downloads on admin interface
- Fixed downloads stats on admin
- Prevent adding package owner as package collaborator
- Storing package\_type when API package upload
- Collaborators can now access a package's history page
- API docs are back up again
- Refactored mirroring tools

- Fixed incorrect links from feed items

### 2.33.0 - 2017-09-19

#### Added

- SUPERUSER\_SEARCH to set superuser status in LDAP
- File format validation on installer upload
- Show which users are admin in users list
- Use similar settings for typeahead package suggestions
- Require user to be logged in to see user typeahead suggestions
- Cleaned output from test suite
- READ\_ONLY mode setting and admin option
- Added tooltips to social media icons on footer
- Hide license download buttons from add ons page
- PAM authentication support
- Added reCAPTCHA to contact us form

#### Fixed

- Exception in group collaborations list for a package after group delete
- Maintain consistency in redirections after item deletion
- Fix group link in project collaborator view
- Flash message after issues with email validation
- Exception on admin downloads list for a user when package/file was had no owner
- Change dashboard user on item transfer
- Prevent adding current user as a collaborator
- Remove current owner from items ownership transfer options
- Fixed UI issues
- Validate name and version of installers only when full form is submitted
- Fixed some redirections to documentation in Anaconda Cloud
- Hiding delete package for collaborators
- Updated links to slideshare and youtube accounts

### 2.32.9 - 2017-09-15

#### Fixed

- Fixed forgot password link

### 2.32.8 - 2017-09-11

Fixed

- Temporarily disabled contact page for anaconda cloud

### 2.32.7 - 2017-09-07

Fixed

- Exception in token expiration warning code
- Fixed error when displaying a group that no longer exists

### 2.32.6 - 2017-09-06

Added

- Separated package groups collaborations in three tabs (packages, notebooks, environments)
- Added icons to all feed items
- Provided more info on feed for uploaded packages/environments/notebooks
- Unicode validation on signup form
- Package api returns builds and adds filter for search platform
- Validation for profile name
- Added option to upload all packages to a group at once
- Added page to see feed for a user
- Added some reserved names for packages
- Semantic versions validation for installers version field
- Warning header when token is about to expire
- Make favorites page public

Fixed

- Allowing anaconda login under lockdown
- Fixed potential exceptions on old cache code
- Changed typeahead environment query to use dashboard user
- Fixed issues with the upload of previously deleted installers
- Fixed Cache-Control headers on old repodata caching code
- Display all packages by default, not just only conda packages
- Show correct label for Groups & Collaborators depending on type of user
- Changed owner of uploaded installer to current dashboard user
- Remove groups permissions from all items after group delete
- Color schemes of some flashing messages
- Prevent project/installer transfer if recipient already has one with the same name

- Empty environment field from installer created from environment if the environment was deleted
- Fixed email validation when other user is logged in
- Maintain consistency on headers from dashboard
- Fixed token generalizations
- Exception on admin downloads list for a user when package/file was missing
- Fixed “View Docs” URL
- Use dashboard user in redirects after file delete

### 2.32.5 - 2017-08-29

Fixed

- Removed Continuum references

### 2.32.4 - 2017-08-28

Fixed

- Fixed old continuum links

### 2.32.3 - 2017-08-24

Fixed

- Navbar logo responsiveness issues

### 2.32.2 - 2017-08-24

Fixed

- Changed navbar buttons order to the new design schema

### 2.32.1 - 2017-08-24

Fixed

- Bigger logo on the navbar
- Fixed home page screenshot of the site

### 2.32.0 - 2017-08-22

Added

- New top bar button structure
- Added option ‘any’ to display all kind of packages in repo view
- Support for custom user avatar methods

- Updated *cas-mirror* docs
- Create installers uploading an environment file
- Parcel and management packs can be created from installers previously created
- SSL protocol version can now be customized
- Fresh design
- Stats API endpoint
- Updated all flash messages colors

#### Fixed

- Ownership of uploaded environments
- Doc links on the feed
- Styling of installer widget
- Transferred projects now appear in dashboard
- Environment validation
- Environment upload labels
- Show correct package type when transferring package/environment/notebook
- Increased panel sizes in profile and dashboard
- Limited items to display in panels
- Fixed collaborators view
- Potential cache related exception
- Made management packs template order deterministic
- Unsafe redirections
- Removed packages from groups when transferred
- Closed XSS vulnerabilities
- Contact us emails are sent from [contact@anaconda.org](mailto:contact@anaconda.org) with a reply-to header
- Fixed typeahead input field to add package collaborators
- Archive items when all their files are deleted
- Return NotFound on item details page when they don't contain any files
- Fixed stats report admin view
- Replaced occurrences of the word “package” for a more appropriate name depending on the package type

#### 2.31.6 - 2017-08-08

#### Added

- Email notification when added as a collaborator
- Labels regex now distinguishes uppercase characters
- Added site export tool
- Upload option for installers

- Added button to review the build log next to each installer file
- Version specific landing page for packages
- Added group info to site export tool
- Upload option for environments

### Fixed

- Layout issues on dashboard and repo pages
- Remove user from groups when the account is removed
- Remove user as a collaborator for installers/packages/projects/notebooks/environments when is deleted
- Show only projects with files in projects list
- CSV export of users
- Typeahead for multi-type packages
- Added user validation to remove collaborator form
- Metadata display on package API
- Cache key generation and diskcache size limit parameter
- Empty packages will no longer appear in search results

### 2.31.4 - 2017-08-03

### Fixed

- Fixed repodata caching

### 2.31.3 - 2017-07-27

### Fixed

- Fixed label validation

### 2.31.2 - 2017-07-24

### Added

- Tool to check a file's checksum

### Fixed

- Show conda packages install instructions only for available labels
- Solved exception raise by anaconda-server-admin clean-storage
- Hide empty packages/environments/notebooks from dashboard/profile page
- Solved exception raised creating an installer from an empty environment
- Fixed style issues with dashboard/profile page.



- Added help info in profile page
- Show correct icons in objects page
- Removed extra space from groups breadcrumb
- Fixed license not updating
- Hide License expired message overlay during session when alert is closed
- Fixed email sending on forgot password and forgot username

### 2.31.1 - 2017-07-13

#### Added

- Docs for LDAP timeout
- `--clean-platforms` option for `anaconda-server-sync-conda`
- Docs for backup and restore procedures based on the default installation
- Added setting for custom installers location
- Updated FontAwesome to 4.7.0

#### Fixed

- Displays the latest release data on the package page
- Fixed panel size in profile page and added scrollbars on overflow
- Show latest version available for each platform in conda packages
- Custom installers pre-configured to point to repo instance
- Exception when trying to display security log
- Display the correct username on the navigation bar
- Remove unused logging configuration
- Python tags on `environment.yaml` now parsed on installer creation from environment
- Omitting non-conda dependencies on installer creation from environment
- Updated documentation links
- Added missing R packages icons
- Unicode issue on Contact Us form for anaconda cloud
- Fixed CSS issue on Internet Explorer
- Solved issues with labels containing slashes and spaces
- Updated link to conda documentation
- Force pypi mirroring for a new mirror user
- Fixed validation when setting packages to private in bulk
- Fixed some UI issues with long names
- Fixed org creation on mirroring tools

- Labels link takes you to all type package listing
- Package type filter set to 'all' will not show notebooks/environments anymore
- Confirmation of package delete with username input works also using uppercase
- Correct order of search filters
- Fixed typeahead endpoints
- Fixed duplicated channels on custom installers
- Allowing slashes on token name delete action
- Disabled LDAP referrals by default

### 2.31.0 - 2017-06-28

#### Added

- Added USER\_REGEX defaults to reference docs
- Added period (.) as a valid character for the default USER\_REGEX
- Added diskcache based repodata caching
- Added license url validation for packages
- Option to set storage keyname to full path
- Show error message when attempting to add duplicated collaborators

#### Fixed

- CSS fixes on top navbar
- CSS fixes on group names
- Added filter for valid packages in installer creation
- Added support for deleted Strip accounts
- Stops adding/updating labels if the validation fails
- Tokens modal is no longer going below the bottom of the page
- Displaying credit card errors correctly
- Handling LDAP login error
- Fixed highlight of project settings tab
- Updated tqdm version to stop exception on mirror download
- Environments summary is no longer duplicated
- Display correct package summary after update
- Customized success message on upvote depending on package type
- Updated links to docs for labels
- Updated verbose exception
- Fixed notebook revisions links

- Optimized query to get latest package versions
- Updated all references to docs with correct links for cloud
- Removed top-level domain validation from profile URL
- Improved speed of show\_channel endpoint
- Added validation to prevent duplicated packages on installers
- Changed default label filter for packages to 'all'
- Removed distinction of user menu based on username
- CSS issues with long names
- Fixed long project names overlapping

### **2.30.3 - 2017-06-06**

#### **Added**

- Added feeds for kapsel creation/removal/new revision

#### **Fixed**

- Added some more plural forms for flash messages
- Show project description from latest revision instead of project summary
- Fixed window installer configuration files
- Moved project history to settings
- Projects and installers on the same row
- Fixed installer creation under LOCK\_DOWN
- Fixed settings tab highlight on installer admin page
- Fixed handling of empty page param on search page
- Fixed max-age overflow on authentications endpoint
- Fixed project creation time
- Fixed installer form when python package has no releases
- Fixed subscriptions plans link
- Fixed unicode issues on contact form
- Merged LDAP login logic
- CSS clean up for groups with long names

### **## 2.30.2 - 2017-05-24**

- Fixed authentications endpoint

### ## 2.30.1 - 2017-05-24

#### Added

- Warning before deleting a package and all of its messages
- Tool to check orphan files and packages
- Added option to lock down all public pages
- Added link to contact us for custom plans.

#### Fixed

- Display error message when config file is not found
- Fixes resend confirmation email
- Retrying on 502 error while mirroring conda
- Replace non-ascii characters from filename when downloading a file
- Added password validation to password reset form
- Handling 404 on s3 key\_exists
- Removed files and packages will appear on package history
- Using user's name and email on contact emails
- Changed Resend Email label to Password Reset in admin page
- Added placeholder to collaborators form
- Added singular form messages in flash notifications
- Fixed popup label for pkg/nbk/env settings
- Fixed scrollbar blocking content in installers documentation
- Added searchbox on navigation header for non-authenticated users
- Added more database indexes for better query performance
- Removed admin monitor page
- Increased request timeout default to 120 seconds
- Updated the mirror configuration examples
- Fixed URL for pricing info
- Fixed token creation API
- Removed outdated mirror documentation
- Added migration to normalize files data
- Added brand as key in api endpoint
- Declined credit card info is no longer stored
- Improved UI for group members page

**## 2.30.0 - 2017-05-08**

## Added

- Added EULA to the installer
- Contact Us form now sends emails to [support@anaconda.org](mailto:support@anaconda.org)
- Create organization instead of user on mirroring tools

## Fixed

- Fixed anaconda-server-sync-conda settings message
- Secured web helpers views
- Removed unused test endpoints
- Fixed insecure groups endpoint
- Fixed filename too long exception on type filter for installers
- Server side encryption on S3 storage
- Fixed documentation link in /settings/access API token page
- Year in footer matches current year
- Fixed password restrictions checks
- Replaced binstar-\* message for anaconda-server-\* on mirroring script
- Added missing instruction to Project upload instructions
- Fixed the way we load the license data from the database
- Added validation for reserved usernames
- Fixed package set-access on firefox
- Fixed encoding error on package information page
- Changed error message on installer creation form

**## 2.29.1 - 2017-04-19**

## Fixed

- Fixed access to LDAP views
- Removed unused remove\_user view
- Add support for expired marketo access token
- Fixed exception on installer creation

**## 2.29.0 - 2017-04-19**

## Added

- Visibility on Projects feature
- Sortable account list by package count
- Change plan button for organizations

- Add lead source to marketo requests

### Fixed

- Fixed installers downloads
- Set S3 addressing style to “virtual”
- Fixed S3 ETag processing
- Fixed handling of missing arch attribute on search
- Typeahead endpoint access limits
- Changed supervisord runtime files location
- Allowing numeric named installers
- Allows installer creation with environment with url on the channel list
- Fixed typeahead on installer creation form
- Remove unreachable code
- Fixed flake8 findings
- Fixed installer collaborators form
- Fixed remove unlabeled files
- Fixed repo access admin for organizations

## ## 2.28.1 - 2017-04-03

### Added

- Installers can now be created from uploaded environments

### Fixed

- Fixed outdated version badges
- Add “jessie” and “sles12” parcel suffixes
- Only allows alphanumeric characters on installers name
- Fix group installers page
- Fix edition of existing installers

## 2.28 - 2017-03-22

### Added

- Add UI to delete and set access of packages on the repo page
- Add UI to delete files in the files section of the repo page
- Add UI to set and unset superuser and staff status on admin page
- Staff users can now access licensing
- Pagination on history for the account admin page

### Fixed

- Config set using *anaconda-server-config*
- Username on page titles
- Fixed anaconda-server-sync-conda issue with local repos
- CSV export on emails with special characters
- Package label filtering
- Signup password validation error message
- Exception requesting non existing file url
- Fixed email confirmation for organizations
- Text overflow when username is too long
- Remove all user packages in a single action to avoid filling the queue
- Checking user existence on reset password
- Installer URL shows zip extension

#### 2.27.5 - 2017-03-14

Fixed

- Added boto dependency back

#### 2.27.4 - 2017-03-03

Added

- Support for S3 regions that only use V4 signatures
- Support for S3 server-side encryption
- Support for custom PyPI repo sync
- New releases overrides package's description, summary, license and icon
- Update mongodb to 3.4

Fixed

- API endpoint *DELETE /dist/{owner\_login}/{package\_name}/{version}/{\_id}* should delete the file with the associated ID
- Email validation on profile page
- Downloading files with spaces or special characters should result in the correct filename
- Some documentation URLs showed up without styling
- Fixed text overlap in admin deployment page
- */downloads* installers should generate configuration files correctly
- "Not Found" errors are more consistent and clear
- Package search timeout
- Displaying validation in the popup on account's admin page

### 2.27.3 - 2017-03-02

Fixed

- Add support for string license attribute

### 2.27.2 - 2017-02-27

Fixed

- Remove pyc from ambari mpack templates folder

### 2.27.1 - 2017-02-23

Added

- Limit to the cache

Fixed

- Added missing ambari mpack templates folder

### 2.27.0 - 2017-02-15

Added

- Support for generating custom Hortonworks/Ambari management packs
- License and license url to packages api
- Update email confirmation code to more secure and flexible hash
- Support for multiple users with same email (if option enabled)
- Admin support to remove an account
- Admin support to change storage size or change plan to free unlimited
- Package versions on installers and parcels are now optional
- Specify a configuration file with the environment variable ANACONDA\_SERVER\_CONFIG

Fixed

- Noarch repodata should not include files that are missing platform and arch
- Fix attribute errors kapsel unit tests
- Mirror configuration *python\_versions* should not require quotes
- Add link to package on Favorites page breadcrumbs.
- Improve support for POWER and ARM architectures.
- Provide a useful error page when MongoDB is unreachable.
- Fix notebook and env with same name
- Suppress form errors when adding or removing package/channels
- anaconda-server-config will work on the config file you actually have
- Remove temporary redirects on user settings and org groups settings



- Disable empty as a valid label/channel name
- Fix organization name on group membership view
- Disable Reset Password if it is the only button

#### 2.26.5 - 2017-01-30

- Remove experimental feature from display.

#### 2.26.4 - 2017-01-30

##### Fixed

- Some files would not be cleaned up correctly when the corresponding user was deleted in the interface. Added a migration to clean up any existing unused files.
- Add *anaconda-server-admin clean-storage* command to clean up unused files.
- Fix csv column order on package info at the admin page.
- Render URLs in the package summary as links.
- Display correct breadcrumb for a selected environment.
- Sort labels on package page alphabetically.
- Pluralize storage information correctly.

#### 2.26.3 - 2017-01-10

- Added AnacondaCON promo to Anaconda Cloud

#### 2.26.2 - 2017-01-06

##### Added

- Conda repodata is now cached more frequently.
- Constructor installer creation will now be terminated if it takes longer than 60 seconds.

##### Fixed

- An error that occurred when PyPI packages that were deleted were re-uploaded.

#### Anaconda repository 2.26.0 - 2016-12-19

- Anaconda Repository has a new mirroring tool with reproducible results, and improved support for delta mirroring.

#### Anaconda repository 2.25.0 - 2016-11-30

- Anaconda Repository is now distributed as a self-contained installer.

### Anaconda repository 2.24.4 - 2016-11-17

- FIX: issues with async workers PR #3120, #3123
- FIX: Issue with sending forgotten username. PR #3120
- LOGGING: log everything to stdout. supervisord script will now log to file instead of syslog PR #3106
- KAPSEL: Remove kapsel uploader PR #3107

### Anaconda repository 2.24.0 - 2016-11-09

- Documentation updates
- Fix task queue (removed mtq library)
- Improve performance of PyPI simple index page
- Move licensing code to `anaconda_platform.component.licensing`
- Add hotjar (cloud)
- Move username regex to check into settings
- Parcels: Add anaconda and python 2.7 as default packages
- Added AIC (Anaconda Installer Configuration) installers
- Remove Kapsel Execution

### Anaconda repository 2.23.1 - 2016-10-25

Added

- Gevent in as the server worker\_class
- Remove check of key existence in s3 for anaconda.org

### Anaconda repository 2.22.0 - 2016-10-18

Fixed

- API: added correct handling when user is deleted
- DOWNLOADS: allow unlimited storage of download stats
- UI: terms and conditions link was incorrectly escaped
- NOTEBOOKS: fix sorting of notebook versions
- REPO: copied package files would sometimes return 404
- UI: added default sorting to more tables
- REPO: usability and functionality fixes for CDH parcel generation

### Anaconda repository 2.21.0 - 2016-09-29

#### Added

- REPO: users can *create custom CDH parcels through Anaconda Repository*
- UI: standardize sorting on tables
- UI: the software version is included in the footer of Anaconda Repository

#### Fixed

- NOTEBOOKS: added iframe sandboxing to notebooks
- NOTEBOOKS: fixed rendering of thumbnails uploaded by *nb\_anacondacloud*
- REPO: copied package files were sometimes incorrectly garbage collected

#### Changed

- UI: The pages on the *conda.anaconda.org* and *pypi.anaconda.org* domains redirect to *anaconda.org*.

#### Removed

- BUILD: The deprecated build feature has been removed from Anaconda Repository.

### Anaconda repository 2.20.4 - 2016-09-26

#### Fixed

- NOTEBOOKS: links in the notebook will open in the browser window directly, instead of inside of a frame.

### Anaconda repository 2.20.3 - 2016-09-20

#### Fixed

- Allow numeric usernames

### Anaconda repository 2.20.2 - 2016-08-18

#### Added

- REPO: package types will correctly update from added files (#2492)
- UI: cluster pages now list apps associated with that cluster
- Notebooks larger than 25mb will not be rendered (#2336)
- API: the endpoint `/user/{account}/downloads/{start}--{end}` now provides download activity aggregated by package for an account.

#### Fixed

- Improve the performance of the security feed (#2335)

#### Changed

- UI: the reminder to use beta will be hidden for 24 hours when a user clicks the “close” button.
- BUILD: remove welcome to build message for build deprecation notice.
- UI: rename project to kapsel everywhere (except imports) (#2563)

- Collaborators page updated to new groups API (#2512)

### Anaconda repository 2.19.5 - 2016-08-04

Fixed

- Fixed generation of URLs to user notebook content server over https

### Anaconda repository 2.19.4 - 2016-07-21

Fixed

- DB: improved group migration to handle more corner cases

### Anaconda repository 2.19.2 - 2016-07-07

Fixed

- REPO: package types will correctly update from added files (#2492)

### Anaconda repository 2.19.1 - 2016-07-07

Added

- Basic Cluster Pages
- Conda Caching - Conda endpoints now use Last-Modified/if-modified-since headers

### Anaconda repository 2.18.0 - 2016-06-01

Added

- API: add an endpoint `/user/{account}/downloads/{start}--{end}` that provides an aggregated summary of download activity for an account.
- BUILD: automatically scroll to the bottom of log when new lines are appended
- REPO: improve support for R packages
- WEB: license warning message includes a link to the license configuration page

Fixed

- Users do not need to be logged into GitHub to trigger builds
- BUILD: remote address for workers will be detected correctly when running behind a proxy (#2036)
- API: LDAP users logging in for the first time via *anaconda login* are created correctly.
- PIP v8.1.2 fixed package name lookup

## Anaconda repository 2.17.0 - 2016-04-18

### Added

- Queue administration page that displays build worker details and history (#1847)
- An additional configuration file can be specified with the environment variable `ANACONDA_SERVER_CONFIG` or the command line argument `--config-file`
- Configuration files in the directory `$PREFIX/etc/anaconda-server/` will now be automatically loaded
- Better logging for login logic
- Failed logins are now recorded in the security log
- `docs.anaconda.org` content is now bundled with Anaconda Repository
- New privacy policy
- Project's API
- Show notebooks with nbpresent metadata as presentations (#1583)
- Can now view different versions of notebooks (#1764)
- Complete list of current settings on /admin/deployment (#1928)
- Decorator to validate params in a requests. (#1970)
- `api.anaconda.org` returns `conda_url`, `pypi_url` and `main_url` (#1984)
- `keyname` is displayed for superusers on the file details modal, allowing an administrator to locate a file on disk (#1985)

### Fixed

- Editing package description should not add extra whitespace (#1710)
- Starred packages owned by other users will appear on the dashboard (#1706)
- Notebook output that is too wide will display a scroll-bar (#1581)
- Cleaned up styling on CI settings page (#1713)
- Security log details modal should appear for non-administrator users
- More graceful handling of notebook rendering failure (#1548)
- GitHub OAuth flow in the user settings page (#1931)
- Changed conda install instructions to use short channel name
- Group API exceptions when viewing group members (#1959)
- Fixed error in sample enterprise config file (#1968)

### Changed

- Renamed “upvotes” to “favorites” (#1707)
- adjusted helptext for conda install from specific user channel (#1914)

## Anaconda repository 2.16.6 - 2016-03-28

- Clean up build workers that have been idle too long (#1749)
- Add SMTP support for sending email (#1747)

- Add remote address of build workers to queue status (#1743)
- Toggleable sections in build log output
- Render progress bars in build log correctly
- Fix organization page redirects
- Improve search performance for “type:pypi” query (#1808)
- Fix duplicated build item when resubmitting via CLI (#1805)
- Fix sorting of file sizes (#1783)
- Fix small issue in package files page

### Anaconda repository 2.16.0 - 2016-02-25

- Kerberos Authentication Support
- Several small fixes
- Performance improvements

### Anaconda repository 2.15.5 - 2016-02-06

- Minor fixes and improvements
- Made build a separate component from the server
- Added license code
- Improved UI
- Better support for labels
- Improved performance on user profiles / security pages

### Anaconda repository 2.14.1 - 2016-01-20

- Re-enabled the anaconda copy command
- Release renaming “channels” to “labels”
- Implemented new UI enhancements that included a new user dashboard
- Performed additional bug fixes

### Anaconda repository 2.13.1 - 2016-01-12

- Implemented “My upvotes” page
- Added UI improvements to notebooks
- Implemented error logging fixes
- Performed additional bug fixes

**Anaconda repository 2.12.3 - 2015-12-22**

- Implemented UI Improvements to align with Anaconda branding, making A-Cloud easier to use
- Added confirmation after sending a message to support from the “contact us” page
- Removed left nav on dashboard
- Moved channel manager to the apps dropdown
- Made it easier for Academic users to access features by adding extended subdomain access for institutions
- Created a landing page for bug reporting to help A-Cloud users better self-select which repo for issue logging

**Anaconda repository 2.11 - 2015-12-09**

- Implemented UI Improvements
- Fixed minor issues
- Improved user profile
- Improved password validation
- Updated plans and pricing pages

**Anaconda repository 2.10 - 2015-11-13**

- Implemented UI Improvements

**Anaconda repository 2.9 - 2015-09-28**

- Implemented Upgrade/Setup script
- Offered free MKL Optimizations and free IOPro Addons for academic use
- Added command line scripts for user name changes
- Allowed port number configuration
- The Anaconda Server will subsequently be referred to as Anaconda repository

**Anaconda Server 2.8 - 2015-08-27**

- Added support for Jupyter 4.0
- Made passwords configurable
- Supplied better error messages

**Anaconda Server 2.7 - 2015-07-28**

- Implemented a new environment page
- Offered new channel features

### Anaconda Server 2.6 - 2015-07-23

- Added support for [conda noarch packages](#).
- Exposed additional distribution attributes via the API
- Changed Anaconda Server's underlying webserver from tornado to gunicorn

### Anaconda Server 2.3 - 2015-04-24

- [Increased specificity](#) when mirroring the Anaconda repository including more robust license-blacklisting capacity and new python version-filtering capacity
- Implemented the ability to [upload iPython notebooks](#) to your Anaconda Server user account

### Anaconda Server 2.2 - 2015-04-17

- Improved the user interface for channel-based interactions, which allowed users to manage multiple package and channel interactions from a single dashboard
- Performed additional unit testing
- **Due to a lack of backwards compatibility, this release locks the following two versions of the dependency packages:**
  - flask-wtf=0.8.4
  - werkzeug=0.9.6

## Command reference

Anaconda Client is the command line interface (CLI) to Anaconda Repository. You can use it to log in, log out, manage your account, upload files, generate access tokens, view tokens and other tasks.

The full Client command reference is shown below. You can also view this command reference in a terminal window with the command `anaconda --help` or `anaconda -h`.

See also: [Anaconda Cloud API Reference](#).

- *anaconda*
- *Authentication*
  - *auth*
  - *login*
  - *logout*
  - *whoami*
- *Informational*
  - *show*
  - *search*
  - *config*



- *Package management*

- *package*
- *upload*
- *download*
- *remove*
- *groups*
- *label*
- *copy*
- *move*

## anaconda

```
usage: anaconda [-h] [--disable-ssl-warnings] [--show-traceback] [-v] [-q]
               [-V] [-t TOKEN] [-s SITE]
               ...

Anaconda Repository command line manager

optional arguments:
  -h, --help            show this help message and exit
  -V, --version          show program's version number and exit

output:
  --disable-ssl-warnings  Disable SSL warnings (default: False)
  --show-traceback       Show the full traceback for chalmers user errors
                        (default: False)
  -v, --verbose          print debug information ot the console
  -q, --quiet            Only show warnings or errors the console

anaconda-client options:
  -t TOKEN, --token TOKEN
                        Authentication token to use. May be a token or a path
                        to a file containing a token
  -s SITE, --site SITE  select the anaconda-client site to use

Commands:

  auth                Manage Authorization Tokens
  label               Manage your Anaconda Repository labels
  channel              [DEPRECATED in favor of label] Manage your Anaconda
                        Repository channels
  config              Anaconda client configuration
  copy                Copy packages from one account to another
  download             Download notebooks from Anaconda Repository
  groups              Manage Groups
  login               Authenticate a user
  logout              Log out from Anaconda Repository
  notebook             [DEPRECATED in favor of upload/download] Interact
                        with notebooks in anaconda.org
```

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package	Package utils
remove	Remove an <b>object from Anaconda</b> Repository. Must refer to the formal package name <b>as</b> it appears <b>in</b> the URL of the package. Also use <code>anaconda show &lt;USERNAME&gt;</code> to see <b>list</b> of package names. Example: <code>anaconda remove continuumio/empty-example-notebook</code>
search	Search Anaconda Repository
show	Show information about an <b>object</b>
upload	Upload packages to Anaconda Repository
whoami	Print the information of the current user
build	Anaconda build client <b>for</b> continuous integration, testing <b>and</b> building packages
worker	Anaconda build client <b>for</b> continuous integration, testing <b>and</b> building packages

## Authentication

### auth

```
usage: anaconda auth [-h] [-n NAME] [-o ORGANIZATION]
                   [--strength {strong,weak}] [--strong] [-w] [--url URL]
                   [--max-age MAX_AGE] [-s SCOPES] [--out OUT]
                   (-x | -l | -r NAME [NAME ...] | -c | -i)
```

#### Manage Authorization Tokens

##### optional arguments:

```
-h, --help            show this help message and exit
-n NAME, --name NAME  A unique name so you can identify this token later.
                       View your tokens at anaconda.org/settings/access
-o ORGANIZATION, --org ORGANIZATION, --organization ORGANIZATION
                       Set the token owner (must be an organization)
```

##### token creation arguments:

These arguments are only valid with the `--create` action

```
--strength {strong,weak}
--strong            Create a longer token (default)
-w, --weak          Create a shorter token
--url URL           The url of the application that will use this token
--max-age MAX_AGE   The maximum age in seconds that this token will be
                    valid for
-s SCOPES, --scopes SCOPES
                    Scopes for token. For example if you want to limit
                    this token to conda downloads only you would use
                    --scopes "repo conda:download"
--out OUT
```

##### actions:

```
-x, --list-scopes    list all authentication scopes
-l, --list           list all user authentication tokens
-r NAME [NAME ...], --remove NAME [NAME ...]
                    remove authentication tokens
-c, --create         Create an authentication token
```

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```
-i, --info, --current-info
                        Show information about the current authentication
                        token
Manage Authentication tokens
```

See also *token*.

## login

```
usage: anaconda login [-h] [--hostname HOSTNAME] [--username LOGIN_USERNAME]
                    [--password LOGIN_PASSWORD]

Authenticate a user

optional arguments:
  -h, --help            show this help message and exit
  --hostname HOSTNAME   Specify the host name of this login, this should be
                        unique (default: hq-phone-114.corp.continuum.io)
  --username LOGIN_USERNAME
                        Specify your username. If this is not given, you will
                        be prompted
  --password LOGIN_PASSWORD
                        Specify your password. If this is not given, you will
                        be prompted
```

## logout

```
usage: anaconda logout [-h]

Log out from Anaconda Repository

optional arguments:
  -h, --help  show this help message and exit
```

## whoami

```
usage: anaconda whoami [-h]

Print the information of the current user

optional arguments:
  -h, --help  show this help message and exit
```

## Informational

## show

```
usage: anaconda show [-h] spec

Show information about an object

positional arguments:
  spec                Package written as USER[/PACKAGE[/VERSION[/FILE]]]

optional arguments:
  -h, --help          show this help message and exit

Show information about an object
```

### EXAMPLE:

```
anaconda show anaconda
anaconda show anaconda/python
anaconda show anaconda/python/2.7.5
anaconda show anaconda/python/2.7.5/linux-64/python-2.7.5-0.tar.bz2
```

## search

```
usage: anaconda search [-h] [-t {conda,pypi}]
                        [-p {osx-32,osx-64,win-32,win-64,linux-32,linux-64,linux-
↳armv6l,linux-armv7l,linux-ppc64le,noarch}]
                        name

Search Anaconda Repository

positional arguments:
  name                Search string

optional arguments:
  -h, --help          show this help message and exit
  -t {conda,pypi}, --package-type {conda,pypi}
                        only search for packages of this type
  -p {osx-32,osx-64,win-32,win-64,linux-32,linux-64,linux-armv6l,linux-armv7l,linux-
↳ppc64le,noarch}, --platform {osx-32,osx-64,win-32,win-64,linux-32,linux-64,linux-
↳armv6l,linux-armv7l,linux-ppc64le,noarch}
                        only search for packages of the chosen platform

Search Anaconda Repository for packages
```

## config

```
usage: anaconda config [-h] [--type TYPE] [--set name value] [--get name]
                        [--remove REMOVE] [--show] [-f] [--show-sources] [-u]
                        [-s]

Anaconda client configuration

optional arguments:
```

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```

-h, --help            show this help message and exit
--type TYPE           The type of the values in the set commands

actions:
  --set name value    sets a new variable: name value
  --get name          get value: name
  --remove REMOVE     removes a variable
  --show              show all variables
  -f, --files         show the config file names
  --show-sources      Display all identified config sources

location:
  -u, --user          set a variable for this user
  -s, --system, --site set a variable for all users on this machine

anaconda-client configuration

Get, Set, Remove or Show the anaconda-client configuration.

##### anaconda-client sites

anaconda-client sites are a mechanism to allow users to quickly switch
between Anaconda Repository instances. This can be used with the on-site Anaconda
Enterprise.

* Invoke the anaconda command with the '-s/--site' option like this:

    anaconda -s site_name whoami

* Set a site as the default:

    anaconda config --set default_site site_name
    anaconda whoami

##### Add an anaconda-client site

After installing Anaconda Enterprise
you can add a site named **site_name** like this:

    anaconda config --set sites.site_name.url "http://<anaconda-enterprise-ip>:<port>/
    ↪api"
    anaconda config --set default_site site_name

##### Site Options VS Global Options

All options can be set as global options that affect all sites
or site options that affect only one site.

By default, options are set globally:

    anaconda config --set OPTION VALUE

If you want the option to be limited to a single site,
prefix the option with 'sites.site_name':

    anaconda config --set sites.site_name.OPTION VALUE

```

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```
##### Common anaconda-client configuration options

* `url`: Set the anaconda api url (default: https://api.anaconda.org)
* `ssl_verify`: Perform ssl validation on the https requests.
    ssl_verify may be `True`, `False` or a path to a root CA pem file.

##### Toggle auto_register when doing anaconda upload

The default is yes, automatically create a new package when uploading.
If no, then an upload will fail if the package name does not already exist on the
server.

    anaconda config --set auto_register yes|no
```

## Package management

### package

```
usage: anaconda package [-h]
                        (--add-collaborator user | --list-collaborators | --create)
                        [--summary SUMMARY] [--license LICENSE]
                        [--license-url LICENSE_URL] [--personal | --private]
                        USER/PACKAGE

Anaconda Repository package utilities

positional arguments:
  USER/PACKAGE          Package to operate on

optional arguments:
  -h, --help            show this help message and exit

actions:
  --add-collaborator user
                        username of the collaborator you want to add
  --list-collaborators list
                        list all of the collaborators in a package
  --create              Create a package

metadata arguments:
  --summary SUMMARY    Set the package short summary
  --license LICENSE    Set the package license
  --license-url LICENSE_URL
                        Set the package license url

privacy:
  --personal           Set the package access to personal This package will
                        be available only on your personal registries
  --private            Set the package access to private This package will
                        require authorized and authenticated access to install
```

## upload

```
usage: anaconda upload [-h] [-c CHANNELS] [-l LABELS] [--no-progress]
                        [-u USER] [--all] [-p PACKAGE] [-v VERSION]
                        [-s SUMMARY] [-t PACKAGE_TYPE] [-d DESCRIPTION]
                        [--thumbnail THUMBNAIL] [--private]
                        [--no-register | --register] [--build-id BUILD_ID]
                        [-i | -f | --force]
                        files [files ...]
```

Upload packages to Anaconda Repository

positional arguments:

- files Distributions to upload

optional arguments:

- h, --help show this help message **and** exit
- c CHANNELS, --channel CHANNELS  
[DEPRECATED] Add this file to a specific channel.  
**Warning:** **if** the file channels do **not** include "main",  
the file will **not** show up **in** your user channel
- l LABELS, --label LABELS  
Add this file to a specific label. **Warning:** **if** the  
file labels do **not** include "main", the file will **not**  
show up **in** your user label
- no-progress Don't show upload progress
- u USER, --user USER User account **or** Organization, defaults to the current  
user
- all Use conda convert to generate packages **for** all  
platforms **and** upload them
- no-register Don't create a new package namespace if it does not  
exist
- register Create a new package namespace **if** it does **not** exist
- build-id BUILD\_ID Anaconda Repository Build ID (internal only)
- i, --interactive Run an interactive prompt **if** any packages are missing
- f, --fail Fail **if** a package **or** release does **not** exist (default)
- force Force a package upload regardless of errors

metadata options:

- p PACKAGE, --package PACKAGE  
Defaults to the package name **in** the uploaded file
- v VERSION, --version VERSION  
Defaults to the package version **in** the uploaded file
- s SUMMARY, --summary SUMMARY  
Set the summary of the package
- t PACKAGE\_TYPE, --package-type PACKAGE\_TYPE  
Set the package **type** [ipynb, env]. Defaults to  
autodetect
- d DESCRIPTION, --description DESCRIPTION  
description of the file(s)
- thumbnail THUMBNAIL  
Notebook's **thumbnail image**
- private Create the package **with** private access

```
anaconda upload CONDA_PACKAGE_1.bz2
anaconda upload notebook.ipynb
anaconda upload environment.yml
```

See also:

- *Uploading a conda package.*
- *Uploading PyPI packages.*

### download

```
usage: anaconda download [-h] [-f] [-o OUTPUT] handle

Download packages from Anaconda Repository

positional arguments:
  handle                user/notebook

optional arguments:
  -h, --help            show this help message and exit
  -f, --force            Overwrite
  -o OUTPUT, --output OUTPUT
                        Download as

Usage:
  anaconda download notebook
  anaconda download user/notebook
```

### remove

```
usage: anaconda remove [-h] [-f] specs [specs ...]

Remove an object from Anaconda Repository

example::

    anaconda remove sean/meta/1.2.0/meta.tar.gz

positional arguments:
  specs                Package written as <user>[/<package>[/<version>[/<filename>]]]

optional arguments:
  -h, --help          show this help message and exit
  -f, --force          Do not prompt removal
```

### groups

```
usage: anaconda groups [-h] [--perms {read,write,admin}]
                        {add,show,members,add_member,remove_member,packages,add_
↪package,remove_package}
                        spec

positional arguments:
  {add,show,members,add_member,remove_member,packages,add_package,remove_package}
                        The group management command to execute
```

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```

spec                <organization>/<group_name>/<member>

optional arguments:
  -h, --help            show this help message and exit
  --perms {read,write,admin}
                        The permission the group should provide

```

## label

```

usage: anaconda label [-h] [-o ORGANIZATION]
                    (--copy LABEL LABEL | --list | --show LABEL | --lock LABEL | --
↪unlock LABEL | --remove LABEL)

```

Manage your Anaconda Repository channels

```

optional arguments:
  -h, --help            show this help message and exit
  -o ORGANIZATION, --organization ORGANIZATION
                        Manage an organizations labels
  --copy LABEL LABEL
  --list                list all labels for a user
  --show LABEL          Show all of the files in a label
  --lock LABEL          Lock a label
  --unlock LABEL        Unlock a label
  --remove LABEL        Remove a label

```

## copy

```

usage: anaconda copy [-h] [--to-owner TO_OWNER] [--from-label FROM_LABEL]
                    [--to-label TO_LABEL]
                    spec

```

Copy packages **from one** account to another

```

positional arguments:
  spec                Package - written as user/package/version[/filename]
                        If filename is not given, copy all files in the
                        version

optional arguments:
  -h, --help            show this help message and exit
  --to-owner TO_OWNER   User account to copy package to (default: your
                        account)
  --from-label FROM_LABEL
                        Label to copy packages from
  --to-label TO_LABEL   Label to put all packages into

```

## move

```
usage: anaconda move [-h] [--from-label FROM_LABEL] [--to-label TO_LABEL] spec
```

Move packages between labels.

positional arguments:

spec	Package - written <b>as</b> user/package/version[/filename]
	If filename <b>is not</b> given, move <b>all</b> files <b>in</b> the version

optional arguments:

-h, --help	show this help message <b>and</b> exit
--from-label FROM_LABEL	Label to move packages <b>from</b>
--to-label TO_LABEL	Label to move packages <b>to</b>

## Glossary

- *Anaconda*
- *Anaconda Client CLI*
- *Anaconda Repository*
- *conda*
- *conda build*
- *conda package*
- *label*
- *Miniconda*
- *namespace*
- *noarch package*
- *on-site repository*
- *organization account*
- *package*
- *package manager*
- *project*
- *repository*
- *source package*
- *token*

## Anaconda

An easy-to-install, free collection of open source packages, including Python and the conda package manager. Over 150 packages are installed with Anaconda. After installing Anaconda, you can install or update over 250 additional open source packages contained in the Anaconda Repository using the `conda install PACKAGE` command.

NOTE: Replace `PACKAGE` with the name of the desired package.

## Anaconda Client CLI

The Anaconda Client command line interface (CLI) allows you to log into Anaconda Repository directly from your Terminal window or Anaconda Prompt and manage your account. It is not necessary for downloading or installing packages from Repository.

## Anaconda Repository

Repository hosts hundreds of useful Python packages, notebooks and environments for a wide variety of applications. You do not need to be logged in, or even need a Repository account, to search for packages, download and install them.

## conda

The conda package manager and environment manager program that installs and updates packages and their dependencies, and lets you easily switch between environments on your local computer.

## conda build

The command line interface that lets you build packages for your local operating system.

## conda package

A compressed file containing system-level libraries, Python modules, executable programs or other components. The file uses the tarball format.

## label

Part of the URLs for Repository where conda looks for packages. Labels are searched only if you specify a label.

The default label is “main,” so packages that are uploaded without specifying a label are automatically labeled “main.” The version labeled main is also downloaded by default, unless a user specifies a different label. So, if a file is labeled main, then the label name may be omitted from the URL.

EXAMPLE: The following repositories are equivalent:

```
https://<your-anaconda-repo>/sean/label/main
https://<your-anaconda-repo>/sean
```

Commands such as `conda install` can be used with a channel, or used with a channel and a label:

```
conda install --channel sean selenium
conda install --channel sean/label/dev selenium
conda install --channel sean/label/stable selenium
```

Using Anaconda Client, *package* developers can create labels such as development `labels/dev`, test `labels/test` or other labels that are searched only if the user specifies the label.

EXAMPLE: The following search examples use a *namespace* of “travis”:

- <https://<your-anaconda-repo>/travis/labels/main>—the label searched by default.
- <https://<your-anaconda-repo>/travis>—same as default label with `main` implicit.
- <https://<your-anaconda-repo>/travis/labels/dev>—contains the packages in development.
- <https://<your-anaconda-repo>/travis/labels/test>—contains packages ready to test.
- <https://<your-anaconda-repo>/travis/labels/any-custom-label>—any label you want to use.

### Miniconda

A minimal installer for [conda](#). Like [Anaconda](#), Miniconda is a software package that includes the conda package manager and Python and its dependencies, but does not include any other packages. Once conda is installed by installing either Anaconda or Miniconda, you can install other software packages directly from the command line using `conda install`.

### namespace

Each user and organization has their own location called a “namespace” where they may host packages. You can view the public packages in a user or organization’s namespace by navigating to their user page.

EXAMPLE: The “travis” user namespace located at <https://<your-anaconda-repo>/travis> contains packages that were uploaded and shared by the user whose account is named “travis.”

### noarch package

A conda package that contains nothing specific to any system architecture, so it may be installed on any system. When conda searches for packages on any system in a channel, conda always checks both the system-specific subdirectory—such as `linux-64`—and the `noarch` directory.

### on-site repository

Repository is powered by Anaconda Server. You can run your own server behind firewalls or in air gapped environments. For more information, contact [sales@anaconda.com](mailto:sales@anaconda.com).

### organization account

An organization account is a type of account on Repository that allows multiple individual users to administer packages and control package access to different user groups. It also includes a large amount of storage space.

Use organization accounts to:

- Share packages, environments or notebooks under an organization’s account rather than your personal account.
- Assign multiple account administrators.
- Assign different access permissions to groups of users and customize per-package access by group.

## package

All files uploaded to Repository are stored in packages. Each Repository package is visible at its own unique URL based on the name of the user who owns the package and the name of the package.

EXAMPLE: If a user “travis” uploads a test package named “testpkg,” it is visible at:

```
https://<your-anaconda-repo>/travis/testpkg
```

Repository packages may contain multiple files, and these files may be data files such as comma separated value (CSV), tab separated value (TSV), or text (TXT), or package files such as conda packages, PyPI packages or R packages.

## package manager

A tool that facilitates the process of installing, upgrading, configuring and removing packages on Repository. Repository supports two package managers, *conda* and *PyPI*.

For more information, see *Using package managers*.

## project

Anaconda Project is an open source tool created by Anaconda that delivers light-weight, efficient encapsulation and portability of data science projects.

## repository

A storage location from which software packages may be retrieved and installed on a computer.

## source package

“Source” packages are source code only, not yet built for any specific platform, and might be compatible with all, some or only one of the platforms.

## token

An access control token is a random alphanumeric string that is inserted into a URL that you give to another Repository user. The token allows them to download a package or add a channel that you have marked private. Only those users with the correct access token can access the private file. You can use Client to generate tokens to give other users specifically scoped access to packages and collections.

## Previous versions

This documentation is provided for the use of our customers who have not yet upgraded to the current version. Your version number is located in the footer.\*

**Anaconda Repository 2.32**

**User guide (AER 2.32)**

**Quickstart (AER 2.32)**

**Managing Your Account (AER 2.32)**

**Using Anaconda Repository (AER 2.32)**

**Parcels, Management Packs, and Installers (AER 2.32)**

**Reference (AER 2.32)**

**Command Reference (AER 2.32)**

**Admin and install guide (AER 2.32)**

**Install Anaconda Repository (AER 2.32)**

**Online Installation (AER 2.32)**

**Offline Installation (AER 2.32)**

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## Maintenance and configuration concerns

### User administration

### Anaconda repository requirements and verification

### Client configuration

### Anaconda repository command line interface

### Command line interface

### Adding a PyPI or Anaconda mirror to your Anaconda repository installation

You can create a local copy of the PyPI or Anaconda repositories. Included here you will find an explanation of how to use Anaconda repository's convenient syncing tools to create and configure local mirrors:

- Mirroring an Anaconda repository
- Mirroring a PyPI repository
- Configuring your mirror
- *Customizing your PyPI or Anaconda repository mirror - v 2.2.0 or earlier*

### Mirroring an Anaconda repository

### Mirroring a PyPI repository

### Configuring your PyPI or Anaconda Repository mirror

### Customizing your PyPI or Anaconda repository mirror - v 2.2.0 or earlier

### Cross platform ("Noarch") package support in Anaconda repository

### Jupyter notebook support in Anaconda repository

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\* Anaconda Repository Versions 2.21.0 and earlier do not contain the version number in the footer. Please contact your Enterprise Support representative to get your version number.

## 4.1.2 Anaconda Enterprise 4 Notebooks

*Empower the Data Science Team with cross-collaboration*

AEN is a browser-based Python data analysis environment and visualization tool from Anaconda®. AEN is a ready-to-use, powerful, fully-configured data analytics environment all in a secure, governed environment.

AEN allows data science team members to create and share private notebooks, manage access, control notebook revisions, compare and identify differences across notebook versions, search notebooks for keywords and packages, use enhanced collaborative notebook features—including revision control and locking—and to access an on-premises and/or cloud collaborative notebook server.

The current version of AEN is 4.3.3, released on November 5th, 2019.

### User guide

AEN's browser-based management of private packages, notebooks, and environments allows data science team members to:

- Create, share and manage private notebooks.
- Control notebook revisions.
- Compare and identify differences across notebook versions.
- Search notebooks for keywords and packages.
- Use enhanced collaborative notebook features including revision control and locking.
- Access on-premises and/or cloud-based collaborative notebook servers.
- Utilize multiple language kernels like Python and R language in the same notebook.
- Create new notebook environments on the fly without leaving the notebook or entering commands in a prompt.
- Publish results to business stakeholders as interactive visualizations and presentations.

To quickly get up and running with AEN, see [Getting started](#).

Download the [Cheat sheet](#) for easy reference.

### Concepts

- [Projects](#)
- [Team collaboration](#)
- [Access control](#)
- [Sharing projects](#)
- [Project tags](#)

### Projects

AEN users interact with the system predominantly through projects.

A project is a set of conda environments, Jupyter Notebooks, and other files.

Each project has a project drive that all team members can access. The size of the drive is not limited by AEN. Contact your system administrator if you find you do not have sufficient space.

Each project has a separate project directory on the project drive.

The project directory is a directory for project files and data that is separate from the project owner's and team members' home directories, so that team members can share and have equal access.

The path to your project directory is `/projects/<project_owner>/<project_name>`.

For administrative information about projects, directories, and permissions, see [Projects and permissions](#).

## Team collaboration

Teams collaborate in AEN using projects. Projects allow a team to easily come together by sharing the resources, applications, and environments that are necessary to collaborate effectively.

The AEN project owner and any team members connected to their project will have access to the same:

- Shared files and home directories.
- Shared Python and R environments.
- Shared nodes and hardware.
- Common applications.
- Web user interface.

For more information, see [Working with projects](#).

## Access control

AEN access controls allow you to:

- Add and remove project access for new team members.
- Limit the access to specific folders and files to members of your project team.
- Use permissions to extend execute access to team members. By default, all of the team members on a project have read and write access to all project assets.

Access control is performed from each project's Workbench application.

For more information, see [Controlling access to your project](#).

## Sharing projects

AEN supports both public and private sharing.

A project can be “public,” which means that anyone with access to the system can view the project assets.

Any content placed in the `public` folder in a project is publicly accessible using its URL.

A project can be “private,” which means that only the project owner and team members can view the project assets.

You can also [limit who can access specific files](#).

### Sharing Jupyter Notebooks

In addition to general project sharing capabilities, you can also publish Jupyter Notebooks to Anaconda Repository. This automatically versions the notebook and allows you to define who can view the notebook.

### Project tags

Tags are used to:

- Group similar or related projects.
- Identify your project so that it is easier to find.
- Let others know about your project.

You can *add and remove tags* for any project that you have access to.

### Getting started

This section contains information and tasks for first-time AEN users.

In this getting started guide, you will:

- *1. Download the AEN cheat sheet*
- *2. Access your user home page*
- *3. Create a new project*
- *4. Add collaborators*
- *5a. Open an example notebook, OR*
- *5b. Create a new environment and notebook*
- *6. Create checkpoints for version control*
- *7. Share your notebook and environment with others*
- *8. See what to do next*

#### 1. Download the AEN cheat sheet

Before you start, download and print the *AEN cheat sheet* for easy reference.

#### 2. Access your user home page

After your administrator has set up your server and new Anaconda account, you will receive a welcome email.

1. Click the link in the email to open the AEN login page.

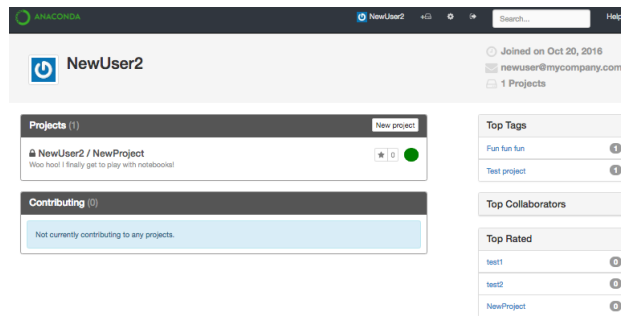
NOTE: Use the domain name and not the IP address when you connect to AEN. Using the IP address can cause TLS and security certificate errors.

2. Enter your AEN account username and password.

NOTE: Some administrators allow you to create your own account. If your administrator has allowed this, in the create a new account section, create your own username and password.

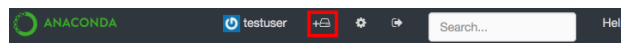
3. Click the Login button.

Your user home page, where all good things happen, is displayed:

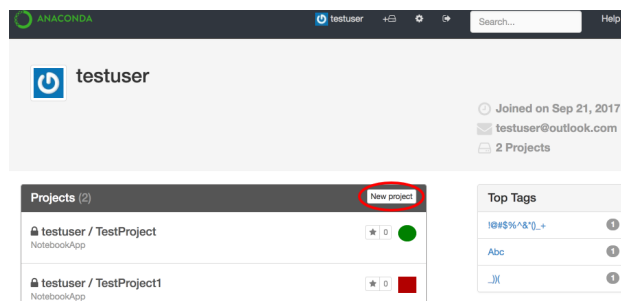


### 3. Create a new project

1. There are 2 ways to create a new project in AEN:
  - On the right side of the AEN task bar, click on the New Project icon:



- On your home page, click the New project button:



2. On the Project page that is displayed, type a name for your project, such as “Testing.”

**New Project**  
Create your project here!

Project Name

Project names must start with a letter and contain only alphanumeric characters.

Summary

☐ Public  
 Anyone can see this project. Collaborators have write access.

☒ Private  
 No one can see this project except collaborators.

Next

3. Type a summary of the project so you can recognize it later.
4. Select whether your project will be public or private.
5. Verify that the default data center is selected.

TIP: You can update the project summary and description at any time from the **Project** menu in the Project Settings. To return to your project at any time, click the project name.

6. Click the Next button.

Your new project's home page is displayed:

**testuser / TestProject1**  
NotebookApp

workbench viewer jupyterlab terminal notebook Compute Resource Config

**Description**  
We recommend that each repository have a description. Treat it like a README of your project for the new developer.

**Public Folder**  
This project does not have contents in its public folder yet!

7. To change the project settings, click the Project Settings icon on at the top right.

**testuser / TestProject1**  
NotebookApp

Project Settings icon highlighted with a red box.

8. Modify the summary or add a description of the project.



TIP: A project description is recommended, and may be written in Markdown syntax (plain text valid Markdown).

To see how Markdown will be displayed, in the description area, click the **Preview** tab.

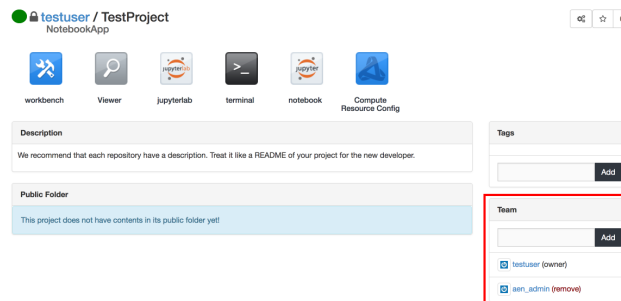
## 4. Add collaborators

You can add team members to your project as collaborators. Adding team members to your projects makes collaboration easy because they have full access to the project's applications, files and services.

When you add team members, their home directory is mounted in the project. There is no need to download and email data or scripts—team members can work on the same files in the same environment in which you are working.

To add collaborators to your project:

1. From your project home page, in the Team box, begin typing a teammate's username.
2. In the list that is displayed, select the teammate's username.
3. Click the Add button.

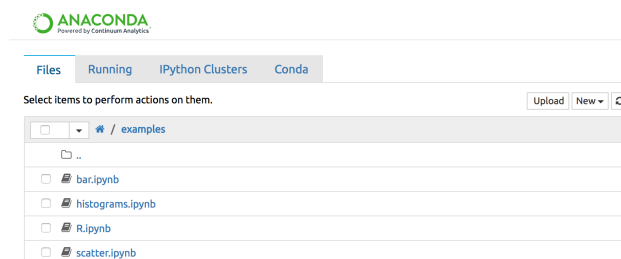


1. Repeat these steps for each team member you want to add as a collaborator.

TIP: You can add or remove team members any time from the **Team** menu in Project Settings. You can also modify a team member's read, write or execute permissions at any time from the *Using Workbench*.

## 5a. Open an example notebook, OR

1. From your project home page, click the Jupyter Notebooks icon.
2. On the File View page, click the Examples folder.



1. Select any of the example notebooks.

2. To see the default results of the formulas used in the displayed notebook, in the **Cell** menu, select Run All.
3. To experiment with changing the notebook, edit any of the formulas in the notebook.
4. In the **Cell** menu, select Run All.

Any differences resulting from your edits are displayed.

## 5b. Create a new environment and notebook

If you are already familiar with creating notebooks, you can easily set up a new environment with the programs you need—like SciPy and NumPy—then open a new notebook and make your edits.

To create a new environment:

1. From your project home page, click the Jupyter Notebooks icon.
2. On the File View page, click the **Conda** tab.
3. To add a new conda environment, on the top right of the **Conda** tab, click the + icon.
4. Type a name for your environment.
5. Select Python 2, Python 3 or R language kernel.
6. Click the Create button.
7. To activate your new environment, click its name.

The packages that are available and installed in your new environment are displayed.

## Adding SciPy and Numpy packages

1. In the available packages section, search for the package name `numpy`—all lower case.
2. In the results section, next to `numpy`, select the checkbox.

The screenshot shows the Anaconda Cloud interface. At the top, there are tabs for Files, Running, IPython Clusters, and Conda. The Conda tab is active. Below the tabs, there is a section for '3 Conda environments'. It contains a table with columns: Action, Name, Default?, and Directory. The environments listed are 'root', 'default', and 'myenv'. The 'default' environment is marked as the default.

Below the environments section, there is a search bar with 'numpy' entered. To the left of the search bar, it says '2 available packages'. To the right, it says '39 installed packages in environment "myenv"'. Below the search bar, there are two tables. The first table shows available packages for 'numpy' with columns: Name, Version, and Channel. The second table shows installed packages for 'myenv' with columns: Name, Version, Build, and Available.

Name	Version	Channel
<input checked="" type="checkbox"/> numpy	1.13.1	defaults
<input type="checkbox"/> numpydoc	0.7.0	defaults

Name	Version	Build	Available
<input type="checkbox"/> anaconda-client	1.6.3	py36_0	
<input type="checkbox"/> certifi	2016.2.28	py36_0	
<input type="checkbox"/> clyent	1.2.2	py36_0	
<input type="checkbox"/> decorator	4.1.2	py36_0	
<input type="checkbox"/> ipykernel	4.6.1	py36_0	
<input type="checkbox"/> ipython	6.1.0	py36_0	

1. Click the Install icon.

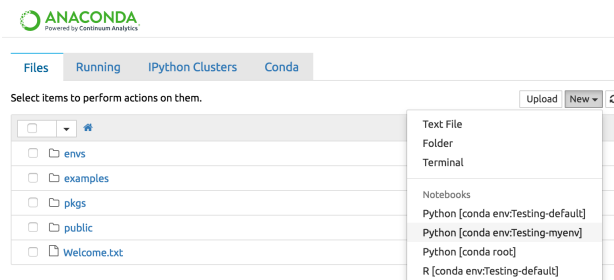
2. To confirm your installation, click the Install button.

Numpy is displayed in the installed packages section—if not, click the Refresh button. Repeat these steps to install the Scipy package—searching for `scipy` in step 1.

TIP: You can return to this screen at any time to add additional packages to this environment.

## Creating a new notebook in your environment

1. From the AEN homepage, click the **Files** tab.
2. On the top right of the **Files** tab, click the New button.
3. Under Notebooks, select the Python environment with the name you entered while *creating a new environment*.



NOTE: If you do not see your new environment listed under Notebooks, next to the New button, click the Refresh button.

A new locked notebook is displayed. Paste or write some code to execute when you are ready.

## 6. Create checkpoints for version control

Whether you are exploring an existing notebook, or creating a new one, you can easily create checkpoints, return to an earlier version, compare two different versions and save them for reference.

To create a checkpoint, in the **File** menu, select Save and Checkpoint:

To revert your notebook to a previous checkpoint, in the **File** menu, select Revert to Checkpoint.

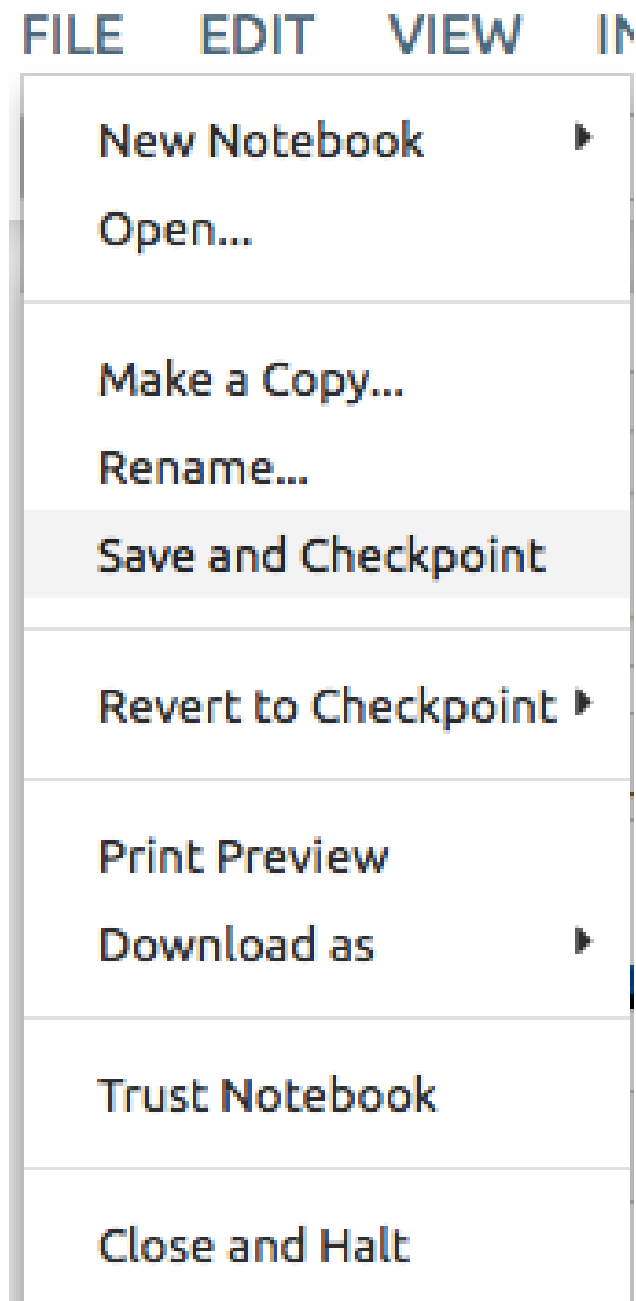
NOTE: For more information about revision control features, including creating commits and comparing differences, see *Using the Revision Control Mechanism extension*.

## 7. Share your notebook and environment with others

See *Sharing projects and notebooks*.

## 8. See what to do next

Now that you have completed the Getting Started guide, you are ready to move on to *basic tasks* and *advanced tasks*.



## Basic tasks

This section contains information and tasks that use the web browser to manage projects and is best-suited for any beginning AEN user:

### Working with projects

Almost everything in AEN starts by opening an existing project or creating a new one.

After that, you can set up a special environment with the packages you want, set their access permissions and modify your project settings.

### Searching for a project or file

- *Types of files searched*
- *Search indexing*
- *Using search constructs*
- *Searching metadata fields*
- *Searching a project*
- *Saving a search*
- *Removing a saved search*

To search for projects and files, use the Search box in the AEN navigation bar. The search provides different results depending on which page you search from:

- On a project home page, search results include any files that match your search criteria within the current project.
- On any other AEN page, search results include any files that match your search criteria within all projects.

**TIP:** Your search results include only files and projects that you can view: public projects, and private projects to which you have a minimum of view access.

### Types of files searched

The following types of files are included in search results:

- `.py`—Python source files.
- `.ipynb`—IPython/Jupyter notebooks.
- `.txt`—plain text files.
- `.md`—Markdown files.

### Search indexing

Files that are modified while a project is running are automatically re-indexed shortly after the files are modified. If you create or update a large number of files—such as cloning a git repository or copying a directory—search results may take several minutes to update.

Files that are modified while the project is not running are re-indexed only after the project is started.

## Using search constructs

You can use the following search constructs:

- Ordinary words will match the full-text contents of any file.
- Wildcards are permitted.

EXAMPLE: `John*` will match John and Johnny. These are glob patterns and are similar to their usage in the command line.

- Combine queries using AND or OR, and group them using parentheses `()`.

Regular expression patterns can be embedded in the query string by wrapping them in forward-slashes `/`:

```
name:/joh?n(ath[oa]n)/
```

The supported regular expression syntax is explained in [the Elasticsearch reference](#).

NOTE: Wildcards apply inside a regular expression. A query string such as `/.*n/` would force the search to visit every term in the index.

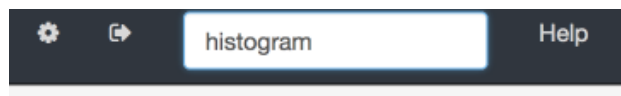
## Searching metadata fields

You can search in specific metadata fields:

- `imports:name`—matches files that import the module name.
- `uses:name`—matches files that reference the identifier name. Referenced names include any functions and globals imported from other modules, as well as the names of any methods invoked on any object.
- `defines:name`—matches files that define the identifier name. Defined names include functions defined at global scope, class names, and method names within classes.
- `acl:user`—matches files in which the named user has read access or higher.

## Searching a project

1. In the Search box, type a string of text:

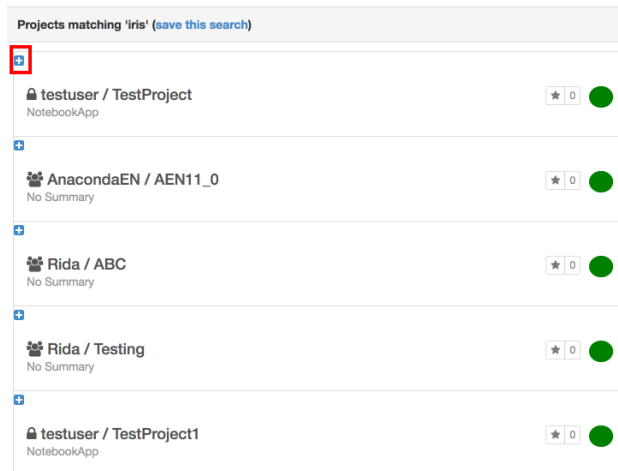


TIP: Search by glob patterns, which are similar to file matching in the command line.

EXAMPLE: To find projects in the test family that are numbered from 00 to 99, search for `Test-??`. To find all projects whose name ends with “Stats,” search for `*Stats`.

2. Press Enter.

3. In the search results, click the plus + icon above a project name to show a list of matching files in the selected project:



TIP: Click the project name to open the project's home page.

4. To view a file, click its file name in the matching files list:



## Saving a search

1. At the top of the search results, click Save this search:

The “save this search” text changes to “stored” and your search is saved. Your saved searches are listed on your home page.

## Removing a saved search

On your home page, in the Saved searches section, click X next the saved search that you want to remove:

Projects matching 'iris' **Stored**

+

testuser / TestProject

NotebookApp

★ 0

+

AnacondaEN / AEN11\_0

No Summary

★ 0

+

Rida / ABC

No Summary

★ 0

+

Rida / Testing

No Summary

★ 0

+

testuser / TestProject1

NotebookApp

★ 0

Projects (2) 

New project

testuser / TestProject

NotebookApp

★ 0

testuser / TestProject1

NotebookApp

★ 0

Contributing (0)

Not currently contributing to any projects.

Top Tags

l@#\$%^&\*0\_+ 1

Abc 1

\_)({ 1

Top Collaborators

aan\_admin 1

Top Rated

Project 1

Testing 0

AEN11\_0 0

ABC 0

TestProject 0

Saved searches

iris x

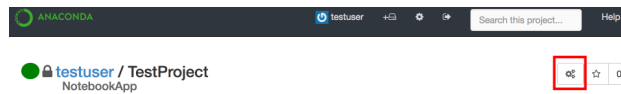
200

Chapter 4. Anaconda Cloud

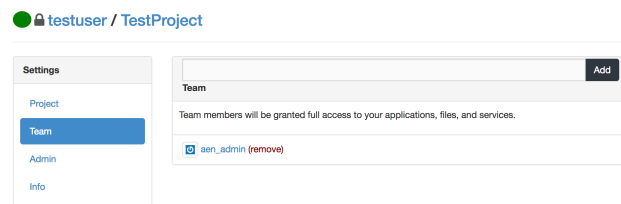


## Adding and removing team members on a project

1. On the project home page, click the Project Settings icon to open the Project Settings page.



2. In the **Settings** menu, select Team.



## Adding a team member

1. In the username box, type in the first few letters of the username for the team member you want to add to the project.
2. In the list of usernames that displays, click the user to add.
3. Click the Add button.

## Removing a team member

Click the red Remove link next to the name of the user you want to remove from the project.

## Controlling access to your project

- *Controlling team member access*
- *Controlling non-team member access*

### Controlling team member access

By default, all of the team members on a project have read and write access permissions for all project assets.

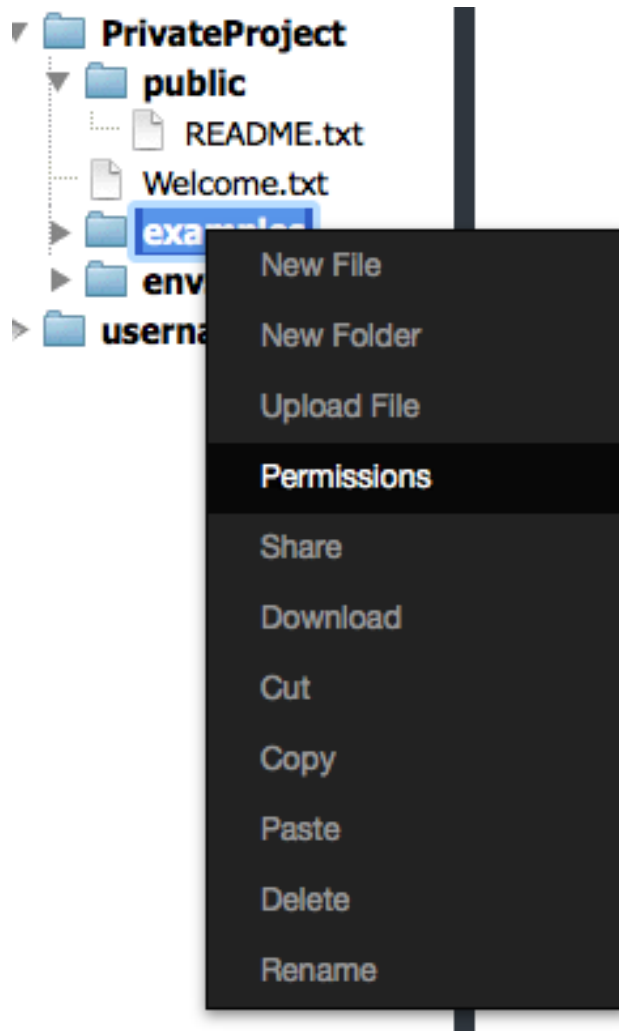
The available permissions are read, write and execute. If you remove all individual or group permissions for a project asset, team members will not be able to access that asset.

To change a project's permissions:

1. Open the project's home page.
2. Click the Workbench icon.
3. In the Workbench app, right-click the file or folder you want to limit access to.

NOTE: When you change a folder's permissions, the permissions of files and folders inside it do not change. You may change the permissions of those files and folders manually.

4. In the menu that displays, select Permissions:



A list of owners and team members who have access to your project is displayed.

- Find the team member you want to change access for:

Permissions for examples

Owner  Group

Who	Type	Read	Write	Execute
owner		<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
group		<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
others		<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>
Mask		true	true	true
<input type="text" value="username"/>	User <input type="button" value="v"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input type="text" value="username"/>	Group <input type="button" value="v"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input type="text" value="username2"/>	User <input type="button" value="v"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>
<input type="text" value="username2"/>	Group <input type="button" value="v"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
<input type="text" value="username3"/>	User <input type="button" value="v"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
<input type="text" value="username3"/>	Group <input type="button" value="v"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

- Next to the team member's name, select or deselect the permissions for that user.

NOTE: You can add a team member and set their access at the same time by typing their name in a username box, setting their permissions, and then clicking the Add button.

- Click the Submit button.

The selected permissions are added, and the deselected permissions are removed.

NOTE: If a team member is in the Workbench application when you give them access, they must refresh their browser window to see their current permissions.

## Controlling non-team member access

You can choose to grant file or folder access to someone who is not part of the project team, as long as that person has an AEN account.

Sharing with individuals outside the team is a four step process:

- Copy or move the file or folder to your home directory.*
- Give the user read and execute access to your home directory.*
- Add the user to the file's permissions.*
- Have the user add your directory to their workbench.*

## Copying a file or folder to your home directory

Your home directory is displayed at the bottom of the File Manager pane in the Workbench.

To protect the other files and folders in your home directory—those you are not providing permissions to a user to access—we recommended that you:

1. Create a sub-folder.
2. Rename the folder with the name of the user you are granting access to.
3. Copy or move the file you want to grant permissions for to the renamed folder.

The file is copied or moved to the new location and is ready for you to update the file permissions.

### Granting file access

You must select read and execute access for a user to be able to view, but not edit, the files or folders.

1. Right-click the name of the file or folder you are granting access to.
2. In the menu that is displayed, select Permissions.
3. Click the Add button.
4. Type the username of the user to whom you are granting file access and press Enter.

**TIP:** If you grant access to a folder instead of a specific file, you only have to set permissions the first time you share the folder with each user, unless you need to update the permissions.

### Adding file permissions for a user

Once a user is included in your Permissions list, you must *add the correct permissions* for the user, in the same way as you would for a team member.

Once complete, depending on the access granted, the user will be able to view, read, change, and execute the file.

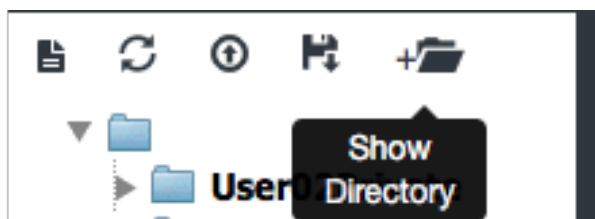
**NOTE:** If you change permissions for a folder instead of a file, the user will be able to see and access any files within that folder.

### Adding a directory to a user's workbench

The user can now add your home directory to their Workbench File Manager.

To add your home directory to another user's workbench, have the other user follow these steps:

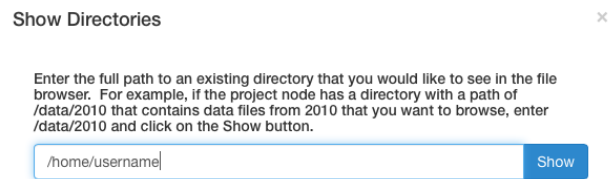
1. Click the Show Directory button at the top of the Workbench File Manager:



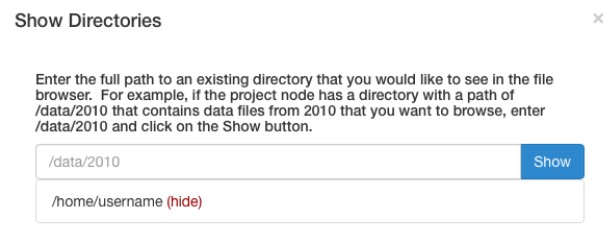
The Show Directories dialog box displays.

2. In the text box, type `/home/[yourusername]`.

NOTE: Replace `[yourusername]` with your AEN username.

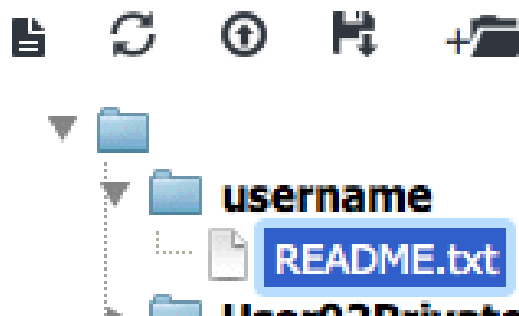


3. Click the Show button.
4. Verify that the folder is now displayed below the text box:



5. Close the Show Directories dialog box by clicking the X in the upper-right corner or by clicking anywhere outside the box.
6. Click the Refresh button.

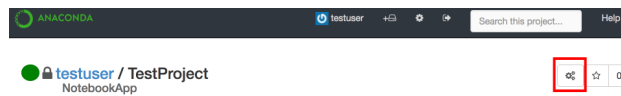
The shared file is displayed in the File Manager:



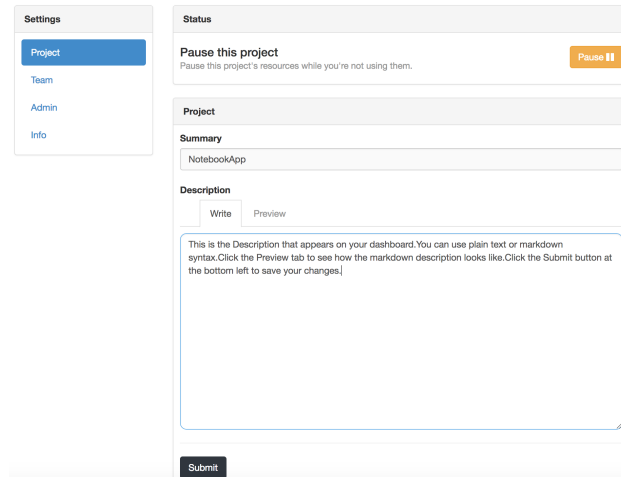
## Starting and stopping a project

TIP: Stopping a project stops all the applications launched for that project that use resources when running, such as memory and compute cycles. It is best to stop projects when they are not in use.

1. On the project home page, click the Project Settings icon to open the Project Settings page.



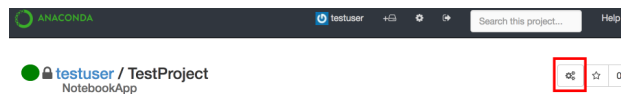
2. In the **Settings** menu, select Project.



3. In the Status section, click the Start or Stop button to toggle between manually starting and stopping your project.

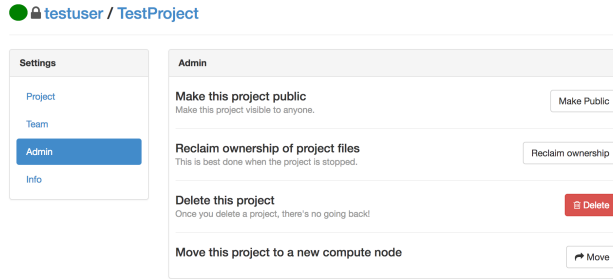
## Making a project public or private

1. On the project home page, click the Project Settings icon to open the Project Settings page.



2. In the **Settings** menu, select Admin.

3. Click the Make Public button.



4. If the project is already public and you want to make it private, click the Make Private button.

## Tagging a project

Existing tags assigned to a project are listed in the Tags section on the project's home page.

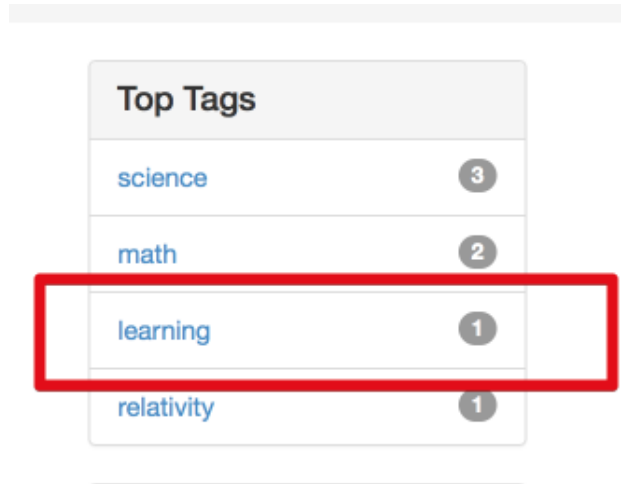
## Adding a tag

1. In the Tags box, type the name of the tag you want to add:

2. Click the Add button.

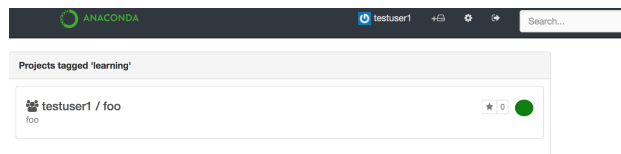
The new tag is added to the Tags list:

If the tag was not already in the Top Tags list on your user home page, it is added. If the tag was already listed because another project used it, the number next to the tag is incremented:



## Removing a tag

1. On your user home page, in the Top Tags list, click the tag name.



1. In the Tags list, click the X button next to tag name.

## Starring a project (rating)

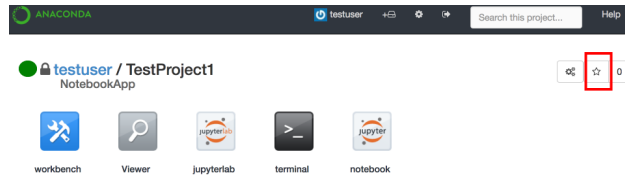
Starring a project makes it appear on your user home page in the Top Rated list.

Adding or removing stars for a project does not affect the stars added by other users.

1. Open the project that you want to star.
2. On the project home page, click the Star icon at the upper right:

3. To unstar a project, click the Star icon again.

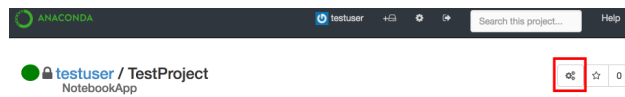




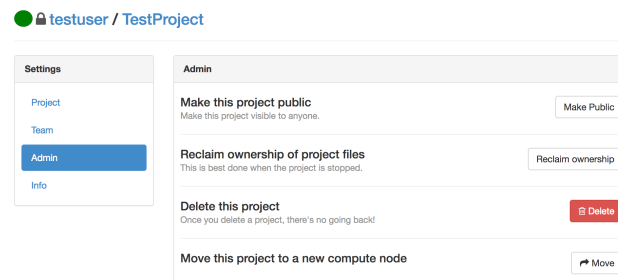
## Claim ownership of a project

When you claim ownership of a project, ownership of all files and folders created by the team members on the project is transferred to you. Project files and folders are copied and renamed.

1. *Stop the project* to prevent team members from making changes while you are changing ownership.
2. On the project home page, click the Project Settings icon to open the Project Settings page.



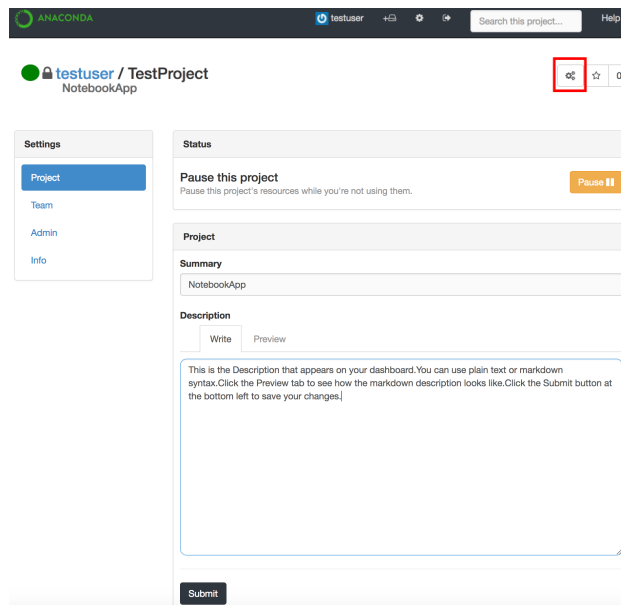
3. In the **Settings** menu, select Admin.



4. Click the Reclaim ownership button.

## Changing a project's summary or description

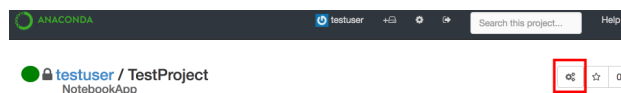
1. On the project home page, click the Project Settings icon to open the Project Settings page.
2. In the **Settings** menu, select Project.



3. Update your project's summary using plain text or its description using Markdown syntax.
4. Click the **Preview** tab to see a preview of the Markdown description.
5. Click the Submit button.

## Viewing a project's status

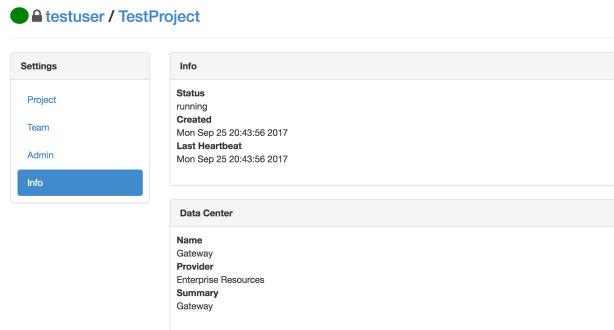
1. On the project home page, click the Project Settings icon to open the Project Settings page.



2. In the **Settings** menu, select Info.

On the Info page, you can see:

- Whether the project is currently running or stopped.
- When the project was created.
- When the project was last accessed.



- The data center in which the project is running.

## Viewing related projects

Related projects are listed on a project's home page.

These are projects that contain fields that are most similar to the current project.

**TIP:** You will only see projects to which you have been granted access: public projects, and private projects on which you are a team member.

## How related projects are identified

To determine which projects should be listed in Related Projects:

1. The recommendation engine scans the current project's files and weights the terms found to determine which of them to use for the likeness search.
2. The engine performs a search, with extra weight given to the "uses" and "imports" keywords.
3. The engine finds the files and projects that are most similar to the current project and scores the results.
4. The top-scoring matches are displayed in Related Projects. Only public projects and private projects to which you have access are included.

## Viewing top-rated projects

Top-rated projects are listed on your home page:

The number next to a project represents the number of stars that have been given to that project.

Click a project name to view the project's home page.

Team

Add

user02 (owner)

user01 (remove)

Related Projects

user01 / TestProject2

No Summary

user02 / User02Private

No Summary

user01 / TestProject

No Summary

Top Rated	
einstein	2
euler	1
laplace	1
plank	1
Public_project	1

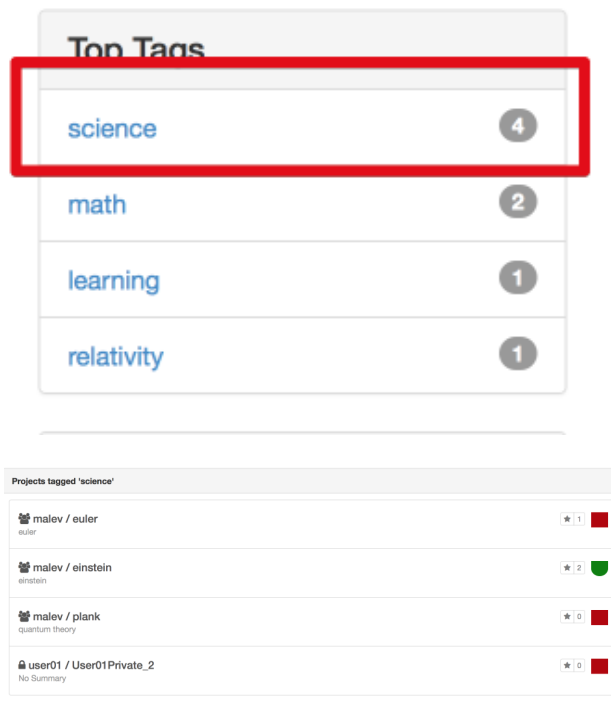
## Using tags to find a project

The top tags used on your projects are listed on your home page:

The screenshot shows the Anaconda user interface for a user named NewUser2. The interface includes a sidebar with 'Projects (1)' and 'Contributing (0)'. The main content area displays a project titled 'NewUser2 / NewProject' with a description 'Woo hoo! I finally get to play with notebooks!'. On the right, there are sections for 'Top Tags' (Fun fun fun, Test project), 'Top Collaborators', and 'Top Rated' (test1, test2, NewProject).

To list all projects that share a specific tag, click the tag name:

A list of projects with the selected tag is displayed:

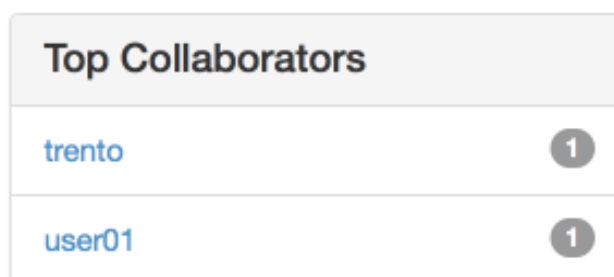


**TIP:** The list includes only projects that you have access to: public projects, and private projects on which you are a team member.

Click a project name to open the project's home page.

### Viewing your top collaborators

Your top collaborators are listed on your home page:



These are the team members who have the most projects in common with you.

To view a collaborator's home page—where you can see all public projects and the private projects they have shared with you—click the collaborator's name.

## Sharing projects and notebooks

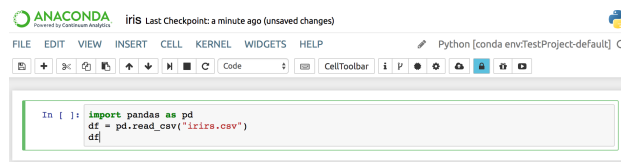
For information on sharing projects via the project settings and access control, see [Sharing projects](#).

To upload a Jupyter Notebook to Anaconda Repository:

1. Log in to Repository by running the `anaconda login` command or by using the login user interface provided by the [nbextension](#).

CAUTION: If you are not using a secure connection, we strongly recommended that you use the command line to log in.

2. To share your notebook environment, select the Attach conda environment checkbox. This ensures that your team members will have the right environment for your notebook.
3. Click the Upload button to upload your notebook to your local Repository or to [Anaconda.org](#), depending on how your administrator has set up AEN:



NOTE: If you have not yet logged into Repository or Anaconda Cloud, or have not created an account, you will be asked to do so.

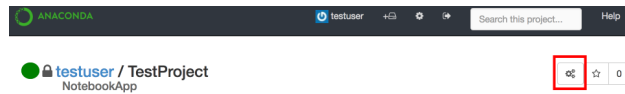
## Other ways to share a notebook

- Print—In the **File** menu, select Print.
- Download and share—In the **File** menu, select one of the following options:
  - Download as Notebook.
  - Download as Python.
  - Download as HTML.
  - Download as Markdown.
  - Download as ReStructured Text.
  - Download as PDF.
- Share and control team members' direct access to read, write and/or execute your notebook file or folder. For more information, see [Controlling access to your project](#).
- Share and control non-team members' file or folder access. For more information, see [Controlling access to your project](#).
- Create a presentation with [NBPresent 4.1](#).

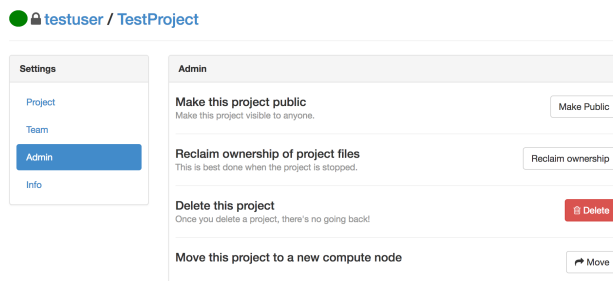
## Deleting a project

CAUTION: Deleting a project deletes all project files and information! There is no undo option.

1. Download a copy of any project files that you need to save.
2. On the project home page, click the Project Settings icon to open the Project Settings page.



3. In the **Settings** menu, select Admin.



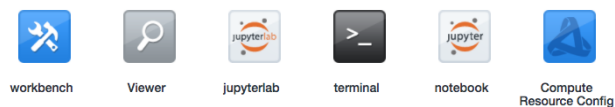
4. Click the Delete button.

## Using AEN applications

The applications in your project make it easy for you to interact with your files and data, manage your project's resources and to customize your AEN experience.

To use applications, log into AEN, then select the project you want to work on or create a new project and open it.

On the project home page, the following application icons are displayed:



TIP: Each application opens in a new browser tab. You can run multiple applications at the same time in your project. For more information on each AEN application, see:



- *Using Workbench*—File viewer and manager, including permissions settings.
- *Using Viewer*—View-only versions of notebooks and other text files.
- *Using JupyterLab*—Alpha preview of the next generation notebook.
- *Using Terminal*—Basic bash shell Terminal.
- *Using Jupyter Notebook*—Jupyter Notebooks with extensions.
- *Using Compute Resource Configuration*—Project information, view and manage applications.

## Using Workbench

- *Opening Workbench*
- *Using File Manager*
- *Opening the Workbench terminal*

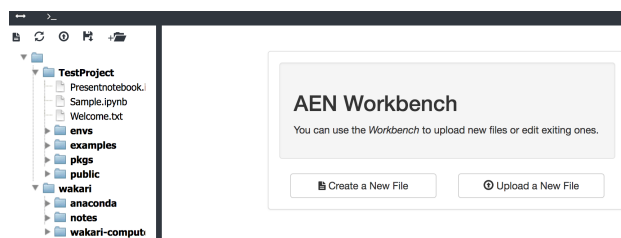
Workbench is a file viewer and manager that includes a file editor and file permissions manager.

You can use Workbench to:

- Upload and download files using the *File Manager*.
- Create new files and folders using the *File Manager*.
- Copy and move files to new locations using the *File Manager*.
- Rename files and/or folders using the *File Manager*.
- Manage the *access permissions* of team members.
- Grant or revoke *access to non-team members*.

Workbench also includes a simple Terminal application, which is convenient because the File Manager is always visible, making navigation simple.

When you first open Workbench, the File Manager is displayed in the left pane, and the Create a New File and Upload a New File buttons are in the right pane:



When you open a file or Workbench Terminal, it is displayed in the right pane. To make the Create or Upload a file options re-appear, refresh your browser window.

Two small icons are displayed in the black navigation bar at the top of the Workbench page. Hovering over them displays tool tips that describe their use:

- The Toggle icon displays or hides the File Manager.
- The Terminal icon opens a simple terminal window.

### Opening Workbench

To open Workbench:

1. Log in to AEN.
2. Select the project you want to work on, or create a new project and open it.
3. On the project home page, click the Workbench icon:



Workbench opens in a new browser window.

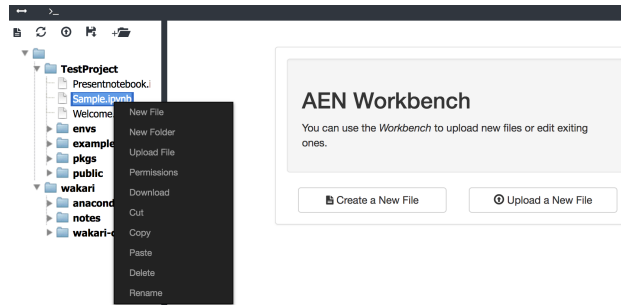
### Using File Manager

The File Manager is an intuitive way to interact with your files and folders.

### Using the options drop-down menu

To perform any of the actions described below:

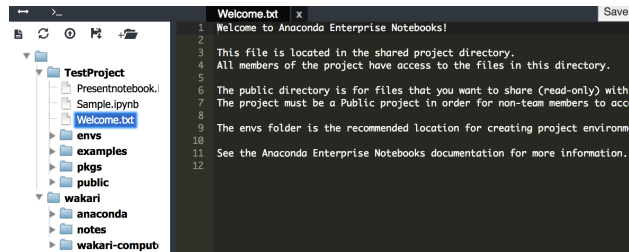
1. Right-click on any folder to display the options drop-down menu.
2. Select one of the following options:
  - New File—Create and edit a new file.
  - New Folder—Create a new folder.
  - Upload File—Upload a file to the selected folder. You can also drag a file to the folder.
  - Permissions—*Control access to files and folders.*
  - Cut—Cut the selected file or folder.
  - Copy—Copy the selected file or folder.
  - Paste—Paste a previously cut or copied file or folder.
  - Delete—Delete the highlighted file or folder.
  - Rename—Rename the highlighted file or folder.



## Editing files using the File Editor

1. Double-click any text file in the File Manager.

The File Editor opens in the right pane:

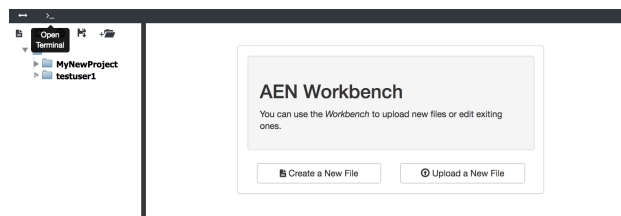


2. When you finish editing the file, click the Save button.

NOTE: To close the file without saving, click the X at the top of the page under the file name.

## Opening the Workbench terminal

In the navigation bar, click the Open terminal icon:



A Terminal—bash shell—is displayed in the right pane.

**TIP:** You can open additional terminals by clicking the Open terminal icon again, or by clicking the Plus + icon at the top of an open terminal.

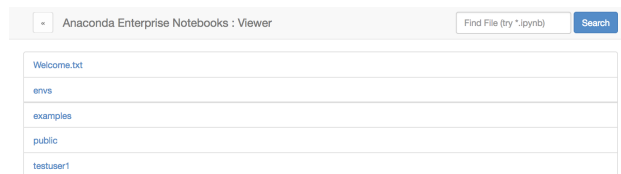
To move between terminal windows, click the **Terminal** tab in the navigation bar, then select the number of the terminal window you want to work in.

### Using Viewer

The Viewer application displays a static, view-only version of your notebooks and other text files by rendering the text files directly and using the NBConvert tool to convert notebooks to static HTML.

1. Log in to AEN.
2. Select the project you want to work on, or create a new project and open it.
3. On the project home page, click the Viewer icon.

Viewer opens in a new browser window:



4. Click any folder to view its contents, or click any filename to view the file.
5. To search for a file or folder name, type text in the Find File box, then press the Enter key. This is not a full-text search, but wildcards are permitted.

### Using JupyterLab

JupyterLab is an early alpha-preview of the next generation of the Jupyter Notebook. It is included so that you can take a tour and play with its capabilities.

**CAUTION:** JupyterLab is experimental. It is not yet intended for production work.

JupyterLab does not include any of the notebook extensions that are available in the *Jupyter Notebook app*.

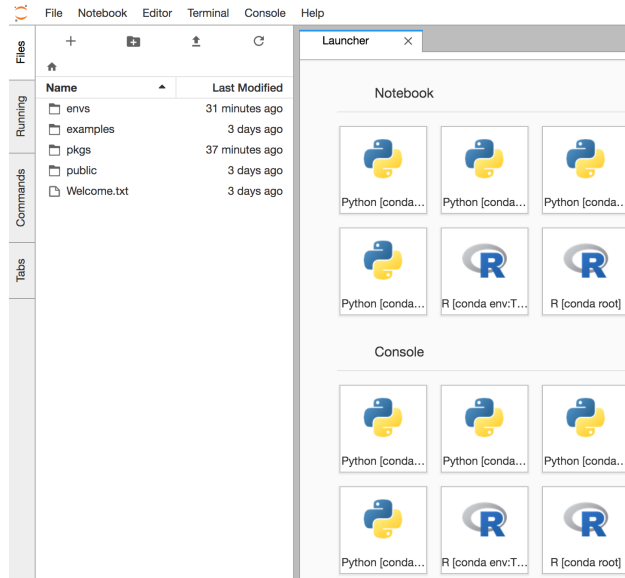
For more information about JupyterLab, see the [documentation](#).

You can also download and print a `Jupyter cheat sheet` on using Jupyter Notebook and the new JupyterLab.

To open JupyterLab:

1. Log in to AEN.
2. Select the project you want to work on, or create a new project and open it.
3. On the project home page, click on the JupyterLab icon.

JupyterLab opens in a new browser window:



Experiment with the application on your own, using the **Notebook**, **Editor**, **Terminal** and **Console** menus.

To review a guided tour of all of the features JupyterLab will contain when it is ready for production, click the Take a tour link in the right pane.

## Using Terminal

The Terminal application is a simple bash shell terminal that runs in your browser:

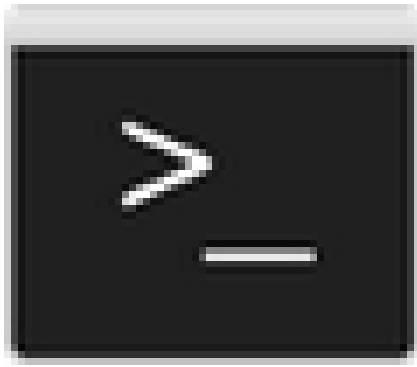
```

+ 1 bash
(/projects/aen_admin/TestProject/envs/default) ls
envs examples pkgs Presentnotebook.ipynb public Sample.ipynb Welcome
(/projects/aen_admin/TestProject/envs/default)

```

Using Terminal, you can:

- Access your home directory and your project drive.
  - Open multiple shells within one instance of Terminal.
  - Open multiple instances of Terminal in the same browser window.
1. Log in to AEN.
  2. Select a project you want to work on, or create a new project and open it.
  3. On the project home page, click the Terminal icon:



## Terminal

Terminal opens the project directory in a new browser window.

By default, the project directory is `/projects/username/project-name`.

EXAMPLE: `/projects/TestUser/MyFirstNotebook`

4. To see the physical path of your directory, run the Print Working Directory command `pwd -P`.

TIP: The physical path `-P` is important because project attaches data to the beginning of your virtual path to keep your project files together.

5. To navigate out of your project directory to your home directory, run the command `cd`.
6. To return to your project directory, run the command `cd/projects/username/project-name`.

TIP: If you are new to navigating in a terminal, you may want to use *the Workbench terminal*, which includes a visual navigation tree in the File Manager.

### Using multiple Terminals

You can open as many terminals as you want.

To open another shell in the terminal, in the upper left of the pane, click the plus `+` icon.



A corresponding number appears after the plus + icon and 1.

To move to another Terminal, click the corresponding number.

The color of the number tab changes to show which terminal is currently selected.

## Using Jupyter Notebook

- *Opening the Jupyter Notebook application*
- *Using example notebooks*
- *Creating a new Jupyter Notebook*

The Jupyter Notebook application allows you to create and edit documents that display the input and output of a Python or R language script. Once saved, you can share these files with others.

NOTE: Python and R language are included by default, but with customization, Notebook can run several other kernel environments.

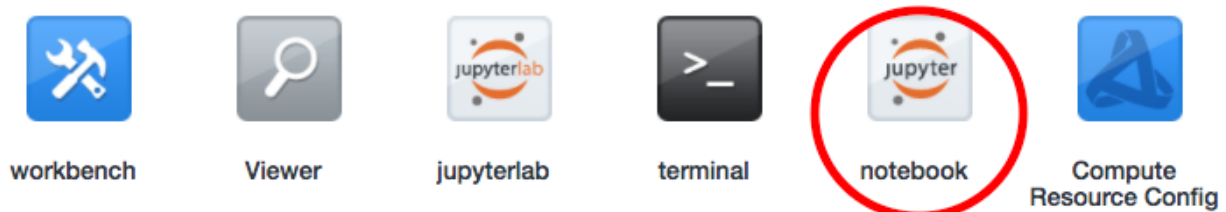
This page provides a brief introduction to Jupyter Notebooks for AEN users.

For the official Jupyter Notebook user instructions, see [Jupyter documentation](#).

For information on the notebook extensions available in AEN, see [Using Jupyter Notebook extensions](#).

## Opening the Jupyter Notebook application

1. Log in to AEN.
2. Select the project you want to work on, or create a new project and open it.
3. On the project home page, click the Jupyter Notebook icon:



Jupyter Notebook opens in a new browser window:

TIP: You can see the same *File Manager* in the Terminal, Workbench, and Viewer applications.



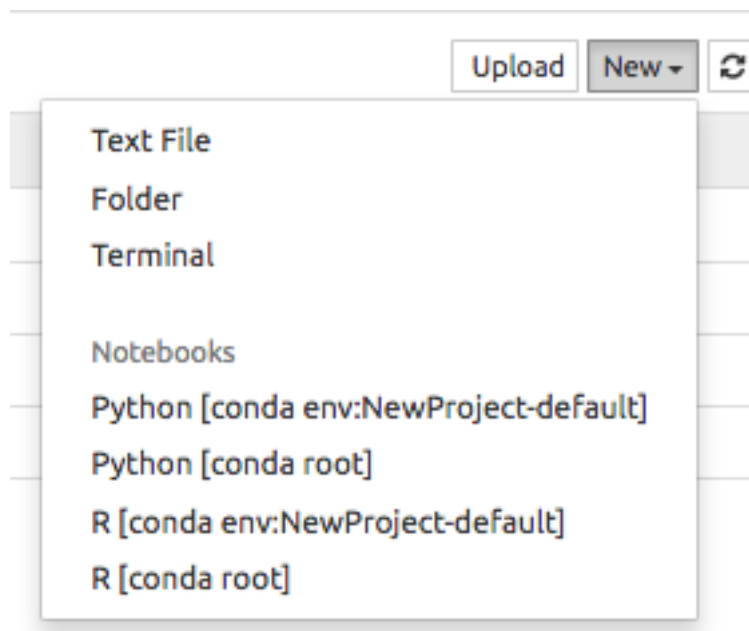
## Using example notebooks

The `Examples` folder in Jupyter Notebook contains several types of Notebook examples created in Python—and one with R language—kernel environments.

Open any example notebook to experiment and see how it works.

## Creating a new Jupyter Notebook

1. At the top right of the **Files** tab, click the New button.





2. Select the kernel environment to create your new notebook in.

NOTE: Customizable Python and R Language kernel environments are automatically created for you during project creation.

- Your project's default conda env kernels are a cloned copy of the root environment. You can customize them and install and delete additional packages.
- Root environment is managed by your Administrator. You cannot make or save any changes to it.
- You can switch between Python, R language and any other custom kernels in the notebook as you work in your notebook. For more information, see [Using the Synchronize Environments extension](#).

The new notebook is saved in the related project directory and displayed.

## Using Jupyter Notebook extensions

The following extensions are available for use with AEN's Jupyter Notebook application:

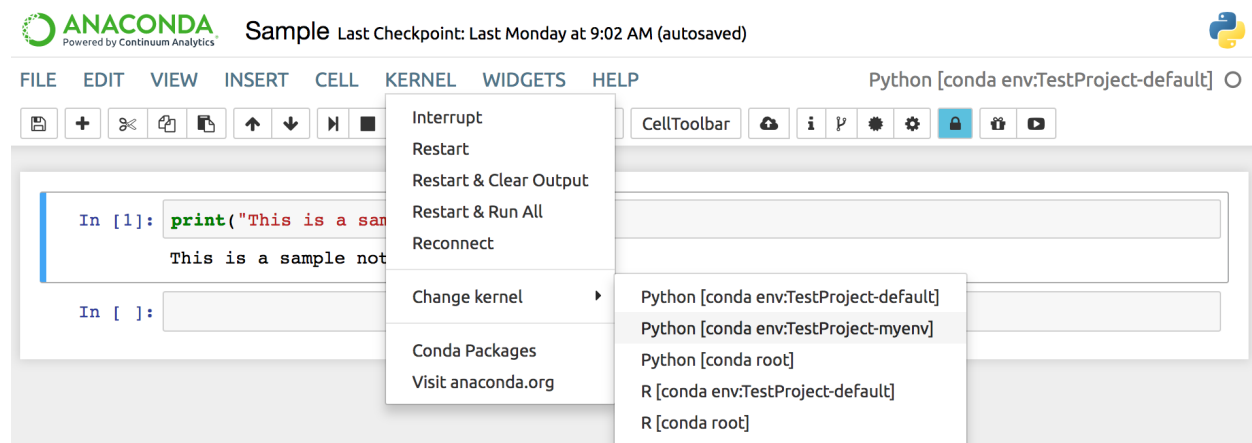
- [Synchronize Environments](#) with Jupyter from the **Kernel** menu.
- [Locking](#) adds multi-user capability from the Lock button.
- [Revision Control Mechanism \(RCM\)](#) adds Status, Checkout and Commit buttons.
- [Conda environment and package management](#) tab.
- [Conda notebook](#) adds conda management inside Notebook from the Kernel > Conda Packages menu option.
- [Anaconda Cloud integration](#) from the Publish to cloud button.
- [Notebook Present](#) turns your notebook into a PowerPoint-style presentation.

## Using the Synchronize Environments extension

The Synchronize Environments extension allows you to apply a Python, R language or any other custom environment inside your current notebook session, without needing to start up several Notebook instances using each of the selected environments.

To change environments:

1. Open the **Kernel** menu.



2. Click the Change kernel option.
3. From the list, select the environment to use.

NOTE: In AEN 4.1+ the default kernel for projects is `default`. In versions prior to 4.0, the default kernel for projects is `root Python`.

## Using the Locking extension

Multi-user capabilities are engaged in AEN when multiple users work in the same notebook file.

The Locking extension allows you to lock a notebook to prevent multiple team members from making changes at the same time. Notebooks are automatically locked when you open them.

If team members open a notebook and make changes while it is locked, their save capability is disabled, and they cannot overwrite the notebook.

To override the lock, they must actively take control of the locked file by clicking the Lock icon in the Notebook menu bar:



NOTE: This is a soft locking model. Team members can choose to override your lock to save their work. If you give team members write access to your files, confirm that they understand that they should never unlock your file unless they are making meaningful, non-destructive team contributions.

## Using the Revision Control Mechanism extension

The Revision Control Mechanism (RCM) Jupyter Notebook extension provides simple version control for notebook files. It uses the internal Jupyter functionality to perform tasks.

On the surface, RCM uses a simple linear model, but beneath that is a more complex git-based branching model. To prevent merge conflicts, this model uses a “latest wins” policy as its main merging strategy.

The RCM Jupyter Notebook extension adds four buttons:



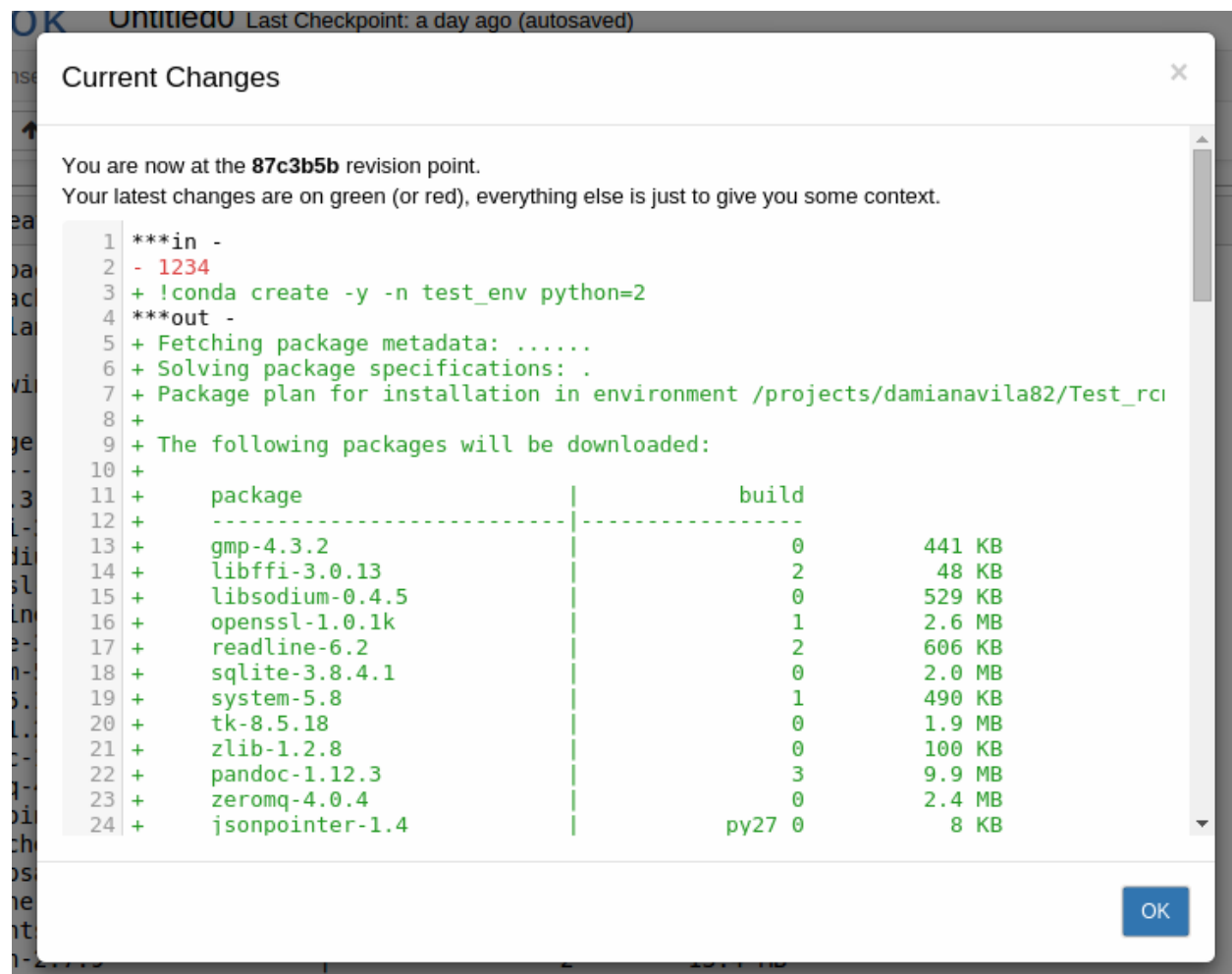
- *Status.*
- *Checkout.*
- *Commit.*
- *Configure git.*

TIP: If you do not see the RCM buttons, see *Setting up RCM for the first time.*

## Using the Status button

The Status button allows you to see what revision you are on.

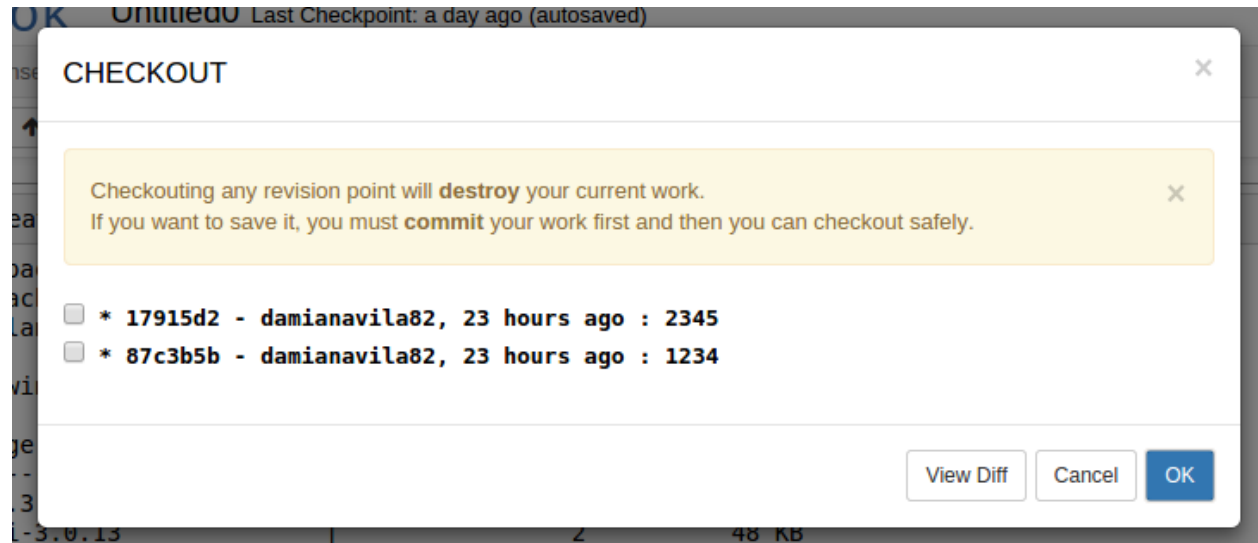
Clicking the Status button displays:



## Using the Checkout button

The Checkout button allows you to view a list of the previous revision points, check out a previous revision or compare differences between revisions.

Clicking the Checkout button displays:



## Checking out a previous revision

To checkout a notebook at an earlier revision point:

1. Select the checkbox next to the desired revision point.
2. Click the OK button.

A copy of the notebook at the selected revision point is displayed.

NOTE: If you have not saved the work in your current project window, checking out a previous revision destroys it. If in doubt, click the Cancel button and save your work before reverting to a previous revision point.

## Comparing revisions

To compare 2 previous revision points:

1. Select the checkboxes of the revision points to compare.
2. Click the View Diff button.

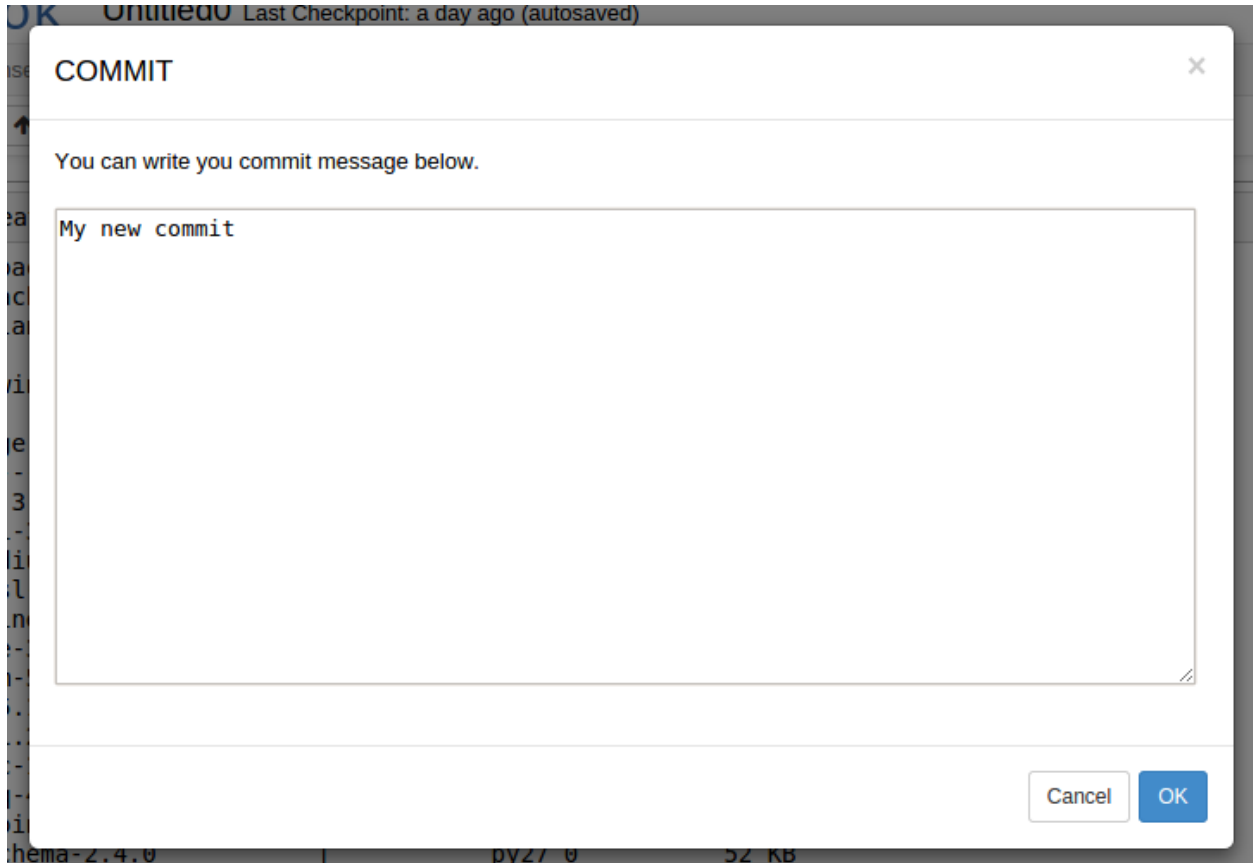
A side-by-side comparison is displayed.

Click the Cancel button to close the differences window.

## Using the Commit button

The Commit button allows you to save or persist the current changes, keeping a permanent record of any changes that are introduced, so that you do not have to worry about losing important data.

Clicking the Commit button displays:



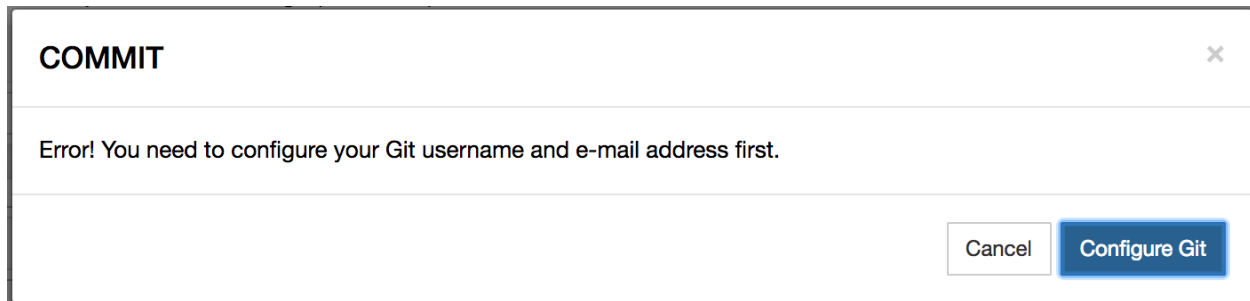
1. Enter a description of the changes in the commit as a reminder in case you need to revert back to it later.
2. Click the OK button.

Your changes are committed and a revision point is created.

If Git user name and user email are not set, the following window appears:

Configure Git and then try to commit again.

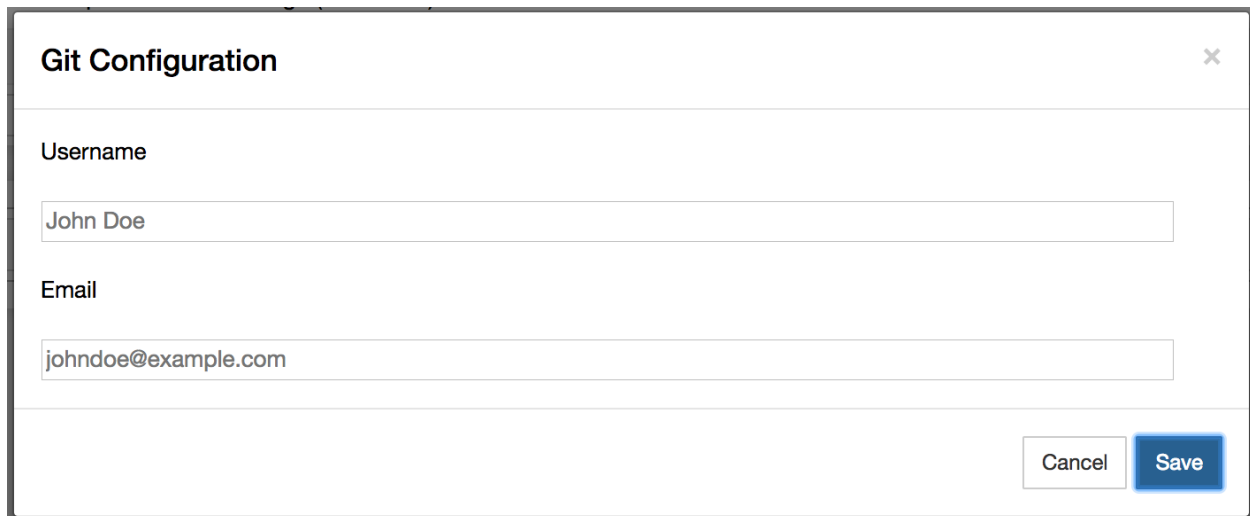
TIP: You can roll back committed changes by *checking out a previous version*.



### Using the Configure git button

The Configure git button allows you to configure Git user name and email values.

After clicking the Configure Git button, the following window appears:



Enter user name and e-mail address. Click the OK button when finished.

### Setting up RCM for the first time

If you do not see the RCM buttons in your notebook:

1. Go to the project home page.
2. Open the Terminal application.
3. In the terminal window, run:

```
git config --global user.email "you@example.com"  
git config --global user.name "Your Name"
```

NOTE: Change `you@example.com` to your email address, and `Your Name` to your actual name.

4. Open Jupyter Notebook and refresh the page.

## Using the NBConda extension

The NBConda extension adds a Conda tab to your notebook for easy environment and package management from within the notebook.



Files

Running

IPython Clusters

Conda

2 Conda environments

Action	Name	Default?	Directory
	root		/opt/wakari/anaconda
	default	✓	/projects/aen_admin/TestProject/envs/default

1143 available packages

Search...

→

376 installed packages in environment "default"

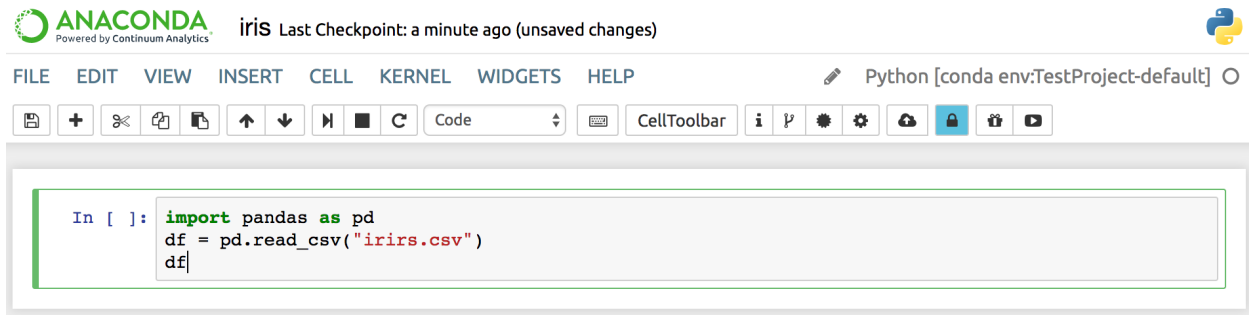
Name	Version	Channel
<input type="checkbox"/> _license	1.1	defaults
<input type="checkbox"/> _nb_ext_conf	0.4.0	defaults
<input type="checkbox"/> abstract-rendering	0.5.1	defaults
<input type="checkbox"/> accelerate	2.3.1	defaults
<input type="checkbox"/> accelerate_cudalib	2.0	defaults
<input type="checkbox"/> aen-app-jupyterlab	0.4.0	wakari

Name	Version	Build	Available
<input type="checkbox"/> _license	1.1	py27_1	
<input type="checkbox"/> alabaster	0.7.10	py27_0	
<input type="checkbox"/> anaconda	custom	py27_0	
<input type="checkbox"/> anaconda-client	1.5.1	py27_0	
<input type="checkbox"/> anaconda-project	0.6.0	py27_0	
<input type="checkbox"/> asn1crypto	0.22.0	py27_0	

Click the Conda tab in a notebook to display:

- Conda environments list—export, clone or delete an environment in the action column, or create a new environment by clicking the plus + icon. Switch to an environment by clicking it; packages for that environment are displayed below in the installed packages list.
- Conda available packages list—for the selected environment in currently configured channels, search for packages and click a package name to install it.
- Installed packages list—in the selected environment, check for updates, update or delete selected packages.

**TIP:** While you are in any notebook, you can jump to the NBConda extension for that environment by clicking the **Kernel** menu and selecting Conda Packages:



## Using the Conda Notebook extension

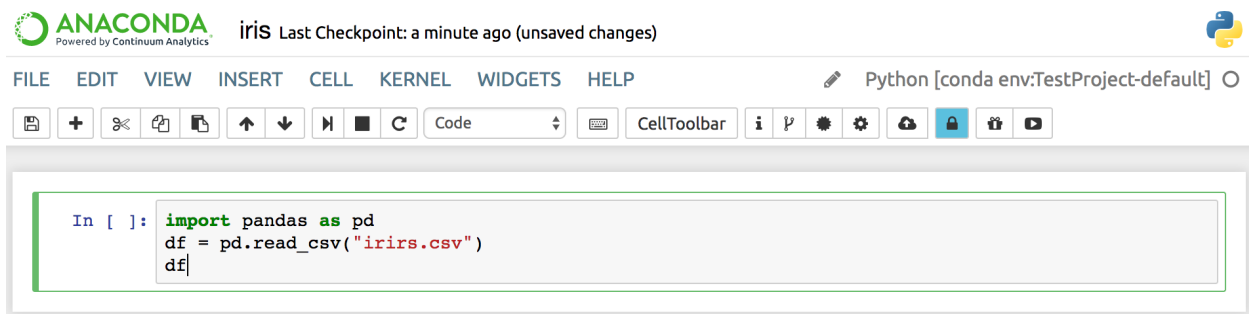
The Conda Notebook extension adds the Conda Packages option to the **Kernel** menu.

Select the Conda Packages option to display a list of all of the Conda packages that are currently used in the environment associated with the running kernel, as well as any available packages.

From the Conda Packages option, you can perform all of the tasks available in the *Conda tab*, but they will only apply to the current environment.

## Using the Anaconda Cloud extension

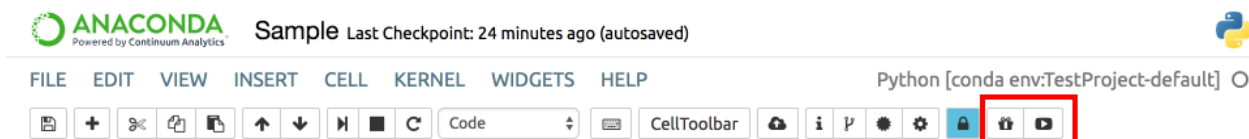
The Anaconda Cloud extension adds the Cloud button to your notebook, allowing you to easily upload your notebook to Cloud:



## Using the Notebook Present extension

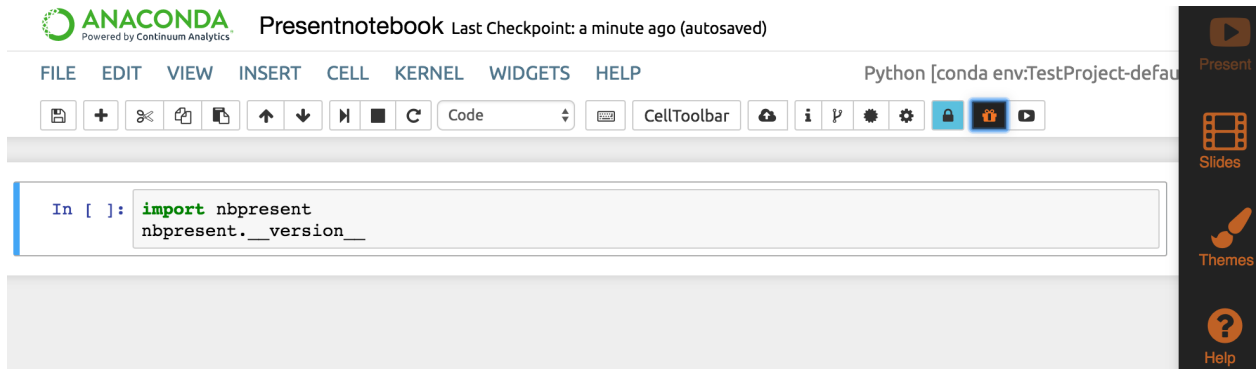
The AEN Notebook Present extension turns your notebook into a Microsoft PowerPoint-style presentation.

The Present extension adds 2 buttons to Notebook's menu bar—Edit Presentation and Show Presentation:





To begin using Notebook Present, click the Edit Presentation button.

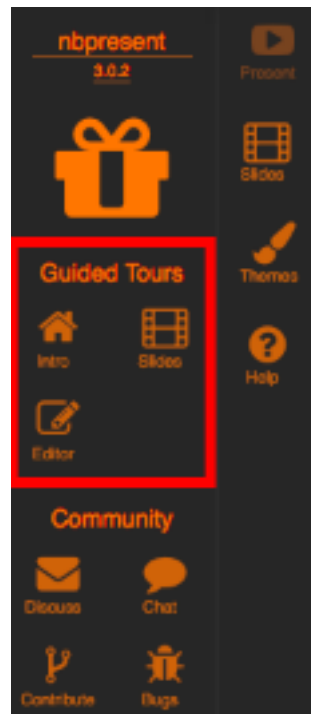


The Notebook Present sidebar is displayed on the right side of your browser:

Clicking each icon changes the menu and layout of your notebook.

Clicking the Help icon displays 3 tours—demonstrations—of the main features of Present:

- *Intro tour.*
- *Slides tour.*
- *Editor tour.*



Select one of the tours to view a short presentation regarding the specifics of that feature.

### Intro tour

The Intro tour is a 2-minute presentation that explains how to use the main features of Present, including a description of each button's purpose.

NOTE: At any time, you can pause, go back to the previous or move forward to the next slide.

The following information is covered in the Intro tour:

- **App Bar**—When Authoring, this allows you control the content and style of your presentation. It also can be used to activate several keyboard shortcuts for editing:
- **Stop Authoring**—Clicking the Edit Presentation button again stops Authoring, and removes all keyboard shortcuts.
- **Show Presentation**—If you just want to run your presentation without using any Authoring tools, just click the Show Presentation button.
- **Presenting/Authoring**—Once you've made some slides, start Presenting, where you can use most Notebook functions with the Theme we have defined, as well as customize slides on the fly.
- **Slides button**—Slides, made of Regions linked to Cell Parts are the bread and butter of any presentation, and can be imported, created, linked, reordered, and edited here.
- **Theming**—Theming lets you select from existing colors, typography, and backgrounds to make distinctive presentations. The first theme you select will become the default, while you can choose custom themes for a particular slide, like a title.
- **Saving**—Whenever you save your Notebook, all your presentation data will be stored right in the Notebook .ipynb file.
- **Downloading**—After you've made a presentation, you can download it as an HTML page by choosing Download → Download As: Presentation (.html) in the menu.
- **Help**—Activate Help at any time to try other tours, connect with the Present developers and community, and other information.

## Keyboard shortcuts



The Jupyter Notebook has two different keyboard input modes. **Edit mode** allows you to type code/text into a cell and is indicated by a green cell border. **Command mode** binds the keyboard to notebook level actions and is indicated by a grey cell border with a blue left margin.

Mac OS X modifier keys:

: Command

: Control

: Option

: Shift

: Return

: Space

: Tab

### Command Mode (press to enable)

: find and replace

: previous slide

: next slide

: next slide

: enter edit mode

: open the command palette

: run cell, select below

: run selected cells

: run cell, insert below

: to code

: to markdown

: extend selected cells above

: extend selected cells above

: extend selected cells below

: extend selected cells below

: insert cell above

: insert cell below

: cut selected cells

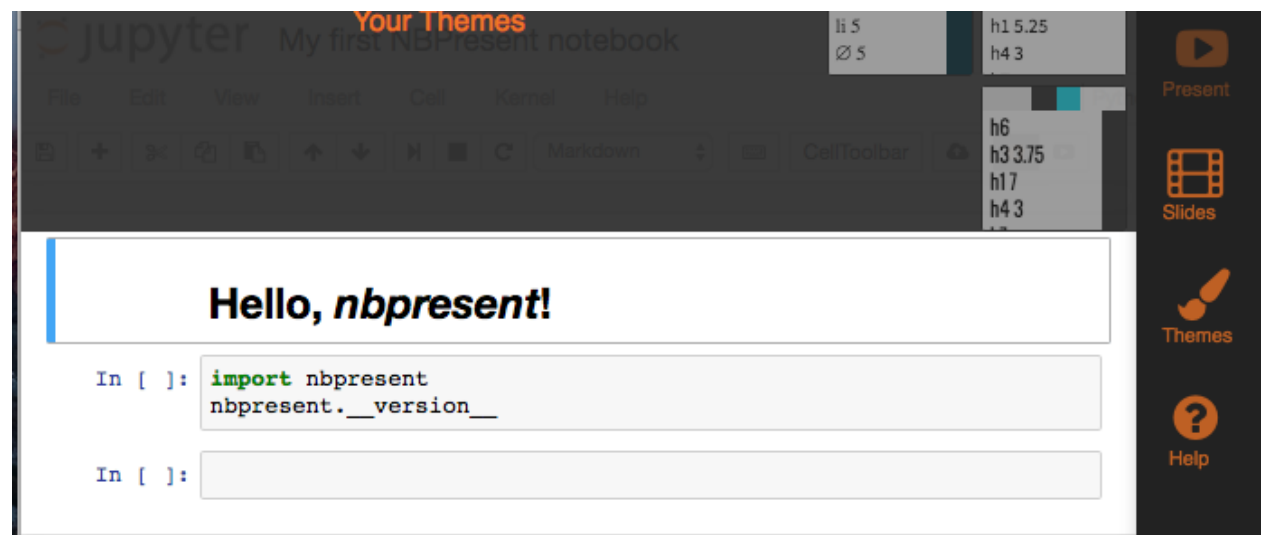
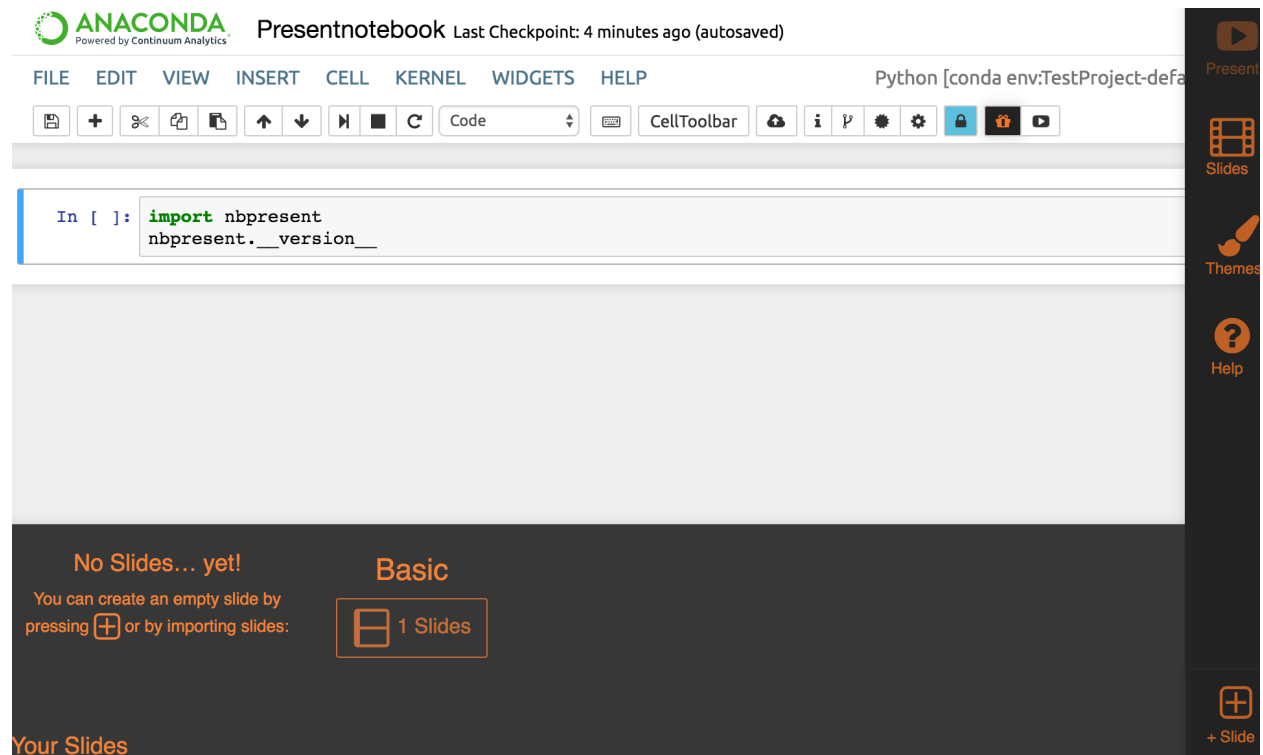
: copy selected cells

: paste cells above

: paste cells below

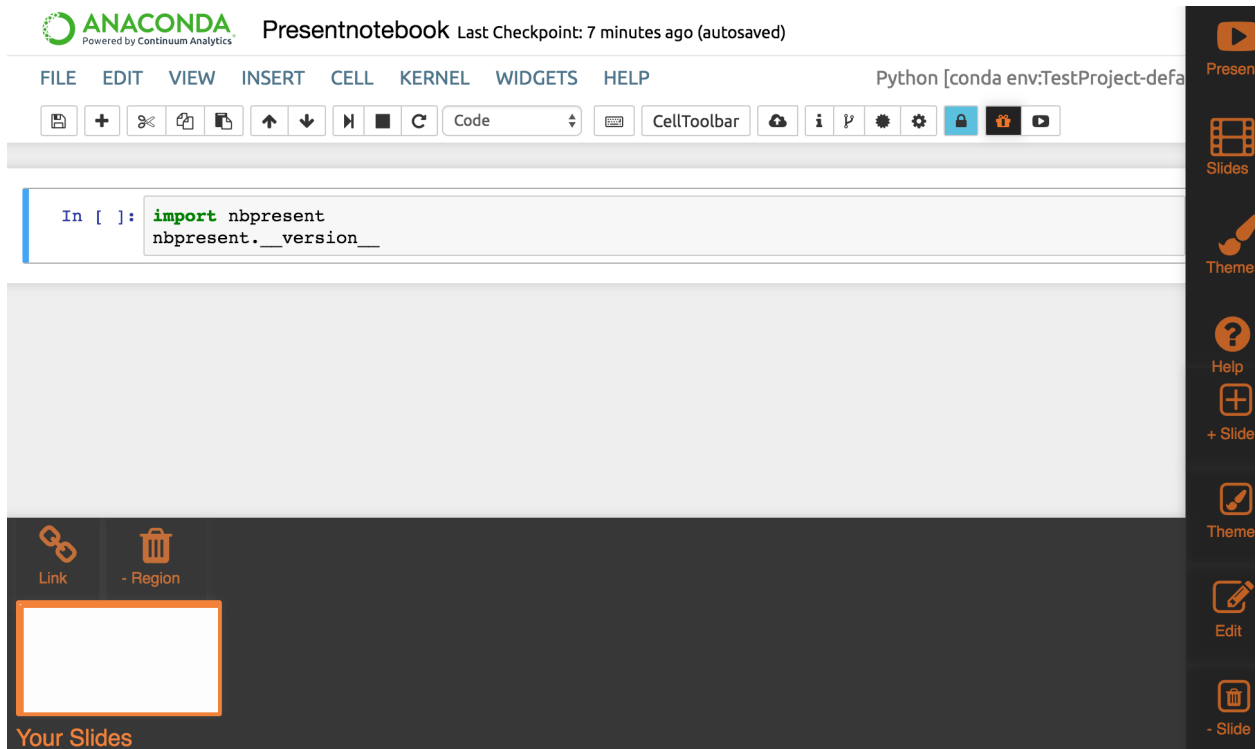
: undo cell deletion

Close



## Slides tour

Slides make up a presentation. Clicking Slides toggles the sorter view and the Slide Toolbar on and off:



The Slides tour explains how to create and manage slides, including the following information:

- Slide Toolbar—Create a new slide. Clicking + Slide will offer some choices for creating your new slide.
- Import—The quickest way to create a presentation is to import each cell as a slide. If you’ve already created slides with the official slideshow cell toolbar or RISE, you can import most of that content.
- Template Library—You can create a presentation from an existing template.
  - Reuse Slide as Template—You can create a presentation based on an existing slide.
  - Simple Template—A common template is the Quad Chart, with four pieces of content arranged in a grid.
- Region—The Quad Chart has four Regions. To select a region, click it.
  - Link a Region to a Cell Part—Each Region can be linked to a single Cell Part using the Link Overlay, which shows all of the parts available.
    - \* Cell Part: Source (blue)—Source, such as code and Markdown text.
    - \* Cell Part: Outputs (red)—Outputs, such as rich figures and script results.
    - \* Cell Part: Widgets (purple)—Jupyter widgets, interactive widgets that provide both visualization and user input.

- **Cell Part: Whole (orange)**—Finally, a Whole Cell, including its Source, Widgets and Outputs can be linked to a single region.
- **Unlink a region from a Cell Part**—Unlinking removes the connection between a region and a cell part, without deleting either one.
- **Region: Trashing**—Trashing a Region permanently deletes it, without affecting any linked Cell Part.
- **Part Thumbnail**—We'll try to draw a part thumbnail. It can only be reliably updated when a linked Cell Part is on-screen when you mouse over it, but you should usually be able to get an idea of what you're seeing. The colors of the regions correspond to the cell types.
- **Presenting**—Clicking the Present button while editing brings up the Presenter with editing mode still enabled:
  - Linked inputs and widgets are still interactive.
  - **Go forward**—Click to go to the next slide
  - **Go back**—Click to go back to the previous slide
  - **Go back to the beginning**—Click to go back to the first slide
  - **My work is done here**—Click to go back to the Notebook.

## Editor tour

Once you've made a few slides, you'll likely want to customize them. The Editor tour explains how to edit your notebook, including the following information:

- **Editing Slides**—Activate the Slide Editor by double-clicking it, or by clicking Edit Slide.
- **Region Editor**—Click to drag Regions around and resize them.
- **Region Tree**—Reorder Regions and see the details of how Regions will show their linked Parts.
- **Add Region**—Add new regions.
- **Attribute Editor**—Edit the properties of a region.
- **Data Layouts**—In addition to manually moving regions, you can apply these layouts to automatically fill your slides.
- **More Regions**—Add more regions—with a weight of 1.
- **Tree Weight**—Make a Region bigger or smaller, based on its relative weight.
- **12 Grid**—A compromise between the Free and Treemap layouts, the 12 Grid option rounds all of the values in a layout to a factor of 12.

## Using Compute Resource Configuration

The Compute Resource Configuration (CRC) application displays information about the current project and allows you to set a custom project environment and view and manage your other AEN applications, including stopping, starting, restarting and viewing the logs of each.

The CRC application screen contains 3 sections:

- *Info.*
- *Conda environment.*
- *Running apps.*

The screenshot shows the Anaconda AEN interface with three main sections:

- Info:** Displays system information including Hostname (davila-aen-test), Project Home (/projects/testuser1/demo), and Project RC file (/projects/testuser1/demo/.projectrc).
- Conda Environment:** Shows the current default environment path (/projects/testuser1/demo/envs/default). A yellow warning box states: "Setting the default environment for this project will affect all users by modifying the .projectrc file. All running apps will be shutdown. Make sure **No one working on this project** has any unsaved documents!". A green "Set Project Environment" button is at the bottom.
- Running Apps:** A table listing active applications.

User	Application	Status	Last Seen	Terminate	Relaunch	Logs
testuser1	terminal	running	1 hours ago	<a href="#">Terminate</a>	<a href="#">Relaunch</a>	<a href="#">Logs</a>

## Info

The Info section displays:

- Hostname—IP address of the host computer.
- Project Home—File path to the project home.
- Project RC file—File path to the project runtime configuration file `.projectrc`. This file is sourced when a user opens any AEN application. It sets several AEN internal environment variables, sets up the project environment and sets additional user environment variables for the project.

## Conda environment

This section displays the path to the default conda environment.

**CAUTION:** Changing the default environment will affect all users. Be sure that no team members have any unsaved documents before changing the project environment.

To change the default conda environment location:

1. Edit the path to point to your preferred conda environment.
2. Click the Set Project Environment button.

Your `.projectrc` file is modified.

## Running apps

The Running Apps section displays a list of users and the applications that are in use, as well as when the app was last modified.

To terminate any individual application, click the Terminate button.

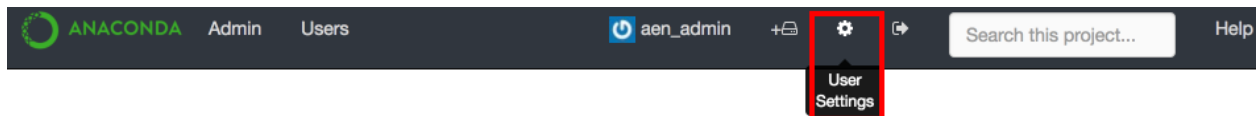
To stop and re-launch any individual application, click the Relaunch button.

To review the run logs of any active application, which may be useful for troubleshooting, click the Logs button.

### Managing your account

- *Updating your public profile*
- *Changing your password*
- *Deleting your AEN account*
- *Viewing account operations*
- *Registering an application*

To access your account information, click the User Settings icon in the AEN navigation bar:



### Updating your public profile

Your public profile is made up of a name, a personal URL, your company and location.

1. In the left navigation pane, click the **Public Profile** tab.
2. To update your profile picture, create a [Gravatar](#) that is associated with the email address you used to create your AEN account. The gravatar will automatically appear.

### Changing your password

1. In the left navigation pane, click the **Account Settings** tab.

### Deleting your AEN account

1. In the left navigation pane, click the **Account Settings** tab.

### Viewing account operations

1. In the left navigation pane, click the **Security Log** tab to view a list of operations performed on your account.



# Settings

Change your account and profile settings.

Public Profile

Account Settings

Security Log

Applications

Security Log

	aen_admin	oauth.authenticate	2017-09-25 04:52:06.713000+00:00
	aen_admin	oauth.authenticate	2017-09-25 04:51:58.954000+00:00
	aen_admin	oauth.authenticate	2017-09-25 04:51:58.720000+00:00
	aen_admin	oauth.authenticate	2017-09-25 04:51:58.490000+00:00
	aen_admin	oauth.authenticate	2017-09-25 04:51:58.259000+00:00
	aen_admin	oauth.authenticate	2017-09-25 04:51:58.033000+00:00
	aen_admin	oauth.authenticate	2017-09-25 04:51:57.802000+00:00

- 2. For more information about an operation, click the Eye icon to the left of the the operation name.

## Registering an application

If you want to create an application for AEN or have already done so, you must register your application.

- 1. In the left navigation pane, click the **Applications** tab.

# Settings

Change your account and profile settings.

Public Profile

Account Settings

Security Log

Applications

Developer Applications

Register New Application

These are applications you have registered to use the Anaconda Enterprise Notebooks API.

Gateway ()

Authorized applications

Gateway ()

revoke

- 2. Click the Register New Application button to open a form for registering your application.

## Advanced tasks

Advanced tasks are best-suited for users who are comfortable working in a Terminal.

## Working with environments

AEN runs on conda, a package management system and environment management system for installing multiple versions of software packages and their dependencies and switching easily between them.

A conda environment usually includes 1 version of Python or R language and some packages.

The ability to have a custom project environment is one of the most powerful features of AEN. Your project environment is integrated so that all of your project applications recognize it and all of your team members have access to it.

This section contains information about:

- *Creating a default conda environment using the Jupyter Notebook application*
- *Creating a default conda environment using the Jupyter Notebook application*
- *Using your conda environment in a notebook*
- *Customizing your conda environment*
- *Installing a conda package using Terminal*
- *Installing a conda package using Notebook*
- *Uninstalling a conda package*

NOTE: This conda environments guide is specific to AEN. For full conda documentation—including cheat sheets, a conda test drive, and command reference—see the [conda documentation](#).

## Creating a default conda environment using the Jupyter Notebook application

You can create, activate, and install packages and deactivate environments from within the Notebook menu bar.

To install from the Notebook menu bar:

1. Click the **Conda** tab and select the plus sign icon.
2. Search for `numpy` in the package search box.
3. Select `numpy` from the search results.

**3 Conda environments**

Action	Name	Default?	Directory
	root		/opt/wakari/anaconda
	default	✓	/projects/aen_admin/TestProject/envs/default
	myenv		/projects/aen_admin/TestProject/envs/myenv

**2 available packages** (search:

Name	Version	Channel
<input checked="" type="checkbox"/> numpy	1.13.1	defaults
<input type="checkbox"/> numpydoc	0.7.0	defaults

**39 installed packages in environment "myenv"**

Name	Version	Build	Available
<input type="checkbox"/> anaconda-client	1.6.3	py36_0	
<input type="checkbox"/> certifi	2016.2.28	py36_0	
<input type="checkbox"/> client	1.2.2	py36_0	
<input type="checkbox"/> decorator	4.1.2	py36_0	
<input type="checkbox"/> ipykernel	4.6.1	py36_0	
<input type="checkbox"/> ipython	6.1.0	py36_0	

1. Click the Install button.

The environment is added to the project's `env` directory.

## Creating a default conda environment using Terminal

In AEN, all new environments created with conda automatically include Python, Jupyter Notebooks and pip. You can specify any other packages you want included in your new environment.

**TIP:** By default, conda creates a new environment in your project's `env` directory—so that all team members have access to the environment. For information about limiting your team member's read, write or execute permissions, see [Workbench](#).

To create a new environment within your AEN account, run the command `conda` in a [Terminal](#) application.

**EXAMPLE:** To create a new environment named `WeatherModel` that contains Python, NumPy, pip and Jupyter Notebooks in your project's `env` directory:

1. Log in to AEN.
2. Open a project.
3. On the project home page, click the Terminal application icon to open a Terminal.
4. Create the environment:

```
conda create -n WeatherModel numpy
```

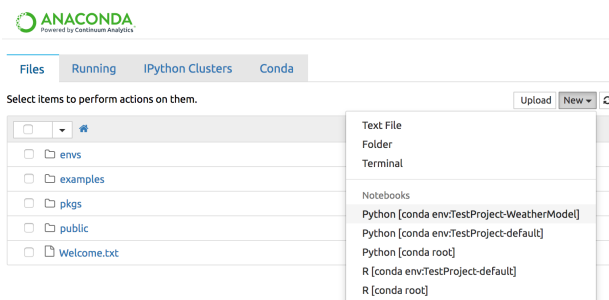
**TIP:** Python, pip and Jupyter Notebooks are automatically installed in each new environment. You only need to specify NumPy in this command.

5. Make the new environment your default:

```
source activate WeatherModel
```

6. To use your new environment with Jupyter Notebooks, open the Notebook application.
7. Click the New button to open a new notebook. In the drop-down menu under Notebooks, the environment you just created is displayed.
8. To activate that environment, select it.

The environment is added to the project's `env` directory.



NOTE: You can deactivate the new environment when you are finished with your notebook by opening the Terminal application and running the command `source deactivate`.

### Using your conda environment in a notebook

Whether you have created an environment using conda in a terminal, or from the **Conda** tab in a notebook, you can use the conda environment in the same way.

When working in a notebook, to select the environment you have created and want to use with that notebook, in the **Kernel** menu, select Change Kernel.

EXAMPLE: If you have an environment named `my_env` in a project named `test1` that includes NumPy and SciPy and you want to use that environment in your notebook, in the **Kernel** menu, select Python [conda env:test1-my\_env].

The notebook code will run in that environment and can import NumPy and SciPy functions.

### Customizing your conda environment

If you need a Python package that AEN doesn't include by default, you can install additional packages into your AEN environment.

TIP: You cannot install packages into the default Anaconda environment. You must create your own environment before installing a new package into that environment.

AEN is built on Anaconda, so you can install additional Python packages using conda or pip—both of which are included with Anaconda.

### Installing a conda package using Terminal

To install a conda package using the Terminal application:

1. Create and activate the environment using the steps in *Creating a default conda environment using the Jupyter Notebook application*.
2. In your Terminal application, run the command `conda install <packagename>`.

NOTE: Be sure to specify the Python version you want when using conda to create the environment, or it will use the same version as root.

EXAMPLE:

```
conda create -n mpy3 python=3 numpy scipy
```

A conda environment named `mpy3`, running on Python 3 and containing NumPy and SciPy is created. All subsequent packages added to this environment will be the Python 3 compatible versions.

### Installing a conda package using Notebook

You can also install the package within your notebook without using the terminal app:

1. From the Notebook application, click the **Conda** tab.
2. Select the environment you wish to use.

3. Search for the package you want to add.
4. Click the Install button.

## Uninstalling a conda package

To uninstall a package using this method, run the command `conda remove <packagename>`.

NOTE: Replace `<packagename>` with the name of the package you are uninstalling.

## Using visualization packages

AEN supports multiple visualization packages for Python and R language.

For Python, the default environment has *Matplotlib* and *Bokeh* installed.

For R language, the default environment has *r-ggplot2* and *r-bokeh* installed.

## Matplotlib

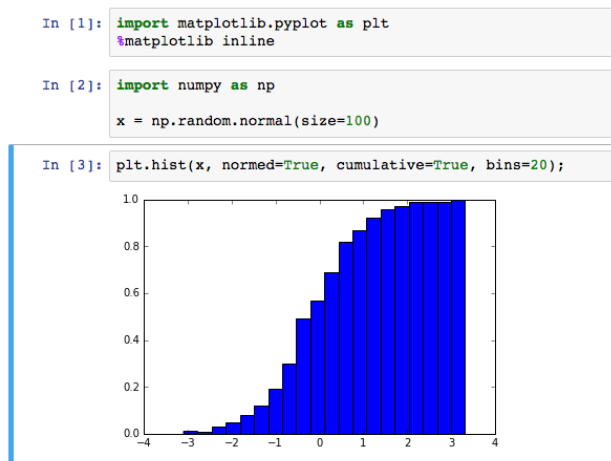
Matplotlib is a Python 2D and 3D plotting and visualization library that produces publication-quality figures in a variety of hardcopy formats and interactive environments across platforms.

To display Matplotlib figures in the output cells of a notebook running the default environment, run:

```
import matplotlib.pyplot as plt
%matplotlib inline
```

Any Matplotlib figures in the notebook are displayed in its output cells.

EXAMPLE: The following screenshot is of a cumulative density function (CDF) plot using values taken from a normal distribution:



For more information, including a [gallery](#), [examples](#), [documentation](#) and a [list of plotting commands](#), see the [Matplotlib website](#).

## Bokeh

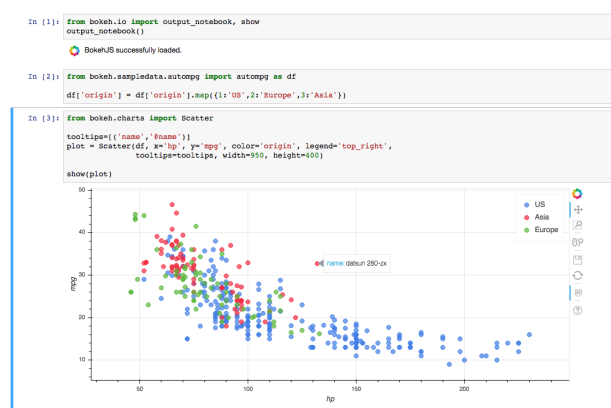
**Bokeh** is an interactive visualization library that targets modern web browsers to provide elegant, concise construction of novel graphics.

To display Bokeh figures in the output cells of a notebook running the default environment, run:

```
from bokeh.io import output_notebook, show
output_notebook()
```

Any Bokeh figures in the notebook are displayed in its output cells.

The following screenshot is of a scatter plot of miles-per-gallon vs. horsepower for 392 automobiles using the `autompg` sample dataset:



## ggplot2

**Ggplot2** is a plotting system for R language which is based on the grammar of graphics. Ggplot2 tries to take only the good parts of base and lattice graphics and none of the bad parts.

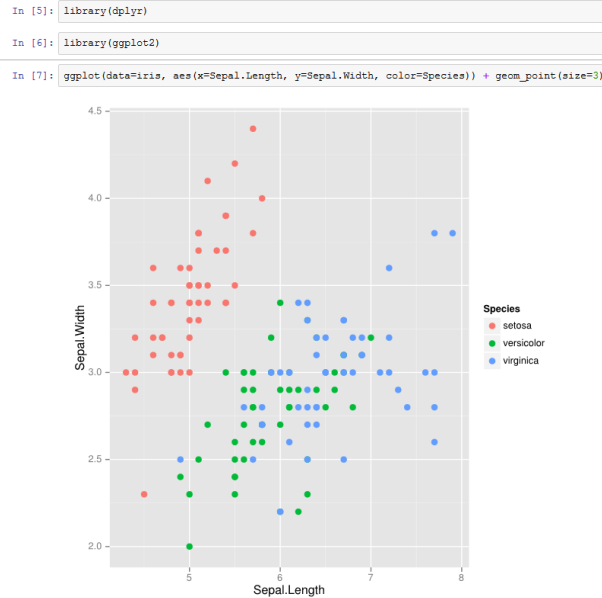
To use ggplot2 with AEN:

1. Open a new Notebook using the R kernel.
2. Load the ggplot2 library with the following code:

```
library(ggplot2)
```

The ggplot2 library is loaded and ready for use in AEN.

The following screenshot is of a scatter plot of sepal width vs sepal length using the `iris` dataset provided by the `dplyr` library:



## Using environment variables

Some Python packages depend on environment variables for correct operation.

EXAMPLE: Theano requires that the directory containing the CUDA compiler is included in the \$PATH environment variable in order for GPU acceleration to be enabled.

To change environment variables for all AEN applications, modify the project runtime configuration file `.projectrc`. For more information, see [Using Compute Resource Configuration](#).

`.projectrc` sets several AEN internal environment variables, sets up the project environment and can set additional user environment variables for that project. This file is sourced when a user opens any AEN application—including Jupyter Notebook—and Jupyter kernels will be able to read the included environment variables.

## Cheat sheet

See the [Anaconda Enterprise Notebooks cheat sheet PDF \(232 KB\)](#) for a single-page summary of the most important information about using AEN.

## Troubleshooting

This troubleshooting guide provides you with ways to deal with issues that may occur with your AEN installation.

### AEN application not working properly

An AEN application is not working as expected.

#### Cause

There are several reasons an application may not work as expected.

### Solution

Most AEN application issues can be resolved by following these steps:

1. Refresh the page.
2. If the issue is not resolved, close and open the application.
3. If the issue is not resolved, *stop and restart your project*.
4. If the issue is not resolved, check that you are using the latest version of your web browser—Chrome, Safari, Edge, or Firefox.
5. Log out of AEN.
6. Restart your browser, and log back in.

If you continue to have issues, then please contact your administrator or enterprise support representative.

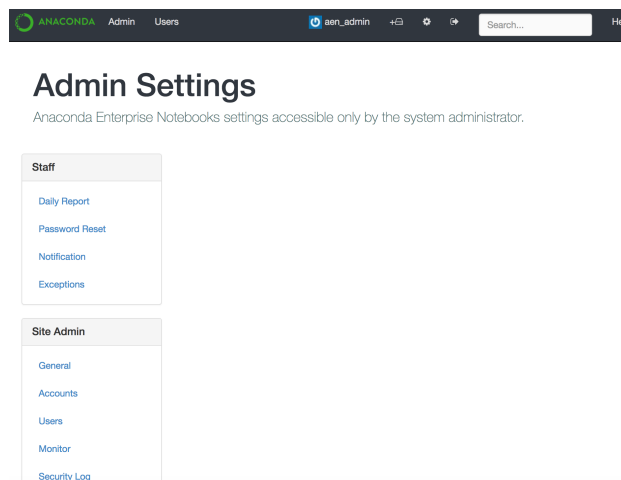
### Admin guide

This administrator guide provides information about the administration of an AEN installation.

Most AEN system management is done from the administrative user interface (admin UI). Some advanced tasks are done *using the command line*.

Any AEN user account can be *upgraded to an administrator account* to have both user and administrator privileges.

Administrators see two additional links in the AEN Navigation bar—Admin and Users:



All of the other navigation bar items are the same as for a user account.

### Concepts



- *System overview*
- *Server node*
- *Gateway node*
- *Compute node(s)*
- *Supervisor and supervisord*
- *Service Account*
- *Anaconda environments*
- *Projects and permissions*

## System overview

The Anaconda Enterprise Notebooks platform consists of 3 main service groups: AEN server, AEN gateway and AEN compute, which are called “nodes”:

- *Server node*—The administrative front-end to the system where users login, user accounts are stored, and administrators manage the system.
- *Gateway node(s)*—A reverse proxy that authenticates users and directs them to the proper compute node for their project. Users will not notice this node after installation as it automatically routes them.
- *Compute nodes*—Where projects are stored and run.

These services can be run on a single machine or distributed across multiple servers.

Organizationally, each AEN installation has exactly 1 server instance and 1 or more gateway instances. Each compute node can only be connected to a single gateway. The collection of compute nodes served by a single gateway is called a **data center**. You can add data centers to the AEN installation at any time.

EXAMPLE: An AEN deployment with 2 data centers, where 1 gateway has a cluster of 20 physical computers, and the second gateway has 30 virtual machines, must have the following services installed and running:

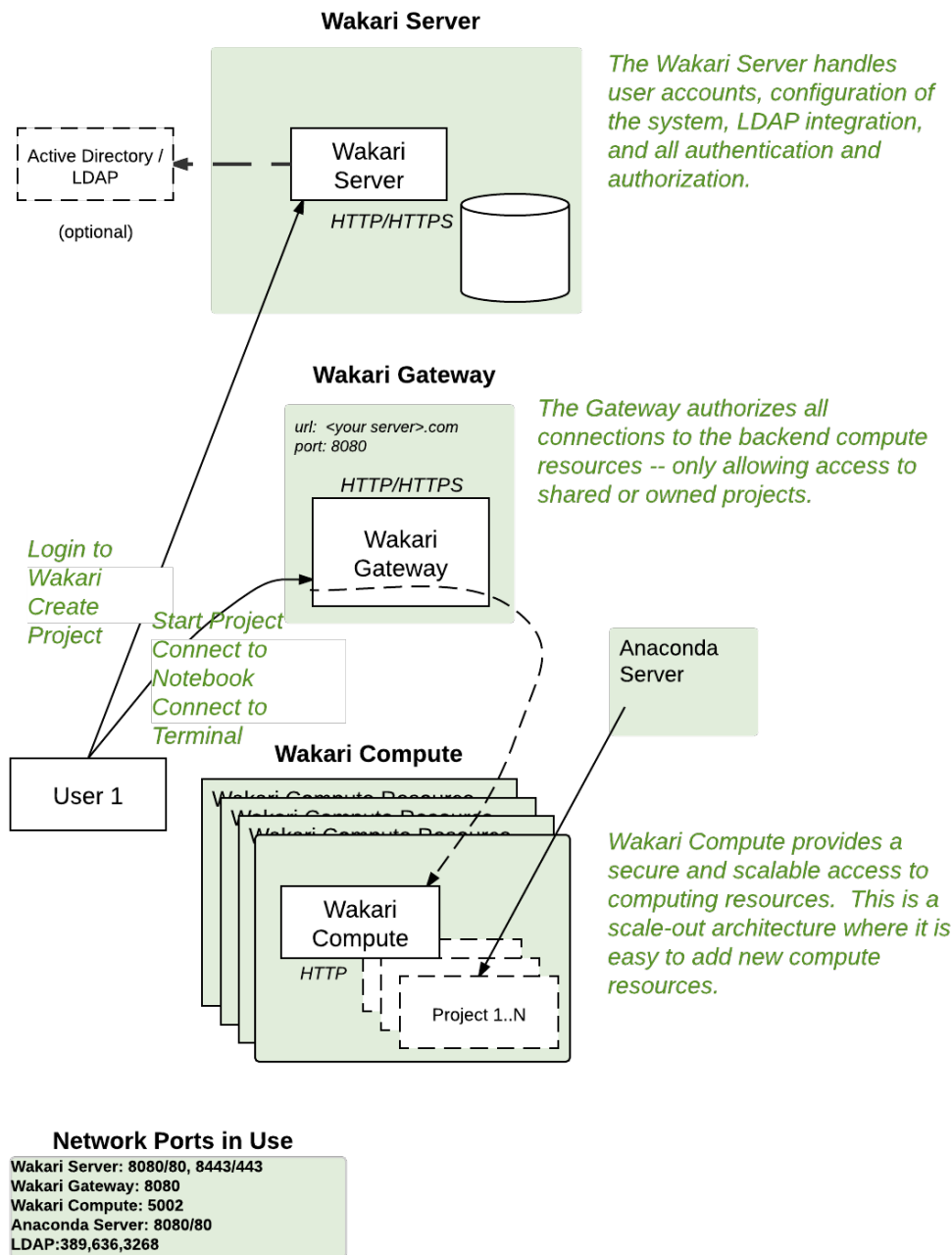
- 1 AEN server instance
- 2 AEN gateway instances
- 50 AEN compute instances (20 + 30)

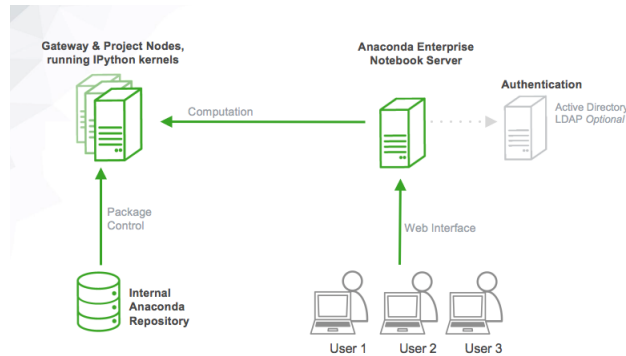
Nodes must be configured and maintained separately.

## Server node

The server node controls login, accounts, admin, project creation and management as well as interfacing with the database. It is the main entry point to AEN for all users. The server node handles project setup and ensures that users

## Anaconda Enterprise Notebooks





are sent to the correct project data center.

Since AEN is web-based, it uses the standard HTTP port 80 or HTTPS port 443 on the server.

AEN uses MongoDB for its internal data persistency. It is typically run on the same host as the server but can also be *installed* on a separate host.

Server nodes use NGINX to handle the user-facing AEN web interface. NGINX acts as a request proxy for the actual server web-process which runs on a high numbered port that only listens on localhost. NGINX is also responsible for static content.

Server is installed in the `/opt/wakari/wakari-server` directory.

## Server processes

When you *view the status of server processes*, you may see the processes explained below.

supervisord	details
description	Manage wakari-worker, multiple processes of wk-server.
user	wakari
configuration	<code>/opt/wakari/wakari-server/etc/supervisord.conf</code>
log	<code>/opt/wakari/wakari-server/var/log/supervisord.log</code>
control	<code>service wakari-server</code>
ports	none

wk-server	details
description	Handles user interaction and passing jobs on to the wakari gateway. Access to it is managed by NGINX.
user	wakari
command	<code>/opt/wakari/wakari-server/bin/wk-server</code>
configuration	<code>/opt/wakari/wakari-server/etc/wakari/</code>
control	<code>service wakari-server</code>
logs	<code>/opt/wakari/wakari-server/var/log/wakari/server.log</code>
ports	Not used in versions after 4.1.2 *

\* AEN 4.1.2 and earlier use port 5000. This port is used only on localhost. Later versions of AEN use Unix sockets instead. The Unix socket path is: `unix:/opt/wakari/wakari-server/var/run/wakari-server.sock`

wakari-worker	details
description	Asynchronously executes tasks from <code>wk-server</code> .
user	wakari
logs	/opt/wakari/wakari-server/var/log/wakari/worker.log
control	service wakari-server

nginx	details
description	Serves static files and acts as proxy for all other requests passed to <code>wk-server</code> process. *
user	nginx
configuration	/etc/nginx/nginx.conf /opt/wakari/wakari-server/etc/conf.d/www.enterprise.conf
logs	/var/log/nginx/woc.log /var/log/nginx/woc-error.log
control	service nginx status
port	80

\* In AEN 4.1.2 and earlier the `wk-server` process runs on port 5000 on localhost only. In later versions of AEN the `wk-server` process uses the Unix socket path `unix:/opt/wakari/wakari-server/var/run/wakari-server.sock`.

NGINX runs at least two processes:

- Master process running as root user.
- Worker processes running as nginx user.

## Gateway node

The gateway node serves as an access point for a given group of compute nodes. It acts as a proxy service and manages the authorization and mapping of URLs and ports to services that are running on those nodes. The gateway nodes provide a consistent uniform interface for the user.

NOTE: The gateway may also be referred to as a data center because it serves as the proxy for a collection of compute nodes.

You can put a gateway in each data center in a tiered scale-out fashion.

AEN gateway is installed in the `/opt/wakari/wakari-gateway` directory.

## Gateway processes

When you *view the status of server processes*, you may see the processes explained below.

supervisord	details
description	Manages the <code>wk-gateway</code> process.
user	wakari
configuration	/opt/wakari/wakari-gateway/etc/supervisord.conf
log	/opt/wakari/wakari-gateway/var/log/supervisord.log
control	service wakari-gateway
ports	none

wakari-gateway	details
description	Passes requests from the AEN Server to the Compute nodes.
user	wakari
configuration	/opt/wakari/wakari-gateway/etc/wakari/wk-gateway-config.json
logs	/opt/wakari/wakari-gateway/var/log/wakari/gateway.application.log /opt/wakari/wakari-gateway/var/log/wakari/gateway.log
working dir	/ (root)
port	8089 (webcache)

## Compute node(s)

Compute nodes are where applications such as Jupyter Notebook and Workbench actually run. They are also the hosts that a user sees when using the Terminal app or when using SSH to access a node. Compute nodes contain all user-visible programs.

Compute nodes only need to communicate with a gateway, so they can be completely isolated by a firewall.

Each project is associated with one or more compute nodes that are part of a single data center.

AEN compute nodes are installed in the `/opt/wakari/wakari-compute` directory.

Each compute node in the AEN system requires a compute launcher service to mediate access to the server and gateway.

## Compute processes

When you *view the status of server processes*, you may see the processes explained below.

supervisord	details
description	Manages the wk-compute process.
user	wakari
configuration	/opt/wakari/wakari-compute/etc/supervisord.conf
log	/opt/wakari/wakari-compute/var/log/supervisord.log
control	service wakari-compute
working dir	/opt/wakari/wakari-compute/etc
ports	none

wk-compute	details
de-scrip-tion	Launches compute processes.
user	wakari
con-figura-tion	/opt/wakari/wakari-compute/etc/wakari/wk-compute-launcher-config.json /opt/wakari/wakari-compute/etc/wakari/scripts/config.json
logs	/opt/wakari/wakari-compute/var/log/wakari/compute-launcher. application.log /opt/wakari/wakari-compute/var/log/wakari/ compute-launcher.log
work-ing dir	/ (root)
con-trol	service wakari-compute
port	5002 (rfe)

Wk-compute loads each of the following configuration files, in this order:

- /etc/wakari/config.json.
- /etc/wakari/compute-launcher-config.json.
- ./compute-launcher-config.json.
- Any configuration file specified by the `-c` option.

If an option is specified in multiple files, the last one encountered takes precedence.

## Supervisor and supervisord

AEN uses a process control system called “Supervisor” to run its services. Supervisor is run by the AEN Service Account user, usually wakari or aen\_admin.

The Supervisor daemon process is called “supervisord”. It runs in the background and should rarely need to be restarted.

## Service Account

AEN must be installed and executed by a Linux account called the AEN Service Account. The username of the AEN Service Account is called the AEN Functional ID (NFI). The AEN Service Account is created during AEN installation—if it does not exist—and is used to run all AEN services.

The default NFI username is wakari. Another popular choice is aen\_admin.

**WARNING:** The Service Account should only be used for administrative tasks, and should not be used for operating AEN the way an ordinary user would. If the Service Account creates or starts projects, the permissions on the AEN package cache will be reset to match the Service Account, which will interfere with the normal operation of AEN for all other users.

## Anaconda environments

Each project has an associated conda environment containing the packages needed for that project. When a project is first started, AEN clones a default environment with the name “default” into the project directory.

Each release of AEN 4 includes specific tested versions of conda and the conda packages included with AEN. These tested conda packages include Python, R, and other packages, and these tested conda packages include all of the packages in Anaconda.

If you upgrade or install different versions of conda or different versions of any of these conda packages, the new packages will not have been tested as part of the AEN 4 release.

These different packages will usually work, especially if they are newer versions, but they are not tested or guaranteed to work, and in some cases they may break product functionality.

You can use a new conda environment to test a new version of a package before installing it in your existing environments.

If using conda to change the version of a package breaks product functionality, you can use conda to change the version of the package back to the version known to work.

For more information about environments, see [Working with environments](#).

## Projects and permissions

AEN users interact with the system predominantly through [projects](#).

Projects are associated with a single data center within the AEN environment. The team of users includes one owner, which is the user that created the project.

Projects live in the `projectRoot` folder on the compute node—by default, `/projects`.

The project directory is created the first time a project is started. The `start-project` script clones it from `/opt/wakari/wakari-compute/lib/node_modules/wakari-compute-launcher/skeleton`.

Project directory permissions are:

```
owner: rwx, user who created the project
group: rwx, group of the owner
other: --x, to allow access to the Public folder
ACL: rwx for any other team members
```

Files and subdirectories within the project directory have the same permissions as the project directory, except:

- The public folder and everything in it are open to anyone.
- Any files hardlinked into the root anaconda environment—`/opt/wakari/anaconda`—are owned by the root or wakari users.

Project file and directory permissions are maintained by the `start-project` script. All files and directories in the project will have their permissions set when the project is started, except for files owned by root or the AEN\_SRVC\_ACCT user—by default, wakari or aen\_admin.

The permissions set for files owned by root or the AEN\_SRVC\_ACCT user are not changed to avoid changing the permissions settings of any linked files in the `/opt/wakari/anaconda` directory.

**CAUTION:** Do not start a project as the AEN\_SRVC\_ACCT user. The permissions system does not correctly manage project files owned by this user.

## Installation

### Installation requirements

- *Hardware requirements*
- *Software requirements*
- *Security requirements*
- *Network requirements*
- *Other requirements*
- *What's next*

### Hardware requirements

AEN server—At least:

- 2+GB RAM.
- 2+CPU cores.
- 20GB storage.

AEN gateway—At least:

- 2 GB RAM.
- 2 CPU cores.

AEN compute (N-machines)—Configured to meet the needs of the projects. At least:

- 2GB RAM.
- 2 CPU cores.
- 20 GB.

NOTE: We recommend putting `/opt/wakari` and `/projects` on the same filesystem. If the project and conda env directories are on separate filesystems then more disk space will be required on compute nodes and performance will be worse.

### Software requirements

- RHEL/CentOS on all nodes. Versions from 6.5 through 7.4 are supported. Other operating systems are supported. However, this document assumes RHEL or CentOS.
- Linux home directories—Jupyter looks in `$HOME` for profiles and extensions.
- Ability to install in AEN directory `/opt/wakari` with at least 10 GB of storage.
- Ability to install in Projects directory `/projects` with at least 20 GB of storage. Size depends on number and size of projects.

NOTE: To install AEN in a different location see *Installing AEN in a custom location*.



## Linux system accounts

Some Linux system accounts (UIDs) are added to the system during installation.

If your organization requires special actions, the following list is available:

- mongod (RHEL) or mongodb (Ubuntu/Debian)—created by the RPM or deb package.
- elasticsearch—created by RPM or deb package.
- nginx—created by RPM or deb package.
- AEN\_SRVC\_ACCT—created during installation of AEN, and defaults to wakari.
- ANON\_USER—An account such as “public” or “anonymous” on the compute node.

NOTE: If ANON\_USER is not found, AEN\_SRVC\_ACCT will attempt to create it. If it fails, the project(s) will fail to start.

- ACL directories need the filesystem mounted with Posix ACL support (Posix.1e).

NOTE: You can verify ACL from the command line by running `mount` and `tune2fs -l /path/to/filesystem | grep options`.

## Software prerequisites

- AEN server:
  - Mongo—Equal to or higher than version 2.6.8 and lower than version 3.0.
  - NGINX—Equal to or higher than version 1.6.2.
  - Elasticsearch—Equal to or higher than version 1.7.2.
  - Oracle JRE version 7 or 8.
  - bzip2.
- AEN Gateway:
  - bzip2.
- AEN compute:
  - git
  - bzip2
  - bash or zsh
  - X Window System

NOTE: If you don’t want to install the whole X Window System, you must install the following packages to have R plotting support:

```
sudo yum install -y libXrender libXext libXdmp libSM libICE libXt \
dejavu-sans-fonts dejavu-serif-fonts dejavu-fonts-common \
fontpackages-filesystem
```

## Security requirements

- Root or sudo access.
- File permissions: `umask 0022` is required during the installation.
- SELinux in permissive or disabled mode.

Edit the following file using either root or sudo access:

```
/etc/sysconfig/selinux
```

Edit the following:

```
# This file controls the state of SELinux on the system.
# SELINUX= can take one of these three values:
#   enforcing - SELinux security policy is enforced.
#   permissive - SELinux prints warnings instead of enforcing.
#   disabled - No SELinux policy is loaded.

SELINUX=enforcing

# SELINUXTYPE= can take one of these two values:
#   targeted - Targeted processes are protected,
#   mls - Multi Level Security protection.

SELINUXTYPE=targeted
```

NOTE: You must reboot for the changes to take effect.

Verify changes with `getenforce`.

## Network requirements

TCP Ports:

Direction	Type	Default Port	Protocol	Optional	Configurable	Comments
Inbound	TCP	80	HTTP or HTTPS	No	Yes	Server
Inbound	TCP	8089	HTTP or HTTPS	No	Yes	Gateway
Inbound	TCP	5002	HTTP	No	Yes	Compute

## Other requirements

As long as the above requirements are met, there are no additional dependencies for AEN.

See also system requirements for Anaconda Repository and Anaconda Scale.

## What's next

*Prepare for installation.*

## Preparing for installation

- *Downloading AEN installers*
- *Gathering IP addresses or FQDNs*
- *Set up variables*
- *What's next*

## Downloading AEN installers

Download the installers and copy them to the corresponding servers.

```
RPM_CDN="https://820451f3d8380952ce65-4cc6343b423784e82fd202bb87cf87cf.ssl.cf1.
↪rackcdn.com"
curl -O $RPM_CDN/aen-server-4.3.3-Linux-x86_64.sh
curl -O $RPM_CDN/aen-gateway-4.3.3-Linux-x86_64.sh
curl -O $RPM_CDN/aen-compute-4.3.3-Linux-x86_64.sh
```

NOTE: The current \$RPM\_CDN server will be confirmed in an email provided by your sales rep.

NOTE: These instructions use *curl* or *wget* to download packages, but you may use other means to move the necessary files into the installation directory.

## Gathering IP addresses or FQDNs

AEN is very sensitive to the IP address or domain name used to connect to the server and gateway nodes. If users will be using the domain name, you should install the nodes using the domain name instead of the IP addresses. The authentication system requires the proper hostnames when authenticating users between the services.

Print this page and fill in the domain names or IP addresses of the nodes below and record the user name and auto-generated password for the administrative user account in the box below after installing the AEN server node:

Node   Name or IP address	Port Number	Username   Password	
AEN server			
AEN gateway			
AEN compute			

NOTE: The values of these IP entries or DNS entries are referred to as <AEN\_SERVER\_IP> or <AEN\_SERVER\_FQDN>, particularly in examples of shell commands. Consider actually assigning those values to environment variables with similar names.

## Set up variables

Certain variables need to have values assigned to them before you start the installation.

### AEN server address

To define an environment variable for the AEN server address—FQDN or IP:

```
export AEN_SERVER=<AEN_SERVER_IP> # <from table above>
```

NOTE: The address—FQDN or IP—specified for the AEN server must be resolvable by your intended AEN users' web clients.

To verify your hostname, run `echo $AEN_SERVER`.

### AEN functional ID

AEN must be installed and executed by a Linux account called the AEN Service Account. The username of the AEN Service Account is called the AEN Functional ID (NFI). The AEN Service Account is created during AEN installation—if it does not exist—and is used to run all AEN services.

The default NFI username is `wakari`. Another popular choice is `aen_admin`.

To set the environment variable `AEN_SRVC_ACCT` to `wakari` or your chosen name before installation, run `export AEN_SRVC_ACCT="aen_admin"`.

This name is now the username of the AEN Service Account and of the AEN administrator account.

When upgrading AEN, set the NFI to the NFI of the current installation.

WARNING: The Service Account should only be used for administrative tasks, and should not be used for operating AEN the way an ordinary user would. If the Service Account creates or starts projects, the permissions on the AEN package cache will be reset to match the Service Account, which will interfere with the normal operation of AEN for all other users.

### AEN functional group

The AEN Functional Group (NFG) may be given any name. Most often, it is set to `aen_admin` or `wakari`. This Linux group includes the AEN service account, so all files and directories that have the owner NFI also have the group NFG.

When upgrading AEN, set the NFG to the NFG of the current installation.

To set the NFG before installation, run:

```
export AEN_SRVC_GRP="<NFG>"
```

NOTE: Replace `<NFG>` with your NFG name.

### AEN install sudo command

During AEN installation the installers perform various operations that require root level privileges. By default, the installers use the `sudo` command to perform these operations.

Before installation, set the `AEN_SUDO_CMD_INSTALL` environment variable to perform root level operations. You can also set it to no command at all if the user running the installer(s) has root privileges and the `sudo` command is not needed or is not available.

EXAMPLES:

```
export AEN_SUDO_CMD_INSTALL=""
export AEN_SUDO_CMD_INSTALL="sudo2"
```

## AEN sudo command

By default the AEN services uses `sudo -u` to perform operations on behalf of other users—including `mkdir`, `chmod`, `cp` and `mv`.

To override the default `sudo` command when `sudo` is not available on the system, before installing, set the `AEN_SUDO_CMD` environment variable.

AEN must have the ability to perform operations on behalf of other users. Therefore, this environment variable cannot be set to an empty string or to `null`.

**CAUTION:** Any command that replaces `AEN_SUDO_CMD` must support the `-u` command line parameter—similarly to the `sudo` command.

**EXAMPLE:**

```
export AEN_SUDO_CMD="sudo2"
```

The optional environmental variable `AEN_SUDO_SH` is another way to customize AEN `sudo` operations. When AEN executes any `sudo` command, it will include the value of `AEN_SUDO_SH`, if it is set.

**EXAMPLE:** If your username is “jsmith” and the values are set as:

```
AEN_SUDO_CMD=sudo
OWNER=jsmith
AEN_SUDO_SH=sudologger
PROJECT_HOME=/projects/jsmith/myproj
```

Then AEN will resolve:

```
$AEN_SUDO_CMD -u ${OWNER} $AEN_SUDO_SH rm -rf $PROJECT_HOME
```

As:

```
sudo -u jsmith sudologger rm -rf /projects/jsmith/myproj
```

In this case the `sudologger` utility could be a pass-through utility that logs all `sudo` usage and then executes the remaining parameters.

## Post-installation Sudo configuration

While `root/sudo` privileges are required during installation, `root/sudo` privileges are not required during normal operations after install, if user accounts are managed outside the software. However `root/sudo` privileges are required to start the services, thus in the service config files there may still need to be an `AEN_SUDO_CMD` entry.

For more information, see [Configuring sudo customizations](#).

## AEN remote database settings

By default AEN server uses a local database. To override the default database location, see [Install AEN connected to a remote Mongo DB instance](#).

### What's next

*Install the AEN server.*

### Installing the AEN server

- *Installing the bzip2 package*
- *Downloading prerequisite RPMs*
- *Installing prerequisite RPMs*
- *Setting variables and changing permissions*
- *Running the AEN server installer*
- *Starting NGINX and Elasticsearch*
- *Testing AEN server installation*
- *Updating your license*
- *What's next*

The AEN server is the administrative front end to the system. This is where users log in to the system, where user accounts are stored, and where admins can manage the system.

Server is installed in the `/opt/wakari/wakari-server` directory.

### Installing the bzip2 package

Be sure you have the *bzip2* package installed. If this package is not installed on your system, install it:

```
sudo yum install bzip2
```

### Downloading prerequisite RPMs

To install AEN on a CentOS 6 server:

```
RPM_CDN="https://820451f3d8380952ce65-4cc6343b423784e82fd202bb87cf87cf.ssl.cf1.
↪rackcdn.com"
curl -O $RPM_CDN/nginx-1.6.2-1.el6ngx.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-tools-2.6.8-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-shell-2.6.8-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-server-2.6.8-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-mongos-2.6.8-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-2.6.8-1.x86_64.rpm
curl -O $RPM_CDN/elasticsearch-1.7.2.noarch.rpm
curl -O $RPM_CDN/jre-8u65-linux-x64.rpm
```

To install AEN on a CentOS 7 server:

```
RPM_CDN="https://820451f3d8380952ce65-4cc6343b423784e82fd202bb87cf87cf.ssl.cf1.
↳rackcdn.com"
curl -O $RPM_CDN/nginx-1.10.2-1.el7ngx.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-tools-2.6.12-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-shell-2.6.12-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-server-2.6.12-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-mongos-2.6.12-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-2.6.12-1.x86_64.rpm
curl -O $RPM_CDN/jre-8u112-linux-x64.rpm
curl -O $RPM_CDN/elasticsearch-1.7.6.noarch.rpm
```

## Installing prerequisite RPMs

Run:

```
sudo yum install -y *.rpm
sudo service mongod start
sudo chkconfig --add elasticsearch
```

## Setting variables and changing permissions

Run:

```
export AEN_SERVER=<FQDN HOSTNAME OR IP ADDRESS> # Use the real FQDN
chmod a+x aen-*.sh # Set installer to be executable
```

NOTE: Change <FQDN HOSTNAME OR IP ADDRESS> to the actual fully qualified domain hostname or IP address.

## Running the AEN server installer

Run:

```
sudo -E ./aen-server-4.3.3-Linux-x86_64.sh -w $AEN_SERVER
<license text>
...
...
PREFIX=/opt/wakari/wakari-server
Logging to /tmp/wakari_server.log
Checking server name
Ready for pre-install steps
Installing miniconda
...
...
Checking server name
Loading config from /opt/wakari/wakari-server/etc/wakari/config.json
Loading config from /opt/wakari/wakari-server/etc/wakari/wk-server-config.json

=====

Created password '<RANDOM_PASSWORD>' for user 'aen_admin'
```

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```
=====
```

```
Starting Wakari daemons...
installation finished.
```

After successfully completing the installation script, the installer creates the administrator account—AEN\_SRVC\_ACCT user—and assigns it a password.

EXAMPLE:

```
Created password '<RANDOM_PASSWORD>' for user 'aen_admin'
```

**TIP:** Record this password. It will be needed in the following steps. It is also available in the installation log file `/tmp/wakari_server.log`.

## Starting NGINX and Elasticsearch

When SELinux is enabled, it blocks NGINX from connecting to the socket created by Gunicorn. If you have SELinux enabled, run these commands to correct these permissions and allow connections between NGINX and Gunicorn:

```
sudo semanage fcontext -a -t httpd_var_run_t "/opt/wakari/wakari-server/var/run/
↪wakari-server.sock"
sudo restorecon -r /opt/wakari/wakari-server/var/run
```

To start NGINX and Elasticsearch to read the new config file:

```
sudo service nginx start
sudo service elasticsearch start
```

**TIP:** If the AEN web page shows an NGINX 404 error, restart NGINX:

```
sudo nginx -s stop
sudo nginx
```

## Testing AEN server installation

Visit [http://\protect\T1\textdollarAEN\\_SERVER](http://\protect\T1\textdollarAEN_SERVER).

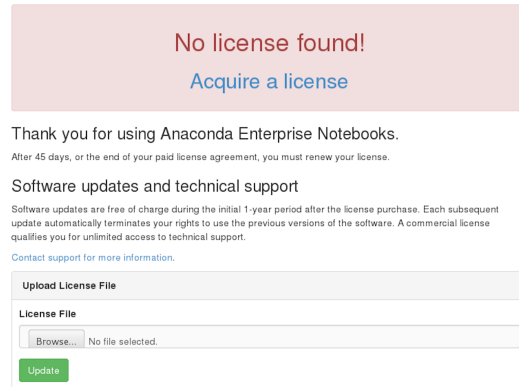
The License expired page is displayed.

## Updating your license

From the License expired page, follow the onscreen instructions to upload your license file.

After your license is submitted, you will see this page:





**No license found!**  
[Acquire a license](#)

Thank you for using Anaconda Enterprise Notebooks.  
 After 45 days, or the end of your paid license agreement, you must renew your license.

**Software updates and technical support**

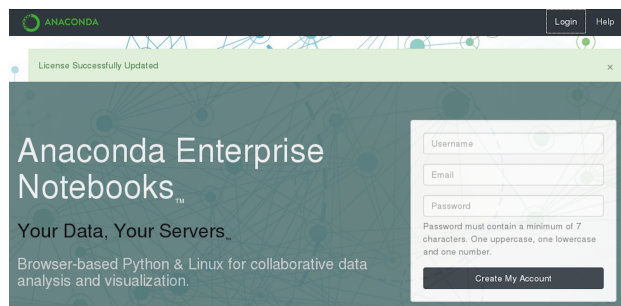
Software updates are free of charge during the initial 1-year period after the license purchase. Each subsequent update automatically terminates your rights to use the previous versions of the software. A commercial license qualifies you for unlimited access to technical support.

[Contact support for more information.](#)

**Upload License File**

License File  
 Browse... No file selected.

[Update](#)



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 Your Data, Your Servers.  
 Browser-based Python & Linux for collaborative data analysis and visualization.

Username  
 Email  
 Password

Password must contain a minimum of 7 characters. One uppercase, one lowercase and one number.

[Create My Account](#)

## What's next

*Install the AEN gateway.*

## Installing the AEN gateway

- *Setting variables and changing permissions*
- *Running the AEN gateway installer*
- *Registering your gateway*
- *What's next*

The gateway is a reverse proxy that authenticates users and automatically directs them to the proper AEN compute node for their project. Users will not notice this node as it automatically routes them.

Gateway is installed in the `/opt/wakari/wakari-gateway` directory.

## Setting variables and changing permissions

Run:

```
export AEN_SERVER=<FQDN HOSTNAME OR IP ADDRESS> # Use the real FQDN
export AEN_GATEWAY_PORT=8089
```

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```
export AEN_GATEWAY=<FQDN HOSTNAME OR IP ADDRESS> # will be needed shortly
chmod a+x aen-*.sh # Set installer to be executable
```

NOTE: Change <FQDN HOSTNAME OR IP ADDRESS> to the actual fully qualified domain hostname or IP address.

NOTE: You must perform the entire procedure before closing the terminal to ensure the variable export persists. If the terminal is closed before successful installation, export the variables to continue with the installation.

## Running the AEN gateway installer

Run:

```
sudo -E ./aen-gateway-4.3.3-Linux-x86_64.sh -w $AEN_SERVER
<license text>
...
...

PREFIX=/opt/wakari/wakari-gateway
Logging to /tmp/wakari_gateway.log
...
...
Checking server name
Please restart the Gateway after running the following command
to connect this Gateway to the AEN Server
...
```

## Registering your gateway

The gateway needs to register with the AEN server.

This needs to be authenticated, so the NFI user's credentials created during the AEN server install must be used.

To write the configuration file `/opt/wakari/wakari-gateway/etc/wakari/wk-gateway-config.json`, run the following as `sudo` or `root`:

```
sudo /opt/wakari/wakari-gateway/bin/wk-gateway-configure \
--server http://$AEN_SERVER --host $AEN_GATEWAY \
--port $AEN_GATEWAY_PORT --name Gateway --protocol http \
--summary Gateway --username $AEN_SRVC_ACCT \
--password '<NFI USER PASSWORD>'
```

NOTE: replace <NFI USER PASSWORD> with the password of the NFI user that was generated during *server installation*.

## Setting permissions

Run:

```
sudo chown $AEN_SRVC_ACCT /opt/wakari/wakari-gateway/etc/wakari/wk-gateway-config.json
```

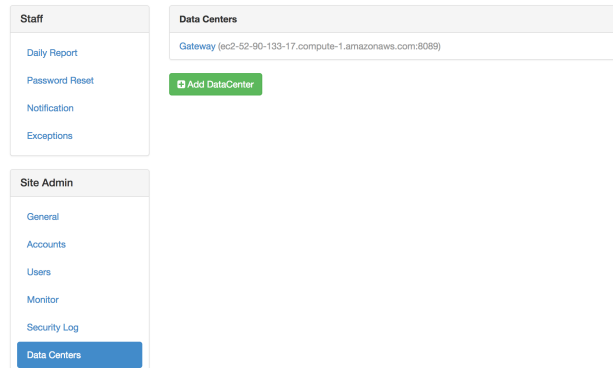
## Starting the gateway

Run:

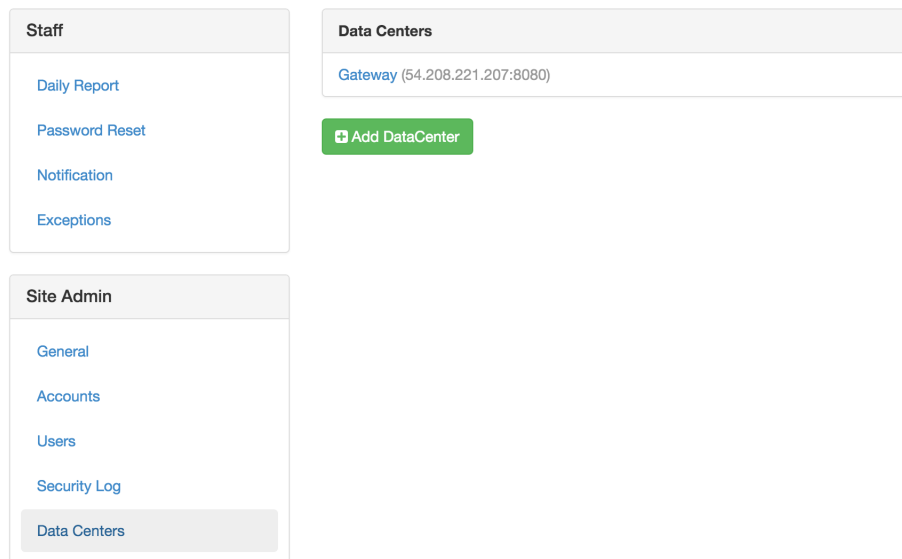
```
sudo service wakari-gateway start
```

## Verifying your gateway registration

1. Log into the AEN server using the Chrome or Firefox browser and the AEN\_SRVC\_ACCT user.
2. In the AEN navigation bar, click Admin to open the Admin Settings page.
3. In the **Site Admin** menu, select Data Centers:



4. Click your data center:



5. Verify that your data center is registered and the status is {"status": "ok", "messages": []}:

Staff

[Daily Report](#)
[Password Reset](#)
[Notification](#)
[Exceptions](#)

Site Admin

[General](#)
[Accounts](#)
[Users](#)
[Monitor](#)
[Security Log](#)
[Data Centers](#)
[Task Queue](#)

Datacenter Gateway

Provider

wk\_server.plugins.providers.enterprise

Client ID

59c119cd3f94c30fe45ff5db

Client Secret

50cc629d-4e8e-44a5-9a2e-a46fee7c1921

Redirect URIs

http://ec2-52-90-133-17.compute-1.amazonaws.com:8089/login/authorized

wk-gateway-config.json

```
{
  "CDN": "http://ec2-204-236-198-47.compute-1.amazonaws.com/static/",
  "SUBDOMAIN_ROUTING": false,
  "client_id": "59c119cd3f94c30fe45ff5db",
  "client_secret": "50cc629d-4e8e-44a5-9a2e-a46fee7c1921",
  "WAKARI_SERVER": "http://ec2-204-236-198-47.compute-1.amazonaws.com",
  "port": 8089
}
```

status

```
{"status": "ok", "messages": []}
```

Back

Remove

## What's next

*Install the AEN compute node(s).*

## Installing the AEN compute node(s)

- *Setting variables and changing permissions*
- *Running the AEN compute installer*
- *Restart the AEN Server*
- *Configuring your compute node(s)*
- *What's next*

Compute nodes are where projects are stored and run.

Adding multiple AEN compute machines allows you to scale-out horizontally to increase capacity. Projects can be created on individual compute nodes to spread the load.

Repeat this procedure on each compute machine.

## Setting variables and changing permissions

Run:

```
export AEN_SERVER=<FQDN HOSTNAME OR IP ADDRESS> # Use the real FQDN
chmod a+x aen-*.sh # Set installer to be executable
```

NOTE: Change <FQDN HOSTNAME OR IP ADDRESS> to the actual fully qualified domain hostname or IP address.

NOTE: You must perform the entire procedure before closing the terminal to ensure the variable export persists.

## Running the AEN compute installer

Run:

```
sudo -E ./aen-compute-4.3.3-Linux-x86_64.sh -w $AEN_SERVER
...
...
PREFIX=/opt/wakari/wakari-compute
Logging to /tmp/wakari_compute.log
Checking server name
...
...
Initial clone of root environment...
Starting Wakari daemons...
installation finished.
Do you wish the installer to prepend the wakari-compute install location
to PATH in your /root/.bashrc ? [yes|no]
[no] >>> yes
```

## Restart the AEN Server

Once configured, restart the AEN server:

```
sudo service wakari-server restart
```

## Configuring your compute node(s)

Once installed, you must configure the compute launcher on your server:

1. In your browser, go to your AEN server.
2. Log in as the AEN\_SRVC\_ACCT user.
3. In the AEN navigation bar, click Admin to open the Admin Settings page.
4. In the **Providers** menu, select Enterprise Resources:
5. Click the Add Resource button to open the new resource form.
6. Select the data center to associate this compute node with.

**Staff**

- Daily Report
- Password Reset
- Notification
- Exceptions

**Resources** [Add Resource](#)

**Gateway**

ec2-54-210-232-251.compute-1.amazonaws.com [remove](#)

**Site Admin**

- General
- Accounts
- Users
- Monitor
- Security Log
- Data Centers
- Task Queue
- License

**Providers**
[Enterprise Resources](#)

Resources / new

**Data Center**

Gateway 59c119cd3f94c30fe45ff5db

**Name**

Compute Node1

**URL**

http://ec2-54-210-232-251.compute-1.amazonaws.com:5002

**Description**

Configuring Compute Node

☒ **Public**  
Uncheck this if you want to control exactly who has access to this compute node

[Add Resource](#)

7. In the URL box, type: `http://$AEN_COMPUTE:5002`.

NOTE: If the compute launcher is located on the same box as the gateway, we recommended that you type `http://localhost:5002` instead.

8. Type a Name and Description for the compute node.
9. Click the Add Resource button to save the changes.

Your AEN compute node is configured.

## What's next

*Configure conda to use your local on-site AEN repository.*

## Configuring conda to use your local on-site AEN repository

You can configure AEN to use a local on-site Anaconda Repository server instead of Anaconda.org.

To configure AEN to use a local on-site Repository, you must:

1. *Edit condarc on the compute node.*
2. *Configure the Anaconda client.*

## Editing condarc on the compute node

NOTE: If there are channels that you haven't mirrored, you must remove them from the configuration.

Edit the file `.condarc` to match the following:

```
#/opt/wakari/anaconda/.condarc
channels:
  - defaults

create_default_packages:
  - anaconda-client
  - ipykernel

# Default channels is needed for when users override the system .condarc
# with ~/.condarc. This ensures that "defaults" maps to your Anaconda Repository and
↪not
# repo.anaconda.com
default_channels:
  - http://<your Anaconda Repository name>:8080/conda/anaconda
  - http://<your Anaconda Repository name>:8080/conda/wakari
  - http://<your Anaconda Repository name>:8080/conda/r-channel

# Note: You must add the "conda" subdirectory to the end
channel_alias: http://<your Anaconda Repository name>:8080/conda
```

NOTE: Replace `<your Anaconda Repository name>` with the actual name or IP address of your local Anaconda Repository installation.

### Configuring the Anaconda client

Anaconda client lets users work with Repository from the command-line—including searching for packages, logging in, uploading packages, and more.

To set the default configuration of anaconda-client for all users on your compute node:

```
sudo /opt/wakari/anaconda/bin/anaconda config --set url http://<your Anaconda_
↳Repository>:8080/api -s
```

NOTE: Sudo is required because the configuration file is written to the root file system: `/etc/xdg/binstar/config.yaml`.

NOTE: Replace `<your Anaconda Repository>` with the actual name or IP address of your local Anaconda Repository installation.

### What's next

Review the *optional configuration* tasks to see if any apply to your system.

### Optional configuration

#### Using configuration files

- *AEN configuration keys*
- *Checking configuration file syntax*

The default locations for each component's configuration files are:

- Server—`/opt/wakari/wakari-server/etc/wakari/config.json`.
- Gateway—`/opt/wakari/wakari-gateway/etc/wakari/config.json`.
- Compute—`/opt/wakari/wakari-compute/etc/wakari/config.json`.

Additionally, service-specific configuration files may also be present in the following locations:

- Server—`/opt/wakari/wakari-server/etc/wakari/wk-server-config.json`.
- Gateway—`/opt/wakari/wakari-gateway/etc/wakari/wk-gateway-config.json`.
- Compute—`/opt/wakari/wakari-compute/etc/wakari/wk-compute-config.json`.

Each service loads each of the configuration files in the following order and updates the AEN configuration at each step:

1. `/etc/wakari/config.json`.
2. `/etc/wakari/wk-gateway-config.json`.
3. `/opt/wakari/wakari-SERVICE/etc/wakari/config.json`.
4. `/opt/wakari/wakari-SERVICE/etc/wakari/wk-SERVICE-config.json`.
5. `./config.json`.
6. `./wk-gateway-config.json`.



## AEN configuration keys

The following is a list of AEN supported configuration keys:

Table 1: Server Configuration Keys

Key	Default	Description
CDN	<code>\$WAKARI_SERVER/static/</code>	The location of static assets.
MONGO_DB	<code>wakari</code>	The name of the AEN database in mongodb.
MONGO_URL	<code>mongodb://localhost/</code>	The URL of your AEN server's mongodb instance. Format: <code>mongodb://&lt;username&gt;:&lt;password&gt;@&lt;host&gt;:&lt;port&gt;/</code>
WAKARI_SERVER		The URL of this AEN server.
DEFAULT_PRIVACY	<code>public</code>	The default project privacy setting—can be either <code>public</code> or <code>private</code> .
SESSION_COOKIE_NAME	<code>wakari.enterprise.session</code>	The Cookie name used to maintain Anaconda Enterprise Notebooks Enterprise login sessions.
SESSION_COOKIE_SECURE	<code>false</code>	This key is automatically set to <code>true</code> when SSL is enabled. It will default to <code>false</code> when SSL is not enabled. Manually changing this value may cause the system to malfunction if it's not configured properly.
PERMANENT_SESSION	<code>True</code>	Sets cookie session to permanent. This will keep the session open after the browser is closed. The session will still expire after the number of minutes set in the <code>SESSION_LIFETIME</code> key.
SESSION_LIFETIME	<code>120</code>	Time in minutes until the session expires. The counter resets with each request.
USE_SES	<code>false</code>	Sets whether AEN will use Amazon SES to send emails.
SMTP		Sets the SMTP email settings.
- host		A SMTP subkey—the SMTP mail server hostname.
- user		SMTP subkey—the username for SMTP server authentication.
- password		SMTP subkey—the password for SMTP server authentication.
- from_addr		SMTP subkey—the From address for emails sent through SMTP.
verify_gateway_certificate	<code>true</code>	A boolean setting that indicates whether your AEN server should verify the gateway SSL certificate.
accounts	<code>wk_server.plugins.accounts.cloud</code>	The account provider class. For LDAP, this should be set to <code>wk_server.plugins.accounts.ldap_accounts</code> .
uniqueEmail	<code>true</code>	A boolean setting that indicates whether unique user email addresses are required. See <a href="#">note below</a> about updating the database when setting <code>uniqueEmail</code> .
has_internet	<code>true</code>	Boolean for retrieving the avatar from the gravatar URL. If <code>false</code> a local default is used instead.
LDAP	<code>389</code>	LDAP configurations.
- SERVER		LDAP subkey—A list of LDAP servers. At least one server name must be listed. The primary server should be listed first. All secondary or fail-over servers should be listed after the primary.
- PORT	<code>389</code>	LDAP subkey—The LDAP port on the LDAP server.

Continued on next page

Table 1 – continued from previous page

Key	Default	Description
- AUTH_TYPE		LDAP subkey—LDAP Authentication types. simple—no encryption not secure. “TLS”—encrypted secure requires the TLS_CERT to be set.
- TLS_CERT		LDAP subkey—the full path to the TLS certificate file. The certificate file must also be provided by the Enterprise.
- BASEDN		LDAP subkey—the LDAP Base DN value.
- OU		LDAP subkey—a list of Organizational Units. Some Enterprises group users by OUs in their LDAP server records. AEN will loop over the list of OUs when authenticating a user. The OU value is a list of lists to support multiple OUs where each OU is a single name or a hierarchy of names.
ANON_USER	anonymous	Username—such as public or anonymous—assigned users who are not logged in to access projects. To disable public access use the special value disabled. For more information, see <a href="#">Configuring sudo customizations</a> .
SEARCH_ENABLED	true	Boolean indicating whether ElasticSearch is enabled
SEARCH_SERVER	'localhost:9200'	IP address or domain name and port of ElasticSearch server
LOG_LEVEL	'DEBUG'	Log verbosity. One of: 'ERROR' 'WARN' 'INFO' 'DEBUG'

NOTE: If you set uniqueEmail to false, you must drop the existing index in the database. EXAMPLE: If the index name is email\_1, run `db.users.dropIndex("email_1")`.

Table 2: Gateway Configuration Keys

Key	Default	Description
WAKARI_SERVER		The URL of the AEN WAKARI_SERVER.
port	8089	The Port number used by the gateway application. Must be a non-privileged port ( $\geq 1024$ ).
client_id		The client ID assigned to this gateway by the server during <code>wk-gateway-configure</code> .
client_secret		The Client secret assigned to this gateway by the server during <code>wk-gateway-configure</code> .
httpTimeout	600	Timeout in seconds. The default is 10 minutes to allow project creation.
logLevel	info	Log verbosity. One of: 'error' 'warn' 'info' 'debug'.
https		Enable SSL encryption. For more information, see <a href="#">Configuring SSL</a> .
- key		A https subkey—Path to gateway key.
- cert		A https subkey—Path to gateway cert.
- ca		A https subkey—Required if cert was signed by a private root CA or signed by an intermediate authority. It must contain separate values for the paths to the CA root, any intermediates and the certificate for the Server.
- passphrase		A https subkey—Passphrase required to decrypt SSL certs.

Table 3: Compute Node Configuration Keys

Key	Default	Description
WAKARI_SERVER		The URL of the AEN WAKARI_SERVER.
MANAGE_ACCOUNTS	true	A boolean setting that indicates whether AEN should manage system user accounts. Set to false for LDAP installations.
identicalGID	false	<b>To make the AEN compute service create groups with the same uid. Set to true</b> /projects folder resides on an NFSv3 volume. For more information, see <i>Group and user permissions for NFS</i> .
port	2227	The port number used by the compute-launcher application. Note that individual applications use dynamic ports.
projectRoot	/projects	The location of project file storage.
logLevel	info	Log verbosity. One of: 'error' 'warn' 'info' 'debug'
logMaxSize	10000000	Max size in bytes of the logfile. Default is 10 MB. If the size is exceeded then a new file is created and a counter will become a suffix of the log file.
logMaxFiles	30	Limit the number of files created when the size of the logfile is exceeded
appIdleTime	172800000 (48 hours)	The amount of idle time before applications will be auto-terminated (in msec).
idleCheckInterval	13600000 (1 hour)	The frequency of idle checks.
numericUsernames	false	A boolean setting that indicates whether numeric usernames are permitted.
httpTimeout	600	The time before a timeout—in seconds. The default is 10 minutes—600 seconds—to allow time for project creation.
ANON_USER	anonymous	Username such as public or anonymous for users who are not logged in to access projects. To disable public access use the special value disabled. For more information, see <i>Configuring sudo customizations</i> .
projDirsAsHome	false	A boolean setting. When false AEN apps use /home/<username> as HOME. When true AEN apps use /projects/<username> as HOME.
emptyDefaultChannels	true	A boolean setting. When true AEN sets default_channels to be an empty list on the project's .condarc preventing the search of packages from the free channel. If you set this option as false, and if you already started a project with this setting as true, you will need to modify the existing project's .condarc and remove the default_channels: [] line.

Table 4: Server Internal Configuration Keys - Do not change

Key	Default	Description
PROVIDERS	<code>["wk_server.plugins.providers.enterprise"]</code>	A list of compute provider classes.
MONGO_ACTION_LOG_SIZE	262144000	The size of the Mongo action log in bytes.
SITE_ADMINS		A list of site administrator email addresses—used for crash notifications and LDAP password reset requests.
FROM_EMAIL_ADDR		The From address for notification emails sent by AEN.
uniqueUserName	true	A boolean setting that indicates whether unique usernames are required.

Table 5: Gateway Internal Configuration Keys - Do not change

Key	Default	Description
CDN	<code>\$WAKARI_SERVER/static/</code>	The location of static assets.
SUBDOMAIN_ROUTING	false	A boolean that indicates whether subdomains are being used.
refreshTokenExpiration	60000	Idle time in milliseconds before the Gateway session expires.

Table 6: Compute Node Internal Configuration Keys - Do not change

Key	Default	Description
CDN	\$WAKARI_SERVER/ static/	The location of static assets.
USE_SES	false	Sets whether AEN will use Amazon SES to send emails.
multiUser	true	A boolean that indicates whether multi-user support is enabled.
multiProject	true	A boolean that indicates whether multi-project support is enabled.
ANACONDA_ROOT	/opt/wakari/ anaconda	The location of your Anaconda installation.
appLogs	/opt/wakari/ wakari- compute/var/ log/wakari/ compute-launcher-apps	The directory where application logs are stored.
appPIDs	/opt/wakari/ wakari-compute/ var/run/ compute-launcher-apps	The directory where application PID files are stored.
applicationLog	/opt/wakari/ wakari-compute/ var/log/ wakari/ compute-launcher- application. log	The path to the compute launcher log.
accessLog	opt/wakari/ wakari-compute/ var/log/ wakari/ compute-launcher- access.log	Path to compute launcher access log

## Checking configuration file syntax

To verify that the configuration file contains valid JSON, run:

```
root@server # python -m json.tool /opt/wakari/wakari-server/etc/wakari/*.json
root@gateway # python -m json.tool /opt/wakari/wakari-gateway/etc/wakari/*.json
root@compute # python -m json.tool /opt/wakari/wakari-compute/etc/wakari/*.json
```

If the file is correct, the contents are displayed.

If there is a syntax error in the file, a “No JSON object could be decoded” message is displayed instead.

To fix any errors, edit the configuration file and verify that it contains the correct JSON syntax.

## Increasing HTTP timeout between gateway and compute nodes

The default HTTP timeout is 600 seconds (10 minutes).

This setting works for HTTP timeout only, not HTTPS.

To modify the HTTP timeout setting:

1. Open the `/opt/wakari/wakari-compute/etc/wakari/wk-compute-launcher-config.json` file and modify the `httpTimeout` key:

```
"httpTimeout": 600
```

2. Update the gateway node by modifying the `httpTimeout` key in the `/opt/wakari/wakari-gateway/etc/wakari/wk-gateway-config.json` file to match the above settings.
3. Restart the AEN compute service:

```
sudo service wakari-compute restart
```

### Installing AEN in a custom location

To install AEN in a custom location:

1. Make the custom install folder owned by `$AEN_SRVC_ACCT`. EXAMPLE: `/data/aen/`.
2. Make a symlink from `/opt/wakari` to `/data/aen`.
3. Run the installers.
4. Move the folder from `/projects` to your chosen custom location. EXAMPLE: `/data/aen/projects`.
5. Make a symlink from `/projects` to `/data/aen/projects`.

NOTE: We recommend putting `/opt/wakari` and `/projects` on the same filesystem. If the project and conda environment directories are on separate filesystems then more disk space will be required on compute nodes and performance will be worse.

### Changing where projects are stored

NOTE: We recommend putting `/opt/wakari` and `/projects` on the same filesystem. If the project and conda env directories are on separate filesystems then more disk space will be required on compute nodes and performance will be worse.

To make `aen-compute` service use a different directory than `/projects` to store your AEN projects:

1. Modify the `/opt/wakari/wakari-compute/etc/wakari/wk-compute-launcher-config.json` file:

```
"projectRoot" : "/nfs/storage/services/wakari/projects",
```

NOTE: The directory `/nfs/storage/services/wakari/projects` specified as `projectRoot` must already exist for this command to resolve properly.

2. Restart the AEN compute service:

```
sudo service wakari-compute restart
```

### Group and user permissions for NFS

To install AEN with multiple compute nodes and a `/projects` folder on an NFSv3 volume, manually pre-create both the anonymous user and the `$AEN_SRVC_ACCOUNT` user on all nodes. Each of these users must have the same user identity number (UID) and group identity number (GID) on all nodes.

By default AEN creates local users with a different GID on each node. To make the AEN compute service create groups with the same GID:

1. In the `/opt/wakari/wakari-compute/etc/wakari/wk-compute-launcher-config.json` file, change the `identicalGID` key value to `true`:

```
, "identicalGID": true
```

If you don't see the `identicalGID` key, add it.

NOTE: You must add the comma at the beginning of the line. If you add this line as the last key, you must remove any comma at the end of the line.

2. Restart the AEN compute service:

```
sudo service wakari-compute restart
```

## Using numeric usernames

1. In the `/opt/wakari/wakari-compute/etc/wakari/wk-compute-launcher-config.json` file, change the `numericUsernames` key value to `true`.

```
, "numericUsernames": true
```

If you don't see the `numericUsernames` key, add it.

NOTE: You must add the comma at the beginning of the line. If you add this line as the last key, you must remove any comma at the end of the line.

2. Restart the AEN compute service:

```
sudo service wakari-compute restart
```

## Using project directories as home directories

The `projDirsAsHome` option changes the AEN home directories from the standard `/home/<username>` location to the project directories and the location `/projects/<username>/<project_name>/<username>/`. This ensures that AEN and AEN apps will not be affected by configuration files in a user's home directory, such as `.bashrc` or configuration files in subdirectories such as `.ipython` and `.jupyter`.

## Package cache locations

AEN version 4.1.3 stores the cache of packages in `/home/<username>`, while AEN versions 4.2.0 and higher store the cache of packages in `/projects/<username>/<project_name>/<username>/`. By moving the package cache to the same filesystem as the project, AEN versions 4.2.0 and higher can use hardlinks and save disk space and time when creating or cloning environments.

These package cache locations are not affected by the `projDirsAsHome` option.

After upgrading from AEN 4.1.3 to AEN 4.2.0 or higher, existing projects will still use the package cache in `/home/<username>`. Do not remove this cache, or the existing projects will break.

When users create new projects or install packages, the newly installed packages will use the new cache location.

If you wish to remove the older package cache in `/home/<username>`:

- Upgrade AEN to 4.2.0 or higher.
- Use `conda remove` to remove every non-default package in every project.
- Use `conda install` to replace them. The replaced packages will link to the new package cache in `/projects/<username>/<project_name>/<username>/`.
- You can now safely remove the older package cache.

## Enabling projDirsAsHome

NOTE: The `projDirsAsHome` option should be enabled immediately after performing the installation process and before any users have logged in to AEN. This ensures that users will not have home directories in different places due to some creating their home directories when the option was disabled and others creating their home directories when the option was enabled.

1. In the `/opt/wakari/wakari-compute/etc/wakari/wk-compute-launcher-config.json` file, add the `projDirsAsHome` key value and set it to `true`.

```
, "projDirsAsHome": true
```

NOTE: You must add the comma at the beginning of the line. If you add this line as the last key, you must remove any comma at the end of the line.

2. Restart the AEN compute service:

```
sudo service wakari-compute restart
```

## Setting up a default project environment

AEN includes a full installation of the Anaconda Python distribution—along with several additional packages—located within the root conda environment in `/opt/wakari/anaconda`.

The first time any new AEN project is started, this default project environment is cloned into the new project's workspace.

To configure a different set of packages than the default:

1. Create a new conda environment in the `/opt/wakari/anaconda/envs/default` directory.

EXAMPLE: Using a Python 3.4 base environment, run:

```
sudo -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda \  
create -p /opt/wakari/anaconda/envs/default python=3.4
```

2. Use `conda` to install any additional packages into the environment.
3. After the environment is created, clone it to ensure that it works correctly:

```
sudo -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda \  
create -p /opt/wakari/testenv --clone /opt/wakari/anaconda/envs/default  
sudo -u $AEN_SRVC_ACCT rm -rf /opt/wakari/testenv
```

For more information and examples about creating a default project environment with Microsoft R Open (MRO), see *Using MRO in AEN*.



## Converting an existing project

1. Run the following command to clone the environment:

```
sudo -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda \
  create -n /projects/owner/project/envs/<ENV_NAME> \
  --clone /opt/wakari/anaconda/envs/default
```

NOTE: Replace `/projects/owner/project/envs/<ENV_NAME>` with the path to the new environment you would like to create within the project.

2. Open the *Compute Resource Configuration application* for your project and set the project environment path there as well.

## Using MRO in AEN

In AEN 4.2.2 and higher, you can choose to create environments with the Microsoft R Open (MRO) interpreter by installing the `mro-base` package, or create environments with the R interpreter by installing the `r-base` package. Unless you request a change, conda will continue to use the existing interpreter in each environment. In AEN `r-base` is the default.

EXAMPLE: To create a custom environment called `mro_env` with MRO and R Essentials:

```
.. code-block:: bash

sudo -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda \
  create -c https://repo.anaconda.com/pkgs/main \
  -n mro_env r-essentials
```

NOTE: Conda 4.4 and higher include the `main` channel by default. Earlier versions of conda do not.

## Making a default project environment with MRO

You can also create an environment with MRO and make this the default AEN project environment.

The first time a new project is started, the default project environment is cloned into the new project's workspace.

1. Create a new conda environment in the `/opt/wakari/anaconda/envs/default` directory.

The command is similar to the one used in the previous example to create a custom environment.

```
sudo -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda \
  create -c https://repo.anaconda.com/pkgs/main \
  -p /opt/wakari/anaconda/envs/default r-essentials
```

2. Use conda to install any additional packages into the environment.
3. After the environment is created, clone it to check that it works correctly, and then clean up the clone.

```
sudo -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda \
  create -p /opt/wakari/testenv --clone /opt/wakari/anaconda/envs/default
sudo -u $AEN_SRVC_ACCT rm -rf /opt/wakari/testenv
```

NOTE: To convert existing projects, see *Converting an existing project*.

## Install AEN connected to a remote Mongo DB instance

To install AEN with a remote database:

1. Connect to the Mongodb instance and create the user for AEN:

```
> user = { user: "<username>",
  pwd: "<super-secure-password>",
  roles: [
    { role: "dbOwner", db: "<db_name>" },
    { role: "dbOwner", db: "<db_name>_mq" }
  ]
}
> db.createUser(user)
Successfully added user: { ... }
```

2. Before installing AEN-server export the database URL and name:

```
$ export MONGO_URL="mongodb://<username>:<password>@<host>:<port>/"
$ export MONGO_DB="<database_name>"
```

3. Continue the installation process: *Install the AEN server.*

## Migrate from local to remote MongoDB

To configure your remote database to work with an already installed AEN server:

1. Stop the server, gateway and compute nodes:

```
sudo service wakari-server stop
sudo service wakari-gateway stop
sudo service wakari-compute stop
```

2. Open the `/opt/wakari/wakari-server/etc/wakari/config.json` file and create the `MONGO_URL` key. For the value parameter, add the database information.

The final file should read:

```
{
  "MONGO_URL": "mongodb://MONGO-USER:MONGO-PASSWORD@MONGO-URL:MONGO-PORT",
  "MONGO_DB": "MONGO-DB-NAME",
  "WAKARI_SERVER": "http://YOUR-IP",
  "USE_SES": false,
  "CDN": "http://YOUR-IP/static/",
  "ANON_USER": "anonymous"
}
```

For more information about configuration keys, see *Using configuration files*.

3. Migrate the data from the former database into the new one. For more information, see the [MongoDB documentation website](#).
4. After migration, restart the nodes:

```
sudo service wakari-server start
sudo service wakari-gateway start
sudo service wakari-compute start
```

## Running SELinux in enforcing mode

To run SELinux in Enforcing mode, a few ports must be set up using the `semanage port` command.

The `semanage` command relies on `policycoreutils-python`. To install `policycoreutils-python`, if needed, run:

```
sudo yum -y install policycoreutils-python
```

Enable ports 9200 and 9300 for Elasticsearch:

```
sudo semanage port -a -t http_port_t -p tcp 9200
sudo semanage port -a -t http_port_t -p tcp 9300
```

## Changing server hostnames

It is possible to change the domain names (hostnames) of the various AEN nodes by updating the configuration files.

NOTE: After the configuration files are updated, the associated nodes need to be restarted.

To edit the information for all of the data centers that you are changing the base domain name for:

1. Go to the Site Admin section of the Admin Settings page.
2. In the Data Centers section, click the Edit button.
3. Make any necessary updates.

NOTE: This must include the service port if it is different from the default—80 for HTTP and 443 for HTTPS.

4. In the Enterprise Resources sub-section of the Providers section, edit each compute node that has a changed domain name.

NOTE: These URLs should include the protocol, hostname and port.

## Authenticating with LDAP

Anaconda Enterprise Notebooks performs local authentication against accounts in the AEN database by default.

To configure AEN to authenticate against accounts in an LDAP (Lightweight Directory Access Protocol) server, follow the instructions below.

## Installing OpenLDAP libraries

The system needs OpenLDAP libraries to be installed and accessible by AEN. AEN uses the OpenLDAP libraries to establish an LDAP connection to your LDAP servers.

To install OpenLDAP on CentOS or Redhat:

```
sudo yum install openldap
```

To install OpenLDAP on Ubuntu or Debian, follow the official [OpenLDAP installation instructions](#).

## Configuring OpenLDAP

1. Open the `/opt/wakari/wakari-server/etc/wakari/wk-server-config.json` file.
2. Add the following LDAP settings:

```
{
  "accounts": "wk_server.plugins.accounts.ldap2",
  "LDAP" : {
    "URI": "ldap://openldap.EXAMPLE.COM",
    "BIND_DN": "cn=Bob Jones,ou=Users,DC=EXAMPLE,DC=COM",
    "BIND_AUTH": "secretpass",
    "USER_SEARCH": { "base": "DC=EXAMPLE,DC=COM",
                     "filter": "(| (& (ou=Payroll)
                                   (uid=%(username)s))
                               (& (ou=Facilities)
                                   (uid=%(username)s)))"
                   },
    "KEY_MAP": { "email": "mail",
                 "name": "cn"
               }
  }
}
```

- **URI**—The IP address or hostname of your OpenLDAP server. For SSL/TLS, use the `ldaps://` prefix and specify a `TLS_CACERT` as described in the SSL/TLS configuration section below.
- **BIND\_DN**—The full directory path of the user you want AEN server to bind as.
- **BIND\_AUTH**—The password of the **BIND\_DN** user.
- **USER\_SEARCH**:
  - **base**—The level at which you want to start the search.
  - **filter**—The default is to search for the `sAMAccountName` attribute, and use its value for the AEN server username field.
- **KEY\_MAP**—Maps user attributes in AEN server to LDAP user attributes.

EXAMPLE: The `mail` attribute in LDAP maps to the `email` attribute in AEN server.

3. Restart AEN server to load new settings.
4. Log in with the admin account. This creates the admin user in the local database.
5. As soon as LDAP is installed, LDAP authentication takes over, so you need to add your admin account again:

```
/opt/wakari/wakari-server/bin/wk-server-admin superuser --add "jsmith"
```

## Configuring Active Directory

Microsoft Active Directory is a server program that provides directory services and uses the open industry standard Lightweight Directory Access Protocol (LDAP).

To enable Active Directory support:

1. Open the `/opt/wakari/wakari-server/etc/wakari/wk-server-config.json` file.
2. Add the following LDAP settings:

```
{
  "accounts": "wk_server.plugins.accounts.ldap2",
  "LDAP" : {
    "URI": "ldap://<ad.EXAMPLE.COM>",
    "BIND_DN": "CN=Bind User,CN=Users,DC=EXAMPLE,DC=COM",
    "BIND_AUTH": "secretpass",
    "USER_SEARCH": { "base": "CN=Users,DC=EXAMPLE,DC=COM",
                     "filter": "sAMAccountName=%(username)s"
                   },
    "KEY_MAP": { "email": "mail",
                 "name": "cn"
               }
  }
}
```

- **URI**—The IP address or hostname of your Active Directory server. Replace `<ad.EXAMPLE.COM>` with the actual URI. For SSL/TLS, use the `ldaps://` prefix and specify a `TLS_CACERT` as described in the SSL/TLS configuration section below.
- **BIND\_DN**—The full directory path of the user you want AEN server to bind as.
- **BIND\_AUTH**—The password of the **BIND\_DN** user.
- **USER\_SEARCH**:
  - **base**—the level at which you want to start the search.
  - **filter**—default is to search for the `sAMAccountName` attribute, and use its value for the AEN server `username` field.
- **KEY\_MAP**—Maps user attributes in AEN server to LDAP user attributes.

EXAMPLE: The `mail` attribute in LDAP maps to the `email` attribute in AEN server.

- Restart AEN server to load new settings.
- Log in with the admin account. This creates the admin user in the local database.
- As soon as LDAP is installed, LDAP authentication takes over, so you need to add your admin account again:

```
/opt/wakari/wakari-server/bin/wk-server-admin superuser --add "jsmith"
```

## Configuring SSL/TLS

AEN uses system-wide LDAP settings, including SSL/TLS support.

- On Redhat/CentOS systems, these settings are located in the `/etc/openldap/ldap.conf` file.
- On Ubuntu/Debian systems, these settings are located in the `/etc/ldap/ldap.conf` file.

Typically, the only configuration necessary is updating the file to read:

```
TLS_CACERT /path/to/CA.cert
```

NOTE: `CA.cert` is the Certificate Authority used to sign the LDAP server's SSL certificate. In the case of a self-signed SSL certificate, this is the path to the SSL certificate itself.

### Testing LDAP configuration

Test your LDAP configuration using `flask-ldap-login-check`:

```
/opt/wakari/wakari-server/bin/flask-ldap-login-check \
  wk_server.wsgi:app \
  -u [username] \
  -p [password]
```

NOTE: `username` is the username of a valid user and `password` is that user's `BIND_AUTH` password.

### Authenticating with PAM

To configure AEN to authenticate with PAM, you need to have LDAP in place and pre-populated with your users. With LDAP, pam does not require to read `/etc/shadow` and it can authenticate successfully without root privileges.

NOTE: PAM on the linux machine needs to be tied to LDAP (`pam_ldap`). You cannot use PAM with local unix accounts because `/etc/shadow` is only readable by the root user, but `pam_ldap` can authenticated against LDAP (non-root).

### Steps

1. Stop the wakari server:

```
sudo service wakari-server stop
```

1. update the configuration file `/opt/wakari/wakari-server/etc/wakari/wk-server-config.json` with the PAM authentication method. Change the entry for the line `"accounts"`: with:

```
"accounts": "wk_server.plugins.accounts.pam",
```

1. Restart the wakari server:

```
sudo service wakari-server start
```

1. In your browser navigate to Anaconda Enterprise Notebooks and attempt to login as a PAM-based user – create and start a project, then open a Jupyter Notebook.
2. Logout then login as an administrator and go to the *Admin* view. Attempt to list users.

### Testing

You can test PAM directly from the Python CLI

```
su - $AEN_USER/opt/wakari/wakari-server/bin/python
```

```
p = pam.pam()
p.authenticate("<username>", "<password>")
True
```

## Troubleshooting

If the server throws an `import error` for the `pam` module, please make sure that the `python-pam==1.8.2` module is installed. If the `.condarc` file includes the `wakari` channel then `python-pam==1.8.2` will be installed automatically.

## Configuring sudo customizations

If your organization's IT security policy does not allow root access or has restrictions on the use of `sudo`, after AEN installation, you may customize AEN to meet their requirements.

Your organization may choose to implement any or all of the following:

- *Remove root access* for AEN service account (Note: this restricts AEN from managing user accounts).
- *Configurable sudo command*.
- *Restrict sudo access to all processes*.

These customizations must be done in a terminal window after copying the files to the server node.

## Removing all root access from the service account

Because root access is required for `useradd`, the following process restricts AEN from managing user accounts.

1. Modify the `/etc/sudoers.d/wakari_sudo` file to read:

```
Defaults:wakari !requiretty, visiblepw
Runas_Alias    OP = ALL,!root
wakari ALL=(OP) NOPASSWD: ALL
```

NOTE: If you used a service account name other than `wakari`, enter that name instead of `wakari`.

2. Modify the `/opt/wakari/wakari-compute/etc/wakari/config.json` file to read:

```
"MANAGE_ACCOUNTS": false,
```

Using this option means that your IT department must create and manage all user accounts at the OS level.

After an OS-level account exists, you may create on the main AEN web page an AEN account using the same name. The password you choose is not linked in any way to the OS-level password for the account.

Alternatively, you can configure the system to *use LDAP for authenticating users*.

## Allowing public users to have access to your AEN projects

A public account is visible to anyone who can access the AEN server. The name of this account can be configured to any name you wish. For example, `public` or `anonymous`. To disable this feature use the special value `disabled`.

1. In the `/opt/wakari/wakari-compute/etc/wakari/wk-compute-launcher-config.json` file, modify the `ANON_USER` line to read:

```
"ANON_USER": "public"
```

2. Restart AEN compute node:

```
sudo service wakari-compute restart
```

3. In the `/opt/wakari/wakari-server/etc/wakari/wk-server-config.json` file, modify the `ANON_USER` line to read:

```
"ANON_USER": "public"
```

4. Restart AEN server:

```
sudo service wakari-server restart
```

For more information about configuration keys, see *Using configuration files*.

## Using a sudo alternative

You can use a sudo alternative as long as it supports the same execution semantics as the original sudo. The alternative must be configured to give the service account permission to run commands on behalf of AEN users.

1. In your terminal window, open the `/opt/wakari/wakari-compute/etc/wakari/config.json` file.
2. Modify the `AEN_SUDO_CMD` line to read:

```
"AEN_SUDO_CMD": "/path/to/alternative/sudo",
```

NOTE: If the alternate sudo command is available on `PATH`, then the full path is not required.

## Restricting sudo access to a single gatekeeper

By default, sudoers is configured to allow AEN to run any command as a particular user which allows the platform to initiate processes as the logged-in end user. If more restrictive control is required, it should be implemented using a suitable sudoers policy. If that is not possible or practical, it is also possible to route all AEN ID-changing operations through a single gatekeeper.

This gatekeeper wraps the desired executable and provides an alternate way to log, monitor, or control which processes can be initiated by AEN on behalf of a user.

CAUTION: Gatekeeper is a special case configuration and should only be used if required.

To configure an AEN gatekeeper:

1. Modify the `/etc/sudoers.d/wakari_sudo` file to contain:

```
Defaults:wakari !requiretty, visiblepw
Runas_Alias    OP = ALL,!root
wakari ALL=(OP) NOPASSWD: /path/to/gatekeeper
```

2. In the `/opt/wakari/wakari-compute/etc/wakari/config.json` file, modify the `AEN_SUDO_SH` line to read:

```
"AEN_SUDO_SH": "/path/to/gatekeeper"
```

EXAMPLE: The gatekeeper can be as simple as a script with contents such as:



```
#!/bin/bash
first_cmd=$1
if [ 'bash' == $1 ]; then
    shift
    export HOME=~
    export SHELL=/bin/bash
    export PATH=$PATH:/opt/wakari/anaconda/bin
    bash "$@"
else
    exec $@
fi
```

## Configuring SSL

The server node uses NGINX to proxy all incoming http(s) requests to the server running on a local port, and uses NGINX for SSL termination. The default setup uses http—non-SSL—since cert files are required to configure SSL and each enterprise will have their own cert files.

The `www.enterprise.conf` file is the default `nginx.conf` file used for AEN. It is copied to the `/etc/nginx/conf.d` directory during server installation.

NOTE: This section describes setting up SSL after your gateway node has been installed and registered with the server node.

## Copying the required files

To configure SSL on AEN, you will need the following files:

- Server certificate and key
- Server CA bundle
- Gateway certificate and key
- Gateway CA bundle

Configure SSL on AEN:

1. Copy the Gateway certificate and key to `/opt/wakari/wakari-gateway/etc/` on the Gateway as `gateway.crt` and `gateway.key`.
2. Copy the Gateway CA bundle to `/opt/wakari/wakari-server/etc/` on the Server.
3. Copy the Server certificate and key to `/etc/nginx` on the Server as `server.crt` and `server.key`.
4. Copy the Server CA bundle to `/opt/wakari/wakari-gateway/etc/` on the Gateway.

If you have a certificate that was signed by a private root CA and/or an intermediate authority:

- The Gateway CA bundle must contain the full chain: root CA, any intermediate authority and the certificate.

```
cat gateway.crt intermediate.crt root.crt >> gateway-crt-int-root.crt
```

- The Server CA bundle must be separated into individual files for the root CA, any intermediate and the certificate.

## Configuring SSL on the server node

The `www.enterprise.https.conf` is an NGINX configuration file for SSL. It is set up to use the `server.crt` and `server.key` cert files.

**CAUTION:** You must change these values to point to the signed cert files for your domain.

**NOTE:** Self-signed certs or those signed by a private root CA require additional configuration.

Perform the following steps as root:

1. Stop NGINX:

```
service nginx stop
```

2. Move the `/etc/nginx/conf.d/www.enterprise.conf` file to a backup directory.

3. Copy the `/opt/wakari/wakari-server/etc/nginx/conf.d/www.enterprise.https.conf` file to `/etc/nginx/conf.d`.

**NOTE:** `/etc/nginx/conf.d` may have `www.enterprise.conf` or `www.enterprise.https.conf` but it may not have both.

4. Edit the `/etc/nginx/conf.d/www.enterprise.https.conf` file and change the `server.crt` and `server.key` values to the names of the real cert and key files if they are different.

5. Restart NGINX by running:

```
service nginx start
```

6. Update the `WAKARI_SERVER` and `CDN` settings to use `https` instead of `http` in the following configuration files:

```
/opt/wakari/wakari-server/etc/wakari/config.json  
/opt/wakari/wakari-gateway/etc/wakari/wk-gateway-config.json  
/opt/wakari/wakari-compute/etc/wakari/config.json
```

7. Copy the gateway certificate, `gateway.crt` to `/opt/wakari/wakari-server/etc/`.

8. In an editor, open `/opt/wakari/wakari-server/etc/wakari/wk-server-config.json` and add:

```
"verify_gateway_certificate": "/opt/wakari/wakari-server/etc/gateway.crt"
```

9. Restart AEN services on the server by running:

```
service wakari-server restart
```

**NOTE:** This step may return an error since the gateway has not yet been configured for SSL.

10. In AEN, verify that the browser uses `https`. On the Admin Settings page, under Data Centers, click Gateway, then select `https`:

# Admin Settings

Anaconda Enterprise Notebooks settings accessible only by the administrator

The screenshot shows two side-by-side panels from the Anaconda Enterprise Admin Settings interface. The left panel, titled 'Staff', contains three links: 'Daily Report', 'Password Reset', and 'Notification'. The right panel, titled 'Data Centers / Register a datacenter', has a 'Name' field with the value 'Gateway 1'. Below this, there are two checkboxes: 'Subdomain Routing' (unchecked) and 'Https' (checked).

## Configuring SSL on the gateway

1. For all types of SSL certificates, in `/opt/wakari/wakari-gateway/etc/wakari/wk-gateway-config.json`, add:

```
{
  EXISTING_CONFIGURATION,
  "https": {
    "key": "/opt/wakari/wakari-gateway/etc/gateway.key",
    "cert": "/opt/wakari/wakari-gateway/etc/gateway.crt"
  }
}
```

2. For a server certificate signed by a private root CA or signed by an intermediate authority, add:

```
{
  EXISTING_CONFIGURATION,
  "https": {
    "key": "/opt/wakari/wakari-gateway/etc/gateway.key",
    "cert": "/opt/wakari/wakari-gateway/etc/gateway.crt",
    "ca": ["/opt/wakari/wakari-gateway/etc/server.crt"]
  }
}
```

**NOTE:** When the certificate chain has more than one intermediate cert signed by a higher root CA authority, you must manually break up the certs in the chain into individual files, and enumerate them in the `ca` key:

```
{
  EXISTING_CONFIGURATION,
  "https": {
    "key": "/opt/wakari/wakari-gateway/etc/gateway.key",
    "cert": "/opt/wakari/wakari-gateway/etc/gateway.crt",
    "ca": ["/opt/wakari/wakari-gateway/etc/server1.crt",
```

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```

        "/opt/wakari/wakari-gateway/etc/server2.crt"
        "/opt/wakari/wakari-gateway/etc/server3.crt"]
    }
}

```

3. For a gateway certificate that is encrypted using a passphrase, add:

```

{
  EXISTING_CONFIGURATION,
  "https": {
    "key": "/opt/wakari/wakari-gateway/etc/gateway.key",
    "cert": "/opt/wakari/wakari-gateway/etc/gateway.crt",
    "passphrase": "mysecretpassphrase"
  }
}

```

NOTE: Alternatively, the passphrase can be passed using an environment variable or entered when the wakari-gateway service is manually started.

#### EXAMPLES:

```

# using an environment variable
AEN_GATEWAY_SSL_PASSPHRASE='mysecretpassphrase' wk-gateway

```

```

# starting wakari-gateway manually
sudo service wakari-gateway start --ask-for-passphrase
Passphrase?

```

4. Restart the gateway:

```

sudo service wakari-gateway restart

```

## Configuring SSL on compute nodes

Anaconda Enterprise does not support direct SSL on Compute Nodes. If you need SSL on Compute Nodes, you must install each Compute Node on the same server as a Gateway using `http://localhost:5002` for the URL value while adding it as a resource, and you must use a Gateway for each and every Compute Node.

### Security reminder

The permissions on the cert files must be set correctly to prevent them from being read by others. Since NGINX is run by the root user, only the root user needs read access to the cert files.

EXAMPLE: If the cert files are called `server.crt` and `server.key`, then use the root account to set permissions:

```

chmod 600 server.key
chmod 600 server.crt

```

## Enabling or disabling the Strict-Transport-Security header

By default, Strict-Transport-Security (STS) is enabled in the `www.enterprise.https.conf` file:

```
add_header Strict-Transport-Security max-age=31536000;
```

It can remain enabled if either of the following is true:

- The gateway is running on a different host than the server.
- or
- SSL has been enabled for the gateway.

You must comment out this line if both of the following are true:

- The gateway is running on the same host as the server.
- and
- SSL has not been enabled for the gateway.

Leaving STS enabled when these conditions are true will cause a mismatch in protocols between the server and gateway, causing your apps to fail to launch correctly.

## Configuring single sign-on

AEN's single sign-on (SSO) capability creates a new authentication provider that defers to your Anaconda Repository for login and authentication cookies.

To enable SSO:

1. Deploy AEN and Repository on the same machine.
2. In the `/opt/wakari/wakari-server/etc/wakari/config.json` file, add:

```
{
  EXISTING_CONFIGURATION,
  "SECRET_KEY": "<repo signing secret>",
  "REPO_LOGIN_URL":
    "http://example_repo.com:8080/account/login?next=http://example_repo.com/"
}
```

3. Copy the `SECRET_KEY` from the Repository configuration file.
4. In the `/opt/wakari/wakari-server/etc/wakari/wk-server-config.json` file, modify:

```
{
  EXISTING_CONFIGURATION,
  "accounts": "wk_server.plugins.accounts.repo",
}
```

5. If you are using Repository version 2.33.3 through 2.33.10, set `USE_SERVER_BASED_SESSIONS: false` in the Repository configuration.

This setting affects the network security properties of AEN and Repository. Specifically, if `USE_SERVER_BASED_SESSIONS` is set to `false`, and if a new cross-site scripting (XSS) vulnerability is discovered, it could expose an additional server fixation vulnerability. Please discuss this with your Anaconda representative and be sure the feature is compatible with your network requirements before setting `USE_SERVER_BASED_SESSIONS: false`.

6. To activate the changes restart `wakari-server`:

```
sudo service wakari-server restart
```

SSO is enabled.

### Adding a third-party extension

Anaconda officially supports and tests functionality of the default environment(s) only for those extensions that ship with AEN.

It is possible to add third-party and custom extensions from conda-forge or pip, but doing so may cause instability in your default project environments or kernels.

CAUTION: Anaconda does not officially support third-party extensions. This section is informational only.

### Installing unofficial Jupyter Notebook extensions for AEN

TIP: Always back up and verify your complete system before installing extensions.

The jupyter-contrib-nbextensions extensions are installed on a compute node.

The default conda executable directory for AEN is `/opt/wakari/anaconda/bin/conda`. If you are installing a Jupyter extension, it must be installed in the `wakari-compute` directory.

EXAMPLE: Run:

```
/opt/wakari/anaconda/bin/conda install -p /opt/wakari/wakari-compute/ -c conda-forge ↵  
↪ jupyter_contrib_nbextension
```

For more information, see [Unofficial Jupyter Notebook Extensions](#).

### Configure search indexing

For search indexing to work correctly, verify that the AEN Compute node can communicate with the AEN Server.

```
curl -m 5 $AEN_SERVER > /dev/null
```

There must be at least one `inotify` watch available for the number of subdirectories within the project root filesystem. Some Linux distributions default to a low number of watches, which can prevent the search indexer from monitoring project directories for changes.

```
cat /proc/sys/fs/inotify/max_user_watches
```

If necessary, increase the number of max user watches with the following command:

```
echo fs.inotify.max_user_watches=100000 | sudo tee -a /etc/sysctl.conf && sudo sysctl ↵  
↪ -p
```

There must be at least one `inotify` user instance available per project.

```
cat /proc/sys/fs/inotify/max_user_instances
```

If necessary, this can be increased with the following command:

```
echo fs.inotify.max_user_instances=1000 | sudo tee -a /etc/sysctl.conf && sudo sysctl ↵  
↪ -p
```

## Create custom Jupyter kernel for Pyspark

These instructions add a custom Jupyter Notebook option to allow users to select PySpark as the kernel.

### Install Spark

The easiest way to install Spark is with [Cloudera CDH](#).

You will use YARN as a resource manager. After installing Cloudera CDH, [install Spark](#). Spark comes with a PySpark shell.

### Create a notebook kernel for PySpark

You may create the kernel as an administrator or as a regular user. Read the instructions below to help you choose which method to use.

#### 1. As an administrator

Create a new kernel and point it to the root env in each project. To do so create a directory 'pyspark' in `/opt/wakari/wakari-compute/share/jupyter/kernels/`.

Create the following kernel.json file:

```
{ "argv": [ "/opt/wakari/anaconda/bin/python",
  "-m", "ipykernel", "-f", "connection_file", "--profile", "pyspark"],
  "display_name": "PySpark", "language": "python" }
```

You may choose any name for the 'display\_name'.

This configuration is pointing to the python executable in the root environment. Since that environment is under admin control, users cannot add new packages to the environment. They will need an admin to help update the environment.

#### 2. As an administrator without IPython profile

To have an admin level PySpark kernel without the user .ipython space:

```
{ "argv":
[ "/opt/wakari/wakari-compute/etc/ipython/pyspark.sh", "-f", "{connection_file}" ],
  "display_name": "PySpark", "language": "python" }
```

NOTE: The pyspark.sh script is defined in *Without IPython profile* section below.

#### 3. As a regular user

Create a new directory in the user's home directory: `.local/share/jupyter/kernels/pyspark/`. This way the user will be using the default environment and able to upgrade or install new packages.

Create the following kernel.json file:

```
{ "argv": [ "/projects/<username>/<project_name>/envs/default/bin/python",
  "-m", "ipykernel", "-f", "connection_file", "--profile", "pyspark"],
  "display_name": "PySpark", "language": "python" }
```

NOTE: Replace “<username>” with the correct user name and “<project\_name>” with the correct project name.

You may choose any name for the ‘display\_name’.

### Create an IPython profile

The above profile call from the kernel requires that we define a particular PySpark profile. This profile should be created for each user that logs in to AEN to use the PySpark kernel.

In the user’s home, create the directory and file `~/ipython/profile_pyspark/startup/00-pyspark-setup.py` with the file contents:

```
import os
import sys

# The place where CDH installed spark, if the user installed Spark locally it can be
↪ changed here.
# Optionally we can check if the variable can be retrieved from environment.

os.environ["SPARK_HOME"] = "/usr/lib/spark"

os.environ["PYSPARK_PYTHON"] = "/opt/wakari/anaconda/bin/python"

# And Python path
os.environ["PYLIB"] = os.environ["SPARK_HOME"] + "/python/lib"
sys.path.insert(0, os.environ["PYLIB"] + "/py4j-0.9-src.zip") #10.4-src.zip")
sys.path.insert(0, os.environ["PYLIB"] + "/pyspark.zip")

os.environ["PYSPARK_SUBMIT_ARGS"] = "--name yarn pyspark-shell"
```

Now log in using the user account that has the PySpark profile.

### Without IPython profile

If it is necessary to avoid creating a local profile for the users, a script can be made to be called from the kernel. Create a bash script that will load the environment variables:

```
sudo -u $AEN_SRVC_ACCT mkdir /opt/wakari/wakari-compute/etc/ipython
sudo -u $AEN_SRVC_ACCT touch /opt/wakari/wakari-compute/etc/ipython/pyspark.sh
sudo -u $AEN_SRVC_ACCT chmod a+x /opt/wakari/wakari-compute/etc/ipython/pyspark.sh
```

The contents of the file should look like:

```
#!/usr/bin/env bash
# setup environment variable, etc.

export PYSPARK_PYTHON="/opt/wakari/anaconda/bin/python"
export SPARK_HOME="/usr/lib/spark"

# And Python path
export PYLIB=$SPARK_HOME:/python/lib
export PYTHONPATH=$PYTHONPATH:$PYLIB:/py4j-0.9-src.zip
export PYTHONPATH=$PYTHONPATH:$PYLIB:/pyspark.zip

export PYSPARK_SUBMIT_ARGS="--name yarn pyspark-shell"
```

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```
# run the ipykernel
exec /opt/wakari/anaconda/bin/python -m ipykernel $@
```

## Using PySpark

When creating a new notebook in a project, now there will be the option to select PySpark as the kernel. When creating such a notebook you'll be able to import pyspark and start using it:

```
from pyspark import SparkConf
from pyspark import SparkContext
```

NOTE: You can always add those lines and any other command you may use frequently in the PySpark setup file 00-pyspark-setup.py as shown above.

## Enabling server-side session management

By default, AEN uses client-side session management which is vulnerable to session replay attacks if an attacker manages to steal a valid session ID of a user.

To enable server-side session management:

1. Modify the /opt/wakari/wakari-server/etc/wakari/wk-server-config.json file:

```
"USE_SERVER_BASED_SESSIONS": true,
```

2. Restart the AEN server service:

```
sudo service wakari-server restart
```

## Terminate terminal sessions on logout

By default, when a user logs out, their open terminal sessions will remain active.

To disable this behavior:

1. Modify the /opt/wakari/wakari-server/etc/wakari/wk-server-config.json file:

```
"TERMINATE_TERMINALS_ON_LOGOUT": true,
```

2. Modify the /opt/wakari/wakari-gateway/etc/wakari/wk-gateway-config.json file:

```
"TERMINATE_TERMINALS_ON_LOGOUT": true,
```

3. Restart the AEN server service:

```
sudo service wakari-server restart
```

4. Restart the AEN gateway service:

```
sudo service wakari-gateway restart
```

### Upgrading AEN

- *Before you upgrade*
- *Upgrading the AEN server node*
- *Upgrading the AEN gateway node*
- *Upgrading AEN compute nodes*
- *After upgrading*

**CAUTION:** These instructions are for upgrading AEN to the current version 4.3.3 from 4.3.2 ONLY. Each version must be upgraded iteratively from the previous version. Do not skip versions.

Upgrade instructions for previous versions:

- *AEN 4.3.2 upgrade instructions*
- *AEN 4.3.1 upgrade instructions*
- *AEN 4.3.0 upgrade instructions*
- *AEN 4.2.2 upgrade instructions*
- *AEN 4.2.1 upgrade instructions*
- *AEN 4.2.0 upgrade instructions*
- *AEN 4.1.3 upgrade instructions*
- *AEN 4.1.2 upgrade instructions*
- *AEN 4.1.1 upgrade instructions.*
- *AEN 4.1.0 upgrade instructions.*
- *AEN 4.0.0 upgrade instructions.*

For upgrades from versions before those listed above, please contact your enterprise support representative.

**NOTE:** Named Service Account functionality is available with AEN 4.0.0+ for new installations only. It is not available for upgraded installations. Contact your enterprise support representative for more information.

An AEN platform update requires that each instance of the 3 node types be upgraded individually:

- AEN Server
- AEN Gateway
- AEN Compute

The upgrade process requires that all AEN service instances be stopped, upgraded, and then restarted.

**NOTE:** Any commands that call for the root user can also be done using `sudo`.

If you encounter any difficulty during the upgrade process, see [Troubleshooting](#) which provides guidance on:

- processes
- configuration files
- log files
- ports

If you are unable to resolve an installation or upgrade problem, please contact your enterprise support representative.

## Before you upgrade

**CAUTION:** Make a tested backup of your installation before starting the upgrade. Upgrading to a higher version of AEN is not reversible. Any errors during the upgrade procedure may result in partial or complete data loss and require restoring data from backups.

**CAUTION:** Terminate all AEN applications and stop all projects before starting the upgrade process.

Before upgrading each service on each host:

1. Suspend the services on each of the nodes:

```
sudo service wakari-server stop
sudo service wakari-gateway stop
sudo service wakari-compute stop
```

2. Set the AEN Functional ID (“NFI”) and AEN Functional Group (“NFG”) to the NFI and NFG of the current installation:

```
export AEN_SRVC_ACCT="wakari"
export AEN_SRVC_GRP="wakari"
```

**NOTE:** The default NFI is wakari, but aen\_admin or any other name may be used instead.

For more information on NFI and NFG, see the [installation instructions](#).

3. Install wget:

```
yum install wget
```

4. Update .condarc files:

/opt/wakari/miniconda/.condarc should be updated with the following content:

```
channels:
  - r
  - https://conda.anaconda.org/wakari
  - http://repo.continuum.io/pkgs/main/
  - defaults

create_default_packages:
  - anaconda-client
  - ipykernel=4.10.0
```

and /opt/wakari/anaconda/.condarc should be updated with the following content:

```
channels:
  - r
  - https://conda.anaconda.org/wakari
  - http://repo.continuum.io/pkgs/main/
  - defaults
create_default_packages:
  - anaconda-client
  - ipykernel=4.10.0
auto_update_conda: false
```

**NOTE:** Both contents are similar but different ones, be sure to update them as indicated.

## Upgrading the AEN server node

NOTE: If you are using LDAP-based authentication, back up the `/opt/wakari/wakari-server/etc/wakari/wk-server-config.json` configuration file. After the server has been upgraded, copy that file back into the same location as before the upgrade.

Complete the following steps on the server host:

1. Stop the Elasticsearch service:

```
sudo service elasticsearch stop
```

2. Remove any previous index:

```
sudo rm -rf /var/lib/elasticsearch/*
```

NOTE: You can choose to keep the old index, but if you detect any issues with the search capabilities after the upgrade, you will need to run the following to start with a clean index:

```
sudo service wakari-server stop
sudo service elasticsearch stop
sudo rm -rf /var/lib/elasticsearch/*
sudo service elasticsearch start
sudo service wakari-server start
```

3. Upgrade the server:

```
pushd /tmp
wget http://j.mp/aen-server-update-4.3.3

sudo -E -u $AEN_SRVC_ACCT /opt/wakari/miniconda/bin/conda install \
    -p /opt/wakari/wakari-server \
    --file aen-server-update-4.3.3

sudo -E -u $AEN_SRVC_ACCT /opt/wakari/miniconda/bin/conda install \
    -p /opt/wakari/wakari-server \
    --no-deps \
    wakari-enterprise-server-conf-update=2.0.13

popd
```

4. Start Elasticsearch:

```
sudo service elasticsearch start
```

Or, if you do not want to use the search features, edit your server's `/opt/wakari/wakari-server/etc/wakari/config.json` file by adding the line `"SEARCH_ENABLED": false`.

5. Restart the *NGINX* server:

AEN server version `>= 4.1.3` uses Unix sockets for communication with NGINX. Restart NGINX to load this new configuration:

```
sudo service nginx restart
```

Alternatively, you can restart NGINX with:

```
sudo nginx -s stop
sudo nginx
```

6. Start the server:

```
sudo service wakari-server start
```

7. Check that the server is running properly:

```
sudo service wakari-server status
```

8. If you see NGINX errors, please check the configuration at `/opt/wakari/wakari-server/etc/nginx/conf.d/www.enterprise.conf:18`.
9. Connect to AEN server using your web browser with the correct protocol (http or https), hostname and port number.

## Upgrading the AEN gateway node

Complete the following steps on each gateway host:

1. Upgrade the gateway:

```
pushd /tmp
wget http://j.mp/aen-gateway-update-4.3.3

sudo -E -u $AEN_SRVC_ACCT /opt/wakari/miniconda/bin/conda install \
    -p /opt/wakari/wakari-gateway \
    --file aen-gateway-update-4.3.3

sudo -E -u $AEN_SRVC_ACCT /opt/wakari/miniconda/bin/conda install \
    -p /opt/wakari/wakari-gateway \
    --no-deps \
    wakari-enterprise-gateway-conf-update=2.0.13

popd
```

2. Start the gateway:

```
sudo service wakari-gateway start
```

3. Check that the gateway is running properly:

```
sudo service wakari-gateway status
```

4. Connect to the gateway using your web browser with the correct http/https, hostname and port number.

## Upgrading AEN compute nodes

Complete the following steps on each host where an AEN compute service is running:

1. Check for any `wakari-indexer` processes running:

```
ps aux | grep wakari-indexer
```

NOTE: If you stopped all the projects, you will not see any `wakari-indexer` processes running.

Terminate any remaining `wakari-indexer` processes:

```
sudo killall wakari-indexer
```

NOTE: The processes killed with `killall` are run by the `$AEN_SRVC_ACCT` user, so they can be killed as root with `sudo killall` or killed as the `$AEN_SRVC_ACCT` user with `sudo -u $AEN_SRVC_ACCT killall`. Example commands show the `sudo killall` option.

2. Check for any AEN applications processes running—Workbench, Viewer, Terminal or Notebook:

```
ps aux | grep wk-app-gateone
ps aux | grep wk-app-workbench
ps aux | grep wk-app-viewer
ps aux | grep wk-app-terminal
ps aux | grep jupyter-notebook
```

NOTE: If you stopped all the projects, you will not see any AEN app processes running.

Terminate any remaining AEN application processes by running one or more of the following:

```
sudo killall wk-app-gateone
sudo killall wk-app-workbench
sudo killall wk-app-viewer
sudo killall wk-app-terminal
sudo killall jupyter-notebook
```

3. Verify the contents of `/opt/wakari/anaconda/.condarc`. Modify it to contain the following entries, and possibly others if you customized the `.condarc` file.

NOTE: Modify the file as the `AEN_SRVC_ACCT` user (or be sure to keep the same ownership).

```
channels:
- https://conda.anaconda.org/t/<TOKEN>/anaconda-nb-extensions
- r
- https://conda.anaconda.org/wakari
- http://repo.continuum.io/pkgs/main/
- defaults
create_default_packages:
- anaconda-client
- ipykernel=4.10.0
auto_update_conda: false
```

NOTE: Contact your enterprise support representative to get your token for the Anaconda channel referenced above. Replace `<TOKEN>` with the actual token from your enterprise support representative.

4. Upgrade *Anaconda* in the root environment:

```
pushd /tmp
wget http://j.mp/aen-anaconda-update-4_3_3

sudo -E -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda remove -p /opt/wakari/
↪anaconda geotiff --yes

sudo -E -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda remove -p /opt/wakari/
↪anaconda iopro --yes

sudo -E -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda remove -p /opt/wakari/
↪anaconda libthrift --yes

sudo -E -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda remove -p /opt/wakari/
↪anaconda basemap --yes

sudo -E -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda install \
```

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(continued from previous page)

```

    -p /opt/wakari/anaconda \
    --file aen-anaconda-update-4_3_3
popd

```

#### 5. Upgrade each compute service:

```

pushd /tmp
wget http://j.mp/aen-compute-update-4.3.3

sudo -E -u $AEN_SRV_C_ACCT /opt/wakari/anaconda/bin/conda install \
    -p /opt/wakari/wakari-compute \
    --file aen-compute-update-4.3.3

sudo -E -u $AEN_SRV_C_ACCT /opt/wakari/anaconda/bin/conda install \
    --no-deps \
    -p /opt/wakari/wakari-compute \
    wakari-enterprise-compute-conf-update=2.0.17
popd

```

NOTE: When upgrading the wakari-compute environment, you may see *ImportError* warnings with some nbextensions. As long as the Validating message is OK, the *ImportError* warnings are harmless—a consequence of the post-link presence on those packages.

#### 6. Initialize the root environment to prime the package cache:

```

sudo -E -u $AEN_SRV_C_ACCT /opt/wakari/anaconda/bin/conda create \
    -p /opt/wakari/testenv \
    --clone root

```

#### 7. Test the offline cloning step:

```

sudo -E -u $AEN_SRV_C_ACCT /opt/wakari/anaconda/bin/conda create \
    -p /opt/wakari/testenvoffline \
    --clone root --offline

```

#### 8. Remove the test environments:

```

sudo rm -rf /opt/wakari/testenv
sudo rm -rf /opt/wakari/testenvoffline

```

#### 9. Install necessary dependencies:

NOTE: Skip this step if you already have these dependencies installed from previous installations.

```

sudo yum groupinstall "X Window System" -y
sudo yum install git -y

```

NOTE: If you don't want to install the whole X Window System, you must install the following packages to have R plotting support:

```

sudo yum install -y libXrender libXext libXdmcp libSM libICE libXt \
    dejavu-sans-fonts dejavu-serif-fonts dejavu-fonts-common \
    fontpackages-filesystem

```

#### 10. Start the compute service:

```
sudo service wakari-compute start
```

11. Verify the compute service is running properly:

```
sudo service wakari-compute status
```

12. Restart the AEN Server with:

```
sudo service wakari-server restart
```

13. Repeat this upgrade procedure for all compute nodes in your Data Center.

## After upgrading

1. Restart the projects and start using AEN applications.
2. If you have a *customized default environment*, you may choose to upgrade it depending on the needs of your users.

Upgrade the customized default environment at `/opt/wakari/anaconda/envs/default` with the `$AEN_SRVC_ACCT` user:

```
pushd /tmp
wget http://j.mp/aen-anaconda-update-4.3.3

sudo -E -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda install \
    -p /opt/wakari/anaconda/envs/default \
    --file aen-anaconda-update-4.3.3

popd
```

To upgrade the customized default environments for every user and every project at `/projects/<USER>/<PROJECT>/envs/default`, run these commands for **every** user as that user:

```
pushd /tmp
wget http://j.mp/aen-anaconda-update-4.3.3

sudo -E -u <USER> /opt/wakari/anaconda/bin/conda install \
    -p /projects/<USER>/<PROJECT>/envs/default \
    --file aen-anaconda-update-4.3.3

popd
```

NOTE: Replace `<USER>` with the user's name. Replace `<PROJECT>` with the project name.

NOTE: Upgrading the default environment at `/opt/wakari/anaconda/envs/default` does NOT automatically upgrade the default environment in the users pre-existing projects. For pre-existing projects, the upgrade, if requested, should be done on a per-user basis.

NOTE: These commands update packages listed in `aen-anaconda-update-4.3.3` and do not update any other package.

3. If you did not stop all your projects before upgrading, then the first time you start an application you will see an error page requesting that you restart the application.
4. Restart the application to complete the upgrade.
5. If you still see old applications or icons after restart, reload the page to reset the browser cache.



## Uninstalling AEN

Each AEN node must be uninstalled separately.

- *Uninstalling a server node*
- *Uninstalling a gateway node*
- *Uninstalling a compute node*
- *OPTIONAL: Removing projects from compute nodes*

Begin by setting the AEN Functional ID (NFI). The NFI is the username of the AEN Service Account which is used to run all AEN services and is also the username of the AEN Admin account. The NFI may be any name. The default NFI is `wakari`. The NFI is also often set to `aen_admin`. The NFI (and AEN Functional Group or NFG) are described in *the installation instructions*.

Set the NFI with this command:

```
export AEN_SRVC_ACCT="aen_admin"
```

Replace the name `aen_admin` with the NFI that was set in your installation of Anaconda Enterprise Notebooks.

### Uninstalling a server node

To remove a server node, run the following commands as root or sudo on the server node's host system:

1. Stop the server processes:

```
service wakari-server stop
```

2. Stop MongoDB:

```
service mongod stop
```

3. Remove AEN server software, AEN database files and NGINX configuration:

```
rm -Rf /opt/wakari/wakari-server
rm -Rf /opt/wakari/miniconda
rm -Rf /var/lib/mongo/wakari*
rm -Rf /etc/nginx/conf.d/www.enterprise.conf
```

NOTE: Remove `/etc/nginx/conf.d/www.enterprise.https.conf` if SSL is enabled on the Server node.

4. Restart MongoDB and NGINX:

```
service mongod restart
service nginx restart
```

5. Check for any outstanding server processes and stop them:

```
ps -ef | grep -e wakari-server -e wk-server
```

6. Remove the AEN Service Account:

```
userdel $AEN_SRVC_ACCT
```

7. Check for and remove any references to “aen” or “wakari” from the root user’s `.condarc` file:

```
grep -i aen ~/.condarc
grep -i wakari ~/.condarc
```

### Uninstalling a gateway node

To uninstall a gateway node, run the following commands as root or sudo on the gateway host system:

1. Stop the gateway processes:

```
service wakari-gateway stop
```

2. Remove gateway software:

```
rm -Rf /opt/wakari/wakari-gateway
```

3. Check for any outstanding gateway processes and stop them:

```
ps -ef | grep -e wakari-gateway -e wk-gateway
```

4. Remove the AEN Service Account:

```
userdel $AEN_SRVC_ACCT
```

5. Check for and remove any references to “aen” or “wakari” from the root user’s `.condarc` file:

```
grep -i aen ~/.condarc
grep -i wakari ~/.condarc
```

### Uninstalling a compute node

To remove a compute node, run the following commands as root or sudo on each compute node host system:

1. Stop the compute processes:

```
service wakari-compute stop
```

2. Remove the compute software:

```
rm -Rf /opt/wakari/wakari-compute
rm -Rf /opt/wakari/miniconda
rm -Rf /opt/wakari/anaconda
```

3. Check for any outstanding compute processes and stop them:

```
ps -ef | grep -e wakari-compute -e wk-compute
```

4. Remove the AEN Service Account:

```
userdel $AEN_SRVC_ACCT
```

5. Check for and remove any references to “aen” or “wakari” from the root user’s `.condarc` file:

```
grep -i aen ~/.condarc  
grep -i wakari ~/.condarc
```

### OPTIONAL: Removing projects from compute nodes

**CAUTION:** This is an extreme measure and is not necessary in most instances. We recommend you create and verify a backup before doing this or any other file removal.

To remove all AEN projects from all of your compute nodes:

```
rm -Rf /projects
```

This is a step-by-step guide to installing an Anaconda Enterprise Notebooks system comprised of a front-end server, a gateway and compute machines.

If you have any questions about these instructions or you encounter any issues while installing AEN, please contact your sales representative or Priority Support team.

When you have completed the installation process, review the *optional configuration tasks* to see if any are appropriate for your system.

### Distributed install

In a distributed install the server and gateway run on separate hosts.

### Single-box install

In a single-box install, both the server and the gateway need separate external ports since they are independent services that are running on the same host in the single-box installation.

Both port 80 and port 8089 must be open on the firewall for a single-box install.

The compute node only receives connections from the gateway and server nodes and typically runs on port 80 or port 443.

### User management

#### Adding or removing an administrative user

An administrator can make any other user an administrator—or remove their administrator permissions—by using administrator commands in the Terminal application.

A user can also be designated as a superuser or as staff, giving them greater administrative privileges within the system.

#### Designating a user as an administrator/superuser

To designate a user as an administrator and superuser:

```
/opt/wakari/wakari-server/bin/wk-server-admin superuser --add <username>
```

NOTE: Replace <username> with the actual username.

EXAMPLE: To give administrative privileges to the user named “jsmith” and set them as a superuser, run:

```
/opt/wakari/wakari-server/bin/wk-server-admin superuser --add jsmith
```

### Removing an administrator/superuser

To remove a user’s administrative privileges:

```
/opt/wakari/wakari-server/bin/wk-server-admin superuser --remove <username>
```

NOTE: Replace <username> with the actual username.

### Allowing and restricting new user registration

When Open Registration is enabled, anyone who has access to the URL of your AEN server can create their own account.

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select Accounts.

The screenshot shows the Admin Settings page. On the left, there are two navigation menus. The 'Staff' menu includes links for 'Daily Report', 'Password Reset', 'Notification', and 'Exceptions'. The 'Site Admin' menu includes links for 'General' and 'Accounts'. The main content area is titled 'Cloud Registration' and contains a checkbox labeled 'Open Registration' with the text 'Allow new user signups' below it. The checkbox is checked. At the bottom of this section is a green 'Update' button.

3. To open user registration, select the Open Registration checkbox. To close registration, clear the checkbox.
4. Click the Update button.

### Resetting a user password

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Staff** menu, select Password Reset:

Anaconda Enterprise Notebooks settings accessible only by the system administrator.

The screenshot shows a web interface for managing staff. On the left is a sidebar with a 'Staff' header and links for 'Daily Report', 'Password Reset', 'Notification', and 'Exceptions'. The 'Password Reset' link is highlighted. The main content area is titled 'Password Reset' and contains a text input field with the value 'guest' and a button labeled 'Generate URL'.

3. Enter the username of the user whose password needs to be reset.
4. Click the Generate URL button.

A password reset link is generated that you can email to the user.

Alternatively you may use the command line interface:

1. Use ssh to log into the server as root.
2. Run:

```
/opt/wakari/wakari-server/bin/wk-server-admin reset-password -u SOME_USER -p SOME_
↪PASSWORD
```

NOTE: Replace SOME\_USER with the username and SOME\_PASSWORD with the password.

3. Log into AEN as the user.

## Managing permissions

This page explains the admin commands used to manage user permissions.

### Checking file ownership

To verify that all files in the `/opt/wakari/anaconda` directory are owned by the `wakari` user or group:

```
root@server # find /opt/wakari/anaconda \! -user wakari -print
root@server # find /opt/wakari/anaconda \! -group wakari -print
```

### Fixing file ownership settings

To fix the ownership settings of any files that are listed in the output:

```
chown -R wakari:wakari /opt/wakari/anaconda
```

## Setting a file owner and permissions

To set a file owner and set its permissions:

```
chown wakari:wakari /opt/wakari/wakari-server/bin/wk-*
chmod 700 /opt/wakari/wakari-server/bin/wk-*
```

## Verifying that POSIX ACLs are enabled

The `acl` option must be enabled on the file system that contains the project root directory.

NOTE: By default, the project root directory is `/projects`.

To determine the project root directory where a custom `projectRoot` is configured:

```
root@compute # grep projectRoot /opt/wakari/wakari-compute/etc/wakari/config.json
```

The mount options or default options listed by `tune2fs` should indicate that the `acl` option is enabled.

EXAMPLE:

```
root@compute # fs=`df /projects | tail -1 | cut -d " " -f 1`
root@compute # mount | grep $fs
/dev/vda on / type ext4 (rw)
root@compute # tune2fs -l $fs | grep options
Default mount options:    user_xattr acl
```

## Viewing a list of users

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select Users:

Staff

[Daily Report](#)
[Password Reset](#)
[Notification](#)
[Exceptions](#)

Site Admin

[General](#)
[Accounts](#)
[Users](#)

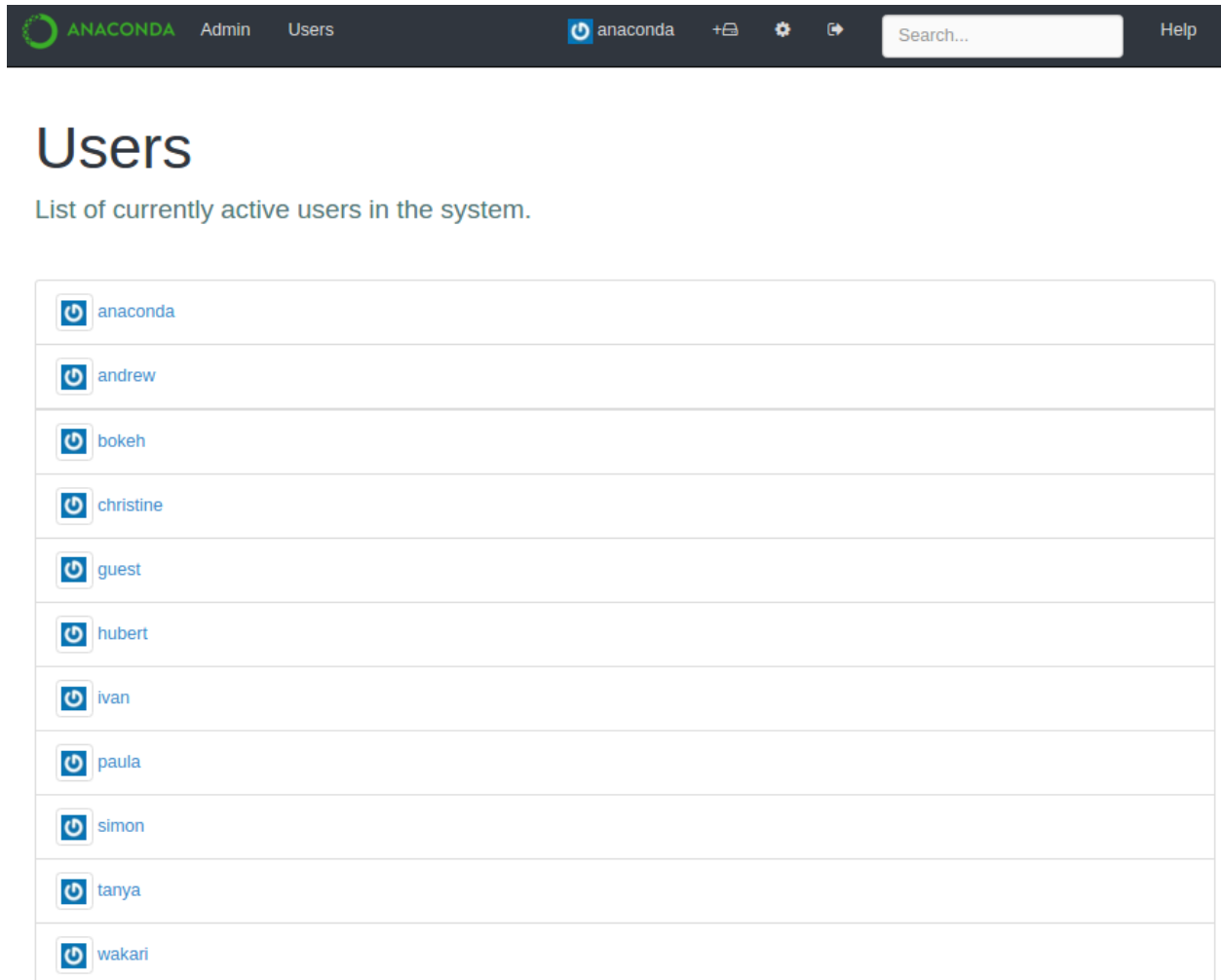
Users

Username	Projects	Last Seen
<a href="#">aen_admin</a>	6	Sep 25, 2017 10:05:58 CDT












The Users section lists the all users who are signed up, the number of projects they have created and the last time they logged on to AEN.

### Viewing a list of currently active users

In the AEN navigation bar, click Users.



The screenshot shows the Anaconda Enterprise (AEN) interface. At the top is a dark navigation bar with the Anaconda logo, 'Admin' and 'Users' links, a search bar, and a 'Help' link. Below the navigation bar, the page title 'Users' is displayed in a large font, followed by the subtitle 'List of currently active users in the system.' Below this is a table listing ten active users, each with a blue power icon and their username.

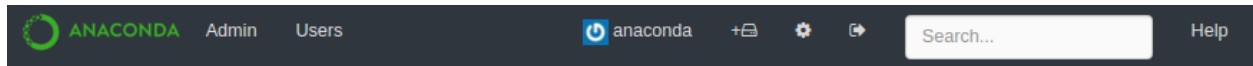
 anaconda
 andrew
 bokeh
 christine
 guest
 hubert
 ivan
 paula
 simon
 tanya
 wakari

Click a username to open the user's profile page.

### Viewing a user profile

A user's profile page includes a summary of the projects created by that user and a list of projects on which the user is a team member.

1. In the AEN navigation bar, click Users to see a list of users who are currently logged into the system.
2. On the Users page, click the username of the user whose profile page you want to view.



## Users

List of currently active users in the system.

 anaconda
 andrew
 bokeh
 christine
 guest
 hubert
 ivan
 paula
 simon
 tanya
 wakari

### Sending a system message

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Staff** menu, select Notification:



**Staff**

[Daily Report](#)  
[Password Reset](#)  
[Notification](#)  
[Exceptions](#)

**Site Admin**

[General](#)  
[Accounts](#)  
[Users](#)  
[Security Log](#)  
[Data Centers](#)  
[Task Queue](#)  
[License](#)

**Providers**

[Enterprise Resources](#)

**Notification Settings**

☒ **Off**  
No email notification will be sent

---

☐ **SES - Amazon Simple Email Service**  
This requires a .boto file in the wakari home dir

---

☐ **SMTP Email Server**

**SMTP Settings**

**SMTP Hostname**

**SMTP Username (optional)**

**SMTP Password (optional)**

**SMTP From Address (optional)**

Update

The Notification Settings section allows you to create a system message that can be relayed to users.

By default, notifications are off.

3. To turn on email notifications, select the radio button for the type of email service to use:

- SES to use Amazon Simple Email Service (SES).
- SMTP Email Server.

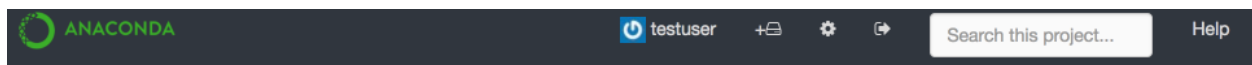
4. If you select SMTP Email Server, complete the SMTP Settings.

NOTE: If you get an error message after changing the SMTP settings, you may need to restart the server.

### Moving a project to another compute node

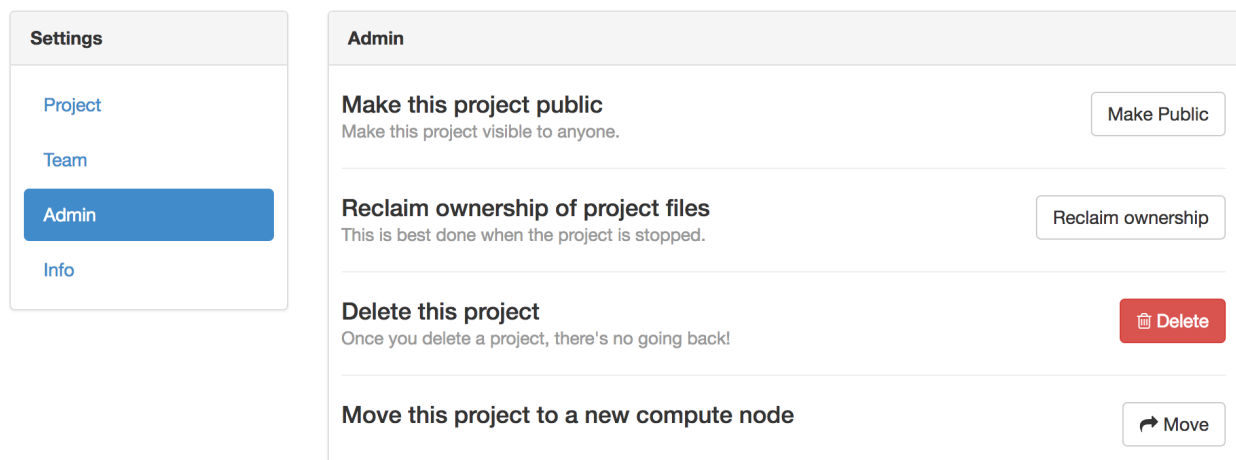
If you have multiple compute nodes available and want to move a project from one to another, the project must exist on both nodes.

1. Verify that the project has been created on both compute nodes. You can use `rsync` for this job unless you have a shared file system like `nfs`.
2. On the project home page, click the Project Settings icon to open the Project Settings page.

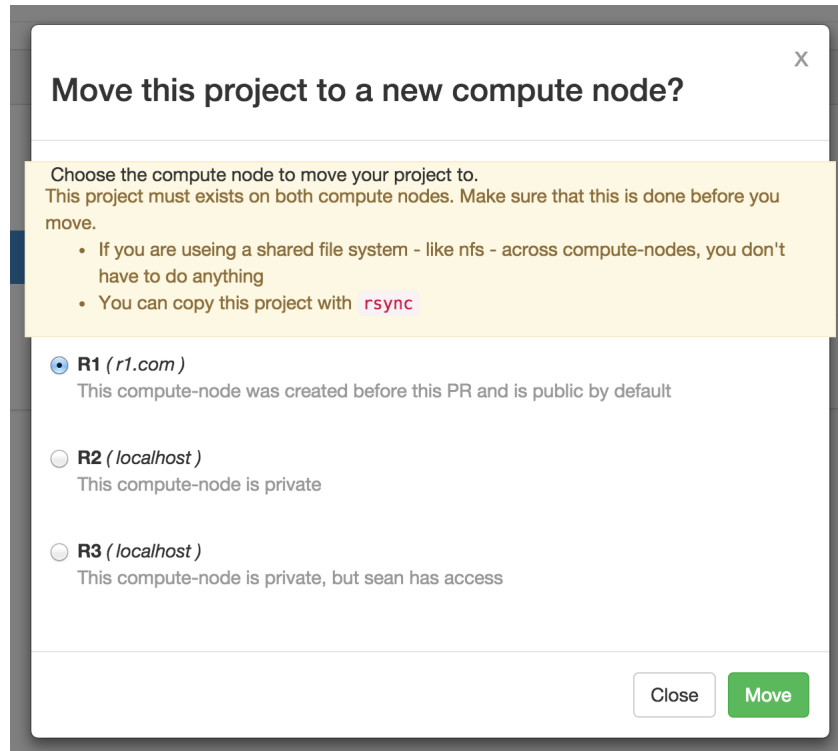


3. In the **Settings** menu, select Admin.

testuser / TestProject



4. Click the Move button.
5. In the move dialog box, click to choose the compute node destination, and click the Move button.



## Deleting a user

To remove a user from the AEN database:

```
/opt/wakari/wakari-server/bin/wk-server-admin remove-user <username>
```

NOTE: Replace <username> with the actual username.

NOTE: Changing the owner of a project requires that both the previous owner and the new owner are still AEN users. Before deleting a user, *change the owner* of that user's projects.

## Deleting a project

To remove a project from the AEN database:

```
/opt/wakari/wakari-server/bin/wk-server-admin remove-project <username> <projectname>
```

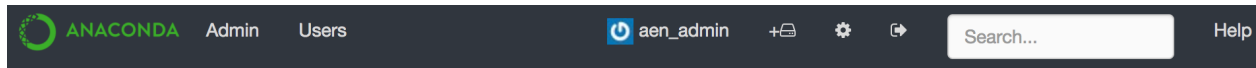
NOTE: Replace <username> with the actual username and <projectname> with the actual project name you are removing.

## System management

### Opening the Admin dashboard

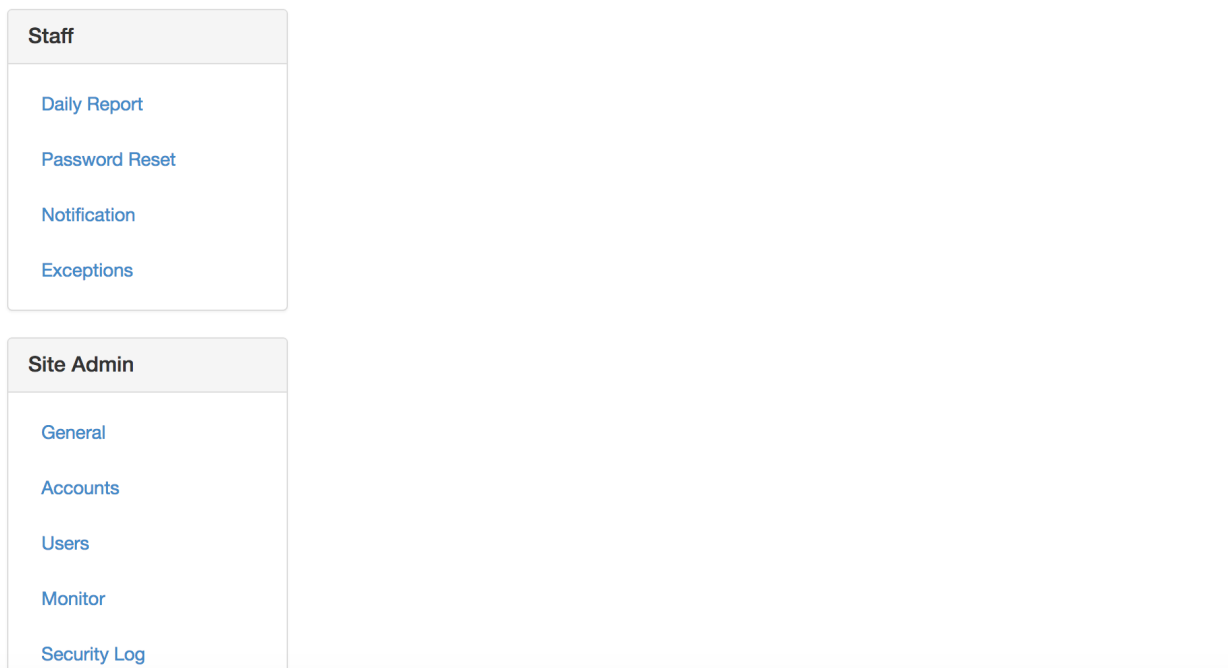
If you have administrator privileges, you see two additional links in the AEN navigation bar—Admin and Users:

To open the Admin dashboard, click the Admin link.



# Admin Settings

Anaconda Enterprise Notebooks settings accessible only by the system administrator.



## Backing up and restoring AEN

- *Document purpose*
- *Important notes*
- *Server component steps*
  - *Backup*

- \* *Mongo database*
- \* *AEN Server config files (including License file)*
- \* *Nginx config (if needed)*
- \* *SSL certificates (if needed)*
- *Restore*
  - \* *Reinstall AEN-Server*
  - \* *Restore Mongo database*
  - \* *AEN Server config files (including License file)*
  - \* *Nginx config (if needed)*
  - \* *SSL certificates (if needed)*
  - \* *Restart server*
- *Gateway component steps*
  - *Backup*
    - \* *Config files*
    - \* *Custom .condarc file (if needed)*
    - \* *SSL certificates (if needed)*
  - *Restore*
    - \* *Reinstall AEN-Gateway*
    - \* *Config files*
    - \* *Custom .condarc file (if needed)*
    - \* *SSL certificates (if needed)*
    - \* *Restart gateway*
- *Compute component steps*
  - *Backup*
    - \* *Config files*
    - \* *Custom Changes (rare)*
    - \* *Create user list*
    - \* *Project files*
    - \* *Full Anaconda (option 1)*
    - \* *Partial Anaconda (option 2)*
  - *Restore*
    - \* *Reinstall AEN-Compute*
    - \* *Config files*
    - \* *Custom changes (rare)*
    - \* *Create users*

- \* *Project files*
- \* *Full Anaconda (option 1)*
- \* *Partial Anaconda (option 2)*
- \* *Custom environments (if needed)*
- \* *Restart compute node*

### Document purpose

This document lays out the steps to backup and restore Anaconda Enterprise Notebooks (AEN) for Disaster Recovery. It is not intended to provide High Availability. Each of the components (Server, Gateway and Compute) has its own instructions and each may be done individually as needed. The steps primarily involve creating tar files of important configuration files and data.

This document is written for a system administrator who is comfortable with basic Linux command line navigation and usage.

To migrate to a new cluster, use these backup and restore instructions to back up the system from the old cluster and restore it to the new cluster.

### Important notes

Review the [Concepts](#) page to become familiar with the different components and how they work together.

Root or sudo access is required for some commands.

**CAUTION:** All commands **MUST** be run by `$AEN_SRVC_ACCT` (the account used to run AEN) except for those commands explicitly indicated to run as root or sudo. If the commands are not run by the correct user, the installation will not work, and a full uninstallation and reinstallation will be required!

These instructions assume that the fully qualified domain name (FQDN) has not changed for any of the component nodes. If any of the FQDNs are not the same, additional steps will be needed.

### Server component steps

#### Backup

##### Mongo database

This will create a single tar file called `aen_mongo_backup.tar` that includes only the database named “wakari” that is used by AEN. It also generates a log of the database backup.

NOTE: These commands must be run by `$AEN_SRVC_ACCT`.

```
mongodump -db wakari -o aen_main >> mongo_backup.log
tar -cvf aen_mongo_backup.tar aen_main
```

##### AEN Server config files (including License file)

Create a tar file of all of the configuration files, including any license files.

NOTE: This command must be run by \$AEN\_SRVC\_ACCT.

```
tar -cvf aen_server_config.tar -C /opt/wakari/ wakari-server/etc/wakari/
```

### Nginx config (if needed)

Make a copy of the nginx configuration file if it has been customized. The default configuration for the AEN server is a symlink.

NOTE: This command must be run by \$AEN\_SRVC\_ACCT.

```
/etc/nginx/conf.d/www.enterprise.conf -> /opt/wakari/wakari-server/etc/nginx/conf.d/  
↪www.enterprise.conf
```

### SSL certificates (if needed)

Make a copy of the SSL certificates files (certfiles) for the server, including the key file, and a copy of the certfile for the gateway, which is needed for verification if using self-signed or private CA signed certs.

## Restore

### Reinstall AEN-Server

See *the instructions for installing the current version of AEN-Server*.

It is not necessary to upload the license, because it will be restored with the config files.

NOTE: The new installation will generate a new password for the local \$AEN\_SRVC\_ACCT account.

### Restore Mongo database

This assumes that mongo was reinstalled as part of the reinstallation of the server component. Untar the mongo database and restore it.

NOTE: These commands must be run by \$AEN\_SRVC\_ACCT.

```
tar -xvf aen_mongo_backup.tar  
mongorestore --drop aen_main
```

NOTE: The --drop option resets the \$AEN\_SRVC\_ACCT user password and restores the database to the exact state it was in at the time of backup. Please see the [MongoDB documentation](#) for more information about mongorestore options for Mongo 2.6.

NOTE: AEN uses Mongo 2.6 by default. If you are using a different version, consult the documentation for your version.

### AEN Server config files (including License file)

Untar the tar file of all of the configuration files, including any license files.

NOTE: This command must be run by \$AEN\_SRVC\_ACCT.

```
tar -xvf aen_server_config.tar -C /opt/wakari/
```

Make sure the files are in `/opt/wakari/wakari-server/etc/wakari/` and are owned by the `$AEN_SRVC_ACCT`.

### Nginx config (if needed)

Make sure any modifications to the nginx configuration are either in `/etc/nginx/conf.d` or in `/opt/wakari/wakari-server/etc/nginx/conf.d/` with a proper symlink.

NOTE: This command must be run by `$AEN_SRVC_ACCT`.

```
/etc/nginx/conf.d/www.enterprise.conf -> /opt/wakari/wakari-server/etc/nginx/conf.d/  
↪www.enterprise.conf
```

### SSL certificates (if needed)

Move any SSL certificate files to the locations indicated in the config files.

### Restart server

Restart the server application.

NOTE: This command must be run as root or with `sudo`.

```
service wakari-server restart
```

## Gateway component steps

### Backup

### Config files

Create a tar file of all of the configuration files.

NOTE: This command must be run by `$AEN_SRVC_ACCT`.

```
tar -cvf aen_gateway_config.tar -C /opt/wakari/ wakari-gateway/etc/wakari/
```

### Custom .condarc file (if needed)

Make a copy of any `/opt/wakari/miniconda/.condarc` if it has been modified.

### SSL certificates (if needed)

Make a copy of SSL certificate files for the gateway (including the key file) and the certfile for the server (needed for verification if using self-signed or private CA signed certs).



## Restore

### Reinstall AEN-Gateway

#### Setting variables and changing permissions

NOTE: These commands must be run by \$AEN\_SRVC\_ACCT.

Run:

```
export AEN_SERVER=<FQDN HOSTNAME OR IP ADDRESS> # Use the real FQDN
export AEN_GATEWAY_PORT=8089
export AEN_GATEWAY=<FQDN HOSTNAME OR IP ADDRESS> # will be needed shortly
chmod a+x aen-*.sh # Set installer to be executable
```

NOTE: Change <FQDN HOSTNAME OR IP ADDRESS> to the actual fully qualified domain hostname or IP address.

NOTE: You must perform the entire procedure before closing the terminal to ensure the variable export persists. If the terminal is closed before successful installation, export the variables to continue with the installation.

#### Running the AEN gateway installer

Run:

```
sudo -E ./aen-gateway-4.3.3-Linux-x86_64.sh -w $AEN_SERVER
<license text>
...
...

PREFIX=/opt/wakari/wakari-gateway
Logging to /tmp/wakari_gateway.log
...
...
Checking server name
Please restart the Gateway after running the following command
to connect this Gateway to the AEN Server
...
```

#### Config files

Untar the configuration files.

NOTE: This command must be run by \$AEN\_SRVC\_ACCT.

```
tar -xvf aen_gateway_config.tar -C /opt/wakari
```

Verify that the files are in /opt/wakari/wakari-gateway/etc/wakari/ and are owned by the \$AEN\_SRVC\_ACCT.

#### Custom .condarc file (if needed)

Move the custom .condarc file to /opt/wakari/miniconda/.condarc.

### SSL certificates (if needed)

Move any SSL certificate files to the locations indicated in the config files.

### Restart gateway

Restart the gateway application.

NOTE: This command must be run as root or with sudo.

```
service wakari-gateway restart
```

### Compute component steps

#### Backup

#### Config files

Create a tar file of all of the configuration files.

NOTE: This command must be run by \$AEN\_SRVC\_ACCT.

```
tar -cvf aen_compute_config.tar -C /opt/wakari/ wakari-compute/etc/wakari
```

### Custom Changes (rare)

Manually backup any custom changes that were applied to the code. One change might be additional files in the skeleton folder:

```
/opt/wakari/wakari-compute/lib/node_modules/wakari-compute-launcher/skeleton
```

### Create user list

AEN uses POSIX access control lists (ACLs) for project sharing, so the backup must preserve the ACL information. This is done with a script that creates a file named `users.lst` containing a list of all users that have access to projects on a given compute node. Download and run the script.

NOTE: These commands must be run by \$AEN\_SRVC\_ACCT.

```
wget https://s3.amazonaws.com/continuum-airgap/misc/wk-compute-get-acl-users.py
chmod 755 wk-compute-get-acl-users.py
./wk-compute-get-acl-users.py
```

### Project files

Create a tar of the projects directory with ACLs enabled. The default projects base location is `/projects`.

NOTE: This command must be run as root or with sudo.

```
tar --acls -cpvf projects.tar -C <projects base location>/*
```

### Full Anaconda (option 1)

If any changes have been made to the default Anaconda installation (additional packages installed or packages removed), it is necessary to backup the entire Anaconda installation.

NOTE: This command must be run by \$AEN\_SRVC\_ACCT.

```
tar -cvf aen_anaconda.tar -C /opt/wakari/anaconda/*
```

If no changes have been made to the default installation of Anaconda, you may just backup the `.condarc` file and any custom environments.

### Partial Anaconda (option 2)

#### Custom `.condarc` file

Make a copy of `/opt/wakari/anaconda/.condarc`.

#### Custom environments (if needed)

Create a tar file of any custom shared environments.

NOTE: This command must be run by \$AEN\_SRVC\_ACCT.

```
tar -cvf aen_compute_envs.tar -C /opt/wakari/ anaconda/envs
```

NOTE: If no custom shared environments have been created, the `envs` folder will not be present.

### Restore

#### Reinstall AEN-Compute

#### Setting variables and changing permissions

NOTE: These commands must be run by \$AEN\_SRVC\_ACCT.

Run:

```
export AEN_SERVER=<FQDN HOSTNAME OR IP ADDRESS> # Use the real FQDN
chmod a+x aen-*.sh # Set installer to be executable
```

NOTE: Change `<FQDN HOSTNAME OR IP ADDRESS>` to the actual fully qualified domain hostname or IP address.

NOTE: You must perform the entire procedure before closing the terminal to ensure the variable export persists.

## Running the AEN compute installer

Run:

```
sudo -E ./aen-compute-4.3.3-Linux-x86_64.sh -w $AEN_SERVER
...
...
PREFIX=/opt/wakari/wakari-compute
Logging to /tmp/wakari_compute.log
Checking server name
...
...
Initial clone of root environment...
Starting Wakari daemons...
installation finished.
Do you wish the installer to prepend the wakari-compute install location
to PATH in your /root/.bashrc ? [yes|no]
[no] >>> yes
```

## Config files

Untar the config files.

NOTE: This command must be run by \$AEN\_SRVC\_ACCT.

```
tar -xvf aen_compute_config.tar -C /opt/wakari
```

NOTE: Verify that they are located in `/opt/wakari/wakari-compute/etc/wakari` and are owned by the \$AEN\_SRVC\_ACCT.

## Custom changes (rare)

Manually restore any custom changes you saved in the backup section. If there are changes in the skeleton directory, these files must be world readable or projects will refuse to start.

## Create users

NOTE: Only create users with these instructions if your Linux machine is not bound to LDAP.

In order for the ACLs to be set properly on restore, all users that have permissions to the files must be available on the machine. Ask your system administrator for the proper way to do this for your system, such as using the “useradd” tool. A list of users that are needed was created in the backup process as a file named `users.lst`.

A process similar to the following `useradd` example will be suitable for most Linux systems.

NOTE: This command must be run by \$AEN\_SRVC\_ACCT.

```
xargs -0 -n 1 useradd --user-group < users.lst
```

## Project files

Create the projects directory in the location specified in `projectRoot` in `wk-compute-launcher-config.json`.

NOTE: By default this directory is `/projects`.

Then untar the projects directory with ACLs.

NOTE: This command must be run as root or with `sudo`:

```
tar --acls -xpvf projects.tar -C <projects base location>
```

### Full Anaconda (option 1)

If you did a full backup of the full Anaconda installation, untar this file to `/opt/wakari/anaconda`.

NOTE: This command must be run by `$AEN_SRVC_ACCT`.

```
tar -xvf aen_anaconda.tar -C /opt/wakari
```

### Partial Anaconda (option 2)

Restore the custom `.condarc` file.

If you did a partial backup of the Anaconda installation, move the copy of the `.condarc` file to `/opt/wakari/anaconda/.condarc`.

### Custom environments (if needed)

Untar any custom environments that were created to `/opt/wakari/anaconda/envs`.

NOTE: This command must be run by `$AEN_SRVC_ACCT`.

```
tar -xvf aen_compute_envs.tar -C /opt/wakari
```

### Restart compute node

Restart the compute-launcher application.

NOTE: This command must be run as root or with `sudo`.

```
service wakari-compute restart
```

### Viewing a list of admin commands

A user who is promoted to administrator can access administrator commands to perform advanced administrator tasks.

NOTE: Utility files are owned by, and should only be executed by, the AEN user who owns the files.

To display a list of all administrator commands:

```
ls -al /opt/wakari/wakari-server/bin/wk-*
```

## Viewing help for admin commands

To view help information for command, run the command followed by `-h` or `--help`.

EXAMPLE: To view help for the `remove-user` command:

```
/opt/wakari/wakari-server/bin/wk-server-admin remove-user -h
/opt/wakari/wakari-server/bin/wk-server-admin remove-project -h
```

## Running daily reports

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Staff** menu, select Daily Report:

Staff

[Daily Report](#)
[Password Reset](#)
[Notification](#)
[Exceptions](#)

Site Admin

[General](#)
[Accounts](#)
[Users](#)
[Monitor](#)
[Security Log](#)
[Data Centers](#)
[Task Queue](#)
[License](#)

Providers

[Enterprise Resources](#)

## Report

Today
Yesterday
This Week
This Month

**From:**  
Sun Sep 24 15:09:03 2017  
**Until:**  
Mon Sep 25 15:09:03 2017  
**Date Range**  
1 day, 0:00:00

### Users

	New	Total
<b>Users</b>	0	1
<b>Projects</b>	0	6

### New User Emails

Username	Email
----------	-------

### Actions

Count	Action
82	<a href="#">oauth.authenticate</a>

The Report section displays the following:

- Users—The number of users and projects.
- New User Emails—If *open registration is enabled*, the user names and emails for new users.
- Actions—The actions—projects created, projects updated, user authentications and added users—that have occurred in during the selected time frame—today, yesterday, this week, or this month.

## Viewing system errors

When an error occurs, a red dot is displayed in the AEN navigation bar next to the Admin link. The red dot is removed when all exceptions are marked as “read.”

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Staff** menu, select Exceptions:

The screenshot shows the AEN Admin Settings interface. On the left, the 'Staff' menu is expanded, and 'Exceptions' is selected. The main content area displays a list of exceptions. The first exception is highlighted with a red box around its radio button. A 'Mark all as read' button is visible in the top right corner of the exceptions list.

Staff	Exceptions
Daily Report	<input checked="" type="radio"/> jinja2.exceptions.UndefinedError: 'wk_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'
Password Reset	<input type="radio"/> jinja2.exceptions.UndefinedError: 'wk_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'
Notification	<input type="radio"/> jinja2.exceptions.UndefinedError: 'wk_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'
Exceptions	<input type="radio"/> jinja2.exceptions.UndefinedError: 'wk_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'
	<input type="radio"/> jinja2.exceptions.UndefinedError: 'wk_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'
	<input type="radio"/> jinja2.exceptions.UndefinedError: 'wk_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'
	<input type="radio"/> jinja2.exceptions.UndefinedError: 'wk_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'
	<input type="radio"/> jinja2.exceptions.UndefinedError: 'wk_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'
	<input type="radio"/> jinja2.exceptions.UndefinedError: 'wk_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'
	<input type="radio"/> jinja2.exceptions.UndefinedError: 'wk_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'
	<input type="radio"/> elasticsearch.exceptions.ConnectionError:
	<input type="radio"/> elasticsearch.exceptions.ConnectionError:
	<input type="radio"/> elasticsearch.exceptions.ConnectionError:
	<input type="radio"/> elasticsearch.exceptions.ConnectionError:

Site Admin

- General
- Accounts
- Users
- Security Log
- Data Centers
- Task Queue
- License

Providers

- Enterprise Resources

The Exceptions section lists all errors that have occurred while AEN is running.

3. To see the details of an error, click the radio button next to the error. This also marks the error as “read.”
4. To mark all errors as read without reviewing each one, click the Mark all as read button.

## Viewing security errors

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select Security Log:

Staff

Daily Report

Password Reset

Notification

Exceptions

Site Admin

General

Accounts

Users

Monitor

Security Log

Security Log

View	Actor	Action	Date
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 25, 2017 09:46:09 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 25, 2017 09:39:17 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 25, 2017 09:22:04 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 25, 2017 09:10:31 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 25, 2017 08:45:50 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 25, 2017 08:43:12 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 25, 2017 08:10:30 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 25, 2017 08:09:38 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 24, 2017 23:52:06 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 24, 2017 23:51:58 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 24, 2017 23:51:58 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 24, 2017 23:51:58 CDT

The Security Log section lists all errors that have occurred that could potentially affect AEN security.

3. To view a user’s profile page, click their username in the Actor column.
4. To see the details of an error, click the Eye icon next to the error.

The error details are displayed:

5. To close the error details, click the Back link.



Public Profile

Account Settings

Security Log

Applications

oauth.authenticate

_id	59c907f03f94c30fe45ffb9e
action	oauth.authenticate
actor_id	59c069b1ae55d1b3fe9fa45e
actor_username	aen_admin
client_id	59c119cd3f94c30fe45ff5db
remote_addr	None
time	2017-09-25 13:43:12.479000+00:00
token_id	59c907f03f94c30fe45ffb9d

⏪ Back

Managing data centers

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select Data Centers:

Staff

Daily Report

Password Reset

Notification

Exceptions

Site Admin

General

Accounts

Users

Monitor

Security Log

Data Centers

Data Centers

Gateway (ec2-52-90-133-17.compute-1.amazonaws.com:8089)

+ Add DataCenter

The Data Centers section displays current data center information.

## Adding a data center

1. Click the Add DataCenter button to display the the Register a datacenter form.
2. In the Name box, type a Name for the new data center:

**Data Centers / Register a datacenter**

**Name**

☐ Subdomain Routing  
☐ Https

**Base Domain Name**

**summary**

**Provider**

3. Select the Subdomain Routing and/or Https checkboxes.
4. In the Base Domain Name box, type the base domain name.
5. In the Summary box, type a description of the data center.
6. In the Provider list, select a provider.
7. Click the Submit button.

## Managing enterprise resources

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Providers** menu, select Enterprise Resources:

Staff

[Daily Report](#)  
[Password Reset](#)  
[Notification](#)  
[Exceptions](#)

Site Admin

[General](#)  
[Accounts](#)  
[Users](#)  
[Monitor](#)  
[Security Log](#)  
[Data Centers](#)  
[Task Queue](#)  
[License](#)

Providers

[Enterprise Resources](#)

Resources

Add Resource

Gateway

[ec2-54-210-232-251.compute-1.amazonaws.com](#)

remove

The Resources section lists your existing cloud and local resources.

### Adding a resource

1. Click the Add Resource button to open the new resource form.
2. Complete the form:

**Resources / new**

**Data Center**  
Gateway 59c119cd3f94c30fe45ff5db

**Name**  
Compute Node1

**URL**  
http://ec2-54-210-232-251.compute-1.amazonaws.com:5002

**Description**  
Configuring Compute Node

☒ **Public**  
Uncheck this if you want to control exactly who has access to this compute node

Add Resource

3. Click the Add Resource button.

### Viewing or changing the resource details

1. Click a resource name to open the Local Resource form.
2. If necessary, change the resource details:

**Data Center**

Gateway 59c119cd3f94c30fe45ff5db

**Name**

ec2-54-210-232-251.compute-1.amazonaws.com

**URL**

http://ec2-54-210-232-251.compute-1.amazonaws.com:5002

**Description****Public**

Uncheck this if you want to control exactly who has access to this compute node

**Update****status**

```
{"status": "ok", "messages": []}
```

3. Click the Update button.

### Making a node public or private

1. Click the resource name to open the Local Resource form.
2. Select or clear the Public checkbox:

**Data Center**  

Gateway 59c119cd3f94c30fe45ff5db

**Name**  

ec2-54-210-232-251.compute-1.amazonaws.com

**URL**  

http://ec2-54-210-232-251.compute-1.amazonaws.com:5002

**Description**

☒ **Public**  
Uncheck this if you want to control exactly who has access to this compute node

Update

**status**  

{"status": "ok", "messages": []}

3. Click the Update button.

## Removing a resource

Click the Remove button next to the resource you want to remove.

NOTE: When you remove a resource assigned to a project, the project becomes orphaned. To fix an orphaned project, *move the project to a valid Compute Resource*.

## Managing services

The tasks on this page assume that the 3 AEN nodes are installed in the following locations:

- Server—`/opt/wakari/wakari-server/`.
- Gateway—`/opt/wakari/wakari-gateway/`.
- Compute-Launcher—`/opt/wakari/wakari-compute/`.

- *Checking the status of server node processes*
- *Checking the status of gateway node processes*
- *Checking the status of compute node processes*
- *Starting AEN services*
- *Verifying that AEN services are set to start with the system*
- *Stopping AEN services*
- *Restarting AEN services*
- *Identifying extraneous processes*
- *Removing extraneous processes*

## Checking the status of server node processes

1. Run:

```
# service wakari-server status
wk-server          RUNNING      pid 20758, uptime 5 days, 0:30:23
worker            RUNNING      pid 20757, uptime 5 days, 0:30:23
```

OR

```
root@server # ps -Hu wakari
  PID TTY          TIME CMD
 20756 ?           00:02:26 .supervisord
 20757 ?           00:05:58 mtq-worker
 20758 ?           00:00:08 wk-server
```

(continues on next page)

(continued from previous page)

```
20765 ?      00:02:00    wk-server
20766 ?      00:01:55    wk-server
20767 ?      00:02:20    wk-server
20770 ?      00:02:02    wk-server
```

## 2. Run:

```
root@server # service nginx status
nginx (pid 26303) is running...
```

For more information on server processes, see *Server processes*.

## Checking the status of gateway node processes

### Run:

```
# service wakari-gateway status
wk-gateway          RUNNING      pid 1137, uptime 5 days, 1:59:28
```

### OR

```
root@gateway # ps -Hu wakari
  PID TTY          TIME CMD
 1136 ?            00:01:59 .supervisord
 1137 ?            00:00:02  wk-gateway
```

For more information on gateway processes, see *Gateway processes*.

## Checking the status of compute node processes

### Run:

```
# service wakari-compute status
wk-compute          RUNNING      pid 22050, uptime 3 days, 1:03:19
```

### OR

```
root@compute # ps -Hu wakari
  PID TTY          TIME CMD
 1150 ?            00:02:01 .supervisord
 1152 ?            00:00:01  wk-compute
```

For more information on compute node processes, see *Compute processes*.

## Starting AEN services

Services should start automatically both when they are first installed and at any point when the system is restarted.

If you need to manually start an AEN service, you must start each node independently, because they may be running on separate machines.

NOTE: The process is basically the same for each node, but the path to the correct commands vary.

To manually start a service:



- On the server node, run:

```
service wakari-server start
```

- On the gateway node, run:

```
service wakari-gateway start
```

- On a compute node, run:

```
service wakari-compute start
```

## Verifying that AEN services are set to start with the system

To verify that AEN services are set up to start automatically:

1. Run the following command on each node:

```
chkconfig --list | grep wakari
```

2. If services are missing, add them:

```
chkconfig --add [wakari-server|wakari-gateway|wakari-compute]
```

3. *Restart the services.*

## Stopping AEN services

CAUTION: Do not stop or kill supervisord without first stopping wk-compute and any other processes that use it.

You must stop services on each node independently, because they may be running on separate machines.

To stop an AEN service:

- On the server node, run:

```
service wakari-server stop
```

- On the gateway node, run:

```
service wakari-gateway stop
```

- On a compute node, run:

```
service wakari-compute stop
```

Compute nodes may have running processes that are not automatically stopped. To stop them, run:

```
sudo /opt/wakari/wakari-compute/bin/wk-compute-apps kill-all
```

## Restarting AEN services

- On the server node, run:

```
service wakari-server restart
```

- On the gateway node, run:

```
service wakari-gateway restart
```

- On a compute node, run:

```
service wakari-compute restart
```

## Identifying extraneous processes

To get a complete list of the processes running under the wakari user account, run `ps -Hu wakari`.

EXAMPLE:

```
root@server # ps -Hu wakari
  PID TTY          TIME CMD
 20756 ?            00:02:26 .supervisord
 20757 ?            00:05:58 mtq-worker
 20758 ?            00:00:08 wk-server
 20765 ?            00:02:00 wk-server
 20766 ?            00:01:55 wk-server
 20767 ?            00:02:20 wk-server
 20770 ?            00:02:02 wk-server

root@server # ps -f -C nginx
UID      PID  PPID  C  STIME TTY          TIME CMD
root    26303    1   0  12:18 ?        00:00:00 nginx: master process /usr/sbin/nginx -c /
→etc/nginx/nginx.conf
nginx   26305 26303   0  12:18 ?        00:00:00 nginx: worker process

root@gateway # ps -Hu wakari
  PID TTY          TIME CMD
 1136 ?            00:01:59 .supervisord
 1137 ?            00:00:02 wk-gateway

root@compute # ps -Hu wakari
  PID TTY          TIME CMD
 1150 ?            00:02:01 .supervisord
 1152 ?            00:00:01 wk-compute
```

- wk-server, wk-gateway and wk-compute should have PIDs reported by supervisorctl.
- The nginx master process should have a PID reported by service nginx status.
- If you have installed more than one AEN node on a single machine, the processes from all of the installed nodes should be displayed for that machine.
- On compute node(s), any AEN applications currently being run by users will be present.

EXAMPLE:

```
root@compute # ps -Hu wakari
  PID TTY          TIME CMD
 1150 ?            00:00:00 .supervisord
 1152 ?            00:00:00 wk-compute
```

(continues on next page)

(continued from previous page)

```
1340 ?      00:00:00 bash
1341 ?      00:00:00  notebookwrapper
```

## Removing extraneous processes

If extra `wk-server`, `wk-gateway`, `wk-compute`, or `supervisord` processes are present, use the `kill` command to remove them to prevent issues with AEN.

You can safely *restart* any process that you remove in error.

## Making sure NGINX and MongoDB are running

In order for AEN to run, the dependencies `mongodb` and `nginx` must be up and running. If either of these fail to start, AEN will not be served on port 80.

Check if `nginx` and `mongod` are both running (RHEL 6x):

```
$ sudo service nginx status
nginx (pid 25956) is running...

$ sudo service mongod status
mongod (pid 25928) is running...
```

If either of these failed to start, tail the log files. The default location of log files is:

```
$ tail -n 50 /var/log/mongodb/mongod.log

# nginx errors reported in error.log
$ tail -n 50 /var/log/nginx/error.log
```

## Viewing, terminating, and relaunching applications

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select Monitor:

The Monitor menu lists started applications by user and project.

The list includes columns for the application name, current running status, running node and last seen date.

3. Use the buttons to terminate or relaunch an application.
4. To view an application's logs, click the Logs button with the document icon.

## Viewing the task queue

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select Task Queue:

Staff

[Daily Report](#)  
[Password Reset](#)  
[Notification](#)  
[Exceptions](#)

Site Admin

[General](#)  
[Accounts](#)  
[Users](#)  
[Monitor](#)

Running Apps								
User	Project	Application	Status	Node	Last Seen	Terminate	Relaunch	Logs
aen_admin	asd	notebook	running	localhost	Jul 24, 2017 15:15:24 CDT	<a href="#">Terminate</a>	<a href="#">Relaunch</a>	<a href="#">Logs</a>
aen_admin	Test	notebook	running	localhost	Jul 25, 2017 11:54:05 CDT	<a href="#">Terminate</a>	<a href="#">Relaunch</a>	<a href="#">Logs</a>

Staff

[Daily Report](#)  
[Password Reset](#)  
[Notification](#)  
[Exceptions](#)

Site Admin

[General](#)  
[Accounts](#)  
[Users](#)  
[Monitor](#)  
[Security Log](#)  
[Data Centers](#)  
[Task Queue](#)

## Task Queue

Workers

ip-172-31-10-196.4053 | [high](#) [default](#) [low](#)

Queues

[high](#)  
Backlog: 0  
Failed: 1

[default](#)  
Backlog: 0  
Failed: 3

The Workers section lists the workers in the task queue and whether each worker is set at high, default or low priority.

The Queues section provides information on the default and high priority queues.

3. To view all the tasks in a particular queue, in the Queues section, click the queue name.

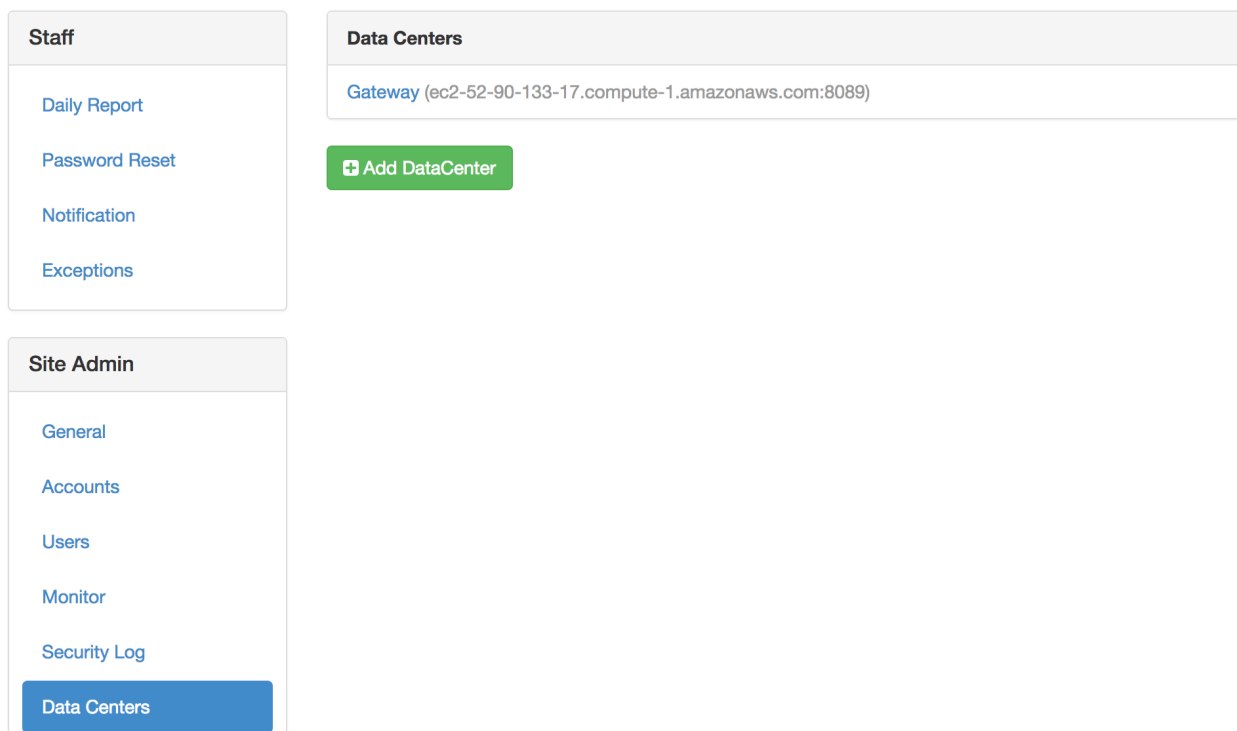
## Checking node connections

When the AEN nodes cannot communicate with each other as intended, it can cause issues with you AEN platform installation.

- *Verifying server to gateway connectivity*
- *Verifying gateway to compute node connectivity*
- *Verifying gateway to server connectivity*

## Verifying server to gateway connectivity

1. On the server, in the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select Data Centers:



3. For each data center in the list, check connectivity from the server to that gateway.

EXAMPLE: The gateway in this example is `http://gateway.example.com:8089`:

```
root@server # curl --connect-timeout 5 http://gateway.example.com:8089 > /dev/null
```

## Verifying gateway to compute node connectivity

1. On the server, in the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Providers** menu, select Enterprise Resources:

The screenshot displays the Admin Settings page in Anaconda Cloud. On the left, the 'Providers' menu is expanded, showing 'Enterprise Resources' as the selected option. The main content area is titled 'Resources' and includes a '+ Add Resource' button. Below this, a 'Gateway' section contains a table with one entry: 'ec2-54-210-232-251.compute-1.amazonaws.com', which has a 'remove' button next to it. The left sidebar also shows other menu items like 'Staff', 'Site Admin', and 'Providers'.

3. Open each compute node in the Resources section.
4. Verify that the contents of the URL field begin with either `http` or `https`.

**Data Center**

Gateway 59c119cd3f94c30fe45ff5db

**Name**

ec2-54-210-232-251.compute-1.amazonaws.com

**URL**

http://ec2-54-210-232-251.compute-1.amazonaws.com:5002

**Description****Public**

Uncheck this if you want to control exactly who has access to this compute node

**Update****status**

```
{"status": "ok", "messages": []}
```

5. Check connectivity to that URL from the corresponding gateway.

EXAMPLE: The gateway in this example is `http://gateway.example.com:8089`:

```
root@gateway # curl --connect-timeout 5 http://compute.example.com:5002 > /dev/
↪null
```

## Verifying gateway to server connectivity

The gateway-to-server path is used by the gateway configuration command `wk-gateway-configure`.

1. Verify that the gateway is linked to the correct server in the configuration file.
2. Verify that the full server URL is specified.
3. Check connectivity to the server:

```
root@gateway # grep WAKARI_SERVER /opt/wakari/wakari-gateway/etc/wakari/wk-
↪gateway-config.json
"WAKARI_SERVER": "http://wakari.example.com",

root@gateway # curl --connect-timeout 5 http://wakari.example.com > /dev/null
root@gateway # curl --connect-timeout 5 http://error.example.com > /dev/null
curl: (7) Failed to connect to error.example.com port 80: Connection refused
```

4. If a connection fails:
  1. Ensure that gateways (data centers) and compute nodes (Enterprise Resources) are correctly configured on the server.
  2. Verify that processes are listening on the configured ports:

```
$ sudo netstat -nplt
Active Internet connections (only servers)
Proto Recv-Q Send-Q Local Address   Foreign Address State  PID/Program
tcp        0      0 *:80             *:*             LISTEN 26409/nginx
tcp        0      0 *:22             *:*             LISTEN 986/sshd
tcp        0      0 127.0.0.1:25     *:*             LISTEN 1063/master
tcp        0      0 *:5000           *:*             LISTEN 26192/python
tcp        0      0 127.0.0.1:27017  *:*             LISTEN 29261/mongod
tcp        0      0 *:22             *:*             LISTEN 986/sshd
tcp        0      0 127.0.0.1:25     *:*             LISTEN 1063/master
```

3. Check the firewall setting and logs on both hosts to ensure that packets are not being blocked or discarded.

## Verifying and tuning search indexing

For search indexing to work correctly, a compute node must be able to communicate with the server. To verify this:

1. Run:

```
curl -m 5 $AEN_SERVER > /dev/null
```

2. Verify that there are sufficient inotify watches available for the number of subdirectories within the project root file system:



```
cat /proc/sys/fs/inotify/max_user_watches
```

NOTE: Some Linux distributions default to a low number of watches, which may prevent the search indexer from monitoring project directories for changes.

3. If necessary, increase the number of watches:

```
echo fs.inotify.max_user_watches=100000 | sudo tee -a /etc/sysctl.conf && sudo  
→ sysctl -p
```

4. Verify that there are sufficient inotify user instances available—at least one per project:

```
cat /proc/sys/fs/inotify/max_user_instances
```

5. If necessary, increase the number of inotify user instances:

```
echo fs.inotify.max_user_instances=1000 | sudo tee -a /etc/sysctl.conf && sudo  
→ sysctl -p
```

## Changing the AEN server URL

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select General:
3. In the Wakari Server box, type the main URL where the site can be viewed.
4. Click the Update button.

## Changing the static URL for JavaScript files

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select General:
3. In the Static URL box, type the static URL where JavaScript files can be accessed.
4. Click the Update button.

## Changing the AEN account type

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select General:

Staff	General Admin Settings
<a href="#">Daily Report</a>	<b>Wakari Server</b> Set the main URL where this site will be accessed <input type="text" value="http://anaconda-enterprise.trl"/>
<a href="#">Password Reset</a>	<b>Static URL</b> Set static URL where the js can be accessed <input type="text" value="http://anaconda-enterprise.trl/static/"/>
<a href="#">Notification</a>	<b>Default Project Access</b> This will be the default when a user creates a project  <input type="radio"/> <b>Public</b> Anyone can see this project. Collaborators have write access  <input checked="" type="radio"/> <b>Private</b> No one can see this project except collaborators.
<a href="#">Exceptions</a>	<b>Account Type</b> <input type="text" value="wk_server.plugins.accounts.cloud"/>
	<input type="button" value="Update"/>
Site Admin	Config Files
<a href="#">General</a>	
<a href="#">Accounts</a>	
<a href="#">Users</a>	
<a href="#">Monitor</a>	
<a href="#">Security Log</a>	
<a href="#">Data Centers</a>	
<a href="#">Task Queue</a>	
<a href="#">License</a>	
Providers	

Staff	General Admin Settings
<a href="#">Daily Report</a>	<b>Wakari Server</b> Set the main URL where this site will be accessed <input type="text" value="http://anaconda-enterprise.trl"/>
<a href="#">Password Reset</a>	<b>Static URL</b> Set static URL where the js can be accessed <input type="text" value="http://anaconda-enterprise.trl/static/"/>
<a href="#">Notification</a>	<b>Default Project Access</b> This will be the default when a user creates a project  <input type="radio"/> <b>Public</b> Anyone can see this project. Collaborators have write access  <input checked="" type="radio"/> <b>Private</b> No one can see this project except collaborators.
<a href="#">Exceptions</a>	<b>Account Type</b> <input type="text" value="wk_server.plugins.accounts.cloud"/>
	<input type="button" value="Update"/>
Site Admin	Config Files
<a href="#">General</a>	
<a href="#">Accounts</a>	
<a href="#">Users</a>	
<a href="#">Monitor</a>	
<a href="#">Security Log</a>	
<a href="#">Data Centers</a>	
<a href="#">Task Queue</a>	
<a href="#">License</a>	
Providers	

<b>Staff</b>	<b>General Admin Settings</b>
<a href="#">Daily Report</a>	<b>Wakari Server</b> Set the main URL where this site will be accessed
<a href="#">Password Reset</a>	<input type="text" value="http://anaconda-enterprise.trl"/>
<a href="#">Notification</a>	
<a href="#">Exceptions</a>	<b>Static URL</b> Set static URL where the js can be accessed
	<input type="text" value="http://anaconda-enterprise.trl/static/"/>
<b>Site Admin</b>	<b>Default Project Access</b> This will be the default when a user creates a project
<b>General</b>	<input type="radio"/> <b>Public</b> Anyone can see this project. Collaborators have write access
<a href="#">Accounts</a>	<input checked="" type="radio"/> <b>Private</b> No one can see this project except collaborators.
<a href="#">Users</a>	
<a href="#">Monitor</a>	<b>Account Type</b>
<a href="#">Security Log</a>	<input type="text" value="wk_server.plugins.accounts.cloud"/>
<a href="#">Data Centers</a>	
<a href="#">Task Queue</a>	<input type="button" value="Update"/>
<a href="#">License</a>	
<b>Providers</b>	<b>Config Files</b>

3. In the Account Type box, select the account type—cloud or LDAP.
4. Click the Update button.

### Changing the default for project access

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select General:

<div>Staff</div> <div>Daily Report</div> <div>Password Reset</div> <div>Notification</div> <div>Exceptions</div>	<div>General Admin Settings</div> <div> <b>Wakari Server</b>  Set the main URL where this site will be accessed  <input type="text" value="http://anaconda-enterprise.trl"/> </div> <div> <b>Static URL</b>  Set static URL where the js can be accessed  <input type="text" value="http://anaconda-enterprise.trl/static/"/> </div> <div> <b>Default Project Access</b>  This will be the default when a user creates a project  <div> <input type="radio"/> <b>Public</b>  Anyone can see this project. Collaborators have write access </div> <div> <input checked="" type="radio"/> <b>Private</b>  No one can see this project except collaborators. </div> </div> <div> <b>Account Type</b>  <input type="text" value="wk_server.plugins.accounts.cloud"/> </div> <div> <input type="button" value="Update"/> </div>
<div>Site Admin</div> <div>General</div> <div>Accounts</div> <div>Users</div> <div>Monitor</div> <div>Security Log</div> <div>Data Centers</div> <div>Task Queue</div> <div>License</div>	<div>Config Files</div>
<div>Providers</div>	

3. Under Default Project Access, select the default access type for new projects: Public or Private.
4. Click the Update button.

## Changing the owner of a project

To change the owner of a project:

1. Collect the project name, the user name of the previous owner, and the user name of the new owner.
2. Run the `wakari-server` executable command `wk-server-admin`:

```
/opt/wakari/wakari-server/bin/wk-server-admin project-owner --project PROJECT --  
↪old OLD_OWNER --new NEW_OWNER --delete --keep-owner
```

- **PROJECT**: The project name.
- **OLD\_OWNER**: The user name of the previous owner.
- **NEW\_OWNER**: The user name of the new owner.
- **--delete**: An optional flag that deletes the old project directory in the `projects` directory of **OLD\_OWNER**. If this flag is not used, the old project directory is preserved but no longer used.
- **--keep-owner**: An optional flag that makes **OLD\_OWNER** a collaborator of the project after it is transferred to **NEW\_OWNER**. If this flag is not used, **OLD\_OWNER** will no longer have collaborator access to the project.

**NOTE:** The **OLD\_OWNER** user must still exist when the project's owner is changed. Before deleting any user, be sure to change the owner of the user's projects.

## Editing configuration files

1. In the AEN navigation bar, click **Admin** to open the Admin Settings page.
2. In the **Site Admin** menu, select **General**.
3. In the **Config Files** section, change the configuration settings for your AEN installation. For more information on configuration files, see [Using configuration files](#).
4. Click the **Update** button.

## Managing your AEN license

1. In the AEN navigation bar, click **Admin** to open the Admin Settings page.
2. In the **Site Admin** menu, select **License**:

The **Current License** section displays information regarding your AEN license, including the name of the product, vendor, license holder's name, end and issued dates, company name, license type, and contact email.

Staff	General Admin Settings
<a href="#">Daily Report</a>	<b>Wakari Server</b> Set the main URL where this site will be accessed <input type="text" value="http://anaconda-enterprise.trl"/>
<a href="#">Password Reset</a>	<b>Static URL</b> Set static URL where the js can be accessed <input type="text" value="http://anaconda-enterprise.trl/static/"/>
<a href="#">Notification</a>	<b>Default Project Access</b> This will be the default when a user creates a project  <input type="radio"/> <b>Public</b> Anyone can see this project. Collaborators have write access <input checked="" type="radio"/> <b>Private</b> No one can see this project except collaborators.
<a href="#">Exceptions</a>	<b>Account Type</b> <input type="text" value="wk_server.plugins.accounts.cloud"/>
	<input type="button" value="Update"/>
Site Admin	Config Files
<a href="#">General</a>	
<a href="#">Accounts</a>	
<a href="#">Users</a>	
<a href="#">Monitor</a>	
<a href="#">Security Log</a>	
<a href="#">Data Centers</a>	
<a href="#">Task Queue</a>	
<a href="#">License</a>	
Providers	

Staff

[Daily Report](#)
[Password Reset](#)
[Notification](#)
[Exceptions](#)

Site Admin

[General](#)
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[Users](#)
[Monitor](#)
[Security Log](#)
[Data Centers](#)
[Task Queue](#)
[License](#)

Current License

You have **166 days** remaining on your current license.

Renew your license

<b>product</b>	Anaconda Enterprise Notebooks
<b>vendor</b>	Continuum Analytics, Inc.
<b>name</b>	Continuum Development
<b>end_date</b>	2018-03-10
<b>issued</b>	2017-03-10
<b>company</b>	Continuum Analytics
<b>type</b>	undefined
<b>email</b>	dev@continuum.io

Upload New License

License File

Choose File

No file chosen

Update

## Renewing your AEN license

1. Click the Renew your license button.
2. In the Upload New License section, click the Choose File button.
3. Select the new license file.
4. Click the Open button.
5. Click the Update button.

Your renewed license information is displayed.

## Cheat sheet

The Admin dashboard includes three menus in the left column: **Staff**, **Site Admin** and **Providers**.

### Staff menu

- Daily Report—See the number of users and projects.
- Password Reset—Reset a user password.
- Notification—Send system messages to users via SES or SMTP.



- Exceptions—If errors are raised while AEN is running, a red dot appears in the AEN navigation bar. Review errors and mark them as read.

## Site Admin menu

- General—Change the configuration settings for your AE Notebook server installation.
- Accounts—Turns on or off Open Registration.
- Users—View usernames, number of projects and last logins.
- Monitor—View status of applications with related data, terminate or restart
- Security Log—View errors that could affect security.
- Data Centers—View current data centers and add a new data center.
- Task Queue—View workers in the task queue and priority.
- License—View current AEN license or upload a new license.

## Providers menu

Enterprise Resources—View, add or remove local or cloud services and designate public or private to control access to a compute node.

## Troubleshooting

This troubleshooting guide provides you with ways to deal with issues that may occur with your AEN installation.

- *General troubleshooting steps*
- *Browser error: too many redirects*
- *Browser error: too many redirects when starting project apps*
- *Exception: exceptions.TypeError: 'NoneType' object has no attribute '\_\_getitem\_\_'*
- *Error: unix:///opt/wakari/wakari-server/etc/supervisor.sock no such file*
- *Error: “Data Center Not Found” when deleting a project*
- *Forgotten administrator password*
- *Log files being deleted*
- *Error: This socket is closed*
- *Service error 502: Cannot connect to the application manager*
- *502 communication error on Amazon web services (AWS)*
- *Invalid username*
- *Notebook Error: Cannot download notebook as PDF via LaTeX*
- *Unresponsive wk-server thread without error messages*
- *Unresponsive wk-gateway thread without error messages*

- *Error starting projects*
- *Changes in .condarc file are ignored*

### General troubleshooting steps

1. Clear browser cookies. When you change the AEN configuration or upgrade AEN, cookies remaining in the browser can cause issues. Clearing cookies and logging in again can help to resolve problems.
2. *Make sure NGINX and MongoDB are running.*
3. Make sure that AEN services are *set to start at boot*, on all nodes.
4. *Make sure that services are running* as expected. If any services are not running or are missing, *restart them*.
5. *Check for and remove extraneous processes.*
6. *Check the connectivity between nodes.*
7. *Check the configuration file syntax.*
8. *Check file ownership.*
9. *Verify that POSIX ACLs are enabled.*

### Browser error: too many redirects

#### Cause

Browser cookies are out of date.

#### Solution

1. Log out.
2. Clear the browser's cookies.
3. Clear the browser cache.
4. Log in.

### Browser error: too many redirects when starting project apps

Browser shows “Too many redirects” when the user tries to start an application.

#### Cause

The project's Compute Resource is invalid or was deleted.

#### Solution

*Move the project to a valid Compute Resource.*

**Exception: exceptions.TypeError: ‘NoneType’ object has no attribute ‘\_\_getitem\_\_’**

This exception appears on the Admin > Exceptions page when a project does not have a Compute Resource assigned.

**Cause**

The project’s Compute Resource is invalid or was deleted.

**Solution**

*Move the project to a valid Compute Resource.*

**Error: unix:///opt/wakari/wakari-server/etc/supervisor.sock no such file**

This is a supervisorctl error.

**Cause**

supervisord is not running on the Server.

**Solution**

Ensure that supervisord is included in the crontab. Then restart supervisord manually.

**Error: “Data Center Not Found” when deleting a project****Cause**

The data center has been removed.

**Solution**

As root, run:

```
/opt/wakari/wakari-server/bin/wk-server-admin remove-project --db-only <user>  
↪<project>
```

**Forgotten administrator password**

1. Use ssh to log into the server as root.
2. Run:

```
/opt/wakari/wakari-server/bin/wk-server-admin reset-password -u SOME_USER -p SOME_  
↪PASSWORD
```

NOTE: Replace SOME\_USER with the administrator username and SOME\_PASSWORD with the password.

3. Log into AEN as the administrator user with the new password.

Alternatively you may add an administrator user:

1. Use ssh to log into the server as root.
2. Run:

```
/opt/wakari/wakari-server/bin/wk-server-admin add-user SOME_USER --admin -p SOME_
↵PASSWORD -e YOUR_EMAIL
```

NOTE: Replace SOME\_USER with the username, replace SOME\_PASSWORD with the password, and replace YOUR\_EMAIL with your email address.

3. Log into AEN as the administrator user with the new password.

### Log files being deleted

Log files are being deleted.

NOTE: Locations of AEN log files for each process and application are shown in the node sections in [Concepts](#).

### Cause

AEN installers log into `/tmp/wakari\__{server,gateway,compute}.log`. If the log files grow too large, they might be deleted.

### Solution

To set the logs to be more or less verbose, Jupyter Notebooks uses `Application.log_level`.

To make the logs less verbose than the default, but still informative, set `Application.log_level` to `ERROR`.

### Error: This socket is closed

You receive the “This socket is closed” error message when you try to start an application.

### Cause

When the `supervisord` process is killed, information sent to the standard output `stdout` and the standard error `stderr` is held in a pipe that will eventually fill up.

Once full, attempting to start any application will cause the “This socket is closed” error.

### Solution

To prevent this issue:

- Follow the instructions in [Managing services](#) to stop and restart processes.
- Do not stop or kill `supervisord` without first stopping `wk-compute` and any other processes that use it.

To resolve the “This socket is closed” error:

1. Stop wk-compute by running `sudo kill -9`.
2. Restart the supervisord and wk-compute processes:

```
sudo /etc/init.d/wakari-compute stop
sudo /etc/init.d/wakari-compute start
```

## Service error 502: Cannot connect to the application manager

Gateway node displays “Service Error 502: Can not connect to the application manager.”

### Cause

A compute node is not responding because the wk-compute process has stopped.

### Solution

Stop and then restart the supervisord and wk-compute processes:

```
sudo /etc/init.d/wakari-compute stop
sudo /etc/init.d/wakari-compute start
```

## 502 communication error on Amazon web services (AWS)

You receive the “502 Communication Error: This gateway could not communicate with the Wakari server” error message.

### Cause

An AEN gateway cannot communicate with the Wakari server on AWS. There may be an issue with the IP address of the Wakari server.

### Solution

Configure your AEN gateway to use the DNS hostname of the server. On AWS this is the DNS hostname of the Amazon Elastic Compute Cloud (EC2) instance.

## Invalid username

### Cause

The username does not follow 1 or more of these rules:

- Must be at least 3 characters and no more than 25 characters.
- The first character must be a letter (A-Z) or a digit (0-9).

- Other characters can be a letter, digit, period (.), underscore (\_) or hyphen (-).
- The [POSIX standard](#) specifies that these characters are the portable filename character set, and that portable usernames have the same character set.

### Solution

Follow the above rules for usernames.

## Notebook Error: Cannot download notebook as PDF via LaTeX

### Cause

LaTeX is not properly installed.

### CentOS/6 Solution

1. Install TeXLive from the [TUG site](#). Follow the described steps. The installation may take some time.
2. Add the installation to the PATH in the file `/etc/profile.d/latex.sh`. Add the following, replacing the year and architecture as needed:

```
PATH=/usr/local/texlive/2017/bin/x86_64-linux:$PATH
```

3. Restart the compute node.

### CentOS/7 Solution

1. Install the missing packages running the command:

```
yum install texlive texlive-xetex texlive-xetexconfig texlive-xetex-def texlive-  
↪adjustbox texlive-upquote texlive-ulem
```

## Unresponsive `wk-server` thread without error messages

### Cause

Two things can cause the `wk-server` thread to freeze without error messages:

- LDAP freezing
- MongoDB freezing

If LDAP or MongoDB are configured with a long timeout, Gunicorn can time out first and kill the LDAP or MongoDB process. Then the LDAP or MongoDB process dies without logging a timeout error.

### Solution

1. Check for frozen LDAP or MongoDB server processes.
2. You may also wish to configure the Gunicorn timeout to more than 30 seconds.

## Unresponsive `wk-gateway` thread without error messages

### Cause

If TLS is configured with a passphrase protected private key, `wk-gateway` will freeze without any error messages.

### Solution

Update the TLS configuration so that it does not use a passphrase protected private key.

## Error starting projects

Project's status page shows "There was an error starting this project".

### Cause

Lack of disk space in compute nodes prevents projects from starting.

### Solution

1. Verify that the project node meets the *system requirements*.
2. Check if there is enough free space on the compute node's partition where `/projects` lives:

```
df -h /projects
```

3. Free up some disk space to meet the system requirements.
4. Restart the project.

## Changes in `.condarc` file are ignored

Changes applied to `.condarc` are ignored by conda.

### Cause

Conda loads its configuration by merging multiple files together.

### Solution

Check if you are applying the changes to the correct file.

To show the merged state that conda is currently using:

```
conda config --show
```

To show all config files that conda is currently reading:

```
conda config --show-sources
```

### Frequently asked questions

- *What is AEN?*
- *Can notebooks be shared with anyone?*
- *Can I disable the option, “publish your notebook to anaconda.org”?*
- *How can I check the version number of my AEN server?*
- *Can I use AEN to access CSV or Amazon S3 data?*
- *Can I install other Python packages?*
- *Can I create a Python environment from the command line?*
- *Can I connect to GitHub with AEN?*
- *Can I print or print preview my Jupyter Notebooks?*
- *Is there a set amount of storage on AEN?*
- *How do I get help, give feedback, suggest features or report a bug?*

### What is AEN?

For information on AEN, see *Anaconda Enterprise 4 Notebooks*.

### Can notebooks be shared with anyone?

Yes. When you share a Jupyter Notebook through AEN, it can be viewed and run without the need to install anything special, regardless of what libraries were used to create the notebook. Each notebook also includes the python environment that it needs to run in.

AEN allows users to clone a shared Jupyter Notebook into their AEN account to make whatever changes or modifications they want. The notebook’s Python environment is also cloned, so it runs in the same environment as the shared Jupyter Notebook unless it is changed.

### Can I disable the option, “publish your notebook to anaconda.org”?

Yes. The upload button in the notebook app executes the option “publish your notebook to anaconda.org”. To disable it, log in as the AEN\_SRVC\_ACCT and run these commands:

```
source activate /opt/wakari/wakari-compute
jupyter-nbextension disable nb_anacondacloud --py --sys-prefix
jupyter-serverextension disable nb_anacondacloud --py --sys-prefix
```



## How can I check the version number of my AEN server?

Go to this URL in a browser: `http://$AEN_SERVER/admin/list`

NOTE: Replace `$AEN_SERVER` with the domain name or the domain name and port number of your AEN server.

## Can I use AEN to access CSV or Amazon S3 data?

Yes. If your data is in CSV files, upload the CSV files to your AEN account using the upload controls in the File Browser of the Workbench Application or the File Transfer Application.

To access data stored on Amazon S3, use the Boto interface from AEN. See the public data files in AEN for examples of how to use Boto to pull your data from Amazon S3 into AEN. For more information, see [Boto documentation](#).

You can also use IOPro to simplify and optimize the conversion of your data into Python arrays.

## Can I install other Python packages?

Yes, by creating a custom environment for your packages within your project.

For more information, see [Using the NBConda extension](#).

## Can I create a Python environment from the command line?

Yes, you can use the `conda create` command to create custom Python environments with whatever packages you choose. All AEN environments are shared with all the team members of a project.

EXAMPLE: In this example, `myenv` is a new environment containing the NumPy package.

```
conda create -n myenv numpy
```

NOTE: Python, Jupyter Notebooks and PIP are installed by default in all new AEN environments.

To use your new environment, activate it by running `source activate myenv`.

## Can I connect to GitHub with AEN?

Yes, you have full access to GitHub through an AEN Terminal application.

To generate an SSH key from your AEN account and add it to your GitHub account:

1. [Generate a GitHub SSH key](#).
2. Copy your key by running `cat ~/.ssh/id_rsa.pub`.
3. Select and copy the contents of the `id_rsa.pub` file to the clipboard.
4. Follow [GitHub's instructions](#) to go to your GitHub account and paste it from your clipboard into the appropriate box in your GitHub settings.

## Can I print or print preview my Jupyter Notebooks?

Yes, you can print your notebooks using your browser's regular printing capabilities.

You can also preview the printed page by clicking the **File** menu and selecting Print Preview.

### Is there a set amount of storage on AEN?

No, there is no set limit for storage in AEN. You are limited only by the size of the disk where AEN is installed.

If you need more storage, contact your system administrator.

### How do I get help, give feedback, suggest features or report a bug?

See *Help and support*.

### Help and support

Priority support is included with the purchase of an Anaconda subscription.

Contact your administrator first if you are having problems. Your administrator has a service level agreement where your issue will be responded to within a specific response time, depending on type and severity.

### Training and consulting

Training and consulting is available for AEN and any other Anaconda product.

For more information, please contact your account representative or [email the sales team](#).

### Providing feedback

Your feedback is very important to us!

Please, send us any [product feedback](#) while you are thinking about it.

TIP: Be sure to select AEN as the Platform Component Name.

### Submitting feature requests

We'd love to hear your ideas for consideration in future releases!

Your ideas help us build a better product. Your administrator can submit a support ticket for you.

NOTE: You can also request new features by using the [product feedback](#) form.

### Reporting a bug

If you think you have found a bug, please contact your administrator immediately. They will open a support ticket for your issue.

### Additional resources

The following resources are useful for getting started with Jupyter Notebooks:

- [Jupyter Notebook quick start guide](#)
- [Jupyter Notebook user documentation](#)

- [GitHub](#) shows the most popular Jupyter notebooks of the [month](#), [week](#), and [day](#).

## Release notes

### v4.3.3 Nov 5th, 2019

Administrator-facing changes:

- Support fetching packages from the `main` channel
- Add a new configuration key `emptyDefaultChannels` to avoid searching packages from the `free` channel
- Documentation updates

User-facing changes:

- Remove `gdal` and `basemap`
- Update `ipykernel`, `jupyter_core` and `jupyter_client`
- Update `astropy`, `scikit-learn`, `dask`, `numba`, `numpy`, `scipy`, `pandas` and `matplotlib`

Internal Fixes:

- Update Python to version 2.7.17
- Update Angular to version 1.7.8
- Update urllib3 to version 1.25.3
- Update Node.js to version 10.15.3
- Replace `pycrypto` with `pycryptodome` 3.8.2
- Update `paramiko` to version 2.60
- Update `jinja2` to version 2.10
- Update `request` to version 2.88
- Update `grunt` to version 1.0.4
- Update `requests` to version 2.22.0
- Update `gunicorn` to version 19.9.0
- Update `openldap` to version 2.4.46
- Update `python-ldap` to version 3.2.0
- Removed `growl` and `superagent` dependencies
- Update `rbase` and `r-essentials` to version 3.5.1

### v4.3.2 May 29, 2019

Internal Fixes:

- Update Bootstrap to version 4.3.1
- Update jQuery to version 3.3.1
- Update jQuery UI to version 1.12.1
- Update notebook to version 5.7.8

- Update ipywidgets to version 7.4.2
- Update ipyparallel to version 6.2.3
- Set Secure flag on xsrf, access\_token, and refresh\_token cookies

### v4.3.1 March 25, 2019

Administrator-facing changes:

- Add option for server-side session management
- Add option to terminate terminal sessions on logout

Internal Fixes:

- Set Secure and HTTPOnly flag on session cookies
- Fix XSS vulnerability

### v4.3.0 October 24, 2018

Administrator-facing changes:

- Fix bug where compute logging wasn't respecting the `logMaxFiles` key
- Log and display a descriptive error message when there is a problem creating the users index
- Log and display a descriptive error message when there is a problem creating a new user with a duplicated e-mail address when the `uniqueEmail` setting is enabled
- Add footer server pages with server host data (IP, AEN version and server version)
- Fix admin script to change the status of private projects
- Fix validation error when updating/editing an existing resource
- Docs: Add KB article about using MongoDB to update old projects with new Data Center information
- Docs: Add restarting service step to SSO documentation
- Docs: Add support for newer versions of MongoDB
- Docs: Add documentation on `uniqueEmail`
- Docs: Add `projDirsAsHome` key to config docs
- Docs: Rewrite the “Using project directories as home directories” section
- Docs: Add full path to admin commands
- Docs: Warn about upgrading away from tested pkgs
- Docs: Add missing steps to “Authenticating with LDAP” section
- Docs: Add troubleshooting documentation about orphaned projects
- Docs: Warn about not using IP address when you connect to AEN
- Docs: Add an entry about ‘Error starting projects’ in the troubleshooting page
- Docs: Rewrite “Group and user permissions for NFS” section and description of the `identicalGID` key in the config pages
- Docs: Add a new section about using MRO packages in AEN

- Docs: Preserve username capitalization when using LDAP/AD
- Docs: Add umask 0022 to security requirements
- Docs: Add new section about changing install location
- Docs: Add note about how to manually break out Root CA for the gateway
- Docs: Add note about upgrading custom environments
- Docs: Add notes about how to find conda config files inside AEN
- Docs: Add note about using `USE_SERVER_BASED_SESSIONS: false` when configuring SSO between AEN and versions 2.33.3 through 2.33.10 of the Repository

#### User-facing changes:

- Increase Workbench file upload limit
- Fix Bokeh examples
- Extend `nb_locker` to detect a server disconnection and generate an alert if it occurs
- Docs: Update the notebook app to correctly point to AEN docs
- Docs: Emphasize that permissions are not applied recursively in the workbench

#### Internal fixes:

- Update Nginx version to v1.12.2
- Remove unused server config file during the compute upgrade process
- Remove already defined compute default settings from the post-script step
- Pin `widgetsnbextension` version to prevent version mismatch issue (ipywidgets)
- Remove `--offline` flag from the conda clone operations
- Support MongoDB 3.4.14 and update pymongo to version 3.2.2
- Fix LDAP username case sensitivity
- Security fixes and enhancements

### v4.2.2 March 1, 2018

#### Administrator-facing changes:

- Add admin command to change project owner
- Server: Add ability to disable public projects
- Gateway: Add support for SSL private key passphrase
- Docs: Add backup and restore runbook to the docs
- Docs: Emphasize backups before upgrading process
- Docs: Recommend putting AEN and projects folder on the same filesystem
- Docs: Add RHEL version 7.4 to supported versions
- Docs: Add troubleshooting instructions to fix problems when downloading notebook as PDF via LaTeX

#### User-facing changes:

- Upgrade bokeh to version 0.12.7

- Upgrade holoviews to version 1.8.3
- Upgrade numba to version 0.35.0
- Upgrade scikit-learn to version 0.19.0

Internal fixes:

- Fix bug in init scripts when requiretty is enabled
- Fix bugs related to AEN\_SUDO\_SSH option
- Fix bug in fix\_ownership function when directories contain spaces
- Docs: Fix error in Active Directory configuration example
- Server: Fix bug when updating user/group in supervisor configuration files in post-install for server and gateway
- Server: Fix bug Admin reports on user totals are inconsistent
- Server: Fix error in login screen when open registration and LDAP are enabled
- Server: Fix bug in Last seen date
- Server: Fix bug Monitor Report blank
- Server: Load JS files from local CDN
- Server: Fix error when terminating or relaunching an application from Monitor
- Server: Fix error creating projects when using Internet Explorer 11
- Compute: Fix 404 errors when using pivottablesjs
- Remove Wakari Cloud leftovers

### **v4.2.1 December 18, 2017**

Administrator-facing changes:

- None

User-facing changes:

- None

Internal fixes:

- Fix undetected “ca” key when using self-signed certificates signed by a private CA
- Fix login redirects when using SSL
- Add verify gateway SSL certificate for get and post requests

### **v4.2.0 November 22, 2017**

Administrator-facing changes:

- Feature/allow remote MongoDB
- Allow for configuration for login timeout and set default
- Add verbose option to conda create clone
- Avoid duplicate name for resources / compute-nodes

- Allow renaming main and message queue databases
- PAM-based authentication module
- Change wakari logos to Anaconda logos
- Replace ‘wakari’ wording
- New config option to move the user’s home directory into the user’s project directory
- Make logging less verbose in AEN
- Documentation for PySpark kernel installation
- Improve SSL documentation

User-facing changes:

- New config option to move the user’s home directory into the user’s project directory
- Package cache was moved from user’s home directory into the user’s project directory
- Change wakari logos to Anaconda logos
- Fix error for deleting tags to work
- Define shell prompt in `.projectrc` template
- Replace ‘wakari’ wording

Internal fixes:

- Move server unix socket from `/tmp` to `/opt/wakari/wakari-server/var/run`
- Make project deletion synchronous for consistency
- Avoid storing `csrf` token in the user profile
- Expire gateway session when server logs out
- Allow log rotation in the three components
- Fix permissions on static files
- Change log level to debug in gateway
- Do not log private keys in gateway
- Save request remote address when logging action
- Unify logs formatting and timezone in compute nodes with Winston
- Several fixes and documentation improvements

#### **v4.1.3 August 16, 2017**

- Upgrade conda to version 4.3.24
- Upgrade anaconda to version 4.4.0
- Admin application monitor
- Block access to package list view
- Add placeholders in password reset form
- Change static content location
- Fix error when checking for package updates in notebook application

- Replace slashes in project tags
- Fix submit errors in password reset form
- Replace/remove “wakari” word from multiple places
- Fix missing commands missing sudo in start-project
- Improve gateway and compute node validators
- Check if bzip2 is installed during server setup process
- Include port number in host header
- Forbid creation of empty tags
- Repair “Create Account” link in login page
- Use UTC for server logs
- Mark datacenters as trusted by default
- Disable heart beating
- Compute resource: Show full path to log file
- Improve init scripts
- Allow deleting all projects
- mtq: Implement exponential backoff on connection error to mongodb
- In the general admin display, do not show the bind password for LDAP
- The accelerate package has been removed from the installation
- Other minor bugfixes

#### **v4.1.2 March 29, 2017**

This is mainly a maintenance release improving internal machinery and upgrading the root packages.

- Upgrade conda to version 4.3.14
- Upgrade Anaconda to 4.3.1
- Upgrade r-base to 3.2.2
- Fixed AEN nb\_conda to be compatible with conda 4.3.x series
- Several documentation fixes
- Other minor bugfixes

#### **v4.1.1 December 15, 2016**

- Added CentOS 7 support
- Support dots in usernames
- More usernames validation
- Fixed creation (through nb\_conda) of single letter environment names
- Environment names (through nb\_conda) validation



- Fixed uploading of notebook using `nb_anacondacloud`
- Fixed attaching of environments in published notebooks through `nb_anacondacloud`
- Several documentation fixes
- Other bugfixes

#### **v4.1.0 October 21, 2016**

- Added JupyterLab application
- Removed GateOne terminal application
- Included additional notebook extensions (`nbpresent` and `nb_anaconda_theme`)
- Updated to conda 4.2.9 in default project environments
- Added HTTP timeout setting for gateway and compute launcher
- Changed default gateway port to 8089
- Added support for all-numeric usernames
- Add R channel to default conda configuration file
- Other bugfixes

#### **v4.0.0 June 30, 2016**

- Customized installation with:
  - AEN Functional ID and Group
  - AEN (installation and run) `sudo` commands
  - Removal of root access from the AEN service account
  - Configurable `sudo` command
  - Restriction of `sudo` access to all the processes
- Upgrade Jupyter to 4.2
- Upgrade the `anaconda-nb-extensions` to the latest versions
- Upgrade Anaconda to 4.0
- Deprecate `wakari-publisher`
- Security enhancements
- SSL configuration documented between all AEN Server components
- Several bugfixes
- Overall documentation revision and general improvement

### v0.10.0 February 2, 2016

- New projects dashboard
- Capability to star and tag a project
- Sticky searches
- New Jupyter Notebook extensions
- Updates to all packages. Highlights: bokeh 0.11, ipython/jupyter 4.1.

### v0.9.1 October 19, 2015

- New Search capability to find projects and files within a project.
- Added “Related Projects” list to the project view, based on code similarity.
- New UI for fine-grained access control of project files in the Workbench app
- Viewer app now renders plain text files correctly
- Updated LDAP configuration docs
- Updates to all packages. Highlights: bokeh 0.10, ipython/jupyter 4.0.

**Note** ElasticSearch, and an Oracle JRE, must be installed on the server in order to use the new search features. Indexing of project files will begin when the project is started (or paused and re-started). If search features are not desired, set "SEARCH\_ENABLED": false in the server configuration file to avoid errors.

### v0.8.0 August 21, 2015

#### New Features

- Updated packages based on Anaconda 2.3, and removed older packages no longer in Anaconda.
- Updated IPython to version 3.2.1
- Documentation is now installed with the server (use the Help link in the top navigation bar)
- Added the ability for the administrator to define a customized default project environment.
- The server has been updated to use python 2.7.10.
- Init scripts are now provided for each Anaconda Enterprise Notebooks service.
- Added relevant links to some error pages

#### Problems Resolved in this Release

- Project status indicators (e.g. starting, pausing) now automatically update.
- If an access is unauthorized, the server now returns a 403 (Unauthorized) status code and prompts the user to log in.
- Modified nginx configuration to support running the server on non-standard ports.
- The server installation no longer uses a default password for the wakari user. A random password is generated and displayed during installation.

- Prevent double-click from attempting to create a project twice
- Removed an obsolete script reference that was causes a 404 error to be logged in the browser console when opening the Terminal app.
- The installer scripts no longer fail if the database already contains the ‘wakari’ user.
- Updated example notebooks to work with latest Bokeh release.
- Fixed terminal app key bindings to allow Mac command key to work normally
- Installers now indicate where the installation logs are stored
- LDAP user attributes containing binary data are now ignored.

## Documentation Updates

- Updated and consolidated Troubleshooting guide.
- Simplified some steps in the installation procedure.
- Updated notebooks in the Examples directory for use with the latest IPython Notebook and Bokeh.
- Added a section on project permissions to the Troubleshooting guide.
- Added notes on how to remove a project if the datacenter has already been removed.

## v0.7.0 June 12, 2015

### New Features

- Updated Bokeh to v0.9
- Ability to list packages installed on the server
- Administrators now have full access to all projects.
- Added automated checking and display of connection status between server, data centers, and compute resources.
- When creating a new project, an environment for the project is automatically created as a clone of the root Anaconda environment.

### Problems Resolved in this Release

- Problem with checking in files with revision control extension
- Revision control extension can’t handle notebook names with spaces
- Problem moving files form one compute node to another if configured for LDAP
- Should default to UTF-8 encoding and warn user if no locale is detected
- Adding a compute resource via the command line admin tool does not work
- The installer now sets `umask 0022` to ensure correct file permissions

### Documentation Updates

- Added a *Troubleshooting* section to the documentation.
- Added notes on how to configure crontab to start the Anaconda Enterprise Notebooks services at startup
- Example SSL config file now has correct log paths
- Added instructions on how to ensure that POSIX ACL support is enabled on the projects directory.
- Fixed syntax problem in sample LDAP config.json
- Added section on how to use self-signed or private CA certificates

### v0.6.3 March 27, 2015

- Updated LDAP module
- LDAP user filtering
- Added Notebook locking
- Added Notebook integrated revision control system
- Move projects between compute nodes
- User-specific binding to compute nodes (private compute nodes)
- Improved installation process and dependency checking
- Incorporated support for SSL for Server and Gateway nodes
- Improved Gateway error handling
- Fixed package dependencies for update process
- Documentation updates

### Previous versions

Documentation for previous versions is provided for users who have not yet upgraded to the current version of AEN.

### Anaconda Enterprise 4 Notebooks

*Empower the Data Science Team with cross-collaboration*

AEN is a browser-based Python data analysis environment and visualization tool from Anaconda®. AEN is a ready-to-use, powerful, fully-configured data analytics environment all in a secure, governed environment.

AEN allows data science team members to create and share private notebooks, manage access, control notebook revisions, compare and identify differences across notebook versions, search notebooks for keywords and packages, use enhanced collaborative notebook features—including revision control and locking—and to access an on-premises and/or cloud collaborative notebook server.

The current version of AEN is 4.3.1, released March 25, 2019.

## User guide

AEN's browser-based management of private packages, notebooks, and environments allows data science team members to:

- Create, share and manage private notebooks.
- Control notebook revisions.
- Compare and identify differences across notebook versions.
- Search notebooks for keywords and packages.
- Use enhanced collaborative notebook features including revision control and locking.
- Access on-premises and/or cloud-based collaborative notebook servers.
- Utilize multiple language kernels like Python and R language in the same notebook.
- Create new notebook environments on the fly without leaving the notebook or entering commands in a prompt.
- Publish results to business stakeholders as interactive visualizations and presentations.

To quickly get up and running with AEN, see [Getting started](#).

Download the [Cheat sheet](#) for easy reference.

## Concepts

- [Projects](#)
- [Team collaboration](#)
- [Access control](#)
- [Sharing projects](#)
- [Project tags](#)

## Projects

AEN users interact with the system predominantly through projects.

A project is a set of conda environments, Jupyter Notebooks, and other files.

Each project has a project drive that all team members can access. The size of the drive is not limited by AEN. Contact your system administrator if you find you do not have sufficient space.

Each project has a separate project directory on the project drive.

The project directory is a directory for project files and data that is separate from the project owner's and team members' home directories, so that team members can share and have equal access.

The path to your project directory is `/projects/<project_owner>/<project_name>`.

For administrative information about projects, directories, and permissions, see [Projects and permissions](#).

### Team collaboration

Teams collaborate in AEN using projects. Projects allow a team to easily come together by sharing the resources, applications, and environments that are necessary to collaborate effectively.

The AEN project owner and any team members connected to their project will have access to the same:

- Shared files and home directories.
- Shared Python and R environments.
- Shared nodes and hardware.
- Common applications.
- Web user interface.

For more information, see [Working with projects](#).

### Access control

AEN access controls allow you to:

- Add and remove project access for new team members.
- Limit the access to specific folders and files to members of your project team.
- Use permissions to extend execute access to team members. By default, all of the team members on a project have read and write access to all project assets.

Access control is performed from each project's Workbench application.

For more information, see [Controlling access to your project](#).

### Sharing projects

AEN supports both public and private sharing.

A project can be “public,” which means that anyone with access to the system can view the project assets.

Any content placed in the `public` folder in a project is publicly accessible using its URL.

A project can be “private,” which means that only the project owner and team members can view the project assets.

You can also *limit who can access specific files*.

### Sharing Jupyter Notebooks

In addition to general project sharing capabilities, you can also publish Jupyter Notebooks to Anaconda Repository. This automatically versions the notebook and allows you to define who can view the notebook.

### Project tags

Tags are used to:

- Group similar or related projects.
- Identify your project so that it is easier to find.

- Let others know about your project.

You can *add and remove tags* for any project that you have access to.

## Getting started

This section contains information and tasks for first-time AEN users.

In this getting started guide, you will:

- 1. *Download the AEN cheat sheet*
- 2. *Access your user home page*
- 3. *Create a new project*
- 4. *Add collaborators*
- 5a. *Open an example notebook, OR*
- 5b. *Create a new environment and notebook*
- 6. *Create checkpoints for version control*
- 7. *Share your notebook and environment with others*
- 8. *See what to do next*

### 1. Download the AEN cheat sheet

Before you start, download and print the *AEN cheat sheet* for easy reference.

### 2. Access your user home page

After your administrator has set up your server and new Anaconda account, you will receive a welcome email.

1. Click the link in the email to open the AEN login page.

NOTE: Use the domain name and not the IP address when you connect to AEN. Using the IP address can cause TLS and security certificate errors.

2. Enter your AEN account username and password.

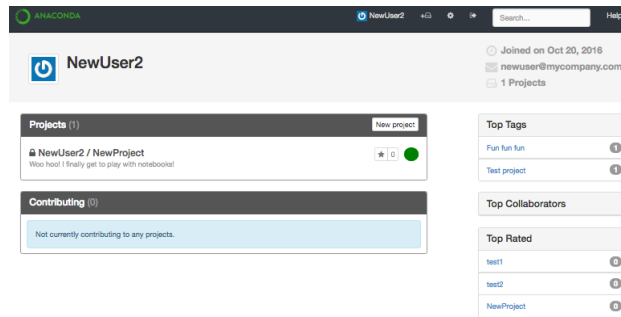
NOTE: Some administrators allow you to create your own account. If your administrator has allowed this, in the create a new account section, create your own username and password.

3. Click the Login button.

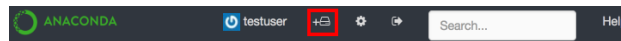
Your user home page, where all good things happen, is displayed:

### 3. Create a new project

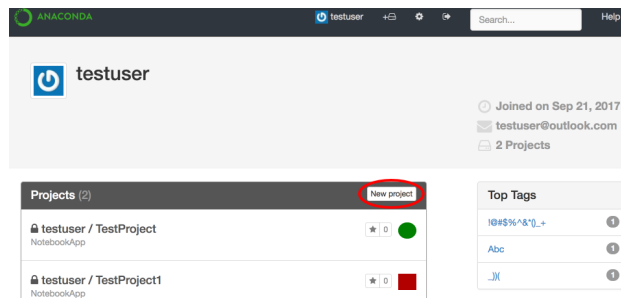
1. There are 2 ways to create a new project in AEN:



- On the right side of the AEN task bar, click on the New Project icon:



- On your home page, click the New project button:



2. On the Project page that is displayed, type a name for your project, such as “Testing.”

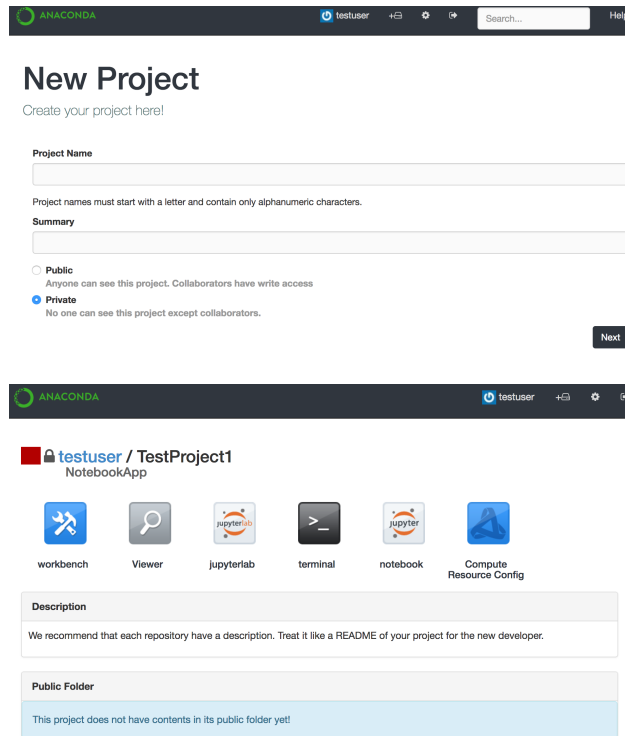
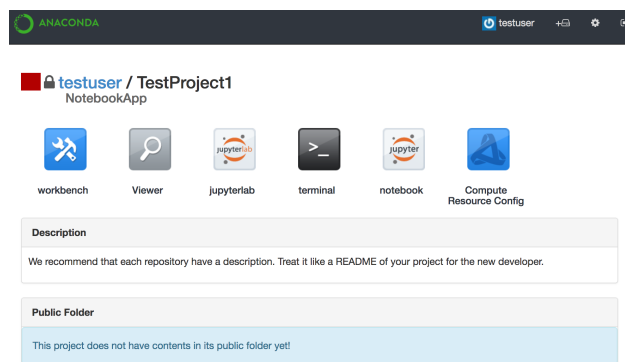
3. Type a summary of the project so you can recognize it later.
4. Select whether your project will be public or private.
5. Verify that the default data center is selected.

**TIP:** You can update the project summary and description at any time from the **Project** menu in the Project Settings. To return to your project at any time, click the project name.

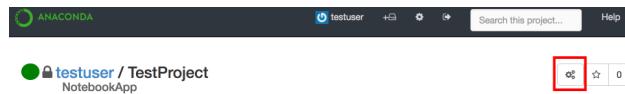
6. Click the Next button.

Your new project’s home page is displayed:



- To change the project settings, click the Project Settings icon on at the top right.



- Modify the summary or add a description of the project.

**TIP:** A project description is recommended, and may be written in Markdown syntax (plain text valid Markdown).

To see how Markdown will be displayed, in the description area, click the **Preview** tab.

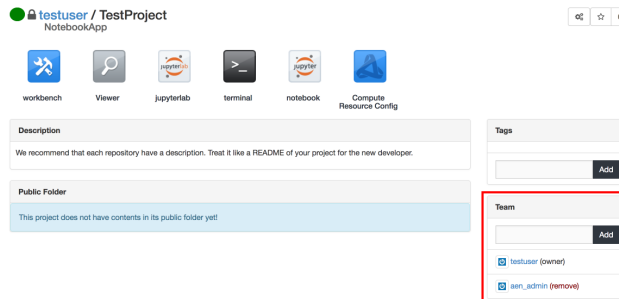
#### 4. Add collaborators

You can add team members to your project as collaborators. Adding team members to your projects makes collaboration easy because they have full access to the project's applications, files and services.

When you add team members, their home directory is mounted in the project. There is no need to download and email data or scripts—team members can work on the same files in the same environment in which you are working.

To add collaborators to your project:

1. From your project home page, in the Team box, begin typing a teammate's username.
2. In the list that is displayed, select the teammate's username.
3. Click the Add button.

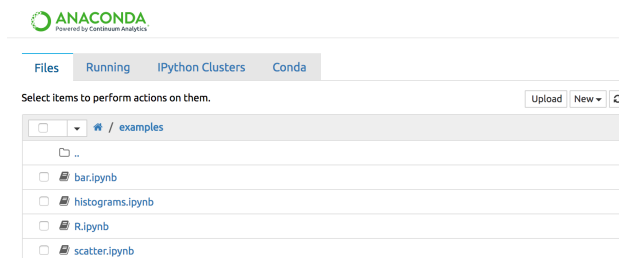


1. Repeat these steps for each team member you want to add as a collaborator.

**TIP:** You can add or remove team members any time from the **Team** menu in Project Settings. You can also modify a team member's read, write or execute permissions at any time from the *Using Workbench*.

## 5a. Open an example notebook, OR

1. From your project home page, click the Jupyter Notebooks icon.
2. On the File View page, click the Examples folder.



1. Select any of the example notebooks.
2. To see the default results of the formulas used in the displayed notebook, in the **Cell** menu, select Run All.
3. To experiment with changing the notebook, edit any of the formulas in the notebook.
4. In the **Cell** menu, select Run All.

Any differences resulting from your edits are displayed.

## 5b. Create a new environment and notebook

If you are already familiar with creating notebooks, you can easily set up a new environment with the programs you need—like SciPy and NumPy—then open a new notebook and make your edits.

To create a new environment:

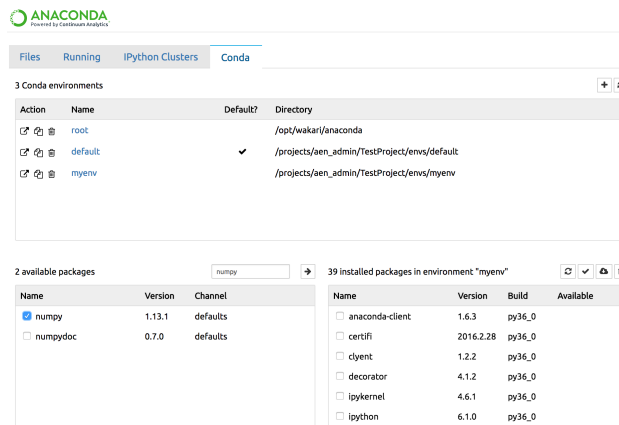
1. From your project home page, click the Jupyter Notebooks icon.

2. On the File View page, click the **Conda** tab.
3. To add a new conda environment, on the top right of the **Conda** tab, click the + icon.
4. Type a name for your environment.
5. Select Python 2, Python 3 or R language kernel.
6. Click the Create button.
7. To activate your new environment, click its name.

The packages that are available and installed in your new environment are displayed.

## Adding SciPy and Numpy packages

1. In the available packages section, search for the package name `numpy`—all lower case.
2. In the results section, next to `numpy`, select the checkbox.



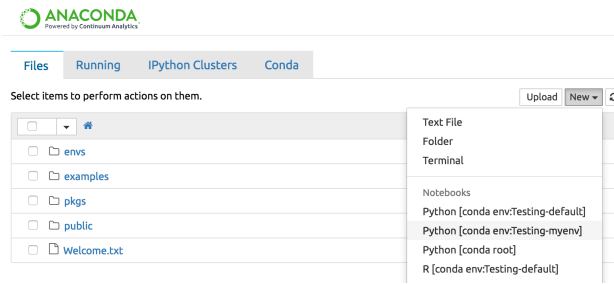
1. Click the Install icon.
2. To confirm your installation, click the Install button.

Numpy is displayed in the installed packages section—if not, click the Refresh button. Repeat these steps to install the Scipy package—searching for `scipy` in step 1.

TIP: You can return to this screen at any time to add additional packages to this environment.

## Creating a new notebook in your environment

1. From the AEN homepage, click the **Files** tab.
2. On the top right of the **Files** tab, click the New button.
3. Under Notebooks, select the Python environment with the name you entered while *creating a new environment*.



NOTE: If you do not see your new environment listed under Notebooks, next to the New button, click the Refresh button.

A new locked notebook is displayed. Paste or write some code to execute when you are ready.

## 6. Create checkpoints for version control

Whether you are exploring an existing notebook, or creating a new one, you can easily create checkpoints, return to an earlier version, compare two different versions and save them for reference.

To create a checkpoint, in the **File** menu, select Save and Checkpoint:

To revert your notebook to a previous checkpoint, in the **File** menu, select Revert to Checkpoint.

NOTE: For more information about revision control features, including creating commits and comparing differences, see [Using the Revision Control Mechanism extension](#).

## 7. Share your notebook and environment with others

See [Sharing projects and notebooks](#).

## 8. See what to do next

Now that you have completed the Getting Started guide, you are ready to move on to [basic tasks](#) and [advanced tasks](#).

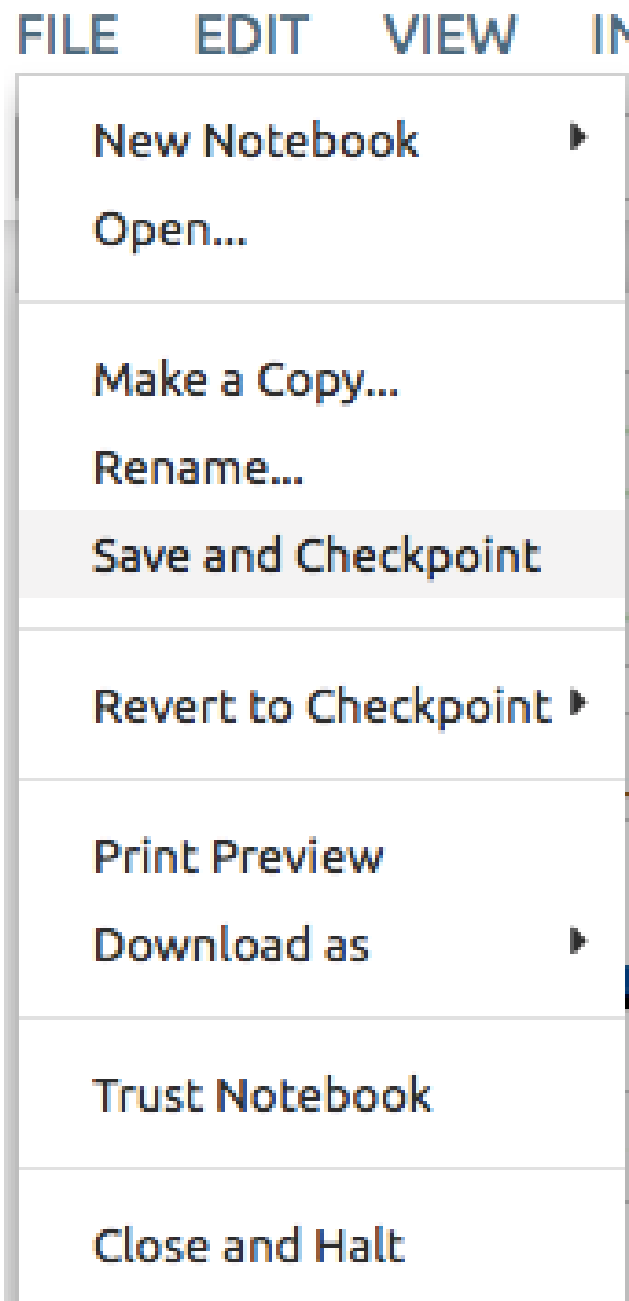
### Basic tasks

This section contains information and tasks that use the web browser to manage projects and is best-suited for any beginning AEN user:

### Working with projects

Almost everything in AEN starts by opening an existing project or creating a new one.

After that, you can set up a special environment with the packages you want, set their access permissions and modify your project settings.



## Searching for a project or file

- *Types of files searched*
- *Search indexing*
- *Using search constructs*
- *Searching metadata fields*
- *Searching a project*
- *Saving a search*
- *Removing a saved search*

To search for projects and files, use the Search box in the AEN navigation bar. The search provides different results depending on which page you search from:

- On a project home page, search results include any files that match your search criteria within the current project.
- On any other AEN page, search results include any files that match your search criteria within all projects.

TIP: Your search results include only files and projects that you can view: public projects, and private projects to which you have a minimum of view access.

### Types of files searched

The following types of files are included in search results:

- `.py`—Python source files.
- `.ipynb`—IPython/Jupyter notebooks.
- `.txt`—plain text files.
- `.md`—Markdown files.

### Search indexing

Files that are modified while a project is running are automatically re-indexed shortly after the files are modified. If you create or update a large number of files—such as cloning a git repository or copying a directory—search results may take several minutes to update.

Files that are modified while the project is not running are re-indexed only after the project is started.

### Using search constructs

You can use the following search constructs:

- Ordinary words will match the full-text contents of any file.
- Wildcards are permitted.

EXAMPLE: `John*` will match John and Johnny. These are glob patterns and are similar to their usage in the command line.

- Combine queries using AND or OR, and group them using parentheses `()`.

Regular expression patterns can be embedded in the query string by wrapping them in forward-slashes (/):

```
name:/joh?n(ath[oa]n)/
```

The supported regular expression syntax is explained in [the Elasticsearch reference](#).

NOTE: Wildcards apply inside a regular expression. A query string such as `/.*n/` would force the search to visit every term in the index.

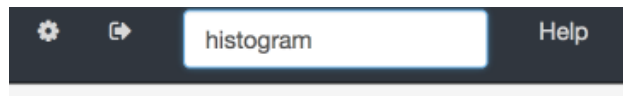
## Searching metadata fields

You can search in specific metadata fields:

- `imports:name`—matches files that import the module name.
- `uses:name`—matches files that reference the identifier name. Referenced names include any functions and globals imported from other modules, as well as the names of any methods invoked on any object.
- `defines:name`—matches files that define the identifier name. Defined names include functions defined at global scope, class names, and method names within classes.
- `acl:user`—matches files in which the named user has read access or higher.

## Searching a project

1. In the Search box, type a string of text:



TIP: Search by glob patterns, which are similar to file matching in the command line.


EXAMPLE: To find projects in the test family that are numbered from 00 to 99, search for `Test-??`. To find all projects whose name ends with “Stats,” search for `*Stats`.






2. Press Enter.
3. In the search results, click the plus + icon above a project name to show a list of matching files in the selected project:

TIP: Click the project name to open the project’s home page.

4. To view a file, click its file name in the matching files list:

Projects matching 'iris' ([save this search](#))

 Projects matching 'iris' ([save this search](#))

 testuser / TestProject NotebookApp	★ 0 ●
 AnacondaEN / AEN11_0 No Summary	★ 0 ●
 Rida / ABC No Summary	★ 0 ●
 Rida / Testing No Summary	★ 0 ●
 testuser / TestProject1 NotebookApp	★ 0 ●


Found 1 files matching 'histogram' in user02/Public\_project. ([save this search](#))






File	Relevance
<a href="#">/examples/histograms.ipynb</a>	42

## Saving a search

1. At the top of the search results, click Save this search:

Projects matching 'iris' **Stored**

 Projects matching 'iris' **Stored**

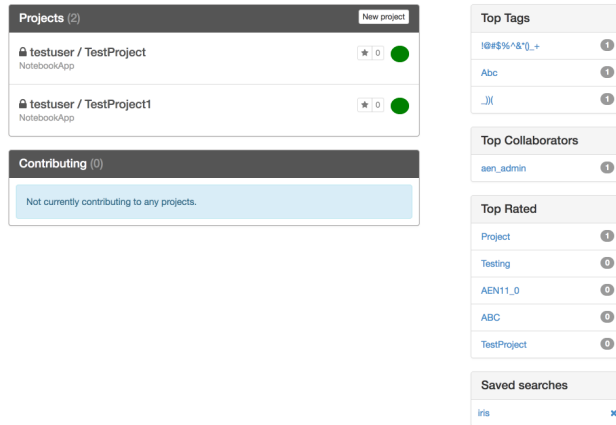
 testuser / TestProject NotebookApp	★ 0 ●
 AnacondaEN / AEN11_0 No Summary	★ 0 ●
 Rida / ABC No Summary	★ 0 ●
 Rida / Testing No Summary	★ 0 ●
 testuser / TestProject1 NotebookApp	★ 0 ●

The “save this search” text changes to “stored” and your search is saved. Your saved searches are listed on your home page.

## Removing a saved search

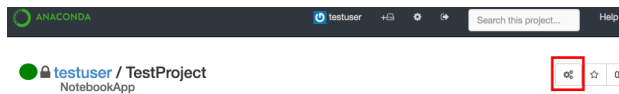
On your home page, in the Saved searches section, click X next the saved search that you want to remove:



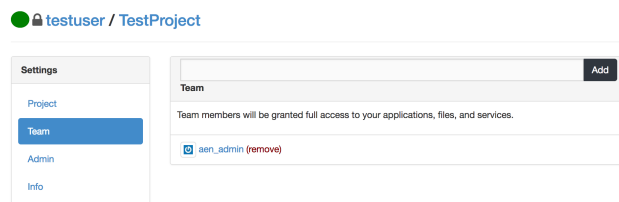


## Adding and removing team members on a project

1. On the project home page, click the Project Settings icon to open the Project Settings page.



2. In the **Settings** menu, select **Team**.



## Adding a team member

1. In the username box, type in the first few letters of the username for the team member you want to add to the project.
2. In the list of usernames that displays, click the user to add.
3. Click the Add button.

### Removing a team member

Click the red Remove link next to the name of the user you want to remove from the project.

### Controlling access to your project

- *Controlling team member access*
- *Controlling non-team member access*

### Controlling team member access

By default, all of the team members on a project have read and write access permissions for all project assets.

The available permissions are read, write and execute. If you remove all individual or group permissions for a project asset, team members will not be able to access that asset.

To change a project's permissions:

1. Open the project's home page.
2. Click the Workbench icon.
3. In the Workbench app, right-click the file or folder you want to limit access to.

NOTE: When you change a folder's permissions, the permissions of files and folders inside it do not change. You may change the permissions of those files and folders manually.

4. In the menu that displays, select Permissions:

A list of owners and team members who have access to your project is displayed.

5. Find the team member you want to change access for:

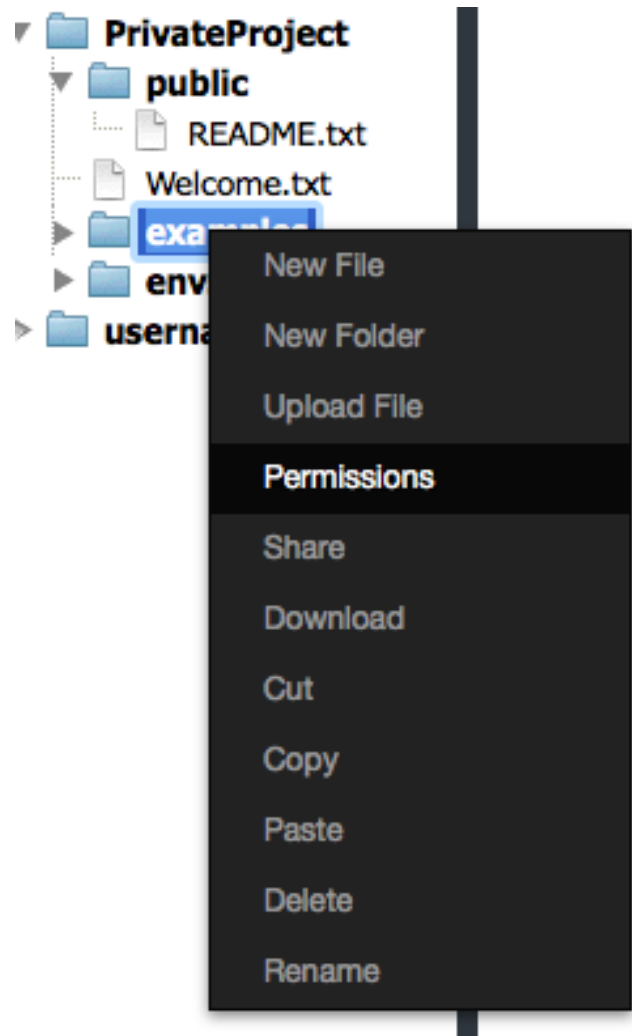
6. Next to the team member's name, select or deselect the permissions for that user.

NOTE: You can add a team member and set their access at the same time by typing their name in a username box, setting their permissions, and then clicking the Add button.

7. Click the Submit button.

The selected permissions are added, and the deselected permissions are removed.

NOTE: If a team member is in the Workbench application when you give them access, they must refresh their browser window to see their current permissions.



Permissions for examples

Owner:  Group:

Who	Type	Read	Write	Execute
owner		<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
group		<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
others		<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>
Mask		true	true	true
<input type="text" value="username"/>	User	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input type="text" value="username"/>	Group	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input type="text" value="username2"/>	User	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>
<input type="text" value="username2"/>	Group	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
<input type="text" value="username3"/>	User	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
<input type="text" value="username3"/>	Group	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

### Controlling non-team member access

You can choose to grant file or folder access to someone who is not part of the project team, as long as that person has an AEN account.

Sharing with individuals outside the team is a four step process:

1. *Copy or move the file or folder to your home directory.*
2. *Give the user read and execute access to your home directory.*
3. *Add the user to the file's permissions.*
4. *Have the user add your directory to their workbench.*

### Copying a file or folder to your home directory

Your home directory is displayed at the bottom of the File Manager pane in the Workbench.

To protect the other files and folders in your home directory—those you are not providing permissions to a user to access—we recommended that you:

1. Create a sub-folder.
2. Rename the folder with the name of the user you are granting access to.
3. Copy or move the file you want to grant permissions for to the renamed folder.

The file is copied or moved to the new location and is ready for you to update the file permissions.

### Granting file access

You must select read and execute access for a user to be able to view, but not edit, the files or folders.

1. Right-click the name of the file or folder you are granting access to.
2. In the menu that is displayed, select Permissions.
3. Click the Add button.
4. Type the username of the user to whom you are granting file access and press Enter.

**TIP:** If you grant access to a folder instead of a specific file, you only have to set permissions the first time you share the folder with each user, unless you need to update the permissions.

### Adding file permissions for a user

Once a user is included in your Permissions list, you must *add the correct permissions* for the user, in the same way as you would for a team member.

Once complete, depending on the access granted, the user will be able to view, read, change, and execute the file.

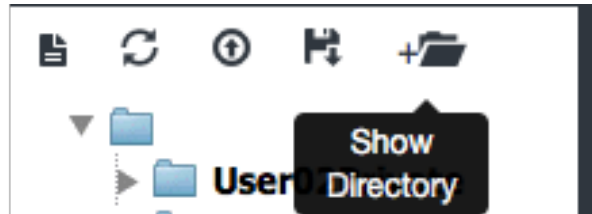
**NOTE:** If you change permissions for a folder instead of a file, the user will be able to see and access any files within that folder.

## Adding a directory to a user's workbench

The user can now add your home directory to their Workbench File Manager.

To add your home directory to another user's workbench, have the other user follow these steps:

1. Click the Show Directory button at the top of the Workbench File Manager:



The Show Directories dialog box displays.

2. In the text box, type `/home/[yourusername]`.

NOTE: Replace `[yourusername]` with your AEN username.

Show Directories
×

Enter the full path to an existing directory that you would like to see in the file browser. For example, if the project node has a directory with a path of `/data/2010` that contains data files from 2010 that you want to browse, enter `/data/2010` and click on the Show button.

Show

3. Click the Show button.
4. Verify that the folder is now displayed below the text box:

Show Directories
×

Enter the full path to an existing directory that you would like to see in the file browser. For example, if the project node has a directory with a path of `/data/2010` that contains data files from 2010 that you want to browse, enter `/data/2010` and click on the Show button.

Show

5. Close the Show Directories dialog box by clicking the X in the upper-right corner or by clicking anywhere outside the box.

- Click the Refresh button.

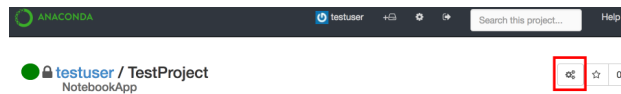
The shared file is displayed in the File Manager:



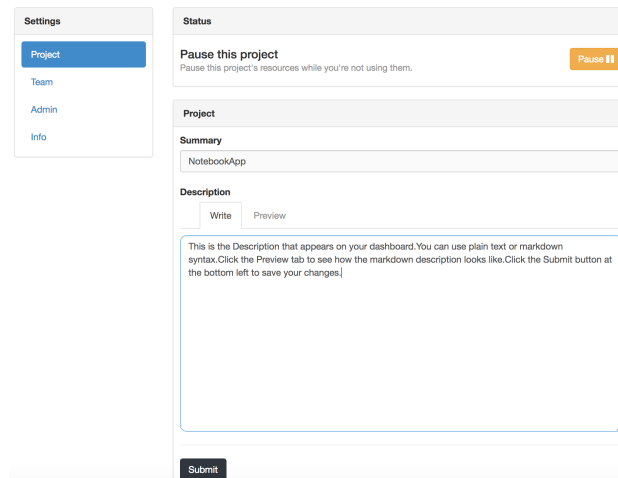
## Starting and stopping a project

**TIP:** Stopping a project stops all the applications launched for that project that use resources when running, such as memory and compute cycles. It is best to stop projects when they are not in use.

- On the project home page, click the Project Settings icon to open the Project Settings page.



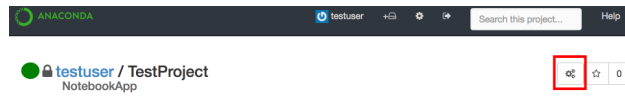
- In the **Settings** menu, select Project.



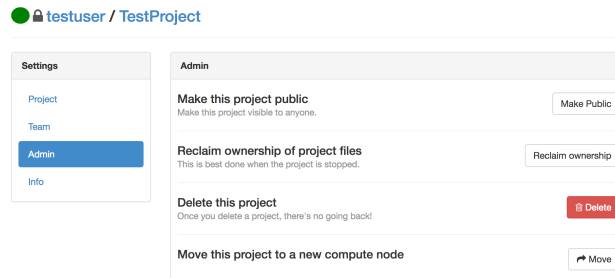
- In the Status section, click the Start or Stop button to toggle between manually starting and stopping your project.

## Making a project public or private

1. On the project home page, click the Project Settings icon to open the Project Settings page.



2. In the **Settings** menu, select Admin.



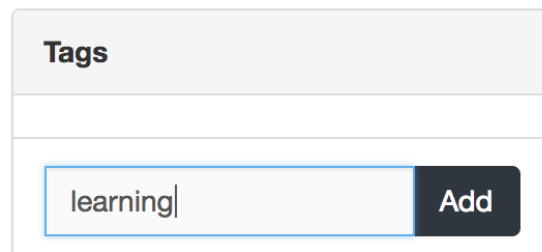
3. Click the Make Public button.
4. If the project is already public and you want to make it private, click the Make Private button.

## Tagging a project

Existing tags assigned to a project are listed in the Tags section on the project's home page.

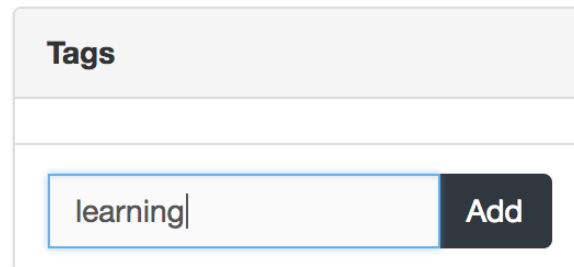
### Adding a tag

1. In the Tags box, type the name of the tag you want to add:



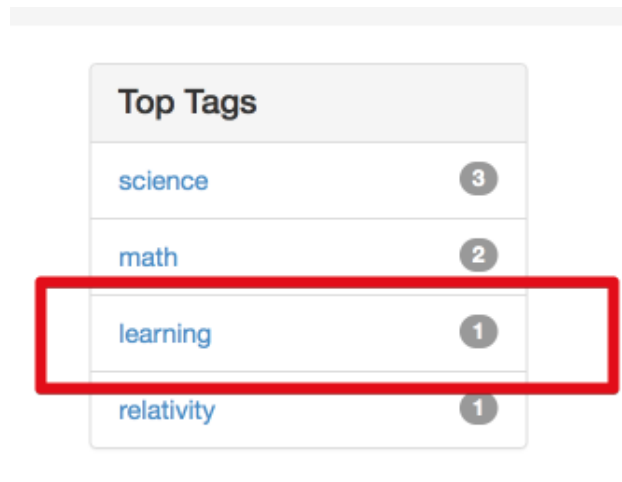
2. Click the Add button.

The new tag is added to the Tags list:



A screenshot of a web interface showing a 'Tags' section. It features a text input field containing the word 'learning' and a dark 'Add' button to its right.

If the tag was not already in the Top Tags list on your user home page, it is added. If the tag was already listed because another project used it, the number next to the tag is incremented:



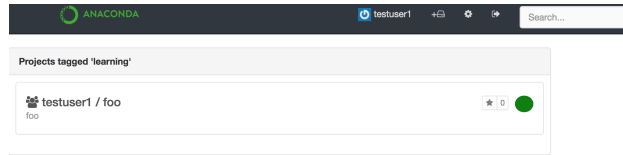
A screenshot of a 'Top Tags' list. The list contains four items: 'science' with a count of 3, 'math' with a count of 2, 'learning' with a count of 1, and 'relativity' with a count of 1. The 'learning' row is highlighted with a red rectangular box.

Top Tags	
science	3
math	2
learning	1
relativity	1

### Removing a tag

1. On your user home page, in the Top Tags list, click the tag name.
1. In the Tags list, click the X button next to tag name.



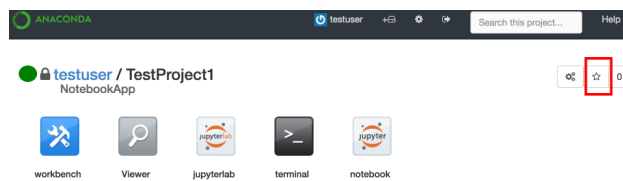


## Starring a project (rating)

Starring a project makes it appear on your user home page in the Top Rated list.

Adding or removing stars for a project does not affect the stars added by other users.

1. Open the project that you want to star.
2. On the project home page, click the Star icon at the upper right:

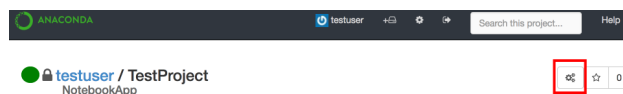


3. To unstar a project, click the Star icon again.

## Claim ownership of a project

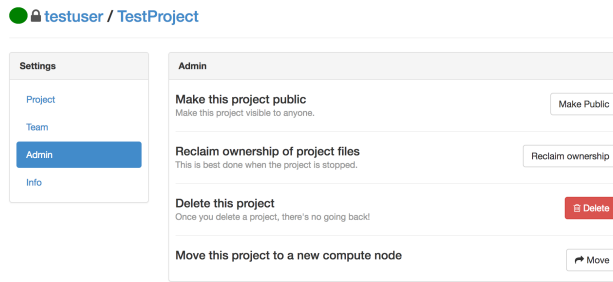
When you claim ownership of a project, ownership of all files and folders created by the team members on the project is transferred to you. Project files and folders are copied and renamed.

1. *Stop the project* to prevent team members from making changes while you are changing ownership.
2. On the project home page, click the Project Settings icon to open the Project Settings page.



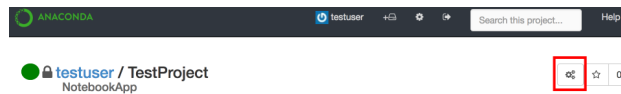
3. In the **Settings** menu, select Admin.

4. Click the Reclaim ownership button.

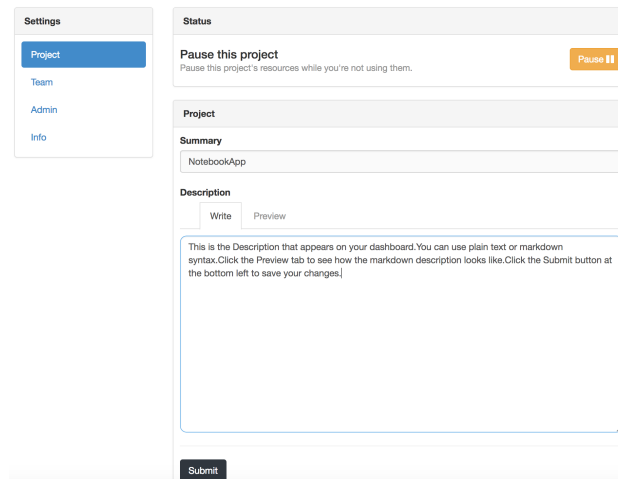


## Changing a project's summary or description

1. On the project home page, click the Project Settings icon to open the Project Settings page.



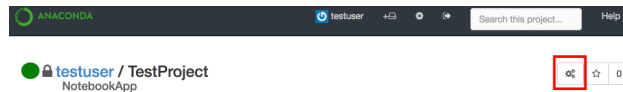
2. In the **Settings** menu, select **Project**.



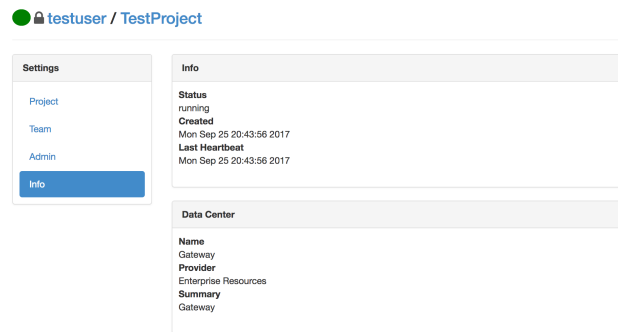
3. Update your project's summary using plain text or its description using Markdown syntax.
4. Click the **Preview** tab to see a preview of the Markdown description.
5. Click the Submit button.

## Viewing a project's status

1. On the project home page, click the Project Settings icon to open the Project Settings page.



2. In the **Settings** menu, select Info.



On the Info page, you can see:

- Whether the project is currently running or stopped.
- When the project was created.
- When the project was last accessed.
- The data center in which the project is running.

## Viewing related projects

Related projects are listed on a project's home page.

These are projects that contain fields that are most similar to the current project.

**TIP:** You will only see projects to which you have been granted access: public projects, and private projects on which you are a team member.

## How related projects are identified

To determine which projects should be listed in Related Projects:

1. The recommendation engine scans the current project's files and weights the terms found to determine which of them to use for the likeness search.

Team

Add

user02 (owner)

user01 (remove)

Related Projects

user01 / TestProject2

No Summary

user02 / User02Private

No Summary

user01 / TestProject

No Summary

2. The engine performs a search, with extra weight given to the “uses” and “imports” keywords.
3. The engine finds the files and projects that are most similar to the current project and scores the results.
4. The top-scoring matches are displayed in Related Projects. Only public projects and private projects to which you have access are included.

### Viewing top-rated projects

Top-rated projects are listed on your home page:

Top Rated	
<a href="#">einstein</a>	2
<a href="#">euler</a>	1
<a href="#">laplace</a>	1
<a href="#">plank</a>	1
<a href="#">Public_project</a>	1

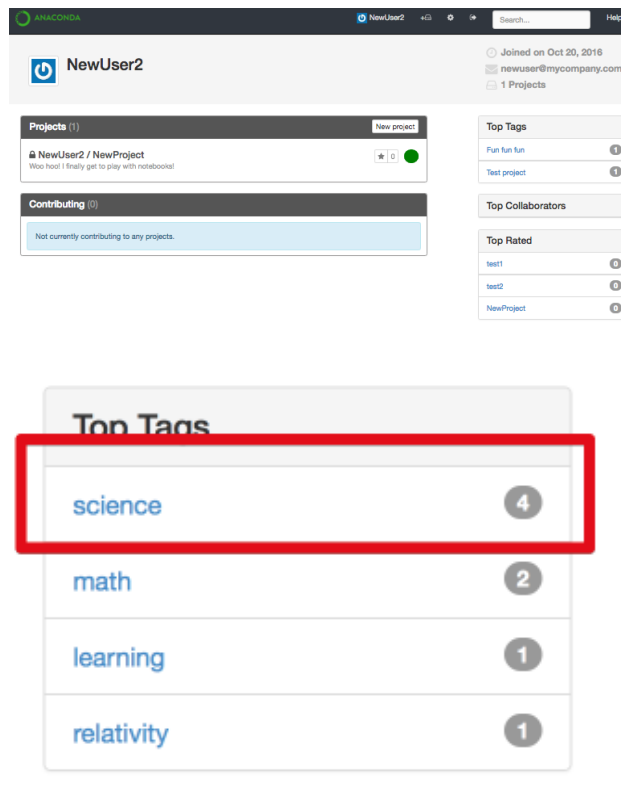
The number next to a project represents the number of stars that have been given to that project.

Click a project name to view the project’s home page.

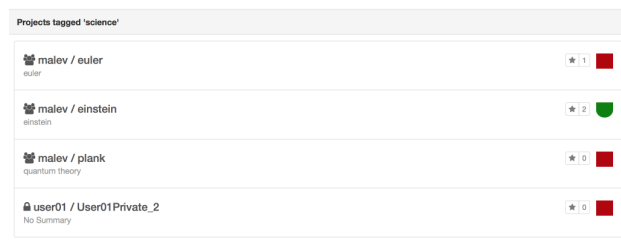
### Using tags to find a project

The top tags used on your projects are listed on your home page:

To list all projects that share a specific tag, click the tag name:



A list of projects with the selected tag is displayed:



**TIP:** The list includes only projects that you have access to: public projects, and private projects on which you are a team member.

Click a project name to open the project's home page.

## Viewing your top collaborators

Your top collaborators are listed on your home page:

Top Collaborators	
trento	1
user01	1

These are the team members who have the most projects in common with you.

To view a collaborator's home page—where you can see all public projects and the private projects they have shared with you—click the collaborator's name.

## Sharing projects and notebooks

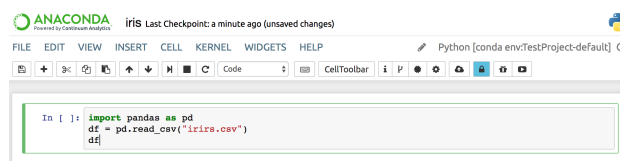
For information on sharing projects via the project settings and access control, see [Sharing projects](#).

To upload a Jupyter Notebook to Anaconda Repository:

1. Log in to Repository by running the `anaconda login` command or by using the login user interface provided by the [nbextension](#).

**CAUTION:** If you are not using a secure connection, we strongly recommended that you use the command line to log in.

2. To share your notebook environment, select the Attach conda environment checkbox. This ensures that your team members will have the right environment for your notebook.
3. Click the Upload button to upload your notebook to your local Repository or to [Anaconda.org](#), depending on how your administrator has set up AEN:



**NOTE:** If you have not yet logged into Repository or Anaconda Cloud, or have not created an account, you will be asked to do so.

## Other ways to share a notebook

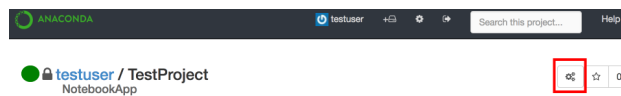
- Print—In the **File** menu, select Print.
- Download and share—In the **File** menu, select one of the following options:
  - Download as Notebook.
  - Download as Python.

- Download as HTML.
- Download as Markdown.
- Download as ReStructured Text.
- Download as PDF.
- Share and control team members' direct access to read, write and/or execute your notebook file or folder. For more information, see [Controlling access to your project](#).
- Share and control non-team members' file or folder access. For more information, see [Controlling access to your project](#).
- Create a presentation with [NBPresent 4.1](#).

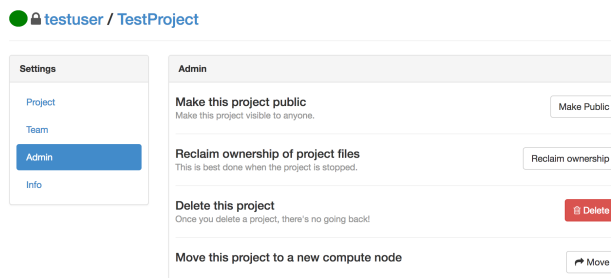
### Deleting a project

CAUTION: Deleting a project deletes all project files and information! There is no undo option.

1. Download a copy of any project files that you need to save.
2. On the project home page, click the Project Settings icon to open the Project Settings page.



3. In the **Settings** menu, select Admin.



4. Click the Delete button.

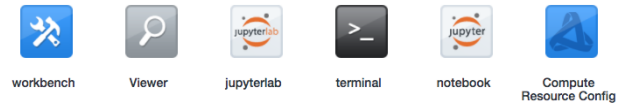
### Using AEN applications

The applications in your project make it easy for you to interact with your files and data, manage your project's resources and to customize your AEN experience.

To use applications, log into AEN, then select the project you want to work on or create a new project and open it.



On the project home page, the following application icons are displayed:



**TIP:** Each application opens in a new browser tab. You can run multiple applications at the same time in your project.

For more information on each AEN application, see:

- *Using Workbench*—File viewer and manager, including permissions settings.
- *Using Viewer*—View-only versions of notebooks and other text files.
- *Using JupyterLab*—Alpha preview of the next generation notebook.
- *Using Terminal*—Basic bash shell Terminal.
- *Using Jupyter Notebook*—Jupyter Notebooks with extensions.
- *Using Compute Resource Configuration*—Project information, view and manage applications.

## Using Workbench

- *Opening Workbench*
- *Using File Manager*
- *Opening the Workbench terminal*

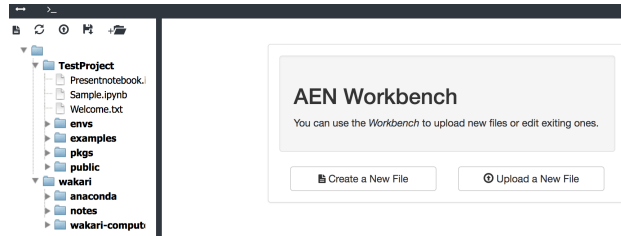
Workbench is a file viewer and manager that includes a file editor and file permissions manager.

You can use Workbench to:

- Upload and download files using the *File Manager*.
- Create new files and folders using the *File Manager*.
- Copy and move files to new locations using the *File Manager*.
- Rename files and/or folders using the *File Manager*.
- Manage the *access permissions* of team members.
- Grant or revoke *access to non-team members*.

Workbench also includes a simple Terminal application, which is convenient because the File Manager is always visible, making navigation simple.

When you first open Workbench, the File Manager is displayed in the left pane, and the Create a New File and Upload a New File buttons are in the right pane:



When you open a file or Workbench Terminal, it is displayed in the right pane. To make the Create or Upload a file options re-appear, refresh your browser window.

Two small icons are displayed in the black navigation bar at the top of the Workbench page. Hovering over them displays tool tips that describe their use:

- The Toggle icon displays or hides the File Manager.
- The Terminal icon opens a simple terminal window.

## Opening Workbench

To open Workbench:

1. Log in to AEN.
2. Select the project you want to work on, or create a new project and open it.
3. On the project home page, click the Workbench icon:



Workbench opens in a new browser window.

## Using File Manager

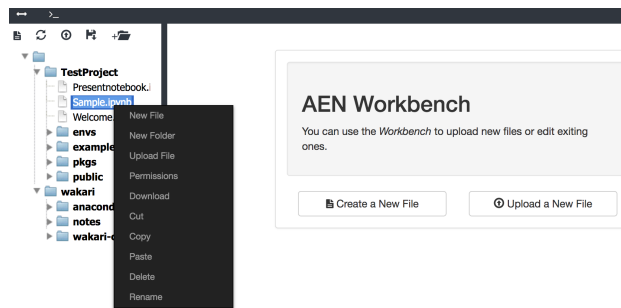
The File Manager is an intuitive way to interact with your files and folders.

## Using the options drop-down menu

To perform any of the actions described below:

1. Right-click on any folder to display the options drop-down menu.
2. Select one of the following options:
  - New File—Create and edit a new file.

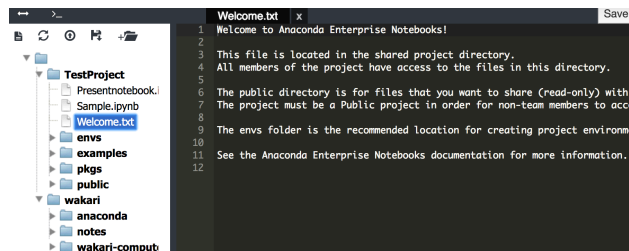
- New Folder—Create a new folder.
- Upload File—Upload a file to the selected folder. You can also drag a file to the folder.
- Permissions—*Control access to files and folders.*
- Cut—Cut the selected file or folder.
- Copy—Copy the selected file or folder.
- Paste—Paste a previously cut or copied file or folder.
- Delete—Delete the highlighted file or folder.
- Rename—Rename the highlighted file or folder.



## Editing files using the File Editor

1. Double-click any text file in the File Manager.

The File Editor opens in the right pane:

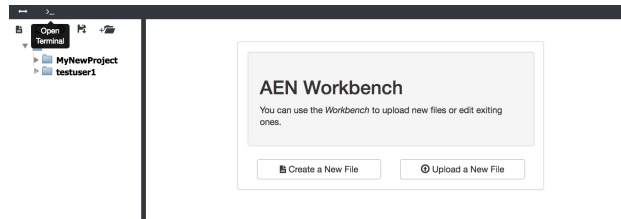


2. When you finish editing the file, click the Save button.

NOTE: To close the file without saving, click the X at the top of the page under the file name.

## Opening the Workbench terminal

In the navigation bar, click the Open terminal icon:



A Terminal—bash shell—is displayed in the right pane.

**TIP:** You can open additional terminals by clicking the Open terminal icon again, or by clicking the Plus + icon at the top of an open terminal.

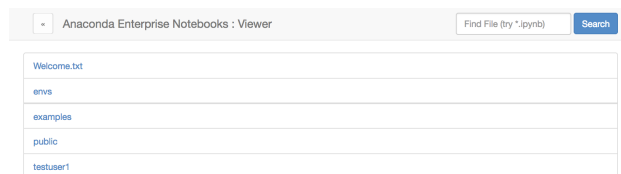
To move between terminal windows, click the **Terminal** tab in the navigation bar, then select the number of the terminal window you want to work in.

## Using Viewer

The Viewer application displays a static, view-only version of your notebooks and other text files by rendering the text files directly and using the NBConvert tool to convert notebooks to static HTML.

1. Log in to AEN.
2. Select the project you want to work on, or create a new project and open it.
3. On the project home page, click the Viewer icon.

Viewer opens in a new browser window:



4. Click any folder to view its contents, or click any filename to view the file.
5. To search for a file or folder name, type text in the Find File box, then press the Enter key. This is not a full-text search, but wildcards are permitted.

## Using JupyterLab

JupyterLab is an early alpha-preview of the next generation of the Jupyter Notebook. It is included so that you can take a tour and play with its capabilities.

**CAUTION:** JupyterLab is experimental. It is not yet intended for production work.

JupyterLab does not include any of the notebook extensions that are available in the *Jupyter Notebook app*.

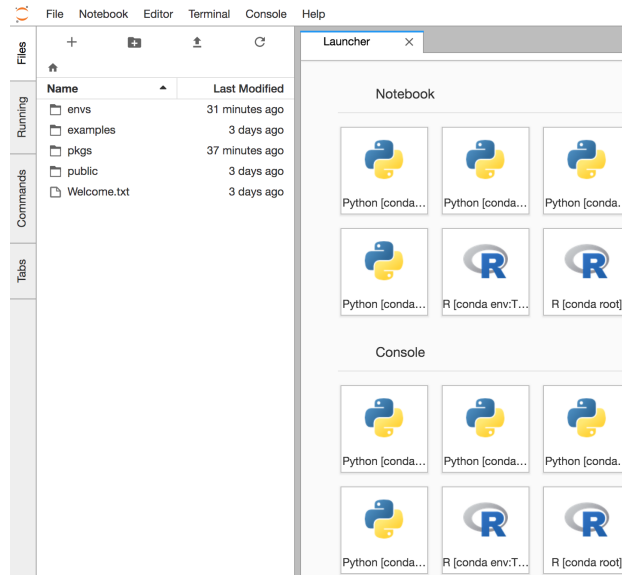
For more information about JupyterLab, see the [documentation](#).

You can also download and print a `Jupyter cheat sheet` on using Jupyter Notebook and the new JupyterLab.

To open JupyterLab:

1. Log in to AEN.
2. Select the project you want to work on, or create a new project and open it.
3. On the project home page, click on the JupyterLab icon.

JupyterLab opens in a new browser window:



Experiment with the application on your own, using the **Notebook**, **Editor**, **Terminal** and **Console** menus.

To review a guided tour of all of the features JupyterLab will contain when it is ready for production, click the [Take a tour](#) link in the right pane.

## Using Terminal

The Terminal application is a simple bash shell terminal that runs in your browser:

```

+ 1 bash
(/projects/aen_admin/TestProject/envs/default) ls
envs examples pkgs Presentnotebook.ipynb public Sample.ipynb Welcome
(/projects/aen_admin/TestProject/envs/default)

```

Using Terminal, you can:

- Access your home directory and your project drive.

- Open multiple shells within one instance of Terminal.
  - Open multiple instances of Terminal in the same browser window.
1. Log in to AEN.
  2. Select a project you want to work on, or create a new project and open it.
  3. On the project home page, click the Terminal icon:



## Terminal

Terminal opens the project directory in a new browser window.

By default, the project directory is `/projects/username/project-name`.

EXAMPLE: `/projects/TestUser/MyFirstNotebook`

4. To see the physical path of your directory, run the Print Working Directory command `pwd -P`.

TIP: The physical path `-P` is important because project attaches data to the beginning of your virtual path to keep your project files together.

5. To navigate out of your project directory to your home directory, run the command `cd`.
6. To return to your project directory, run the command `cd/projects/username/project-name`.

TIP: If you are new to navigating in a terminal, you may want to use [the Workbench terminal](#), which includes a visual navigation tree in the File Manager.

## Using multiple Terminals

You can open as many terminals as you want.

To open another shell in the terminal, in the upper left of the pane, click the plus + icon.



A corresponding number appears after the plus + icon and 1.

To move to another Terminal, click the corresponding number.

The color of the number tab changes to show which terminal is currently selected.

## Using Jupyter Notebook

- *Opening the Jupyter Notebook application*
- *Using example notebooks*
- *Creating a new Jupyter Notebook*

The Jupyter Notebook application allows you to create and edit documents that display the input and output of a Python or R language script. Once saved, you can share these files with others.

NOTE: Python and R language are included by default, but with customization, Notebook can run several other kernel environments.

This page provides a brief introduction to Jupyter Notebooks for AEN users.

For the official Jupyter Notebook user instructions, see [Jupyter documentation](#).

For information on the notebook extensions available in AEN, see [Using Jupyter Notebook extensions](#).

### Opening the Jupyter Notebook application

1. Log in to AEN.
2. Select the project you want to work on, or create a new project and open it.
3. On the project home page, click the Jupyter Notebook icon:



Jupyter Notebook opens in a new browser window:



TIP: You can see the same *File Manager* in the Terminal, Workbench, and Viewer applications.

### Using example notebooks

The `Examples` folder in Jupyter Notebook contains several types of Notebook examples created in Python—and one with R language—kernel environments.

Open any example notebook to experiment and see how it works.

### Creating a new Jupyter Notebook

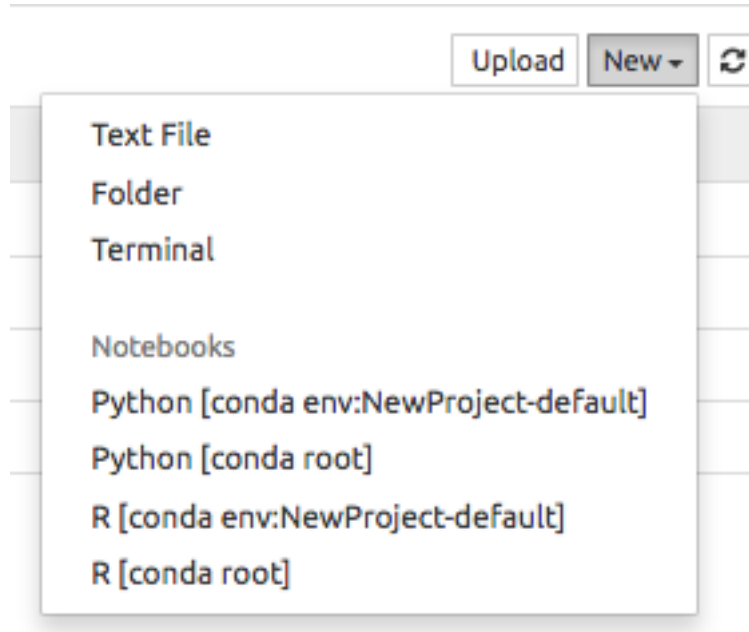
1. At the top right of the **Files** tab, click the New button.

2. Select the kernel environment to create your new notebook in.

NOTE: Customizable Python and R Language kernel environments are automatically created for you during project creation.

- Your project's default conda env kernels are a cloned copy of the root environment. You can customize them and install and delete additional packages.
- Root environment is managed by your Administrator. You cannot make or save any changes to it.





- You can switch between Python, R language and any other custom kernels in the notebook as you work in your notebook. For more information, see [Using the Synchronize Environments extension](#).

The new notebook is saved in the related project directory and displayed.

## Using Jupyter Notebook extensions

The following extensions are available for use with AEN's Jupyter Notebook application:

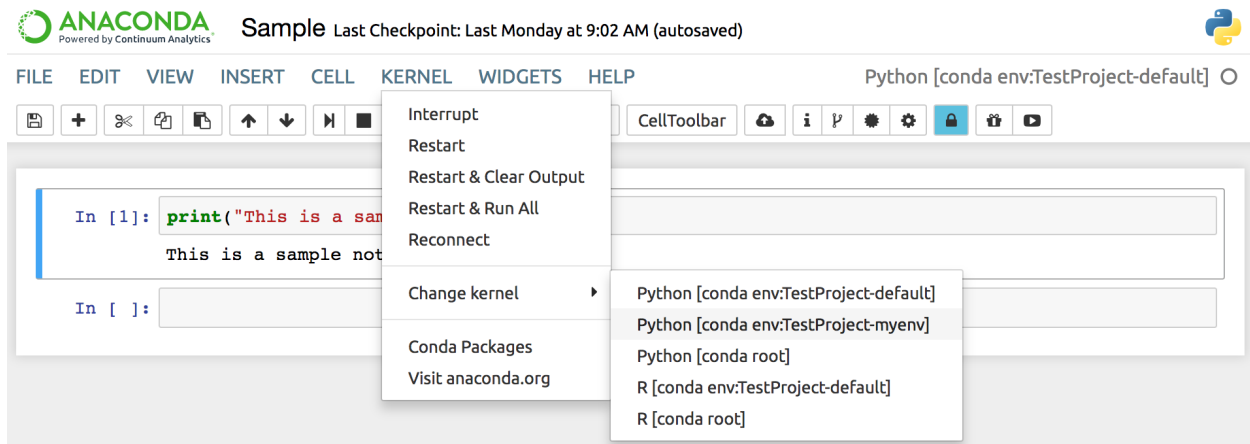
- [Synchronize Environments](#) with Jupyter from the **Kernel** menu.
- [Locking](#) adds multi-user capability from the Lock button.
- [Revision Control Mechanism \(RCM\)](#) adds Status, Checkout and Commit buttons.
- [Conda environment and package management](#) tab.
- [Conda notebook](#) adds conda management inside Notebook from the Kernel > Conda Packages menu option.
- [Anaconda Cloud integration](#) from the Publish to cloud button.
- [Notebook Present](#) turns your notebook into a PowerPoint-style presentation.

## Using the Synchronize Environments extension

The Synchronize Environments extension allows you to apply a Python, R language or any other custom environment inside your current notebook session, without needing to start up several Notebook instances using each of the selected environments.

To change environments:

1. Open the **Kernel** menu.



2. Click the Change kernel option.
3. From the list, select the environment to use.

NOTE: In AEN 4.1+ the default kernel for projects is `default`. In versions prior to 4.0, the default kernel for projects is `root Python`.

## Using the Locking extension

Multi-user capabilities are engaged in AEN when multiple users work in the same notebook file.

The Locking extension allows you to lock a notebook to prevent multiple team members from making changes at the same time. Notebooks are automatically locked when you open them.

If team members open a notebook and make changes while it is locked, their save capability is disabled, and they cannot overwrite the notebook.

To override the lock, they must actively take control of the locked file by clicking the Lock icon in the Notebook menu bar:



NOTE: This is a soft locking model. Team members can choose to override your lock to save their work. If you give team members write access to your files, confirm that they understand that they should never unlock your file unless they are making meaningful, non-destructive team contributions.

## Using the Revision Control Mechanism extension

The Revision Control Mechanism (RCM) Jupyter Notebook extension provides simple version control for notebook files. It uses the internal Jupyter functionality to perform tasks.

On the surface, RCM uses a simple linear model, but beneath that is a more complex git-based branching model. To prevent merge conflicts, this model uses a “latest wins” policy as its main merging strategy.

The RCM Jupyter Notebook extension adds four buttons:



- *Status.*
- *Checkout.*
- *Commit.*
- *Configure git.*

TIP: If you do not see the RCM buttons, see *Setting up RCM for the first time*.

### Using the Status button

The Status button allows you to see what revision you are on.

Clicking the Status button displays:

### Using the Checkout button

The Checkout button allows you to view a list of the previous revision points, check out a previous revision or compare differences between revisions.

Clicking the Checkout button displays:

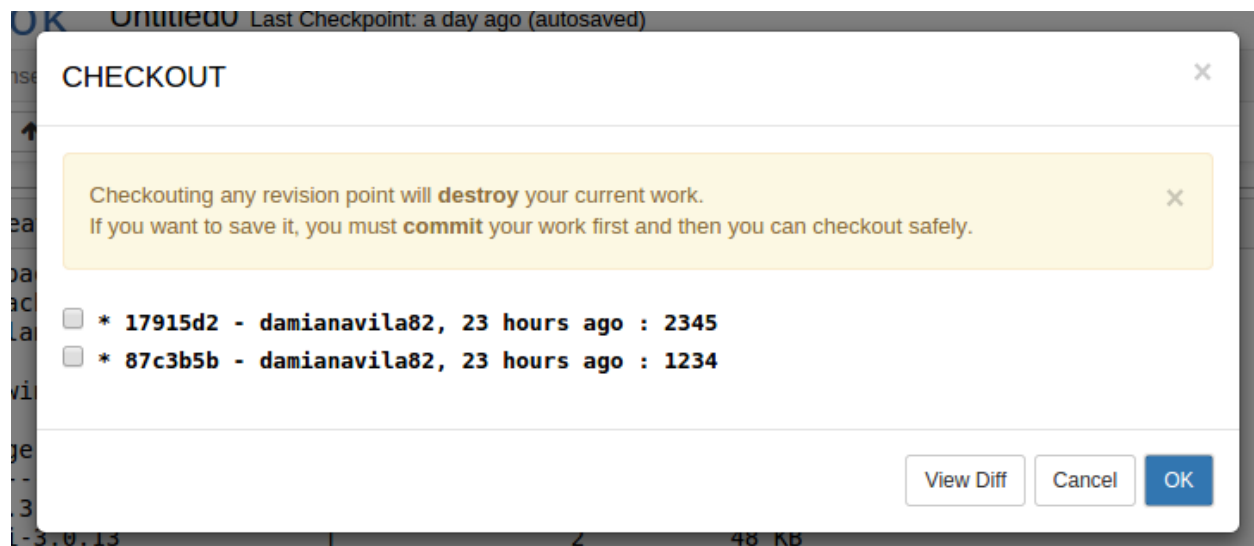
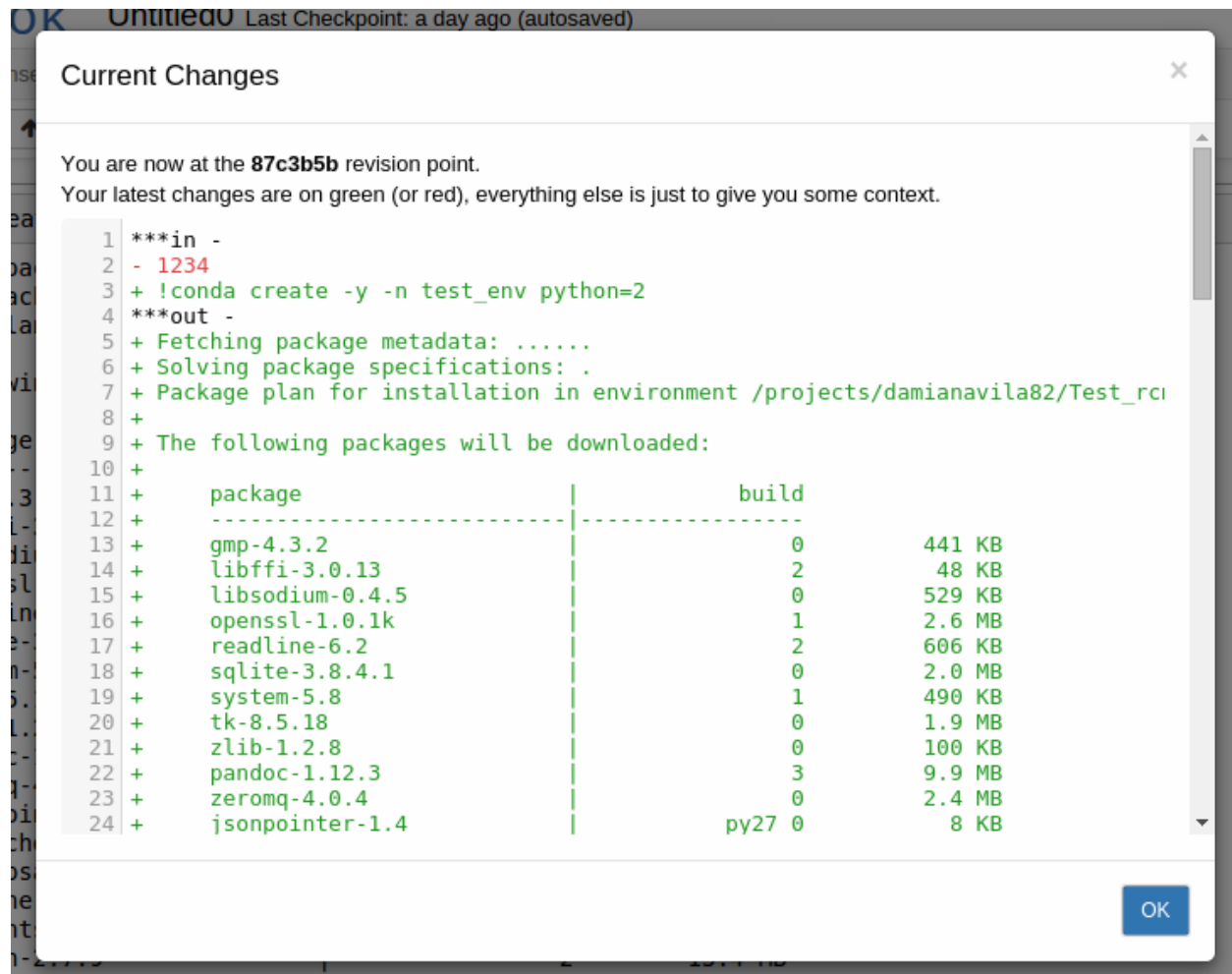
### Checking out a previous revision

To checkout a notebook at an earlier revision point:

1. Select the checkbox next to the desired revision point.
2. Click the OK button.

A copy of the notebook at the selected revision point is displayed.

NOTE: If you have not saved the work in your current project window, checking out a previous revision destroys it. If in doubt, click the Cancel button and save your work before reverting to a previous revision point.



## Comparing revisions

To compare 2 previous revision points:

1. Select the checkboxes of the revision points to compare.
2. Click the View Diff button.

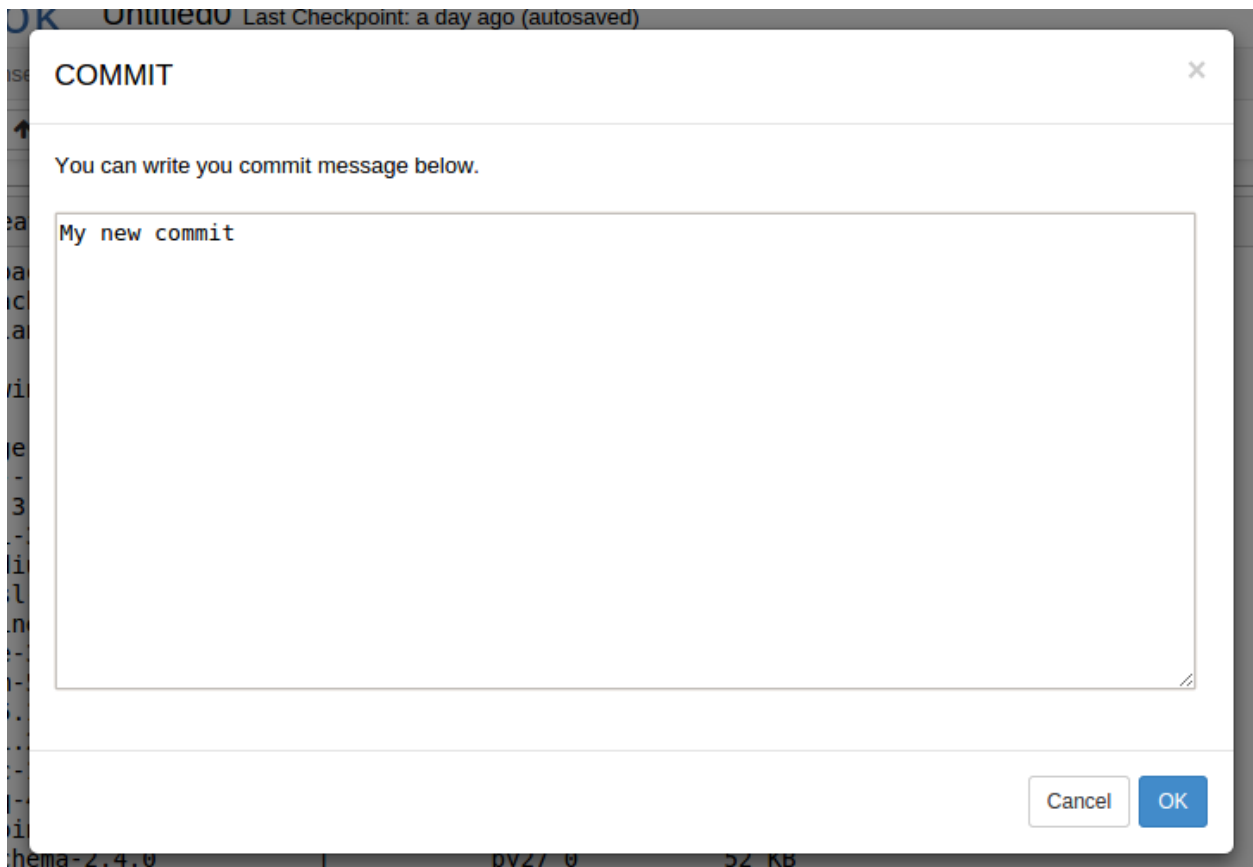
A side-by-side comparison is displayed.

Click the Cancel button to close the differences window.

## Using the Commit button

The Commit button allows you to save or persist the current changes, keeping a permanent record of any changes that are introduced, so that you do not have to worry about losing important data.

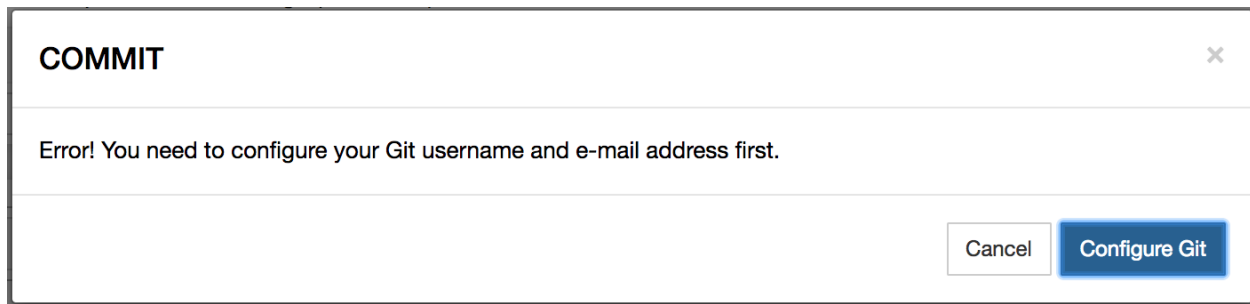
Clicking the Commit button displays:



1. Enter a description of the changes in the commit as a reminder in case you need to revert back to it later.
2. Click the OK button.

Your changes are committed and a revision point is created.

If Git user name and user email are not set, the following window appears:



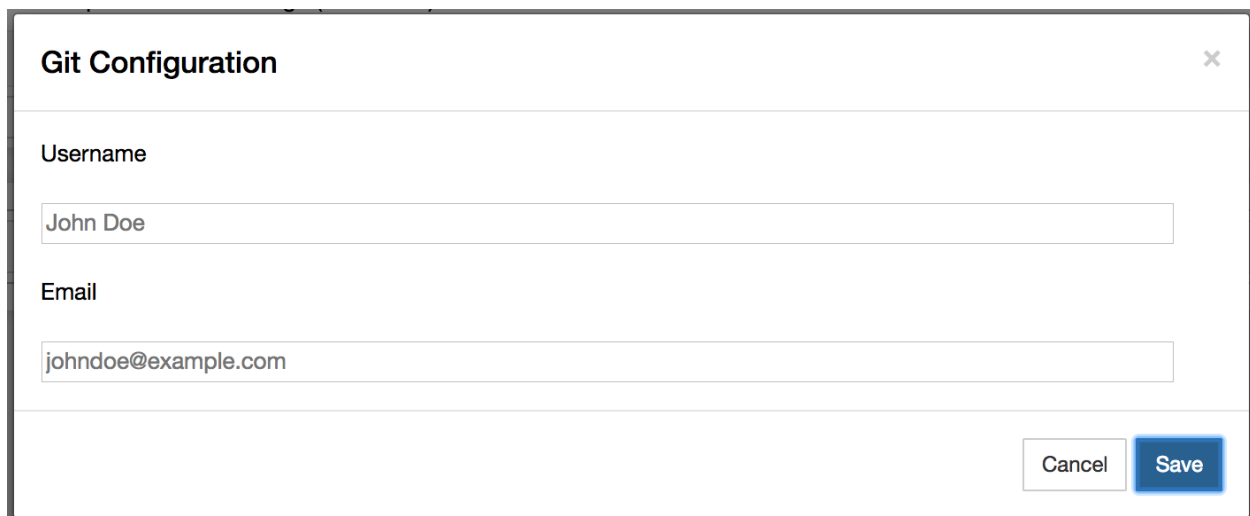
Configure Git and then try to commit again.

TIP: You can roll back committed changes by *checking out a previous version*.

### Using the Configure git button

The Configure git button allows you to configure Git user name and email values.

After clicking the Configure Git button, the following window appears:



Enter user name and e-mail address. Click the OK button when finished.

### Setting up RCM for the first time

If you do not see the RCM buttons in your notebook:

1. Go to the project home page.
2. Open the Terminal application.
3. In the terminal window, run:

```
git config --global user.email "you@example.com"
git config --global user.name "Your Name"
```

NOTE: Change `you@example.com` to your email address, and `Your Name` to your actual name.

4. Open Jupyter Notebook and refresh the page.

## Using the NBConda extension

The NBConda extension adds a Conda tab to your notebook for easy environment and package management from within the notebook.



Files

Running

IPython Clusters

Conda

2 Conda environments + ↺

Action	Name	Default?	Directory
<span>🔗</span> <span>📁</span> <span>🗑️</span>	root		/opt/wakari/anaconda
<span>🔗</span> <span>📁</span> <span>🗑️</span>	default	✓	/projects/aen_admin/TestProject/envs/default

1143 available packages  ➔

Name	Version	Channel
<input type="checkbox"/> _license	1.1	defaults
<input type="checkbox"/> _nb_ext_conf	0.4.0	defaults
<input type="checkbox"/> abstract-rendering	0.5.1	defaults
<input type="checkbox"/> accelerate	2.3.1	defaults
<input type="checkbox"/> accelerate_cudalib	2.0	defaults
<input type="checkbox"/> aen-app-jupyterlab	0.4.0	wakari

376 installed packages in environment "default" ↺ ✓ 📁 🗑️

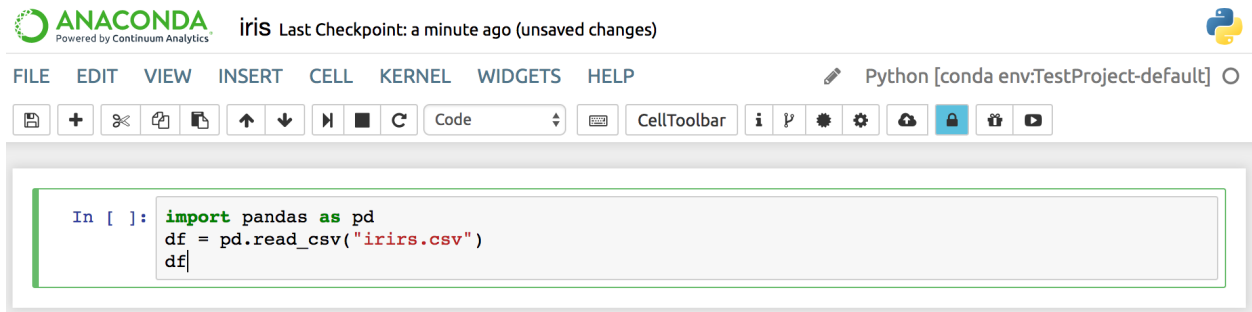
Name	Version	Build	Available
<input type="checkbox"/> _license	1.1	py27_1	
<input type="checkbox"/> alabaster	0.7.10	py27_0	
<input type="checkbox"/> anaconda	custom	py27_0	
<input type="checkbox"/> anaconda-client	1.5.1	py27_0	
<input type="checkbox"/> anaconda-project	0.6.0	py27_0	
<input type="checkbox"/> asn1crypto	0.22.0	py27_0	

Click the Conda tab in a notebook to display:

- Conda environments list—export, clone or delete an environment in the action column, or create a new environment by clicking the plus + icon. Switch to an environment by clicking it; packages for that environment are displayed below in the installed packages list.

- Conda available packages list—for the selected environment in currently configured channels, search for packages and click a package name to install it.
- Installed packages list—in the selected environment, check for updates, update or delete selected packages.

TIP: While you are in any notebook, you can jump to the NBConda extension for that environment by clicking the **Kernel** menu and selecting Conda Packages:



### Using the Conda Notebook extension

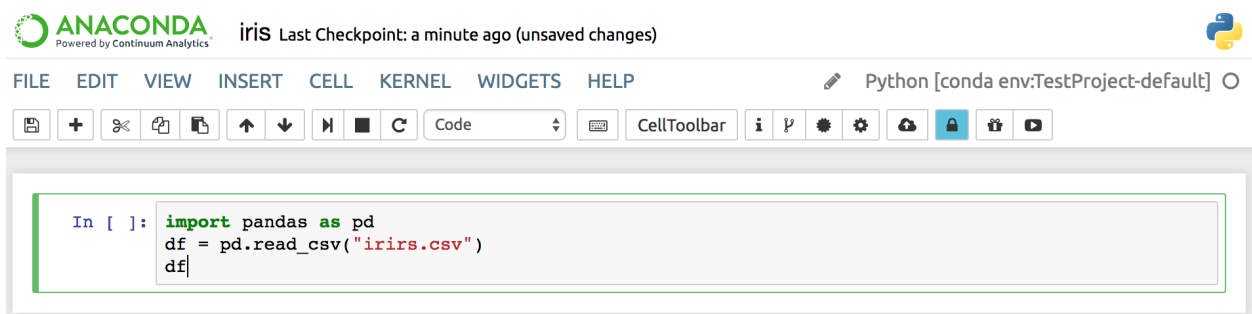
The Conda Notebook extension adds the Conda Packages option to the **Kernel** menu.

Select the Conda Packages option to display a list of all of the Conda packages that are currently used in the environment associated with the running kernel, as well as any available packages.

From the Conda Packages option, you can perform all of the tasks available in the [Conda tab](#), but they will only apply to the current environment.

### Using the Anaconda Cloud extension

The Anaconda Cloud extension adds the Cloud button to your notebook, allowing you to easily upload your notebook to Cloud:

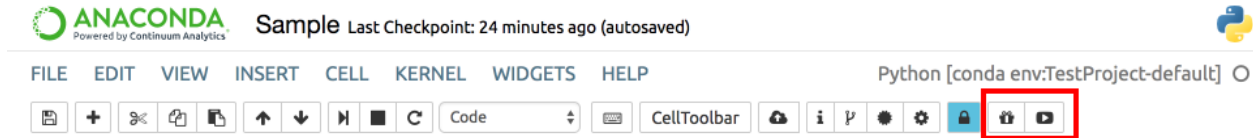




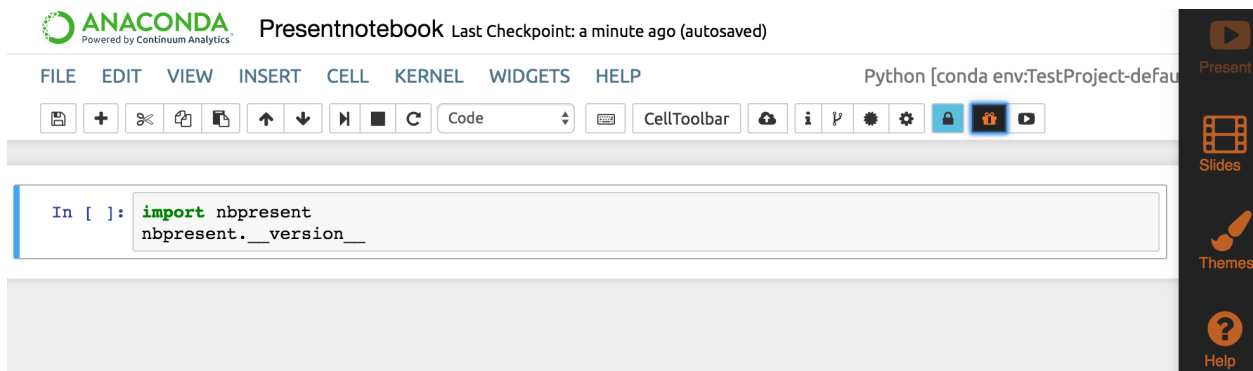
## Using the Notebook Present extension

The AEN Notebook Present extension turns your notebook into a Microsoft PowerPoint-style presentation.

The Present extension adds 2 buttons to Notebook’s menu bar—Edit Presentation and Show Presentation:



To begin using Notebook Present, click the Edit Presentation button.



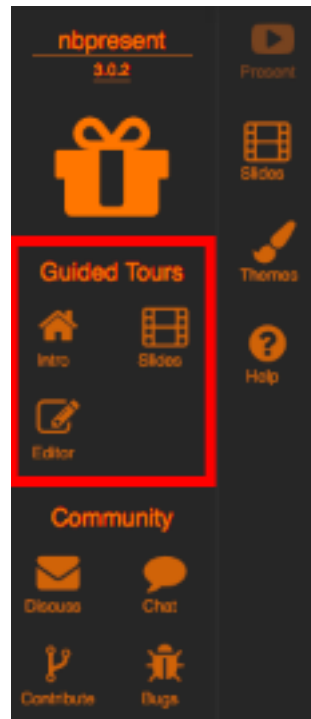
The Notebook Present sidebar is displayed on the right side of your browser:

Clicking each icon changes the menu and layout of your notebook.

Clicking the Help icon displays 3 tours—demonstrations—of the main features of Present:

- *Intro tour.*
- *Slides tour.*
- *Editor tour.*

Select one of the tours to view a short presentation regarding the specifics of that feature.



## Intro tour

The Intro tour is a 2-minute presentation that explains how to use the main features of Present, including a description of each button's purpose.

NOTE: At any time, you can pause, go back to the previous or move forward to the next slide.

The following information is covered in the Intro tour:

- App Bar—When Authoring, this allows you control the content and style of your presentation. It also can be used to activate several keyboard shortcuts for editing:
- Stop Authoring—Clicking the Edit Presentation button again stops Authoring, and removes all keyboard shortcuts.
- Show Presentation—If you just want to run your presentation without using any Authoring tools, just click the Show Presentation button.
- Presenting/Authoring—Once you've made some slides, start Presenting, where you can use most Notebook functions with the Theme we have defined, as well as customize slides on the fly.
- Slides button—Slides, made of Regions linked to Cell Parts are the bread and butter of any presentation, and can be imported, created, linked, reordered, and edited here.

## Keyboard shortcuts



The Jupyter Notebook has two different keyboard input modes. **Edit mode** allows you to type code/text into a cell and is indicated by a green cell border. **Command mode** binds the keyboard to notebook level actions and is indicated by a grey cell border with a blue left margin.

Mac OS X modifier keys:

: Command

: Control

: Option

: Shift

: Return

: Space

: Tab

### Command Mode (press to enable)

: find and replace

: previous slide

: next slide

: next slide

: enter edit mode

: open the command palette

: run cell, select below

: run selected cells

: run cell, insert below

: to code

: to markdown

: extend selected cells above

: extend selected cells above

: extend selected cells below

: extend selected cells below

: insert cell above

: insert cell below

: cut selected cells

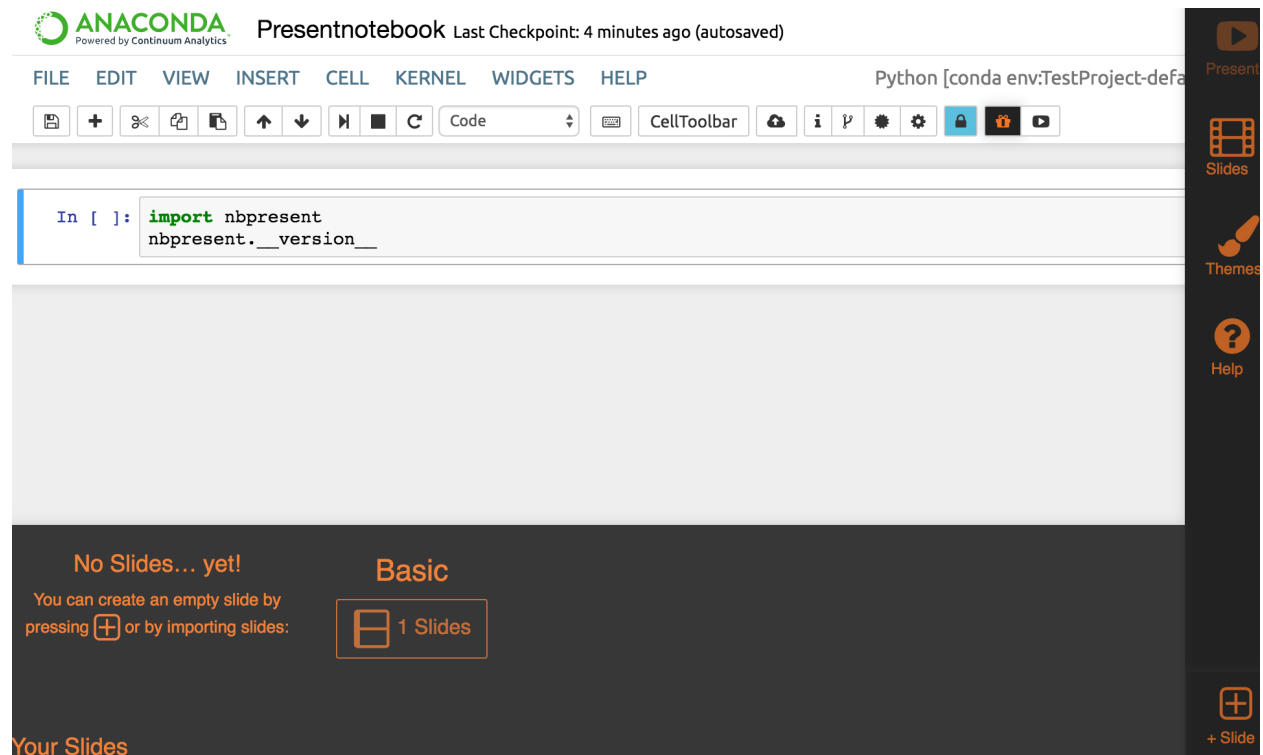
: copy selected cells

: paste cells above

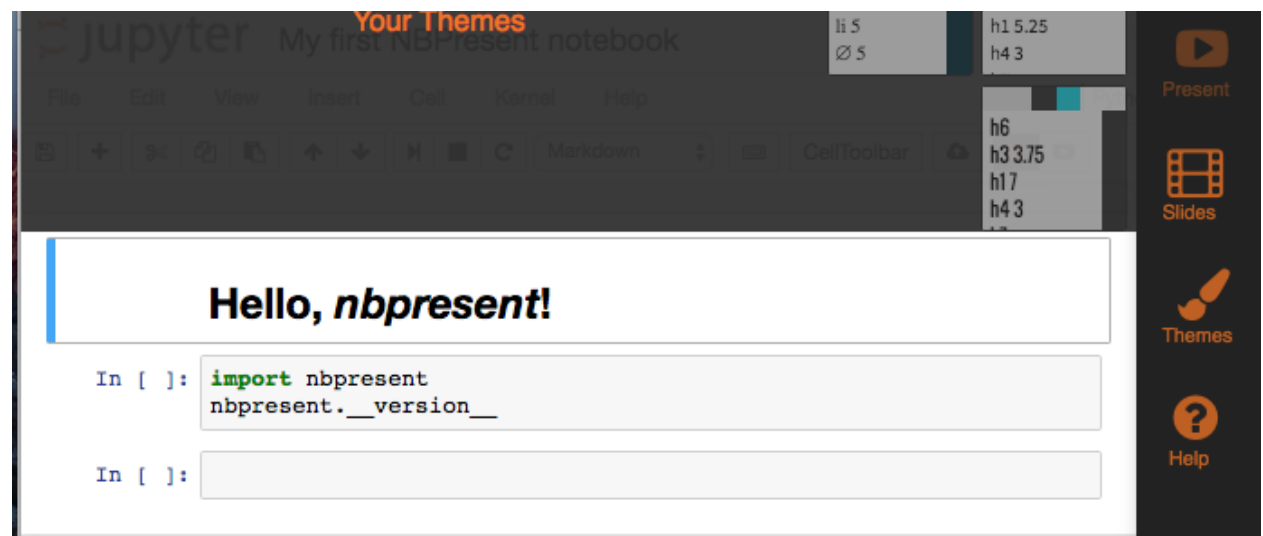
: paste cells below

: undo cell deletion

Close



- Theming—Theming lets you select from existing colors, typography, and backgrounds to make distinctive presentations. The first theme you select will become the default, while you can choose custom themes for a particular slide, like a title.

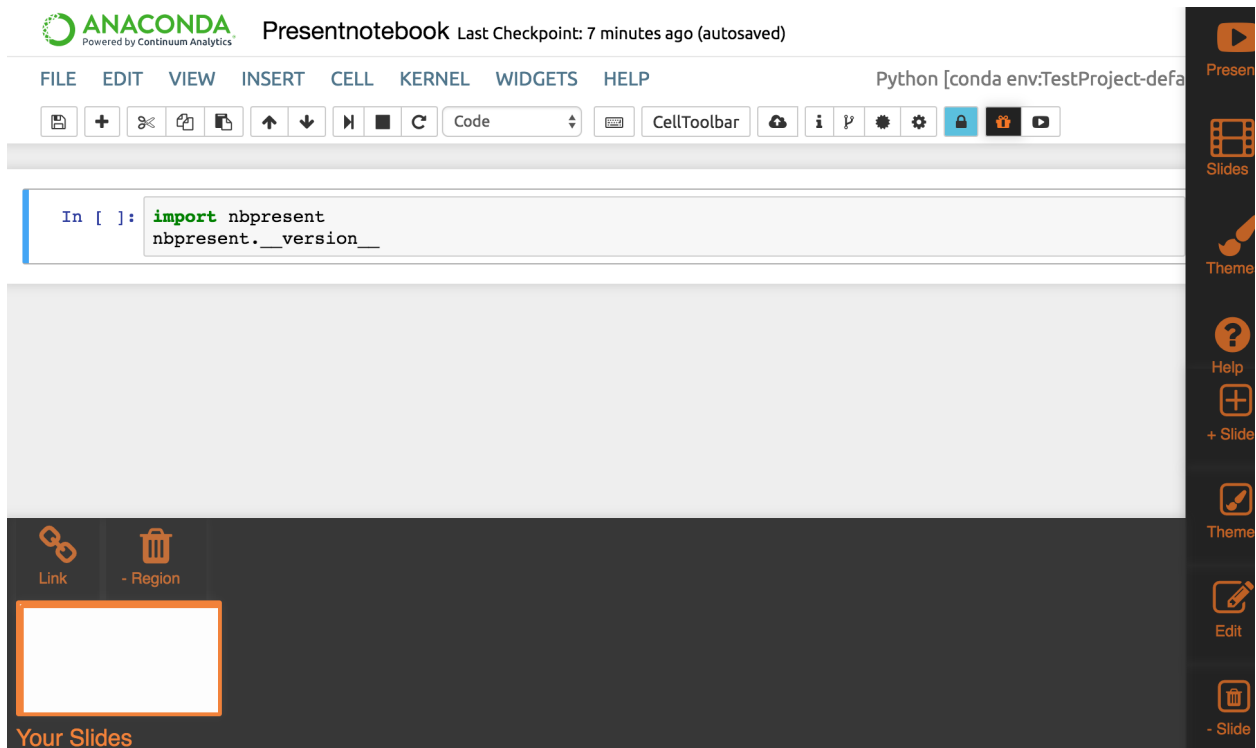


- Saving—Whenever you save your Notebook, all your presentation data will be stored right in the Notebook .ipynb file.

- **Downloading**—After you’ve made a presentation, you can download it as an HTML page by choosing Download → Download As: Presentation (.html) in the menu.
- **Help**—Activate Help at any time to try other tours, connect with the Present developers and community, and other information.

## Slides tour

Slides make up a presentation. Clicking Slides toggles the sorter view and the Slide Toolbar on and off:



The Slides tour explains how to create and manage slides, including the following information:

- **Slide Toolbar**—Create a new slide. Clicking + Slide will offer some choices for creating your new slide.
- **Import**—The quickest way to create a presentation is to import each cell as a slide. If you’ve already created slides with the official slideshow cell toolbar or RISE, you can import most of that content.
- **Template Library**—You can create a presentation from an existing template.
  - **Reuse Slide as Template**—You can create a presentation based on an existing slide.
  - **Simple Template**—A common template is the Quad Chart, with four pieces of content arranged in a grid.
- **Region**—The Quad Chart has four Regions. To select a region, click it.
  - **Link a Region to a Cell Part**—Each Region can be linked to a single Cell Part using the Link Overlay, which shows all of the parts available.
    - \* **Cell Part: Source (blue)**—Source, such as code and Markdown text.

- \* Cell Part: Outputs (red)—Outputs, such as rich figures and script results.
- \* Cell Part: Widgets (purple)—Jupyter widgets, interactive widgets that provide both visualization and user input.
- \* Cell Part: Whole (orange)—Finally, a Whole Cell, including its Source, Widgets and Outputs can be linked to a single region.
- Unlink a region from a Cell Part—Unlinking removes the connection between a region and a cell part, without deleting either one.
- Region: Trashing—Trashing a Region permanently deletes it, without affecting any linked Cell Part.
- Part Thumbnail—We'll try to draw a part thumbnail. It can only be reliably updated when a linked Cell Part is on-screen when you mouse over it, but you should usually be able to get an idea of what you're seeing. The colors of the regions correspond to the cell types.
- Presenting—Clicking the Present button while editing brings up the Presenter with editing mode still enabled:
  - Linked inputs and widgets are still interactive.
  - Go forward—Click to go to the next slide
  - Go back—Click to go back to the previous slide
  - Go back to the beginning—Click to go back to the first slide
  - My work is done here—Click to go back to the Notebook.

### Editor tour

Once you've made a few slides, you'll likely want to customize them. The Editor tour explains how to edit your notebook, including the following information:

- Editing Slides—Activate the Slide Editor by double-clicking it, or by clicking Edit Slide.
- Region Editor—Click to drag Regions around and resize them.
- Region Tree—Reorder Regions and see the details of how Regions will show their linked Parts.
- Add Region—Add new regions.
- Attribute Editor—Edit the properties of a region.
- Data Layouts—In addition to manually moving regions, you can apply these layouts to automatically fill your slides.
- More Regions—Add more regions—with a weight of 1.
- Tree Weight—Make a Region bigger or smaller, based on its relative weight.
- 12 Grid—A compromise between the Free and Treemap layouts, the 12 Grid option rounds all of the values in a layout to a factor of 12.

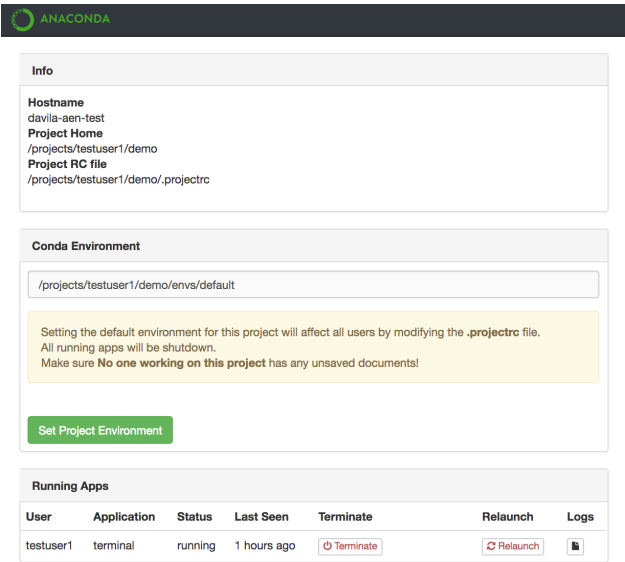
### Using Compute Resource Configuration

The Compute Resource Configuration (CRC) application displays information about the current project and allows you to set a custom project environment and view and manage your other AEN applications, including stopping, starting, restarting and viewing the logs of each.

The CRC application screen contains 3 sections:

- *Info.*

- *Conda environment.*
- *Running apps.*



Info

The Info section displays:

- Hostname—IP address of the host computer.
- Project Home—File path to the project home.
- Project RC file—File path to the project runtime configuration file `.projectrc`. This file is sourced when a user opens any AEN application. It sets several AEN internal environment variables, sets up the project environment and sets additional user environment variables for the project.

Conda environment

This section displays the path to the default conda environment.

CAUTION: Changing the default environment will affect all users. Be sure that no team members have any unsaved documents before changing the project environment.

To change the default conda environment location:

1. Edit the path to point to your preferred conda environment.
2. Click the Set Project Environment button.

Your `.projectrc` file is modified.

### Running apps

The Running Apps section displays a list of users and the applications that are in use, as well as when the app was last modified.

To terminate any individual application, click the Terminate button.

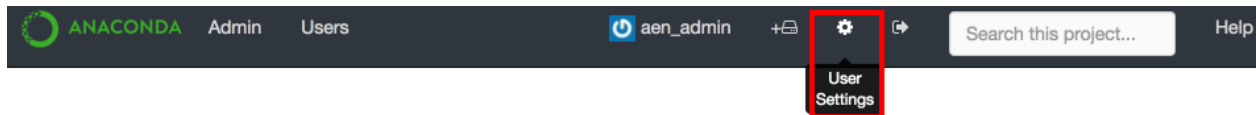
To stop and re-launch any individual application, click the Relaunch button.

To review the run logs of any active application, which may be useful for troubleshooting, click the Logs button.

### Managing your account

- *Updating your public profile*
- *Changing your password*
- *Deleting your AEN account*
- *Viewing account operations*
- *Registering an application*

To access your account information, click the User Settings icon in the AEN navigation bar:



### Updating your public profile

Your public profile is made up of a name, a personal URL, your company and location.

1. In the left navigation pane, click the **Public Profile** tab.
2. To update your profile picture, create a [Gravatar](#) that is associated with the email address you used to create your AEN account. The gravatar will automatically appear.

### Changing your password

1. In the left navigation pane, click the **Account Settings** tab.

### Deleting your AEN account

1. In the left navigation pane, click the **Account Settings** tab.



Viewing account operations

1. In the left navigation pane, click the **Security Log** tab to view a list of operations performed on your account.

# Settings

Change your account and profile settings.

Public Profile

Account Settings

Security Log

Applications

Security Log

	aen_admin	oauth.authenticate	2017-09-25 04:52:06.713000+00:00
	aen_admin	oauth.authenticate	2017-09-25 04:51:58.954000+00:00
	aen_admin	oauth.authenticate	2017-09-25 04:51:58.720000+00:00
	aen_admin	oauth.authenticate	2017-09-25 04:51:58.490000+00:00
	aen_admin	oauth.authenticate	2017-09-25 04:51:58.259000+00:00
	aen_admin	oauth.authenticate	2017-09-25 04:51:58.033000+00:00
	aen_admin	oauth.authenticate	2017-09-25 04:51:57.802000+00:00

2. For more information about an operation, click the Eye icon to the left of the the operation name.

Registering an application

If you want to create an application for AEN or have already done so, you must register your application.

1. In the left navigation pane, click the **Applications** tab.

# Settings

Change your account and profile settings.

Public Profile

Account Settings

Security Log

Applications

Developer Applications

Register New Application

These are applications you have registered to use the Anaconda Enterprise Notebooks API.

Gateway ()

Authorized applications

Gateway ()

revoke

2. Click the Register New Application button to open a form for registering your application.

### Advanced tasks

Advanced tasks are best-suited for users who are comfortable working in a Terminal.

### Working with environments

AEN runs on conda, a package management system and environment management system for installing multiple versions of software packages and their dependencies and switching easily between them.

A conda environment usually includes 1 version of Python or R language and some packages.

The ability to have a custom project environment is one of the most powerful features of AEN. Your project environment is integrated so that all of your project applications recognize it and all of your team members have access to it.

This section contains information about:

- *Creating a default conda environment using the Jupyter Notebook application*
- *Creating a default conda environment using the Jupyter Notebook application*
- *Using your conda environment in a notebook*
- *Customizing your conda environment*
- *Installing a conda package using Terminal*
- *Installing a conda package using Notebook*
- *Uninstalling a conda package*

NOTE: This conda environments guide is specific to AEN. For full conda documentation—including cheat sheets, a conda test drive, and command reference—see the [conda documentation](#).

### Creating a default conda environment using the Jupyter Notebook application

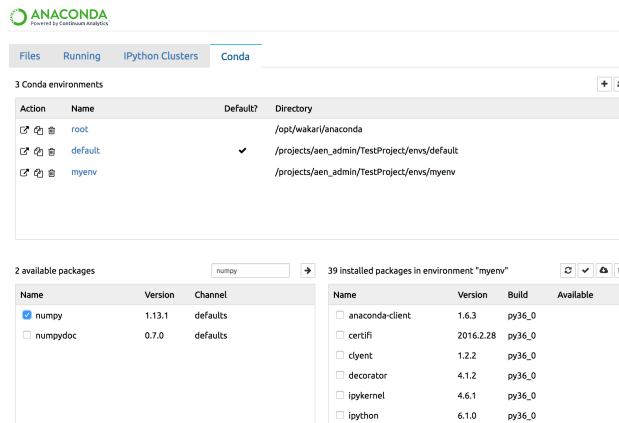
You can create, activate, and install packages and deactivate environments from within the Notebook menu bar.

To install from the Notebook menu bar:

1. Click the **Conda** tab and select the plus sign icon.
2. Search for `numpy` in the package search box.
3. Select `numpy` from the search results.

1. Click the Install button.

The environment is added to the project's `env` directory.



## Creating a default conda environment using Terminal

In AEN, all new environments created with conda automatically include Python, Jupyter Notebooks and pip. You can specify any other packages you want included in your new environment.

**TIP:** By default, conda creates a new environment in your project's `env` directory—so that all team members have access to the environment. For information about limiting your team member's read, write or execute permissions, see [Workbench](#).

To create a new environment within your AEN account, run the command `conda` in a [Terminal](#) application.

**EXAMPLE:** To create a new environment named `WeatherModel` that contains Python, NumPy, pip and Jupyter Notebooks in your project's `env` directory:

1. Log in to AEN.
2. Open a project.
3. On the project home page, click the Terminal application icon to open a Terminal.
4. Create the environment:

```
conda create -n WeatherModel numpy
```

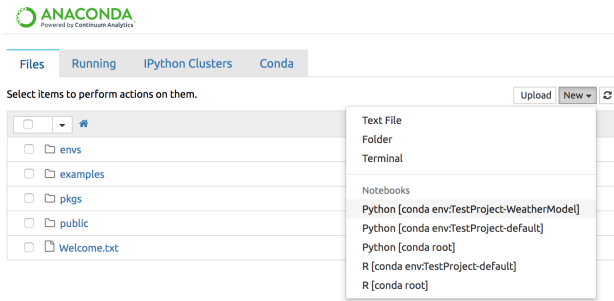
**TIP:** Python, pip and Jupyter Notebooks are automatically installed in each new environment. You only need to specify NumPy in this command.

5. Make the new environment your default:

```
source activate WeatherModel
```

6. To use your new environment with Jupyter Notebooks, open the Notebook application.
7. Click the New button to open a new notebook. In the drop-down menu under Notebooks, the environment you just created is displayed.
8. To activate that environment, select it.

The environment is added to the project's `env` directory.



NOTE: You can deactivate the new environment when you are finished with your notebook by opening the Terminal application and running the command `source deactivate`.

## Using your conda environment in a notebook

Whether you have created an environment using conda in a terminal, or from the **Conda** tab in a notebook, you can use the conda environment in the same way.

When working in a notebook, to select the environment you have created and want to use with that notebook, in the **Kernel** menu, select Change Kernel.

EXAMPLE: If you have an environment named `my_env` in a project named `test1` that includes NumPy and SciPy and you want to use that environment in your notebook, in the **Kernel** menu, select Python [conda env:test1-my\_env].

The notebook code will run in that environment and can import NumPy and SciPy functions.

## Customizing your conda environment

If you need a Python package that AEN doesn't include by default, you can install additional packages into your AEN environment.

TIP: You cannot install packages into the default Anaconda environment. You must create your own environment before installing a new package into that environment.

AEN is built on Anaconda, so you can install additional Python packages using conda or pip—both of which are included with Anaconda.

## Installing a conda package using Terminal

To install a conda package using the Terminal application:

1. Create and activate the environment using the steps in *Creating a default conda environment using the Jupyter Notebook application*.
2. In your Terminal application, run the command `conda install <packagename>`.

NOTE: Be sure to specify the Python version you want when using conda to create the environment, or it will use the same version as root.

EXAMPLE:

```
conda create -n mypy3 python=3 numpy scipy
```

A conda environment named `mypy3`, running on Python 3 and containing NumPy and SciPy is created. All subsequent packages added to this environment will be the Python 3 compatible versions.

## Installing a conda package using Notebook

You can also install the package within your notebook without using the terminal app:

1. From the Notebook application, click the **Conda** tab.
2. Select the environment you wish to use.
3. Search for the package you want to add.
4. Click the Install button.

## Uninstalling a conda package

To uninstall a package using this method, run the command `conda remove <packagename>`.

NOTE: Replace `<packagename>` with the name of the package you are uninstalling.

## Using visualization packages

AEN supports multiple visualization packages for Python and R language.

For Python, the default environment has *Matplotlib* and *Bokeh* installed.

For R language, the default environment has *r-ggplot2* and *r-bokeh* installed.

## Matplotlib

Matplotlib is a Python 2D and 3D plotting and visualization library that produces publication-quality figures in a variety of hardcopy formats and interactive environments across platforms.

To display Matplotlib figures in the output cells of a notebook running the default environment, run:

```
import matplotlib.pyplot as plt
%matplotlib inline
```

Any Matplotlib figures in the notebook are displayed in its output cells.

EXAMPLE: The following screenshot is of a cumulative density function (CDF) plot using values taken from a normal distribution:

For more information, including a [gallery](#), [examples](#), [documentation](#) and a [list of plotting commands](#), see the [Matplotlib website](#).

## Bokeh

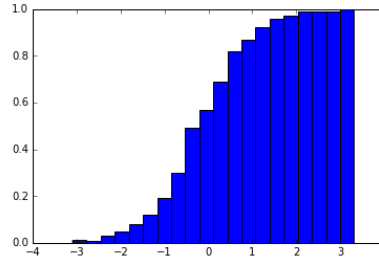
*Bokeh* is an interactive visualization library that targets modern web browsers to provide elegant, concise construction of novel graphics.

To display Bokeh figures in the output cells of a notebook running the default environment, run:

```
In [1]: import matplotlib.pyplot as plt
        %matplotlib inline

In [2]: import numpy as np
        x = np.random.normal(size=100)

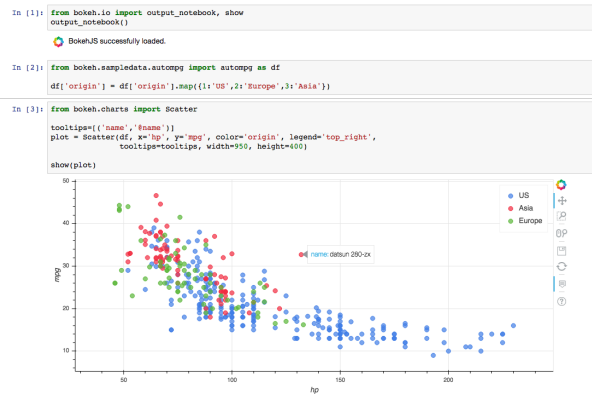
In [3]: plt.hist(x, normed=True, cumulative=True, bins=20);
```



```
from bokeh.io import output_notebook, show
output_notebook()
```

Any Bokeh figures in the notebook are displayed in its output cells.

The following screenshot is of a scatter plot of miles-per-gallon vs. horsepower for 392 automobiles using the `autompg` sample dataset:



## ggplot2

**Ggplot2** is a plotting system for R language which is based on the grammar of graphics. Ggplot2 tries to take only the good parts of base and lattice graphics and none of the bad parts.

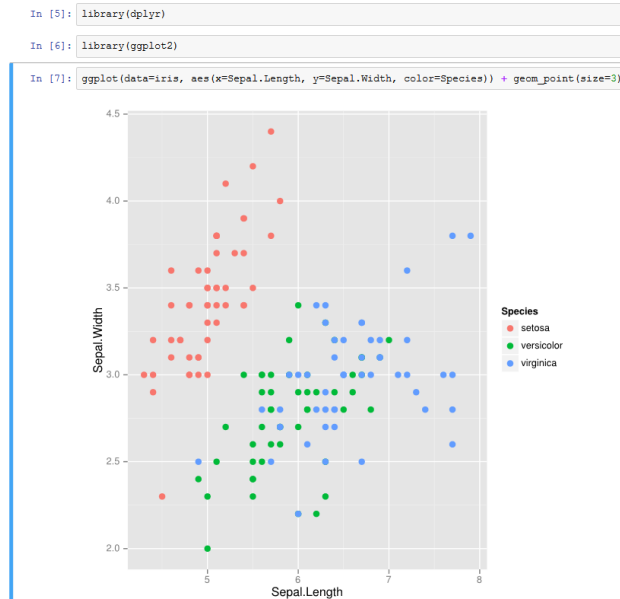
To use ggplot2 with AEN:

1. Open a new Notebook using the R kernel.
2. Load the ggplot2 library with the following code:

```
library(ggplot2)
```

The `ggplot2` library is loaded and ready for use in AEN.

The following screenshot is of a scatter plot of sepal width vs sepal length using the `iris` dataset provided by the `dplyr` library:



## Using environment variables

Some Python packages depend on environment variables for correct operation.

EXAMPLE: Theano requires that the directory containing the CUDA compiler is included in the `$PATH` environment variable in order for GPU acceleration to be enabled.

To change environment variables for all AEN applications, modify the project runtime configuration file `.projectrc`. For more information, see [Using Compute Resource Configuration](#).

`.projectrc` sets several AEN internal environment variables, sets up the project environment and can set additional user environment variables for that project. This file is sourced when a user opens any AEN application—including Jupyter Notebook—and Jupyter kernels will be able to read the included environment variables.

## Cheat sheet

See the [Anaconda Enterprise Notebooks cheat sheet PDF \(232 KB\)](#) for a single-page summary of the most important information about using AEN.

## Troubleshooting

This troubleshooting guide provides you with ways to deal with issues that may occur with your AEN installation.

### AEN application not working properly

An AEN application is not working as expected.

#### Cause

There are several reasons an application may not work as expected.

#### Solution

Most AEN application issues can be resolved by following these steps:

1. Refresh the page.
2. If the issue is not resolved, close and open the application.
3. If the issue is not resolved, *stop and restart your project*.
4. If the issue is not resolved, check that you are using the latest version of your web browser—Chrome, Safari, Edge, or Firefox.
5. Log out of AEN.
6. Restart your browser, and log back in.

If you continue to have issues, then please contact your administrator or enterprise support representative.

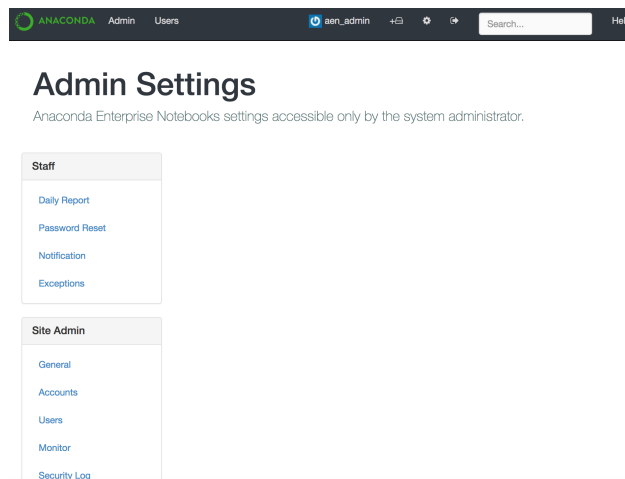
### Admin guide

This administrator guide provides information about the administration of an AEN installation.

Most AEN system management is done from the administrative user interface (admin UI). Some advanced tasks are done *using the command line*.

Any AEN user account can be *upgraded to an administrator account* to have both user and administrator privileges.

Administrators see two additional links in the AEN Navigation bar—Admin and Users:





All of the other navigation bar items are the same as for a user account.

## Concepts

- *System overview*
- *Server node*
- *Gateway node*
- *Compute node(s)*
- *Supervisor and supervisord*
- *Service Account*
- *Anaconda environments*
- *Projects and permissions*

## System overview

The Anaconda Enterprise Notebooks platform consists of 3 main service groups: AEN server, AEN gateway and AEN compute, which are called “nodes”:

- *Server node*—The administrative front-end to the system where users login, user accounts are stored, and administrators manage the system.
- *Gateway node(s)*—A reverse proxy that authenticates users and directs them to the proper compute node for their project. Users will not notice this node after installation as it automatically routes them.
- *Compute nodes*—Where projects are stored and run.

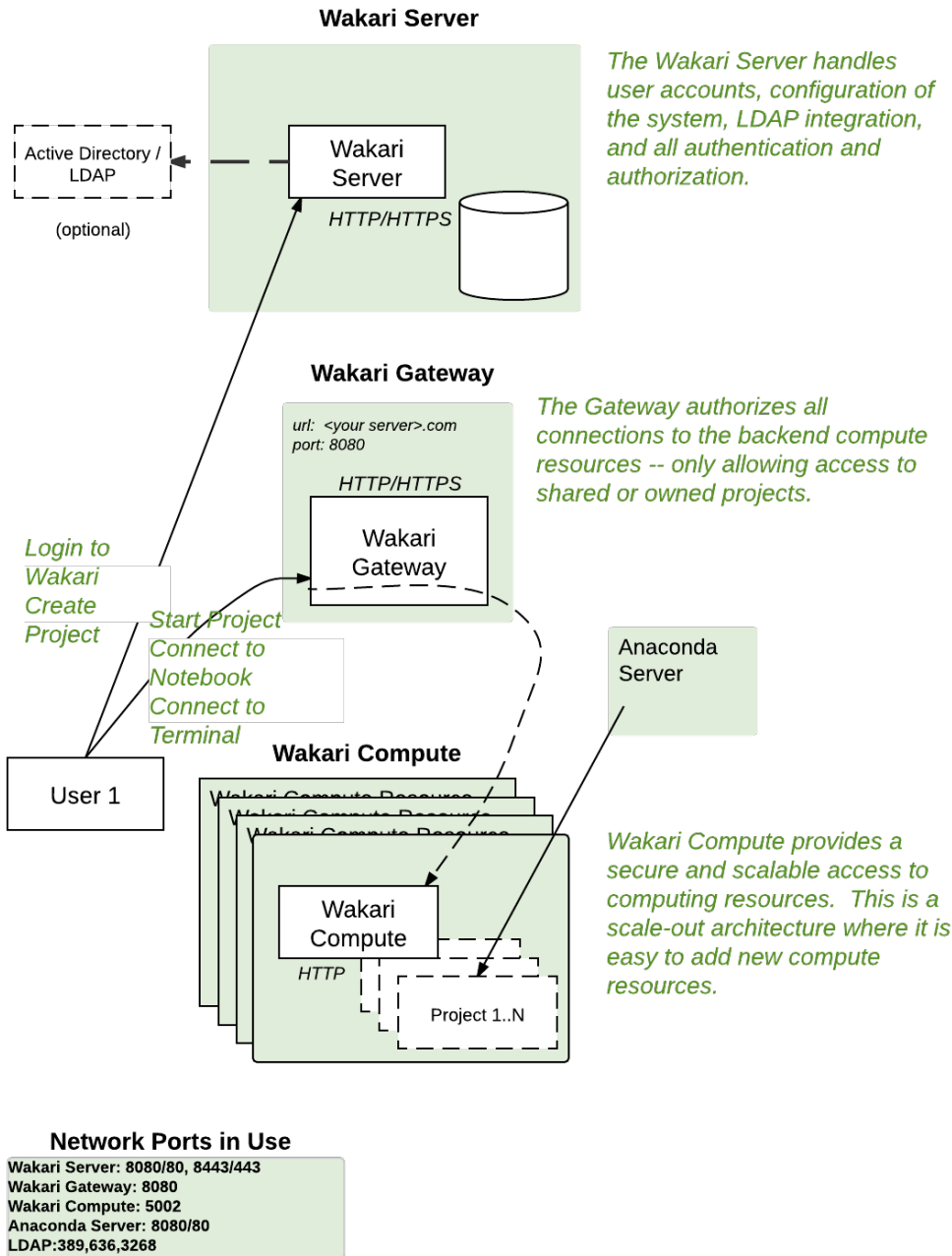
These services can be run on a single machine or distributed across multiple servers.

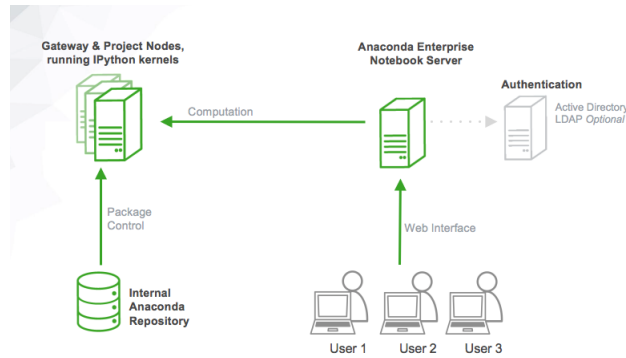
Each AEN installation has exactly 1 server instance and 1 or more gateway instances. Each compute node can only be connected to a single gateway. The collection of compute nodes served by a single gateway is called a **data center**. You can add data centers to the AEN installation at any time.

EXAMPLE: An AEN deployment with 2 data centers, where 1 gateway has a cluster of 20 physical computers, and the second gateway has 30 virtual machines, must have the following services installed and running:

- 1 AEN server instance
- 2 AEN gateway instances

## Anaconda Enterprise Notebooks





- 50 AEN compute instances (20 + 30)

Nodes must be configured and maintained separately.

## Server node

The server node controls login, accounts, admin, project creation and management as well as interfacing with the database. It is the main entry point to AEN for all users. The server node handles project setup, and ensures that users are sent to the correct project data center.

Since AEN is web-based, it uses the standard HTTP port 80 or HTTPS port 443 on the server.

AEN uses MongoDB for internal data persistency. It is typically run on the same host as the server, but can also be *installed on a separate host*.

Server nodes use NGINX to handle the user-facing AEN web interface. NGINX acts as a request proxy for the actual server web process, which runs on a high-numbered port that only listens on localhost. NGINX is also responsible for static content.

AEN server is installed in the `/opt/wakari/wakari-server` directory.

## Server processes

When you *view the status of server processes*, you may see the processes explained below.

supervisord	details
description	Manage wakari-worker, multiple processes of wk-server.
user	wakari
configuration	/opt/wakari/wakari-server/etc/supervisord.conf
log	/opt/wakari/wakari-server/var/log/supervisord.log
control	service wakari-server
ports	none

wk-server	details
description	Handles user interaction and passing jobs on to the wakari gateway. Access to it is managed by NGINX.
user	wakari
command	/opt/wakari/wakari-server/bin/wk-server
configuration	/opt/wakari/wakari-server/etc/wakari/
control	service wakari-server
logs	/opt/wakari/wakari-server/var/log/wakari/server.log
ports	Not used in versions after 4.1.2 *

\* AEN 4.1.2 and earlier use port 5000. This port is used only on localhost. Later versions of AEN use Unix sockets instead. The Unix socket path is `unix:/opt/wakari/wakari-server/var/run/wakari-server.sock`

wakari-worker	details
description	Asynchronously executes tasks from wk-server.
user	wakari
logs	/opt/wakari/wakari-server/var/log/wakari/worker.log
control	service wakari-server

nginx	details
description	Serves static files and acts as proxy for all other requests passed to wk-server process. *
user	nginx
configuration	/etc/nginx/nginx.conf      /opt/wakari/wakari-server/etc/conf.d/www.enterprise.conf
logs	/var/log/nginx/woc.log /var/log/nginx/woc-error.log
control	service nginx status
port	80

\* In AEN 4.1.2 and earlier the wk-server process runs on port 5000 on localhost only. In later versions of AEN the wk-server process uses the Unix socket path `unix:/opt/wakari/wakari-server/var/run/wakari-server.sock`.

NGINX runs at least two processes:

- Master process running as root user.
- Worker processes running as nginx user.

## Gateway node

The gateway node serves as an access point for a given group of compute nodes. It acts as a proxy service, and manages the authorization and mapping of URLs and ports to services that are running on those nodes. The gateway nodes provide a consistent uniform interface for the user.

**NOTE:** The gateway may also be referred to as a data center because it serves as the proxy for a collection of compute nodes.

You can put a gateway in each data center in a tiered scale-out fashion.

AEN gateway is installed in the `/opt/wakari/wakari-gateway` directory.

## Gateway processes

When you *view the status of server processes*, you may see the processes explained below.

supervisord	details
description	Manages the wk-gateway process.
user	wakari
configuration	/opt/wakari/wakari-gateway/etc/supervisord.conf
log	/opt/wakari/wakari-gateway/var/log/supervisord.log
control	service wakari-gateway
ports	none

wakari-gateway	details
description	Passes requests from the AEN Server to the Compute nodes.
user	wakari
configuration	/opt/wakari/wakari-gateway/etc/wakari/wk-gateway-config.json
logs	/opt/wakari/wakari-gateway/var/log/wakari/gateway.application.log /opt/wakari/wakari-gateway/var/log/wakari/gateway.log
working dir	/ (root)
port	8089 (webcache)

## Compute node(s)

Compute nodes are where applications such as Jupyter Notebook and Workbench actually run. They are also the hosts that a user sees when using the Terminal app, or when using SSH to access a node. Compute nodes contain all user-visible programs.

Compute nodes only need to communicate with a gateway, so they can be completely isolated by a firewall.

Each project is associated with one or more compute nodes that are part of a single data center.

AEN compute nodes are installed in the /opt/wakari/wakari-compute directory.

Each compute node in the AEN system requires a compute launcher service to mediate access to the server and gateway.

## Compute processes

When you *view the status of server processes*, you may see the processes explained below.

supervisord	details
description	Manages the wk-compute process.
user	wakari
configuration	/opt/wakari/wakari-compute/etc/supervisord.conf
log	/opt/wakari/wakari-compute/var/log/supervisord.log
control	service wakari-compute
working dir	/opt/wakari/wakari-compute/etc
ports	none

wk-compute	details
de-scrip-tion	Launches compute processes.
user	wakari
con-figura-tion	/opt/wakari/wakari-compute/etc/wakari/wk-compute-launcher-config.json /opt/wakari/wakari-compute/etc/wakari/scripts/config.json
logs	/opt/wakari/wakari-compute/var/log/wakari/compute-launcher. application.log                      /opt/wakari/wakari-compute/var/log/wakari/ compute-launcher.log
work-ing dir	/ (root)
con-trol	service wakari-compute
port	5002 (rfe)

wk-compute loads each of the following configuration files, in this order:

- /etc/wakari/config.json.
- /etc/wakari/compute-launcher-config.json.
- ./compute-launcher-config.json.
- Any configuration file specified by the `-c` option.

If an option is specified in multiple files, the last one encountered takes precedence.

## Supervisor and supervisord

AEN uses a process control system called “Supervisor” to run its services. Supervisor is run by the AEN Service Account user, usually `wakari` or `aen_admin`.

The Supervisor daemon process is called `supervisord`. It runs in the background, and should rarely need to be restarted.

## Service Account

AEN must be installed and executed by a Linux account called the AEN Service Account. The username of the AEN Service Account is called the AEN Functional ID (NFI). The AEN Service Account is created during AEN installation—if it does not exist—and is used to run all AEN services.

The default NFI username is `wakari`. Another popular choice is `aen_admin`.

**WARNING:** The Service Account should be used for administrative tasks only, and should not be used for operating AEN the way an ordinary user would. If the Service Account creates or starts projects, the permissions on the AEN package cache will be reset to match the Service Account, which will interfere with the normal operation of AEN for all other users.

## Anaconda environments

Each project has an associated conda environment containing the packages needed for that project. When a project is first started, AEN clones a default environment with the name `default` into the project directory.

Each release of AEN 4 includes specific tested versions of conda and the conda packages included with AEN. These tested conda packages include Python, R, and other packages, and these tested conda packages include all of the packages in Anaconda.

If you upgrade or install different versions of conda or different versions of any of these conda packages, the new packages will not have been tested as part of the AEN 4 release.

These different packages will usually work, especially if they are newer versions, but they are not tested or guaranteed to work, and in some cases they may break product functionality.

We recommend you use a new conda environment to test a new version of a package, before installing it in your existing environments.

If using conda to change the version of a package breaks product functionality, you can use conda to change the version of the package back to the version known to work.

For more information about environments, see [Working with environments](#).

## Projects and permissions

AEN users interact with the system predominantly through [projects](#).

Projects are associated with a single data center within the AEN environment. The team of users includes one owner, which is the user that created the project.

Projects live in the `projectRoot` folder on the compute node—by default, `/projects`.

The project directory is created the first time a project is started. The `start-project` script clones it from `/opt/wakari/wakari-compute/lib/node_modules/wakari-compute-launcher/skeleton`.

Project directory permissions are:

```
owner: rwx, user who created the project
group: rwx, group of the owner
other: --x, to allow access to the Public folder
ACL: rwx for any other team members
```

Files and subdirectories within the project directory have the same permissions as the project directory, except:

- The public folder and everything in it are open to anyone.
- Any files hardlinked into the root anaconda environment—`/opt/wakari/anaconda`—are owned by the root or wakari users.

Project file and directory permissions are maintained by the `start-project` script. All files and directories in the project will have their permissions set when the project is started, except for files owned by root or the `AEN_SRVC_ACCT` user—by default, `wakari` or `aen_admin`.

The permissions set for files owned by root or the `AEN_SRVC_ACCT` user are not changed to avoid changing the permissions settings of any linked files in the `/opt/wakari/anaconda` directory.

**CAUTION:** Do not start a project as the `AEN_SRVC_ACCT` user. The permissions system does not correctly manage project files owned by this user.

## Installation

### Installation requirements

- *Hardware requirements*
- *Software requirements*
- *Security requirements*
- *Network requirements*
- *Other requirements*
- *What's next*

### Hardware requirements

AEN server—At least:

- 2+GB RAM.
- 2+CPU cores.
- 20GB storage.

AEN gateway—At least:

- 2 GB RAM.
- 2 CPU cores.

AEN compute (N-machines)—Configured to meet the needs of the projects. At least:

- 2GB RAM.
- 2 CPU cores.
- 20 GB.

NOTE: We recommend putting `/opt/wakari` and `/projects` on the same filesystem. If the project and conda env directories are on separate filesystems then more disk space will be required on compute nodes and performance will be worse.

### Software requirements

- RHEL/CentOS on all nodes. Versions from 6.5 through 7.4 are supported. Other operating systems are supported. However, this document assumes RHEL or CentOS.
- Linux home directories—Jupyter looks in `$HOME` for profiles and extensions.
- Ability to install in AEN directory `/opt/wakari` with at least 10 GB of storage.
- Ability to install in Projects directory `/projects` with at least 20 GB of storage. Size depends on number and size of projects.

NOTE: To install AEN in a different location see *Installing AEN in a custom location*.



## Linux system accounts

Some Linux system accounts (UIDs) are added to the system during installation.

If your organization requires special actions, the following list is available:

- mongod (RHEL) or mongodb (Ubuntu/Debian)—created by the RPM or deb package.
- elasticsearch—created by RPM or deb package.
- nginx—created by RPM or deb package.
- AEN\_SRVC\_ACCT—created during installation of AEN, and defaults to wakari.
- ANON\_USER—An account such as “public” or “anonymous” on the compute node.

NOTE: If ANON\_USER is not found, AEN\_SRVC\_ACCT will attempt to create it. If it fails, the project(s) will fail to start.

- ACL directories need the filesystem mounted with Posix ACL support (Posix.1e).

NOTE: You can verify ACL from the command line by running `mount` and `tune2fs -l /path/to/filesystem | grep options`.

## Software prerequisites

- AEN server:
  - Mongo—Equal to or higher than version 2.6.8 and lower than version 3.0.
  - NGINX—Equal to or higher than version 1.6.2.
  - Elasticsearch—Equal to or higher than version 1.7.2.
  - Oracle JRE version 7 or 8.
  - bzip2.
- AEN Gateway:
  - bzip2.
- AEN compute:
  - git
  - bzip2
  - bash or zsh
  - X Window System

NOTE: If you don’t want to install the whole X Window System, you must install the following packages to have R plotting support:

```
sudo yum install -y libXrender libXext libXdmp libSM libICE libXt \
dejavu-sans-fonts dejavu-serif-fonts dejavu-fonts-common \
fontpackages-filesystem
```

## Security requirements

- Root or sudo access.
- File permissions: `umask 0022` is required during the installation.
- SELinux in permissive or disabled mode.

Edit the following file using either root or sudo access:

```
/etc/sysconfig/selinux
```

Edit the following:

```
# This file controls the state of SELinux on the system.
# SELINUX= can take one of these three values:
#   enforcing - SELinux security policy is enforced.
#   permissive - SELinux prints warnings instead of enforcing.
#   disabled - No SELinux policy is loaded.

SELINUX=enforcing

# SELINUXTYPE= can take one of these two values:
#   targeted - Targeted processes are protected,
#   mls - Multi Level Security protection.

SELINUXTYPE=targeted
```

NOTE: You must reboot for the changes to take effect.

Verify changes with `getenforce`.

## Network requirements

TCP Ports:

Direction	Type	Default Port	Protocol	Optional	Configurable	Comments
Inbound	TCP	80	HTTP or HTTPS	No	Yes	Server
Inbound	TCP	8089	HTTP or HTTPS	No	Yes	Gateway
Inbound	TCP	5002	HTTP	No	Yes	Compute

## Other requirements

As long as the above requirements are met, there are no additional dependencies for AEN.

See also system requirements for Anaconda Repository and Anaconda Scale.

## What's next

*Prepare for installation.*

## Preparing for installation

- *Downloading AEN installers*
- *Gathering IP addresses or FQDNs*
- *Set up variables*
- *What's next*

## Downloading AEN installers

Download the installers and copy them to the corresponding servers.

```
RPM_CDN="https://820451f3d8380952ce65-4cc6343b423784e82fd202bb87cf87cf.ssl.cf1.
↪rackcdn.com"
curl -O $RPM_CDN/aen-server-4.3.2-Linux-x86_64.sh
curl -O $RPM_CDN/aen-gateway-4.3.2-Linux-x86_64.sh
curl -O $RPM_CDN/aen-compute-4.3.2-Linux-x86_64.sh
```

NOTE: The current \$RPM\_CDN server will be confirmed in an email provided by your sales rep.

NOTE: These instructions use *curl* or *wget* to download packages, but you may use other means to move the necessary files into the installation directory.

## Gathering IP addresses or FQDNs

AEN is very sensitive to the IP address or domain name used to connect to the server and gateway nodes. If users will be using the domain name, you should install the nodes using the domain name instead of the IP addresses. The authentication system requires the proper hostnames when authenticating users between the services.

Print this page and fill in the domain names or IP addresses of the nodes below and record the user name and auto-generated password for the administrative user account in the box below after installing the AEN server node:

Node   Name or IP address	Port Number	Username   Password	
AEN server			
AEN gateway			
AEN compute			

NOTE: The values of these IP entries or DNS entries are referred to as <AEN\_SERVER\_IP> or <AEN\_SERVER\_FQDN>, particularly in examples of shell commands. Consider actually assigning those values to environment variables with similar names.

## Set up variables

Certain variables need to have values assigned to them before you start the installation.

### AEN server address

To define an environment variable for the AEN server address—FQDN or IP:

```
export AEN_SERVER=<AEN_SERVER_IP> # <from table above>
```

NOTE: The address—FQDN or IP—specified for the AEN server must be resolvable by your intended AEN users' web clients.

To verify your hostname, run `echo $AEN_SERVER`.

### AEN functional ID

AEN must be installed and executed by a Linux account called the AEN Service Account. The username of the AEN Service Account is called the AEN Functional ID (NFI). The AEN Service Account is created during AEN installation—if it does not exist—and is used to run all AEN services.

The default NFI username is `wakari`. Another popular choice is `aen_admin`.

To set the environment variable `AEN_SRVC_ACCT` to `wakari` or your chosen name before installation, run `export AEN_SRVC_ACCT="aen_admin"`.

This name is now the username of the AEN Service Account and of the AEN administrator account.

When upgrading AEN, set the NFI to the NFI of the current installation.

WARNING: The Service Account should only be used for administrative tasks, and should not be used for operating AEN the way an ordinary user would. If the Service Account creates or starts projects, the permissions on the AEN package cache will be reset to match the Service Account, which will interfere with the normal operation of AEN for all other users.

### AEN functional group

The AEN Functional Group (NFG) may be given any name. Most often, it is set to `aen_admin` or `wakari`. This Linux group includes the AEN service account, so all files and directories that have the owner NFI also have the group NFG.

When upgrading AEN, set the NFG to the NFG of the current installation.

To set the NFG before installation, run:

```
export AEN_SRVC_GRP="<NFG>"
```

NOTE: Replace `<NFG>` with your NFG name.

### AEN install sudo command

During AEN installation the installers perform various operations that require root level privileges. By default, the installers use the `sudo` command to perform these operations.

Before installation, set the `AEN_SUDO_CMD_INSTALL` environment variable to perform root level operations. You can also set it to no command at all if the user running the installer(s) has root privileges and the `sudo` command is not needed or is not available.

EXAMPLES:

```
export AEN_SUDO_CMD_INSTALL=""
export AEN_SUDO_CMD_INSTALL="sudo2"
```

## AEN sudo command

By default the AEN services uses `sudo -u` to perform operations on behalf of other users—including `mkdir`, `chmod`, `cp` and `mv`.

To override the default `sudo` command when `sudo` is not available on the system, before installing, set the `AEN_SUDO_CMD` environment variable.

AEN must have the ability to perform operations on behalf of other users. Therefore, this environment variable cannot be set to an empty string or to `null`.

**CAUTION:** Any command that replaces `AEN_SUDO_CMD` must support the `-u` command line parameter—similarly to the `sudo` command.

**EXAMPLE:**

```
export AEN_SUDO_CMD="sudo2"
```

The optional environmental variable `AEN_SUDO_SH` is another way to customize AEN `sudo` operations. When AEN executes any `sudo` command, it will include the value of `AEN_SUDO_SH`, if it is set.

**EXAMPLE:** If your username is “jsmith” and the values are set as:

```
AEN_SUDO_CMD=sudo
OWNER=jsmith
AEN_SUDO_SH=sudologger
PROJECT_HOME=/projects/jsmith/myproj
```

Then AEN will resolve:

```
$AEN_SUDO_CMD -u ${OWNER} $AEN_SUDO_SH rm -rf $PROJECT_HOME
```

As:

```
sudo -u jsmith sudologger rm -rf /projects/jsmith/myproj
```

In this case the `sudologger` utility could be a pass-through utility that logs all `sudo` usage and then executes the remaining parameters.

## Post-installation Sudo configuration

While `root/sudo` privileges are required during installation, `root/sudo` privileges are not required during normal operations after install, if user accounts are managed outside the software. However `root/sudo` privileges are required to start the services, thus in the service config files there may still need to be an `AEN_SUDO_CMD` entry.

For more information, see [Configuring sudo customizations](#).

## AEN remote database settings

By default AEN server uses a local database. To override the default database location, see [Install AEN connected to a remote Mongo DB instance](#).

### What's next

*Install the AEN server.*

### Installing the AEN server

- *Installing the bzip2 package*
- *Downloading prerequisite RPMs*
- *Installing prerequisite RPMs*
- *Setting variables and changing permissions*
- *Running the AEN server installer*
- *Starting NGINX and Elasticsearch*
- *Testing AEN server installation*
- *Updating your license*
- *What's next*

The AEN server is the administrative front end to the system. This is where users log in to the system, where user accounts are stored, and where admins can manage the system.

Server is installed in the `/opt/wakari/wakari-server` directory.

### Installing the bzip2 package

Be sure you have the *bzip2* package installed. If this package is not installed on your system, install it:

```
sudo yum install bzip2
```

### Downloading prerequisite RPMs

To install AEN on a CentOS 6 server:

```
RPM_CDN="https://820451f3d8380952ce65-4cc6343b423784e82fd202bb87cf87cf.ssl.cf1.
↪rackcdn.com"
curl -O $RPM_CDN/nginx-1.6.2-1.el6ngx.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-tools-2.6.8-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-shell-2.6.8-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-server-2.6.8-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-mongos-2.6.8-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-2.6.8-1.x86_64.rpm
curl -O $RPM_CDN/elasticsearch-1.7.2.noarch.rpm
curl -O $RPM_CDN/jre-8u65-linux-x64.rpm
```

To install AEN on a CentOS 7 server:

```
RPM_CDN="https://820451f3d8380952ce65-4cc6343b423784e82fd202bb87cf87cf.ssl.cf1.
↳rackcdn.com"
curl -O $RPM_CDN/nginx-1.10.2-1.el7ngx.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-tools-2.6.12-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-shell-2.6.12-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-server-2.6.12-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-mongos-2.6.12-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-2.6.12-1.x86_64.rpm
curl -O $RPM_CDN/jre-8u112-linux-x64.rpm
curl -O $RPM_CDN/elasticsearch-1.7.6.noarch.rpm
```

## Installing prerequisite RPMs

Run:

```
sudo yum install -y *.rpm
sudo service mongod start
sudo chkconfig --add elasticsearch
```

## Setting variables and changing permissions

Run:

```
export AEN_SERVER=<FQDN HOSTNAME OR IP ADDRESS> # Use the real FQDN
chmod a+x aen-*.sh # Set installer to be executable
```

NOTE: Change <FQDN HOSTNAME OR IP ADDRESS> to the actual fully qualified domain hostname or IP address.

## Running the AEN server installer

Run:

```
sudo -E ./aen-server-4.3.2-Linux-x86_64.sh -w $AEN_SERVER
<license text>
...
...
PREFIX=/opt/wakari/wakari-server
Logging to /tmp/wakari_server.log
Checking server name
Ready for pre-install steps
Installing miniconda
...
...
Checking server name
Loading config from /opt/wakari/wakari-server/etc/wakari/config.json
Loading config from /opt/wakari/wakari-server/etc/wakari/wk-server-config.json

=====

Created password '<RANDOM_PASSWORD>' for user 'aen_admin'
```

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```
=====

Starting Wakari daemons...
installation finished.
```

After successfully completing the installation script, the installer creates the administrator account—AEN\_SRVC\_ACCT user—and assigns it a password.

EXAMPLE:

```
Created password '<RANDOM_PASSWORD>' for user 'aen_admin'
```

**TIP:** Record this password. It will be needed in the following steps. It is also available in the installation log file `/tmp/wakari_server.log`.

## Starting NGINX and Elasticsearch

When SELinux is enabled, it blocks NGINX from connecting to the socket created by Gunicorn. If you have SELinux enabled, run these commands to correct these permissions and allow connections between NGINX and Gunicorn:

```
sudo semanage fcontext -a -t httpd_var_run_t "/opt/wakari/wakari-server/var/run/
↪wakari-server.sock"
sudo restorecon -r /opt/wakari/wakari-server/var/run
```

To start NGINX and Elasticsearch to read the new config file:

```
sudo service nginx start
sudo service elasticsearch start
```

**TIP:** If the AEN web page shows an NGINX 404 error, restart NGINX:

```
sudo nginx -s stop
sudo nginx
```

## Testing AEN server installation

Visit [http://\protect\TI\textdollarAEN\\_SERVER](http://\protect\TI\textdollarAEN_SERVER).

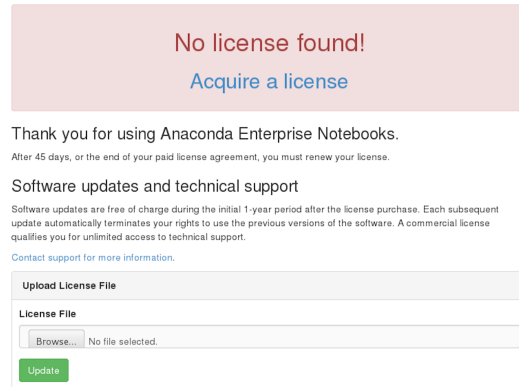
The License expired page is displayed.

## Updating your license

From the License expired page, follow the onscreen instructions to upload your license file.

After your license is submitted, you will see this page:





**No license found!**  
[Acquire a license](#)

Thank you for using Anaconda Enterprise Notebooks.  
After 45 days, or the end of your paid license agreement, you must renew your license.

**Software updates and technical support**

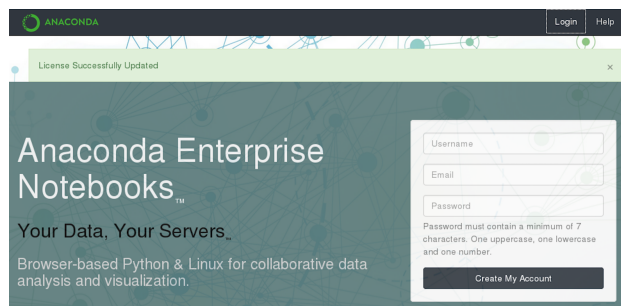
Software updates are free of charge during the initial 1-year period after the license purchase. Each subsequent update automatically terminates your rights to use the previous versions of the software. A commercial license qualifies you for unlimited access to technical support.

[Contact support for more information.](#)

**Upload License File**

License File  
Browse... No file selected.

Update



## What's next

*Install the AEN gateway.*

## Installing the AEN gateway

- *Setting variables and changing permissions*
- *Running the AEN gateway installer*
- *Registering your gateway*
- *What's next*

The gateway is a reverse proxy that authenticates users and automatically directs them to the proper AEN compute node for their project. Users will not notice this node as it automatically routes them.

Gateway is installed in the `/opt/wakari/wakari-gateway` directory.

## Setting variables and changing permissions

Run:

```
export AEN_SERVER=<FQDN HOSTNAME OR IP ADDRESS> # Use the real FQDN
export AEN_GATEWAY_PORT=8089
```

(continues on next page)

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```
export AEN_GATEWAY=<FQDN HOSTNAME OR IP ADDRESS> # will be needed shortly
chmod a+x aen-*.sh # Set installer to be executable
```

NOTE: Change <FQDN HOSTNAME OR IP ADDRESS> to the actual fully qualified domain hostname or IP address.

NOTE: You must perform the entire procedure before closing the terminal to ensure the variable export persists. If the terminal is closed before successful installation, export the variables to continue with the installation.

## Running the AEN gateway installer

Run:

```
sudo -E ./aen-gateway-4.3.2-Linux-x86_64.sh -w $AEN_SERVER
<license text>
...
...

PREFIX=/opt/wakari/wakari-gateway
Logging to /tmp/wakari_gateway.log
...
...
Checking server name
Please restart the Gateway after running the following command
to connect this Gateway to the AEN Server
...
```

## Registering your gateway

The gateway needs to register with the AEN server.

This needs to be authenticated, so the NFI user's credentials created during the AEN server install must be used.

To write the configuration file `/opt/wakari/wakari-gateway/etc/wakari/wk-gateway-config.json`, run the following as `sudo` or `root`:

```
sudo /opt/wakari/wakari-gateway/bin/wk-gateway-configure \
--server http://$AEN_SERVER --host $AEN_GATEWAY \
--port $AEN_GATEWAY_PORT --name Gateway --protocol http \
--summary Gateway --username $AEN_SRVC_ACCT \
--password '<NFI USER PASSWORD>'
```

NOTE: replace <NFI USER PASSWORD> with the password of the NFI user that was generated during *server installation*.

## Setting permissions

Run:

```
sudo chown $AEN_SRVC_ACCT /opt/wakari/wakari-gateway/etc/wakari/wk-gateway-config.json
```

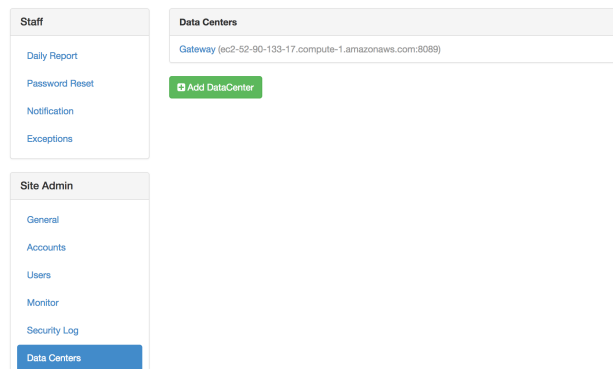
## Starting the gateway

Run:

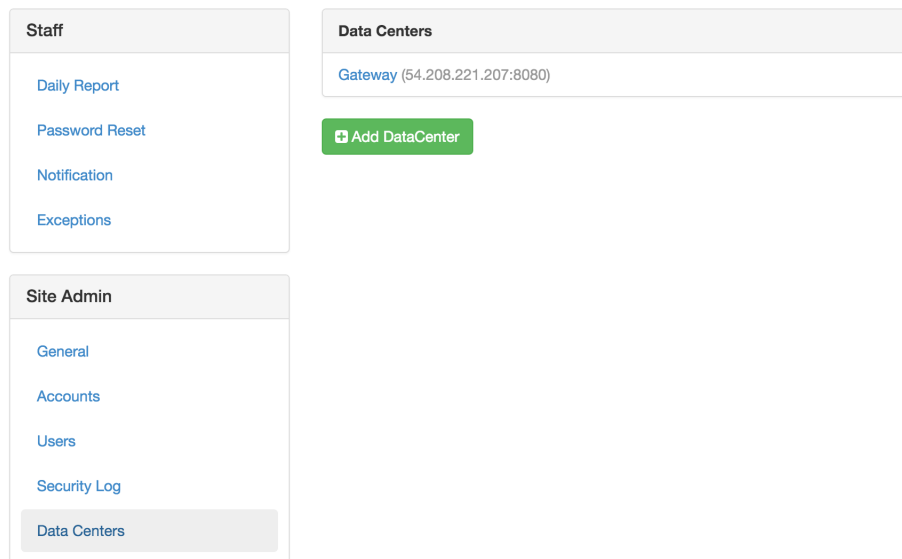
```
sudo service wakari-gateway start
```

## Verifying your gateway registration

1. Log into the AEN server using the Chrome or Firefox browser and the AEN\_SRVC\_ACCT user.
2. In the AEN navigation bar, click Admin to open the Admin Settings page.
3. In the **Site Admin** menu, select Data Centers:



4. Click your data center:



5. Verify that your data center is registered and the status is {"status": "ok", "messages": []}:

Staff

[Daily Report](#)
[Password Reset](#)
[Notification](#)
[Exceptions](#)

Site Admin

[General](#)
[Accounts](#)
[Users](#)
[Monitor](#)
[Security Log](#)
[Data Centers](#)
[Task Queue](#)

Datacenter Gateway

Provider

wk\_server.plugins.providers.enterprise

Client ID

59c119cd3f94c30fe45ff5db

Client Secret

50cc629d-4e8e-44a5-9a2e-a46fee7c1921

Redirect URIs

http://ec2-52-90-133-17.compute-1.amazonaws.com:8089/login/authorized

wk-gateway-config.json

```
{
  "CDN": "http://ec2-204-236-198-47.compute-1.amazonaws.com/static/",
  "SUBDOMAIN_ROUTING": false,
  "client_id": "59c119cd3f94c30fe45ff5db",
  "client_secret": "50cc629d-4e8e-44a5-9a2e-a46fee7c1921",
  "WAKARI_SERVER": "http://ec2-204-236-198-47.compute-1.amazonaws.com",
  "port": 8089
}
```

status

```
{"status": "ok", "messages": []}
```

Back

Remove

## What's next

*Install the AEN compute node(s).*

## Installing the AEN compute node(s)

- *Setting variables and changing permissions*
- *Running the AEN compute installer*
- *Restart the AEN Server*
- *Configuring your compute node(s)*
- *What's next*

Compute nodes are where projects are stored and run.

Adding multiple AEN compute machines allows you to scale-out horizontally to increase capacity. Projects can be created on individual compute nodes to spread the load.

Repeat this procedure on each compute machine.

## Setting variables and changing permissions

Run:

```
export AEN_SERVER=<FQDN HOSTNAME OR IP ADDRESS> # Use the real FQDN
chmod a+x aen-*.sh # Set installer to be executable
```

NOTE: Change <FQDN HOSTNAME OR IP ADDRESS> to the actual fully qualified domain hostname or IP address.

NOTE: You must perform the entire procedure before closing the terminal to ensure the variable export persists.

## Running the AEN compute installer

Run:

```
sudo -E ./aen-compute-4.3.2-Linux-x86_64.sh -w $AEN_SERVER
...
...
PREFIX=/opt/wakari/wakari-compute
Logging to /tmp/wakari_compute.log
Checking server name
...
...
Initial clone of root environment...
Starting Wakari daemons...
installation finished.
Do you wish the installer to prepend the wakari-compute install location
to PATH in your /root/.bashrc ? [yes|no]
[no] >>> yes
```

## Restart the AEN Server

Once configured, restart the AEN server:

```
sudo service wakari-server restart
```

## Configuring your compute node(s)

Once installed, you must configure the compute launcher on your server:

1. In your browser, go to your AEN server.
2. Log in as the AEN\_SRVC\_ACCT user.
3. In the AEN navigation bar, click Admin to open the Admin Settings page.
4. In the **Providers** menu, select Enterprise Resources:
5. Click the Add Resource button to open the new resource form.
6. Select the data center to associate this compute node with.

**Staff**

- Daily Report
- Password Reset
- Notification
- Exceptions

**Resources** [Add Resource](#)

Gateway	
ec2-54-210-232-251.compute-1.amazonaws.com	<a href="#">remove</a>

**Site Admin**

- General
- Accounts
- Users
- Monitor
- Security Log
- Data Centers
- Task Queue
- License

**Providers**

- Enterprise Resources

Resources / new

**Data Center**  
Gateway 59c119cd3f94c30fe45ff5db

**Name**  
Compute Node1

**URL**  
http://ec2-54-210-232-251.compute-1.amazonaws.com:5002

**Description**  

Configuring Compute Node

☒ **Public**  
Uncheck this if you want to control exactly who has access to this compute node

Add Resource

7. In the URL box, type: `http://$AEN_COMPUTE:5002`.

NOTE: If the compute launcher is located on the same box as the gateway, we recommended that you type `http://localhost:5002` instead.

8. Type a Name and Description for the compute node.
9. Click the Add Resource button to save the changes.

Your AEN compute node is configured.

## What's next

*Configure conda to use your local on-site AEN repository.*

## Configuring conda to use your local on-site AEN repository

You can configure AEN to use a local on-site Anaconda repository server instead of Anaconda.org.

To configure AEN to use a local on-site repository, you must:

1. *Edit condarc on the compute node.*
2. *Configure the Anaconda client.*

## Editing condarc on the compute node

**NOTE:** If there are channels that you haven't mirrored, you must remove them from the configuration.

Edit the file `.condarc` to match the following:

```
#/opt/wakari/anaconda/.condarc
channels:
  - defaults

create_default_packages:
  - anaconda-client
  - ipykernel

# Default channels is needed for when users override the system .condarc
# with ~/.condarc. This ensures that "defaults" maps to your Anaconda Repository and
↪not
# repo.anaconda.com
default_channels:
  - http://<your Anaconda Repository name>:8080/conda/anaconda
  - http://<your Anaconda Repository name>:8080/conda/wakari
  - http://<your Anaconda Repository name>:8080/conda/r-channel

# Note: You must add the "conda" subdirectory to the end
channel_alias: http://<your Anaconda Repository name>:8080/conda
```

**NOTE:** Replace `<your Anaconda Repository name>` with the actual name or IP address of your local Anaconda Repository installation.

## Configuring the Anaconda client

Anaconda client lets users work with the repository from the command-line—including searching for packages, logging in, uploading packages, and more.

To set the default configuration of `anaconda-client` for all users on your compute node, run the following command, replacing `<your Anaconda Repository>` with the actual name or IP address of your local Anaconda Repository installation:

```
sudo /opt/wakari/anaconda/bin/anaconda config --set url http://<your Anaconda_
↪Repository>:8080/api -s
```

**NOTE:** Sudo access is required because the configuration file is written to the root file system: `/etc/xdg/binstar/config.yaml`.

## What's next

Review the *optional configuration* tasks to see if any apply to your system.

## Optional configuration

### Using configuration files

- *AEN configuration keys*
- *Checking configuration file syntax*

The default locations for each component's configuration files are:

- **Server**—`/opt/wakari/wakari-server/etc/wakari/config.json`.
- **Gateway**—`/opt/wakari/wakari-gateway/etc/wakari/config.json`.
- **Compute**—`/opt/wakari/wakari-compute/etc/wakari/config.json`.

Additionally, service-specific configuration files may also be present in the following locations:

- **Server**—`/opt/wakari/wakari-server/etc/wakari/wk-server-config.json`.
- **Gateway**—`/opt/wakari/wakari-gateway/etc/wakari/wk-gateway-config.json`.
- **Compute**—`/opt/wakari/wakari-compute/etc/wakari/wk-compute-config.json`.

Each service loads each of the configuration files in the following order and updates the AEN configuration at each step:

1. `/etc/wakari/config.json`.
2. `/etc/wakari/wk-gateway-config.json`.
3. `/opt/wakari/wakari-SERVICE/etc/wakari/config.json`.
4. `/opt/wakari/wakari-SERVICE/etc/wakari/wk-SERVICE-config.json`.
5. `./config.json`.
6. `./wk-gateway-config.json`.



## AEN configuration keys

The following is a list of AEN supported configuration keys:

Table 7: Server Configuration Keys

Key	Default	Description
CDN	\$WAKARI_SERVER/ static/	The location of static assets.
MONGO_DB	wakari	The name of the AEN database in mongodb.
MONGO_URL	mongodb:// localhost/	The URL of your AEN server's mon- godb instance. Format: mongodb:// <username>:<password>@<host>:<port>/
WAKARI_SERVER		The URL of this AEN server.
DEFAULT_PRIVACY	public	The default project privacy setting—can be either public or private.
SESSION_COOKIE_NAME	wk. enterprise. session	The Cookie name used to maintain Anaconda Enterprise Note- books Enterprise login sessions.
PERMANENT_SESSION	true	Sets cookie session to permanent. This will keep the session open after the browser is closed. The session will still expire af- ter the number of minutes set in the SESSION_LIFETIME key.
SESSION_LIFETIME	120	Time in minutes until the session expires. The counter resets with each request.
USE_SES	false	Sets whether AEN will use Amazon SES to send emails.
SMTP		Sets the SMTP email settings.
- host		A SMTP subkey—the SMTP mail server hostname.
- user		SMTP subkey—the username for SMTP server authentication.
- password		SMTP subkey—the password for SMTP server authentication.
- from_addr		SMTP subkey—the From address for emails sent through SMTP.
verify_gateway_certificate	true	A boolean setting that indicates whether your AEN server should verify the gateway SSL certificate.
accounts	wk_server. plugins .accounts.cloud	The account provider class. For LDAP, this should be set to wk_server.plugins.accounts.ldap_accounts.
uniqueEmail	true	A boolean setting that indicates whether unique user email ad- dresses are required. See <a href="#">note below</a> about updating the database when setting uniqueEmail.
has_internet	true	Boolean for retrieving the avatar from the gravatar URL. If false a local default is used instead.
LDAP	389	LDAP configurations.
- SERVER		LDAP subkey—A list of LDAP servers. At least one server name must be listed. The primary server should be listed first. All secondary or fail-over servers should be listed after the pri- mary.
- PORT	389	LDAP subkey—The LDAP port on the LDAP server.
- AUTH_TYPE		LDAP subkey—LDAP Authentication types. simple—no encryption not secure. “TLS”—encrypted secure requires the TLS_CERT to be set.
- TLS_CERT		LDAP subkey—the full path to the TLS certificate file. The cer- tificate file must also be provided by the Enterprise.
- BASEDN		LDAP subkey—the LDAP Base DN value.
- OU		LDAP subkey—a list of Organizational Units. Some Enterprises group users by OUs in their LDAP server records. AEN will loop over the list of OUs when authenticating a user. The OU value is a list of lists to support multiple OUs where each OU is a single name or a hierarchy of names.
ANON_USER	anonymous	Username—such as public or anonymous—assigned users who are not logged in to access projects. To disable public access use the special value disable. For more information, see <a href="#">Configuring sudo customizations</a> .
SEARCH_ENABLED	true	Boolean indicating whether ElasticSearch is enabled
SEARCH_SERVER	'localhost:9200'	IP address or domain name and port of ElasticSearch server

NOTE: If you set `uniqueEmail` to `false`, you must drop the existing index in the database. EXAMPLE: If the index name is `email_1`, run `db.users.dropIndex("email_1")`.

Table 8: Gateway Configuration Keys

Key	Default	Description
<code>WAKARI_SERVER</code>		The URL of the AEN <code>WAKARI_SERVER</code> .
<code>port</code>	8089	The Port number used by the gateway application. Must be a non-privileged port ( $\geq 1024$ ).
<code>client_id</code>		The client ID assigned to this gateway by the server during <code>wk-gateway-configure</code> .
<code>client_secret</code>		The Client secret assigned to this gateway by the server during <code>wk-gateway-configure</code> .
<code>httpTimeout</code>	600	Timeout in seconds. The default is 10 minutes to allow project creation.
<code>logLevel</code>	info	Log verbosity. One of: 'error' 'warn' 'info' 'debug'.
<code>https</code>		Enable SSL encryption. For more information, see <a href="#">Configuring SSL</a> .
- <code>key</code>		A https subkey-Path to gateway key.
- <code>cert</code>		A https subkey-Path to gateway cert.
- <code>ca</code>		A https subkey-Required if cert was signed by a private root CA or signed by an intermediate authority. It must contain separate values for the paths to the CA root, any intermediates and the certificate for the Server.
- <code>passphrase</code>		A https subkey-Passphrase required to decrypt SSL certs.

Table 9: Compute Node Configuration Keys

Key	Default	Description
WAKARI_SERVER		The URL of the AEN WAKARI_SERVER.
MANAGE_ACCOUNTS	true	A boolean setting that indicates whether AEN should manage system user accounts. Set to false for LDAP installations.
identicalGID	false	<b>To make the AEN compute service create groups with the same uid. Set to true</b> /projects folder resides on an NFSv3 volume. For more information, see <i>Group and user permissions for NFS</i> .
port	2227	The port number used by the compute-launcher application. Note that individual applications use dynamic ports.
projectRoot	/projects	The location of project file storage.
logLevel	info	Log verbosity. One of: 'error' 'warn' 'info' 'debug'
logMaxSize	10000000	Max size in bytes of the logfile. Default is 10 MB. If the size is exceeded then a new file is created and a counter will become a suffix of the log file.
logMaxFiles	30	Limit the number of files created when the size of the logfile is exceeded
appIdleTime	172800000 (48 hours)	The amount of idle time before applications will be auto-terminated (in msec).
idleCheckInterval	13600000 (1 hour)	The frequency of idle checks.
numericUsernames	false	A boolean setting that indicates whether numeric usernames are permitted.
httpTimeout	600	The time before a timeout—in seconds. The default is 10 minutes—600 seconds—to allow time for project creation.
ANON_USER	anonymous	Username such as public or anonymous for users who are not logged in to access projects. To disable public access use the special value disabled. For more information, see <i>Configuring sudo customizations</i> .
projDirsAsHome	false	A boolean setting. When false AEN apps use /home/<username> as HOME. When true AEN apps use /projects/<username> as HOME.

Table 10: Server Internal Configuration Keys - Do not change

Key	Default	Description
PROVIDERS	["wk_server. plugins providers. enterprise"]	A list of compute provider classes.
MONGO_ACTION_LOG_SIZE	262144000	The size of the Mongo action log in bytes.
SITE_ADMINS		A list of site administrator email addresses—used for crash notifications and LDAP password reset requests.
FROM_EMAIL_ADDR		The From address for notification emails sent by AEN.
uniqueUserName	true	A boolean setting that indicates whether unique usernames are required.

Table 11: Gateway Internal Configuration Keys - Do not change

Key	Default	Description
CDN	\$WAKARI_SERVER/ static/	The location of static assets.
SUBDOMAIN_ROUTING	false	A boolean that indicates whether subdomains are being used.
refreshTokenExpiration	60000	Idle time in milliseconds before the Gateway session expires.

Table 12: Compute Node Internal Configuration Keys - Do not change

Key	Default	Description
CDN	\$WAKARI_SERVER/ static/	The location of static assets.
USE_SES	false	Sets whether AEN will use Amazon SES to send emails.
multiUser	true	A boolean that indicates whether multi-user support is enabled.
multiProject	true	A boolean that indicates whether multi-project support is enabled.
ANACONDA_ROOT	/opt/wakari/ anaconda	The location of your Anaconda installation.
appLogs	/opt/wakari/ wakari- compute/var/ log/wakari/ compute-launcher-apps	The directory where application logs are stored.
appPIDs	/opt/wakari/ wakari-compute/ var/run/ compute-launcher-apps	The directory where application PID files are stored.
applicationLog	/opt/wakari/ wakari-compute/ var/log/ wakari/ compute-launcher. application. log	The path to the compute launcher log.
accessLog	opt/wakari/ wakari-compute/ var/log/ wakari/ compute-launcher. access.log	Path to compute launcher access log

## Checking configuration file syntax

To verify that the configuration file contains valid JSON, run:

```
root@server # python -m json.tool /opt/wakari/wakari-server/etc/wakari/*.json
root@gateway # python -m json.tool /opt/wakari/wakari-gateway/etc/wakari/*.json
root@compute # python -m json.tool /opt/wakari/wakari-compute/etc/wakari/*.json
```

If the file is correct, the contents are displayed.

If there is a syntax error in the file, a “No JSON object could be decoded” message is displayed instead.

To fix any errors, edit the configuration file and verify that it contains the correct JSON syntax.

### Increasing HTTP timeout between gateway and compute nodes

The default HTTP timeout is 600 seconds (10 minutes).

This setting works for HTTP timeout only, not HTTPS.

To modify the HTTP timeout setting:

1. Open the `/opt/wakari/wakari-compute/etc/wakari/wk-compute-launcher-config.json` file and modify the `httpTimeout` key:

```
"httpTimeout": 600
```

2. Update the gateway node by modifying the `httpTimeout` key in the `/opt/wakari/wakari-gateway/etc/wakari/wk-gateway-config.json` file to match the above settings.
3. Restart the AEN compute service:

```
sudo service wakari-compute restart
```

### Installing AEN in a custom location

To install AEN in a custom location:

1. Make the custom install folder owned by `$AEN_SRVC_ACCT`. **EXAMPLE:** `/data/aen/`.
2. Make a symlink from `/opt/wakari` to `/data/aen`.
3. Run the installers.
4. Move the folder from `/projects` to your chosen custom location. **EXAMPLE:** `/data/aen/projects`.
5. Make a symlink from `/projects` to `/data/aen/projects`.

**NOTE:** We recommend putting `/opt/wakari` and `/projects` on the same filesystem. If the project and conda environment directories are on separate filesystems then more disk space will be required on compute nodes and performance will be worse.

### Changing where projects are stored

**NOTE:** We recommend putting `/opt/wakari` and `/projects` on the same filesystem. If the project and conda env directories are on separate filesystems then more disk space will be required on compute nodes and performance will be worse.

To make `aen-compute` service use a different directory than `/projects` to store your AEN projects:

1. Modify the `/opt/wakari/wakari-compute/etc/wakari/wk-compute-launcher-config.json` file:

```
"projectRoot" : "/nfs/storage/services/wakari/projects",
```

**NOTE:** The directory `/nfs/storage/services/wakari/projects` specified as `projectRoot` must already exist for this command to resolve properly.

2. Restart the AEN compute service:

```
sudo service wakari-compute restart
```

## Group and user permissions for NFS

To install AEN with multiple compute nodes and a `/projects` folder on an NFSv3 volume, manually pre-create both the anonymous user and the `$AEN_SRVC_ACCOUNT` user on all nodes. Each of these users must have the same user identity number (UID) and group identity number (GID) on all nodes.

By default AEN creates local users with a different GID on each node. To make the AEN compute service create groups with the same GID:

1. In the `/opt/wakari/wakari-compute/etc/wakari/wk-compute-launcher-config.json` file, change the `identicalGID` key value to `true`:

```
, "identicalGID": true
```

If you don't see the `identicalGID` key, add it.

NOTE: You must add the comma at the beginning of the line. If you add this line as the last key, you must remove any comma at the end of the line.

2. Restart the AEN compute service:

```
sudo service wakari-compute restart
```

## Using numeric usernames

1. In the `/opt/wakari/wakari-compute/etc/wakari/wk-compute-launcher-config.json` file, change the `numericUsernames` key value to `true`.

```
, "numericUsernames": true
```

If you don't see the `numericUsernames` key, add it.

NOTE: You must add the comma at the beginning of the line. If you add this line as the last key, you must remove any comma at the end of the line.

2. Restart the AEN compute service:

```
sudo service wakari-compute restart
```

## Using project directories as home directories

The `projDirsAsHome` option changes the AEN home directories from the standard `/home/<username>` location to the project directories and the location `/projects/<username>/<project_name>/<username>/`. This ensures that AEN and AEN apps will not be affected by configuration files in a user's home directory, such as `.bashrc` or configuration files in subdirectories such as `.ipython` and `.jupyter`.

## Package cache locations

AEN version 4.1.3 stores the cache of packages in `/home/<username>`, while AEN versions 4.2.0 and higher store the cache of packages in `/projects/<username>/<project_name>/<username>/`. By moving the

package cache to the same filesystem as the project, AEN versions 4.2.0 and higher can use hardlinks and save disk space and time when creating or cloning environments.

These package cache locations are not affected by the `projDirsAsHome` option.

After upgrading from AEN 4.1.3 to AEN 4.2.0 or higher, existing projects will still use the package cache in `/home/<username>`. Do not remove this cache, or the existing projects will break.

When users create new projects or install packages, the newly installed packages will use the new cache location.

If you wish to remove the older package cache in `/home/<username>`:

- Upgrade AEN to 4.2.0 or higher.
- Use `conda remove` to remove every non-default package in every project.
- Use `conda install` to replace them. The replaced packages will link to the new package cache in `/projects/<username>/<project_name>/<username>/`.
- You can now safely remove the older package cache.

### Enabling `projDirsAsHome`

NOTE: The `projDirsAsHome` option should be enabled immediately after performing the installation process and before any users have logged in to AEN. This ensures that users will not have home directories in different places due to some creating their home directories when the option was disabled and others creating their home directories when the option was enabled.

1. In the `/opt/wakari/wakari-compute/etc/wakari/wk-compute-launcher-config.json` file, add the `projDirsAsHome` key value and set it to `true`.

```
, "projDirsAsHome": true
```

NOTE: You must add the comma at the beginning of the line. If you add this line as the last key, you must remove any comma at the end of the line.

2. Restart the AEN compute service:

```
sudo service wakari-compute restart
```

### Setting up a default project environment

AEN includes a full installation of the Anaconda Python distribution—along with several additional packages—located within the root conda environment in `/opt/wakari/anaconda`.

The first time any new AEN project is started, this default project environment is cloned into the new project's workspace.

To configure a different set of packages than the default:

1. Create a new conda environment in the `/opt/wakari/anaconda/envs/default` directory.

EXAMPLE: Using a Python 3.4 base environment, run:

```
sudo -u $AEN_SRV_ACCT /opt/wakari/anaconda/bin/conda \
  create -p /opt/wakari/anaconda/envs/default python=3.4
```

2. Use `conda` to install any additional packages into the environment.
3. After the environment is created, clone it to ensure that it works correctly:



```
sudo -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda \
  create -p /opt/wakari/testenv --clone /opt/wakari/anaconda/envs/default
sudo -u $AEN_SRVC_ACCT rm -rf /opt/wakari/testenv
```

For more information and examples about creating a default project environment with Microsoft R Open (MRO), see *Using MRO in AEN*.

## Converting an existing project

1. Run the following command to clone the environment:

```
sudo -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda \
  create -n /projects/owner/project/envs/<ENV_NAME> \
  --clone /opt/wakari/anaconda/envs/default
```

NOTE: Replace `/projects/owner/project/envs/<ENV_NAME>` with the path to the new environment you would like to create within the project.

2. Open the *Compute Resource Configuration application* for your project and set the project environment path there as well.

## Using MRO in AEN

In AEN 4.2.2 and higher, you can choose to create environments with the Microsoft R Open (MRO) interpreter by installing the `mro-base` package, or create environments with the R interpreter by installing the `r-base` package. Unless you request a change, conda will continue to use the existing interpreter in each environment. In AEN `r-base` is the default.

EXAMPLE: To create a custom environment called `mro_env` with MRO and R Essentials:

```
.. code-block:: bash

sudo -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda \
  create -c https://repo.anaconda.com/pkgs/main \
  -n mro_env r-essentials
```

NOTE: Conda 4.4 and higher include the `main` channel by default. Earlier versions of conda do not.

## Making a default project environment with MRO

You can also create an environment with MRO and make this the default AEN project environment.

The first time a new project is started, the default project environment is cloned into the new project's workspace.

1. Create a new conda environment in the `/opt/wakari/anaconda/envs/default` directory.

The command is similar to the one used in the previous example to create a custom environment.

```
sudo -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda \
  create -c https://repo.anaconda.com/pkgs/main \
  -p /opt/wakari/anaconda/envs/default r-essentials
```

2. Use `conda` to install any additional packages into the environment.
3. After the environment is created, clone it to check that it works correctly, and then clean up the clone.

```
sudo -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda \
    create -p /opt/wakari/testenv --clone /opt/wakari/anaconda/envs/default
sudo -u $AEN_SRVC_ACCT rm -rf /opt/wakari/testenv
```

NOTE: To convert existing projects, see *Converting an existing project*.

## Install AEN connected to a remote Mongo DB instance

To install AEN with a remote database:

1. Connect to the Mongodb instance and create the user for AEN:

```
> user = { user: "<username>",
  pwd: "<super-secure-password>",
  roles: [
    { role: "dbOwner", db: "<db_name>" },
    { role: "dbOwner", db: "<db_name>_mq" }
  ]
}
> db.createUser(user)
Successfully added user: { ... }
```

2. Before installing AEN-server export the database URL and name:

```
$ export MONGO_URL="mongodb://<username>:<password>@<host>:<port>/"
$ export MONGO_DB="<database_name>"
```

3. Continue the installation process: *Install the AEN server*.

## Migrate from local to remote MongoDB

To configure your remote database to work with an already installed AEN server:

1. Stop the server, gateway and compute nodes:

```
sudo service wakari-server stop
sudo service wakari-gateway stop
sudo service wakari-compute stop
```

2. Open the `/opt/wakari/wakari-server/etc/wakari/config.json` file and create the `MONGO_URL` key. For the value parameter, add the database information.

The final file should read:

```
{
  "MONGO_URL": "mongodb://MONGO-USER:MONGO-PASSWORD@MONGO-URL:MONGO-PORT",
  "MONGO_DB": "MONGO-DB-NAME",
  "WAKARI_SERVER": "http://YOUR-IP",
  "USE_SES": false,
  "CDN": "http://YOUR-IP/static/",
  "ANON_USER": "anonymous"
}
```

For more information about configuration keys, see *Using configuration files*.

3. Migrate the data from the former database into the new one. For more information, see the [MongoDB documentation website](#).
4. After migration, restart the nodes:

```
sudo service wakari-server start
sudo service wakari-gateway start
sudo service wakari-compute start
```

## Running SELinux in enforcing mode

To run SELinux in Enforcing mode, a few ports must be set up using the `semanage port` command.

The `semanage` command relies on `polycoreutils-python`. To install `polycoreutils-python`, if needed, run:

```
sudo yum -y install polycoreutils-python
```

Enable ports 9200 and 9300 for Elasticsearch:

```
sudo semanage port -a -t http_port_t -p tcp 9200
sudo semanage port -a -t http_port_t -p tcp 9300
```

## Changing server hostnames

It is possible to change the domain names (hostnames) of the various AEN nodes by updating the configuration files.

**NOTE:** After the configuration files are updated, the associated nodes need to be restarted.

To edit the information for all of the data centers that you are changing the base domain name for:

1. Go to the Site Admin section of the Admin Settings page.
2. In the Data Centers section, click the Edit button.
3. Make any necessary updates.

**NOTE:** This must include the service port if it is different from the default—80 for HTTP and 443 for HTTPS.

4. In the Enterprise Resources sub-section of the Providers section, edit each compute node that has a changed domain name.

**NOTE:** These URLs should include the protocol, hostname and port.

## Authenticating with LDAP

Anaconda Enterprise Notebooks performs local authentication against accounts in the AEN database by default.

To configure AEN to authenticate against accounts in an LDAP (Lightweight Directory Access Protocol) server, follow the instructions below.

## Installing OpenLDAP libraries

The system needs OpenLDAP libraries to be installed and accessible by AEN. AEN uses the OpenLDAP libraries to establish an LDAP connection to your LDAP servers.

To install OpenLDAP on CentOS or Redhat:

```
sudo yum install openldap
```

To install OpenLDAP on Ubuntu or Debian, follow the official [OpenLDAP installation instructions](#).

## Configuring OpenLDAP

1. Open the `/opt/wakari/wakari-server/etc/wakari/wk-server-config.json` file.
2. Add the following LDAP settings:

```
{
  "accounts": "wk_server.plugins.accounts.ldap2",
  "LDAP" : {
    "URI": "ldap://openldap.EXAMPLE.COM",
    "BIND_DN": "cn=Bob Jones,ou=Users,DC=EXAMPLE,DC=COM",
    "BIND_AUTH": "secretpass",
    "USER_SEARCH": { "base": "DC=EXAMPLE,DC=COM",
                     "filter": "(| (& (ou=Payroll)
                                   (uid=%(username)s))
                               (& (ou=Facilities)
                                   (uid=%(username)s)))"
                   },
    "KEY_MAP": { "email": "mail",
                 "name": "cn"
               }
  }
}
```

- **URI**—The IP address or hostname of your OpenLDAP server. For SSL/TLS, use the `ldaps://` prefix and specify a `TLS_CACERT` as described in the SSL/TLS configuration section below.
- **BIND\_DN**—The full directory path of the user you want AEN server to bind as.
- **BIND\_AUTH**—The password of the **BIND\_DN** user.
- **USER\_SEARCH**:
  - **base**—The level at which you want to start the search.
  - **filter**—The default is to search for the `sAMAccountName` attribute, and use its value for the AEN server username field.
- **KEY\_MAP**—Maps user attributes in AEN server to LDAP user attributes.

EXAMPLE: The `mail` attribute in LDAP maps to the `email` attribute in AEN server.

3. Restart AEN server to load new settings.
4. Log in with the admin account. This creates the admin user in the local database.
5. As soon as LDAP is installed, LDAP authentication takes over, so you need to add your admin account again:

```
/opt/wakari/wakari-server/bin/wk-server-admin superuser --add "jsmith"
```

## Configuring Active Directory

Microsoft Active Directory is a server program that provides directory services and uses the open industry standard Lightweight Directory Access Protocol (LDAP).

To enable Active Directory support:

1. Open the `/opt/wakari/wakari-server/etc/wakari/wk-server-config.json` file.
2. Add the following LDAP settings:

```
{
  "accounts": "wk_server.plugins.accounts.ldap2",
  "LDAP" : {
    "URI": "ldap://<ad.EXAMPLE.COM>",
    "BIND_DN": "CN=Bind User,CN=Users,DC=EXAMPLE,DC=COM",
    "BIND_AUTH": "secretpass",
    "USER_SEARCH": { "base": "CN=Users,DC=EXAMPLE,DC=COM",
                     "filter": "sAMAccountName=%(username)s"
                   },
    "KEY_MAP": { "email": "mail",
                 "name": "cn"
               }
  }
}
```

- **URI**—The IP address or hostname of your Active Directory server. Replace `<ad.EXAMPLE.COM>` with the actual URI. For SSL/TLS, use the `ldaps://` prefix and specify a `TLS_CACERT` as described in the SSL/TLS configuration section below.
- **BIND\_DN**—The full directory path of the user you want AEN server to bind as.
- **BIND\_AUTH**—The password of the **BIND\_DN** user.
- **USER\_SEARCH**:
  - **base**—the level at which you want to start the search.
  - **filter**—default is to search for the `sAMAccountName` attribute, and use its value for the AEN server `username` field.
- **KEY\_MAP**—Maps user attributes in AEN server to LDAP user attributes.

EXAMPLE: The `mail` attribute in LDAP maps to the `email` attribute in AEN server.

3. Restart AEN server to load new settings.
4. Log in with the admin account. This creates the admin user in the local database.
5. As soon as LDAP is installed, LDAP authentication takes over, so you need to add your admin account again:

```
/opt/wakari/wakari-server/bin/wk-server-admin superuser --add "jsmith"
```

## Configuring SSL/TLS

AEN uses system-wide LDAP settings, including SSL/TLS support.

- On Redhat/CentOS systems, these settings are located in the `/etc/openldap/ldap.conf` file.
- On Ubuntu/Debian systems, these settings are located in the `/etc/ldap/ldap.conf` file.

Typically, the only configuration necessary is updating the file to read:

```
TLS_CACERT /path/to/CA.cert
```

**NOTE:** `CA.cert` is the Certificate Authority used to sign the LDAP server's SSL certificate. In the case of a self-signed SSL certificate, this is the path to the SSL certificate itself.

### Testing LDAP configuration

Test your LDAP configuration using `flask-ldap-login-check`:

```
/opt/wakari/wakari-server/bin/flask-ldap-login-check \
wk_server.wsgi:app \
-u [username] \
-p [password]
```

**NOTE:** `username` is the username of a valid user and `password` is that user's `BIND_AUTH` password.

### Configuring sudo customizations

If your organization's IT security policy does not allow root access or has restrictions on the use of `sudo`, after AEN installation, you may customize AEN to meet their requirements.

Your organization may choose to implement any or all of the following:

- *Remove root access* for AEN service account (Note: this restricts AEN from managing user accounts).
- *Configurable sudo command*.
- *Restrict sudo access to all processes*.

These customizations must be done in a terminal window after copying the files to the server node.

### Removing all root access from the service account

Because root access is required for `useradd`, the following process restricts AEN from managing user accounts.

1. Modify the `/etc/sudoers.d/wakari_sudo` file to read:

```
Defaults:wakari !requiretty, visiblepw
Runas_Alias    OP = ALL,!root
wakari ALL=(OP) NOPASSWD: ALL
```

**NOTE:** If you used a service account name other than `wakari`, enter that name instead of `wakari`.

2. Modify the `/opt/wakari/wakari-compute/etc/wakari/config.json` file to read:

```
"MANAGE_ACCOUNTS": false,
```

Using this option means that your IT department must create and manage all user accounts at the OS level.

After an OS-level account exists, you may create on the main AEN web page an AEN account using the same name. The password you choose is not linked in any way to the OS-level password for the account.

Alternatively, you can configure the system to *use LDAP for authenticating users*.

## Allowing public users to have access to your AEN projects

A public account is visible to anyone who can access the AEN server. The name of this account can be configured to any name you wish. For example, `public` or `anonymous`. To disable this feature use the special value `disabled`.

1. In the `/opt/wakari/wakari-compute/etc/wakari/wk-compute-launcher-config.json` file, modify the `ANON_USER` line to read:

```
"ANON_USER": "public"
```

2. Restart AEN compute node:

```
sudo service wakari-compute restart
```

3. In the `/opt/wakari/wakari-server/etc/wakari/wk-server-config.json` file, modify the `ANON_USER` line to read:

```
"ANON_USER": "public"
```

4. Restart AEN server:

```
sudo service wakari-server restart
```

For more information about configuration keys, see [Using configuration files](#).

## Using a sudo alternative

You can use a sudo alternative as long as it supports the same execution semantics as the original sudo. The alternative must be configured to give the service account permission to run commands on behalf of AEN users.

1. In your terminal window, open the `/opt/wakari/wakari-compute/etc/wakari/config.json` file.
2. Modify the `AEN_SUDO_CMD` line to read:

```
"AEN_SUDO_CMD": "/path/to/alternative/sudo",
```

NOTE: If the alternate sudo command is available on `PATH`, then the full path is not required.

## Restricting sudo access to a single gatekeeper

By default, sudoers is configured to allow AEN to run any command as a particular user which allows the platform to initiate processes as the logged-in end user. If more restrictive control is required, it should be implemented using a suitable sudoers policy. If that is not possible or practical, it is also possible to route all AEN ID-changing operations through a single gatekeeper.

This gatekeeper wraps the desired executable and provides an alternate way to log, monitor, or control which processes can be initiated by AEN on behalf of a user.

CAUTION: Gatekeeper is a special case configuration and should only be used if required.

To configure an AEN gatekeeper:

1. Modify the `/etc/sudoers.d/wakari_sudo` file to contain:

```
Defaults:wakari !requiretty, visiblepw
Runas_Alias    OP = ALL,!root
wakari ALL=(OP) NOPASSWD: /path/to/gatekeeper
```

2. In the `/opt/wakari/wakari-compute/etc/wakari/config.json` file, modify the `AEN_SUDO_SH` line to read:

```
"AEN_SUDO_SH": "/path/to/gatekeeper"
```

EXAMPLE: The gatekeeper can be as simple as a script with contents such as:

```
#!/bin/bash
first_cmd=$1
if [ 'bash' == $1 ]; then
    shift
    export HOME=~
    export SHELL=/bin/bash
    export PATH=$PATH:/opt/wakari/anaconda/bin
    bash "$@"
else
    exec $@
fi
```

## Configuring SSL

The server node uses NGINX to proxy all incoming http(s) requests to the server running on a local port, and uses NGINX for SSL termination. The default setup uses http—non-SSL—since cert files are required to configure SSL and each enterprise will have their own cert files.

The `www.enterprise.conf` file is the default `nginx.conf` file used for AEN. It is copied to the `/etc/nginx/conf.d` directory during server installation.

NOTE: This section describes setting up SSL after your gateway node has been installed and registered with the server node.

## Copying the required files

To configure SSL on AEN, you will need the following files:

- Server certificate and key
- Server CA bundle
- Gateway certificate and key
- Gateway CA bundle

Configure SSL on AEN:

1. Copy the Gateway certificate and key to `/opt/wakari/wakari-gateway/etc/` on the Gateway as `gateway.crt` and `gateway.key`.
2. Copy the Gateway CA bundle to `/opt/wakari/wakari-server/etc/` on the Server.
3. Copy the Server certificate and key to `/etc/nginx` on the Server as `server.crt` and `server.key`.
4. Copy the Server CA bundle to `/opt/wakari/wakari-gateway/etc/` on the Gateway.

If you have a certificate that was signed by a private root CA and/or an intermediate authority:



- The Gateway CA bundle must contain the full chain: root CA, any intermediate authority and the certificate.

```
cat gateway.crt intermediate.crt root.crt >> gateway-crt-int-root.crt
```

- The Server CA bundle must be separated into individual files for the root CA, any intermediate and the certificate.

## Configuring SSL on the server node

The `www.enterprise.https.conf` is an NGINX configuration file for SSL. It is set up to use the `server.crt` and `server.key` cert files.

**CAUTION:** You must change these values to point to the signed cert files for your domain.

**NOTE:** Self-signed certs or those signed by a private root CA require additional configuration.

Perform the following steps as root:

1. Stop NGINX:

```
service nginx stop
```

2. Move the `/etc/nginx/conf.d/www.enterprise.conf` file to a backup directory.
3. Copy the `/opt/wakari/wakari-server/etc/nginx/conf.d/www.enterprise.https.conf` file to `/etc/nginx/conf.d`.  
**NOTE:** `/etc/nginx/conf.d` may have `www.enterprise.conf` or `www.enterprise.https.conf` but it may not have both.
4. Edit the `/etc/nginx/conf.d/www.enterprise.https.conf` file and change the `server.crt` and `server.key` values to the names of the real cert and key files if they are different.
5. Restart NGINX by running:

```
service nginx start
```

6. Update the `WAKARI_SERVER` and `CDN` settings to use `https` instead of `http` in the following configuration files:

```
/opt/wakari/wakari-server/etc/wakari/config.json
/opt/wakari/wakari-gateway/etc/wakari/wk-gateway-config.json
/opt/wakari/wakari-compute/etc/wakari/config.json
```

7. Copy the gateway certificate, `gateway.crt` to `/opt/wakari/wakari-server/etc/`.
8. In an editor, open `/opt/wakari/wakari-server/etc/wakari/wk-server-config.json` and add:

```
"verify_gateway_certificate": "/opt/wakari/wakari-server/etc/gateway.crt"
```

9. Restart AEN services on the server by running:

```
service wakari-server restart
```

**NOTE:** This step may return an error since the gateway has not yet been configured for SSL.

10. In AEN, verify that the browser uses `https`. On the Admin Settings page, under Data Centers, click Gateway, then select `https`:

# Admin Settings

Anaconda Enterprise Notebooks settings accessible only by the administrator

The screenshot shows two side-by-side panels from the Anaconda Enterprise Admin Settings interface.

- Staff Panel:** Contains three links: "Daily Report", "Password Reset", and "Notification".
- Data Centers / Register a datacenter Panel:**
  - Has a "Name" field with the value "Gateway 1".
  - Has two checkboxes: "Subdomain Routing" (unchecked) and "Https" (checked).

## Configuring SSL on the gateway

1. For all types of SSL certificates, in `/opt/wakari/wakari-gateway/etc/wakari/wk-gateway-config.json`, add:

```
{
  EXISTING_CONFIGURATION,
  "https": {
    "key": "/opt/wakari/wakari-gateway/etc/gateway.key",
    "cert": "/opt/wakari/wakari-gateway/etc/gateway.crt"
  }
}
```

2. For a server certificate signed by a private root CA or signed by an intermediate authority, add:

```
{
  EXISTING_CONFIGURATION,
  "https": {
    "key": "/opt/wakari/wakari-gateway/etc/gateway.key",
    "cert": "/opt/wakari/wakari-gateway/etc/gateway.crt",
    "ca": ["/opt/wakari/wakari-gateway/etc/server.crt"]
  }
}
```

**NOTE:** When the certificate chain has more than one intermediate cert signed by a higher root CA authority, you must manually break up the certs in the chain into individual files, and enumerate them in the `ca` key:

```
{
  EXISTING_CONFIGURATION,
  "https": {
```

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```

    "key": "/opt/wakari/wakari-gateway/etc/gateway.key",
    "cert": "/opt/wakari/wakari-gateway/etc/gateway.crt",
    "ca": ["/opt/wakari/wakari-gateway/etc/server1.crt",
           "/opt/wakari/wakari-gateway/etc/server2.crt",
           "/opt/wakari/wakari-gateway/etc/server3.crt"]
  }
}

```

3. For a gateway certificate that is encrypted using a passphrase, add:

```

{
  EXISTING_CONFIGURATION,
  "https": {
    "key": "/opt/wakari/wakari-gateway/etc/gateway.key",
    "cert": "/opt/wakari/wakari-gateway/etc/gateway.crt",
    "passphrase": "mysecretpassphrase"
  }
}

```

NOTE: Alternatively, the passphrase can be passed using an environment variable or entered when the wakari-gateway service is manually started.

#### EXAMPLES:

```

# using an environment variable
AEN_GATEWAY_SSL_PASSPHRASE='mysecretpassphrase' wk-gateway

```

```

# starting wakari-gateway manually
sudo service wakari-gateway start --ask-for-passphrase
Passphrase?

```

4. Restart the gateway:

```

sudo service wakari-gateway restart

```

## Configuring SSL on compute nodes

Anaconda Enterprise does not support direct SSL on Compute Nodes. If you need SSL on Compute Nodes, you must install each Compute Node on the same server as a Gateway using `http://localhost:5002` for the URL value while adding it as a resource, and you must use a Gateway for each and every Compute Node.

## Security reminder

The permissions on the cert files must be set correctly to prevent them from being read by others. Since NGINX is run by the root user, only the root user needs read access to the cert files.

EXAMPLE: If the cert files are called `server.crt` and `server.key`, then use the root account to set permissions:

```

chmod 600 server.key
chmod 600 server.crt

```

## Enabling or disabling the Strict-Transport-Security header

By default, Strict-Transport-Security (STS) is enabled in the `www.enterprise.https.conf` file:

```
add_header Strict-Transport-Security max-age=31536000;
```

It can remain enabled if either of the following is true:

- The gateway is running on a different host than the server.
- or
- SSL has been enabled for the gateway.

You must comment out this line if both of the following are true:

- The gateway is running on the same host as the server.
- and
- SSL has not been enabled for the gateway.

Leaving STS enabled when these conditions are true will cause a mismatch in protocols between the server and gateway, causing your apps to fail to launch correctly.

## Configuring single sign-on

AEN's single sign-on (SSO) capability creates a new authentication provider that defers to your Anaconda Repository for login and authentication cookies.

To enable SSO:

1. Deploy AEN and Repository on the same machine.
2. In the `/opt/wakari/wakari-server/etc/wakari/config.json` file, add:

```
{
  EXISTING_CONFIGURATION,
  "SECRET_KEY": "<repo signing secret>",
  "REPO_LOGIN_URL":
    "http://example_repo.com:8080/account/login?next=http://example_repo.com/"
}
```

3. Copy the `SECRET_KEY` from the Repository configuration file.
4. In the `/opt/wakari/wakari-server/etc/wakari/wk-server-config.json` file, modify:

```
{
  EXISTING_CONFIGURATION,
  "accounts": "wk_server.plugins.accounts.repo",
}
```

5. If you are using Repository version 2.33.3 through 2.33.10, set `USE_SERVER_BASED_SESSIONS: false` in the Repository configuration.

This setting affects the network security properties of AEN and Repository. Specifically, if `USE_SERVER_BASED_SESSIONS` is set to false, and if a new cross-site scripting (XSS) vulnerability is discovered, it could expose an additional server fixation vulnerability. Please discuss this with your Anaconda representative and be sure the feature is compatible with your network requirements before setting `USE_SERVER_BASED_SESSIONS: false`.

6. To activate the changes restart `wakari-server`:

```
sudo service wakari-server restart
```

SSO is enabled.

## Adding a third-party extension

Anaconda officially supports and tests functionality of the default environment(s) only for those extensions that ship with AEN.

It is possible to add third-party and custom extensions from `conda-forge` or `pip`, but doing so may cause instability in your default project environments or kernels.

**CAUTION:** Anaconda does not officially support third-party extensions. This section is informational only.

## Installing unofficial Jupyter Notebook extensions for AEN

**TIP:** Always back up and verify your complete system before installing extensions.

The `jupyter-contrib-nbextensions` extensions are installed on a compute node.

The default conda executable directory for AEN is `/opt/wakari/anaconda/bin/conda`. If you are installing a Jupyter extension, it must be installed in the `wakari-compute` directory.

EXAMPLE: Run:

```
/opt/wakari/anaconda/bin/conda install -p /opt/wakari/wakari-compute/ -c conda-forge_
↪ jupyter_contrib_nbextension
```

For more information, see [Unofficial Jupyter Notebook Extensions](#).

## Configure search indexing

For search indexing to work correctly, verify that the AEN Compute node can communicate with the AEN Server.

```
curl -m 5 $AEN_SERVER > /dev/null
```

There must be at least one `inotify` watch available for the number of subdirectories within the project root filesystem. Some Linux distributions default to a low number of watches, which can prevent the search indexer from monitoring project directories for changes.

```
cat /proc/sys/fs/inotify/max_user_watches
```

If necessary, increase the number of max user watches with the following command:

```
echo fs.inotify.max_user_watches=100000 | sudo tee -a /etc/sysctl.conf && sudo sysctl_
↪ -p
```

There must be at least one `inotify` user instance available per project.

```
cat /proc/sys/fs/inotify/max_user_instances
```

If necessary, this can be increased with the following command:

```
echo fs.inotify.max_user_instances=1000 | sudo tee -a /etc/sysctl.conf && sudo sysctl_
↪-p
```

### Create custom Jupyter kernel for Pyspark

These instructions add a custom Jupyter Notebook option to allow users to select PySpark as the kernel.

### Install Spark

The easiest way to install Spark is with [Cloudera CDH](#).

You will use YARN as a resource manager. After installing Cloudera CDH, [install Spark](#). Spark comes with a PySpark shell.

### Create a notebook kernel for PySpark

You may create the kernel as an administrator or as a regular user. Read the instructions below to help you choose which method to use.

#### 1. As an administrator

Create a new kernel and point it to the root env in each project. To do so create a directory 'pyspark' in */opt/wakari/wakari-compute/share/jupyter/kernels/*.

Create the following kernel.json file:

```
{ "argv": [ "/opt/wakari/anaconda/bin/python",
  "-m", "ipykernel", "-f", "connection_file", "--profile", "pyspark"],
  "display_name": "PySpark", "language": "python" }
```

You may choose any name for the 'display\_name'.

This configuration is pointing to the python executable in the root environment. Since that environment is under admin control, users cannot add new packages to the environment. They will need an admin to help update the environment.

#### 2. As an administrator without IPython profile

To have an admin level PySpark kernel without the user .ipython space:

```
{ "argv":
  [ "/opt/wakari/wakari-compute/etc/ipython/pyspark.sh", "-f", "{connection_file}" ],
  "display_name": "PySpark", "language": "python" }
```

NOTE: The pyspark.sh script is defined in *Without IPython profile* section below.

#### 3. As a regular user

Create a new directory in the user's home directory: *.local/share/jupyter/kernels/pyspark/*. This way the user will be using the default environment and able to upgrade or install new packages.

Create the following kernel.json file:

```
{ "argv": [ "/projects/<username>/<project_name>/envs/default/bin/python",
  "-m", "ipykernel", "-f", "connection_file", "--profile", "pyspark"],
  "display_name": "PySpark", "language": "python" }
```

NOTE: Replace “<username>” with the correct user name and “<project\_name>” with the correct project name.

You may choose any name for the ‘display\_name’.

## Create an IPython profile

The above profile call from the kernel requires that we define a particular PySpark profile. This profile should be created for each user that logs in to AEN to use the PySpark kernel.

In the user’s home, create the directory and file ~/.ipython/profile\_pyspark/startup/00-pyspark-setup.py with the file contents:

```
import os
import sys

# The place where CDH installed spark, if the user installed Spark locally it can be
↪ changed here.
# Optionally we can check if the variable can be retrieved from environment.

os.environ["SPARK_HOME"] = "/usr/lib/spark"

os.environ["PYSPARK_PYTHON"] = "/opt/wakari/anaconda/bin/python"

# And Python path
os.environ["PYLIB"] = os.environ["SPARK_HOME"] + "/python/lib"
sys.path.insert(0, os.environ["PYLIB"] + "/py4j-0.9-src.zip") #10.4-src.zip")
sys.path.insert(0, os.environ["PYLIB"] + "/pyspark.zip")

os.environ["PYSPARK_SUBMIT_ARGS"] = "--name yarn pyspark-shell"
```

Now log in using the user account that has the PySpark profile.

## Without IPython profile

If it is necessary to avoid creating a local profile for the users, a script can be made to be called from the kernel. Create a bash script that will load the environment variables:

```
sudo -u $AEN_SRVC_ACCT mkdir /opt/wakari/wakari-compute/etc/ipython
sudo -u $AEN_SRVC_ACCT touch /opt/wakari/wakari-compute/etc/ipython/pyspark.sh
sudo -u $AEN_SRVC_ACCT chmod a+x /opt/wakari/wakari-compute/etc/ipython/pyspark.sh
```

The contents of the file should look like:

```
#!/usr/bin/env bash
# setup environment variable, etc.

export PYSPARK_PYTHON="/opt/wakari/anaconda/bin/python"
export SPARK_HOME="/usr/lib/spark"
```

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```
# And Python path
export PYLIB=$SPARK_HOME:/python/lib
export PYTHONPATH=$PYTHONPATH:$PYLIB:/py4j-0.9-src.zip
export PYTHONPATH=$PYTHONPATH:$PYLIB:/pyspark.zip

export PYSARK_SUBMIT_ARGS="--name yarn pyspark-shell"

# run the ipykernel
exec /opt/wakari/anaconda/bin/python -m ipykernel $@
```

## Using PySpark

When creating a new notebook in a project, now there will be the option to select PySpark as the kernel. When creating such a notebook you'll be able to import pyspark and start using it:

```
from pyspark import SparkConf
from pyspark import SparkContext
```

NOTE: You can always add those lines and any other command you may use frequently in the PySpark setup file 00-pyspark-setup.py as shown above.

## Enabling server-side session management

By default, AEN uses client-side session management which is vulnerable to session replay attacks if an attacker manages to steal a valid session ID of a user.

To enable server-side session management:

1. Modify the /opt/wakari/wakari-server/etc/wakari/wk-server-config.json file:

```
"USE_SERVER_BASED_SESSIONS": true,
```

2. Restart the AEN server service:

```
sudo service wakari-server restart
```

## Terminate terminal sessions on logout

By default, when a user logs out, their open terminal sessions will remain active.

To disable this behavior:

1. Modify the /opt/wakari/wakari-server/etc/wakari/wk-server-config.json file:

```
"TERMINATE_TERMINALS_ON_LOGOUT": true,
```

2. Modify the /opt/wakari/wakari-gateway/etc/wakari/wk-gateway-config.json file:

```
"TERMINATE_TERMINALS_ON_LOGOUT": true,
```

3. Restart the AEN server service:



```
sudo service wakari-server restart
```

4. Restart the AEN gateway service:

```
sudo service wakari-gateway restart
```

## Upgrading AEN

- *Before you upgrade*
- *Upgrading the AEN server node*
- *Upgrading the AEN gateway node*
- *Upgrading AEN compute nodes*
- *After upgrading*

**CAUTION:** These instructions are for upgrading AEN to the current version 4.3.2 from 4.3.1 **ONLY**. Each version must be upgraded iteratively from the previous version. Do not skip versions.

Upgrade instructions for previous versions:

- *AEN 4.3.1 upgrade instructions*
- *AEN 4.3.0 upgrade instructions*
- *AEN 4.2.2 upgrade instructions*
- *AEN 4.2.1 upgrade instructions*
- *AEN 4.2.0 upgrade instructions*
- *AEN 4.1.3 upgrade instructions*
- *AEN 4.1.2 upgrade instructions*
- *AEN 4.1.1 upgrade instructions.*
- *AEN 4.1.0 upgrade instructions.*
- *AEN 4.0.0 upgrade instructions.*

For upgrades from versions before those listed above, please contact your enterprise support representative.

**NOTE:** Named Service Account functionality is available with AEN 4.0.0+ for new installations only. It is not available for upgraded installations. Contact your enterprise support representative for more information.

An AEN platform update requires that each instance of the 3 node types be upgraded individually:

- AEN Server
- AEN Gateway
- AEN Compute

The upgrade process requires that all AEN service instances be stopped, upgraded, and then restarted.

**NOTE:** Any commands that call for the root user can also be done using `sudo`.

If you encounter any difficulty during the upgrade process, see [Troubleshooting](#) which provides guidance on:

- processes

- configuration files
- log files
- ports

If you are unable to resolve an installation or upgrade problem, please contact your enterprise support representative.

### Before you upgrade

**CAUTION:** Make a tested backup of your installation before starting the upgrade. Upgrading to a higher version of AEN is not reversible. Any errors during the upgrade procedure may result in partial or complete data loss and require restoring data from backups.

**CAUTION:** Terminate all AEN applications and stop all projects before starting the upgrade process.

Before upgrading each service on each host:

1. Suspend the services on each of the nodes:

```
sudo service wakari-server stop
sudo service wakari-gateway stop
sudo service wakari-compute stop
```

2. Set the AEN Functional ID (“NFI”) and AEN Functional Group (“NFG”) to the NFI and NFG of the current installation:

```
export AEN_SRVC_ACCT="wakari"
export AEN_SRVC_GRP="wakari"
```

**NOTE:** The default NFI is wakari, but aen\_admin or any other name may be used instead.

For more information on NFI and NFG, see the [installation instructions](#).

3. Install wget:

```
yum install wget
```

### Upgrading the AEN server node

**NOTE:** If you are using LDAP-based authentication, back up the /opt/wakari/wakari-server/etc/wakari/wk-server-config.json configuration file. After the server has been upgraded, copy that file back into the same location as before the upgrade.

Complete the following steps on the server host:

1. Stop the Elasticsearch service:

```
sudo service elasticsearch stop
```

2. Remove any previous index:

```
sudo rm -rf /var/lib/elasticsearch/*
```

**NOTE:** You can choose to keep the old index, but if you detect any issues with the search capabilities after the upgrade, you will need to run the following to start with a clean index:

```
sudo service wakari-server stop
sudo service elasticsearch stop
sudo rm -rf /var/lib/elasticsearch/*
sudo service elasticsearch start
sudo service wakari-server start
```

### 3. Upgrade the server:

```
pushd /tmp
wget http://j.mp/aen-server-update-4.3.2

sudo -E -u $AEN_SRVC_ACCT /opt/wakari/miniconda/bin/conda install \
    -p /opt/wakari/wakari-server \
    --file aen-server-update-4.3.2

sudo -E -u $AEN_SRVC_ACCT /opt/wakari/miniconda/bin/conda install \
    -p /opt/wakari/wakari-server \
    --no-deps \
    wakari-enterprise-server-conf-update=2.0.12

popd
```

### 4. Start Elasticsearch:

```
sudo service elasticsearch start
```

Or, if you do not want to use the search features, edit your server's `/opt/wakari/wakari-server/etc/wakari/config.json` file by adding the line `"SEARCH_ENABLED": false`.

### 5. Restart the NGINX server:

AEN server version `>= 4.1.3` uses Unix sockets for communication with NGINX. Restart NGINX to load this new configuration:

```
sudo service nginx restart
```

Alternatively, you can restart NGINX with:

```
sudo nginx -s stop
sudo nginx
```

### 6. Start the server:

```
sudo service wakari-server start
```

### 7. Check that the server is running properly:

```
sudo service wakari-server status
```

8. If you see NGINX errors, please check the configuration at `/opt/wakari/wakari-server/etc/nginx/conf.d/www.enterprise.conf:18`.
9. Connect to AEN server using your web browser with the correct protocol (http or https), hostname and port number.

## Upgrading the AEN gateway node

Complete the following steps on each gateway host:

## 1. Upgrade the gateway:

```
pushd /tmp
wget http://j.mp/aen-gateway-update-4.3.2

sudo -E -u $AEN_SRVC_ACCT /opt/wakari/miniconda/bin/conda install \
    -p /opt/wakari/wakari-gateway \
    --file aen-gateway-update-4.3.2

sudo -E -u $AEN_SRVC_ACCT /opt/wakari/miniconda/bin/conda install \
    -p /opt/wakari/wakari-gateway \
    --no-deps \
    wakari-enterprise-gateway-conf-update=2.0.12

popd
```

## 2. Start the gateway:

```
sudo service wakari-gateway start
```

## 3. Check that the gateway is running properly:

```
sudo service wakari-gateway status
```

## 4. Connect to the gateway using your web browser with the correct http/https, hostname and port number.

## Upgrading AEN compute nodes

Complete the following steps on each host where an AEN compute service is running:

## 1. Check for any wakari-indexer processes running:

```
ps aux | grep wakari-indexer
```

NOTE: If you stopped all the projects, you will not see any wakari-indexer processes running.

Terminate any remaining wakari-indexer processes:

```
sudo killall wakari-indexer
```

NOTE: The processes killed with `killall` are run by the `$AEN_SRVC_ACCT` user, so they can be killed as root with `sudo killall` or killed as the `$AEN_SRVC_ACCT` user with `sudo -u $AEN_SRVC_ACCT killall`. Example commands show the `sudo killall` option.

## 2. Check for any AEN applications processes running—Workbench, Viewer, Terminal or Notebook:

```
ps aux | grep wk-app-gateone
ps aux | grep wk-app-workbench
ps aux | grep wk-app-viewer
ps aux | grep wk-app-terminal
ps aux | grep jupyter-notebook
```

NOTE: If you stopped all the projects, you will not see any AEN app processes running.

Terminate any remaining AEN application processes by running one or more of the following:

```
sudo killall wk-app-gateone
sudo killall wk-app-workbench
```

(continues on next page)

(continued from previous page)

```
sudo killall wk-app-viewer
sudo killall wk-app-terminal
sudo killall jupyter-notebook
```

3. Verify the contents of `/opt/wakari/anaconda/.condarc`. Modify it to contain the following entries, and possibly others if you customized the `.condarc` file.

NOTE: Modify the file as the `AEN_SRVC_ACCT` user (or be sure to keep the same ownership).

```
channels:
- https://conda.anaconda.org/t/<TOKEN>/anaconda-nb-extensions
- r
- https://conda.anaconda.org/wakari
- defaults

create_default_packages:
- anaconda-client
- ipykernel
```

NOTE: Contact your enterprise support representative to get your token for the Anaconda channel referenced above. Replace `<TOKEN>` with the actual token from your enterprise support representative.

4. Upgrade *Anaconda* in the root environment:

```
pushd /tmp
wget http://j.mp/aen-anaconda-update-4_3_2

sudo -E -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda install \
    -p /opt/wakari/anaconda \
    --file aen-anaconda-update-4_3_2

popd
```

5. Upgrade each compute service:

```
pushd /tmp
wget http://j.mp/aen-compute-update-4.3.2

sudo -E -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda install \
    -p /opt/wakari/wakari-compute \
    --file aen-compute-update-4.3.2

sudo -E -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda install \
    --no-deps \
    -p /opt/wakari/wakari-compute \
    wakari-enterprise-compute-conf-update=2.0.16

popd
```

NOTE: When upgrading the `wakari-compute` environment, you may see `ImportError` warnings with some `nbextensions`. As long as the `Validating` message is OK, the `ImportError` warnings are harmless—a consequence of the post-link presence on those packages.

6. Initialize the root environment to prime the package cache:

```
sudo -E -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda create \
    -p /opt/wakari/testenv \
    --clone root
```

7. Test the offline cloning step:

```
sudo -E -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda create \  
    -p /opt/wakari/testenvoffline \  
    --clone root --offline
```

8. Remove the test environments:

```
sudo rm -rf /opt/wakari/testenv  
sudo rm -rf /opt/wakari/testenvoffline
```

9. Install necessary dependencies:

NOTE: Skip this step if you already have these dependencies installed from previous installations.

```
sudo yum groupinstall "X Window System" -y  
sudo yum install git -y
```

NOTE: If you don't want to install the whole X Window System, you must install the following packages to have R plotting support:

```
sudo yum install -y libXrender libXext libXdmcp libSM libICE libXt \  
dejavu-sans-fonts dejavu-serif-fonts dejavu-fonts-common \  
fontpackages-filesystem
```

10. Start the compute service:

```
sudo service wakari-compute start
```

11. Verify the compute service is running properly:

```
sudo service wakari-compute status
```

12. Restart the AEN Server with:

```
sudo service wakari-server restart
```

13. Repeat this upgrade procedure for all compute nodes in your Data Center.

### After upgrading

1. Restart the projects and start using AEN applications.
2. If you have a *customized default environment*, you may choose to upgrade it depending on the needs of your users.

Upgrade the customized default environment at `/opt/wakari/anaconda/envs/default` with the `$AEN_SRVC_ACCT` user:

```
pushd /tmp  
wget http://j.mp/aen-anaconda-update-4.3.2  
  
sudo -E -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda install \  
    -p /opt/wakari/anaconda/envs/default \  
    --file aen-anaconda-update-4.3.2  
popd
```

To upgrade the customized default environments for every user and every project at `/projects/<USER>/<PROJECT>/envs/default`, run these commands for **every** user as that user:

```
pushd /tmp
wget http://j.mp/aen-anaconda-update-4.3.2

sudo -E -u <USER> /opt/wakari/anaconda/bin/conda install \
    -p /projects/<USER>/<PROJECT>/envs/default \
    --file aen-anaconda-update-4.3.2

popd
```

NOTE: Replace <USER> with the user's name. Replace <PROJECT> with the project name.

NOTE: Upgrading the default environment at `/opt/wakari/anaconda/envs/default` does NOT automatically upgrade the default environment in the users pre-existing projects. For pre-existing projects, the upgrade, if requested, should be done on a per-user basis.

NOTE: These commands update packages listed in `aen-anaconda-update-4.3.2` and do not update any other package.

3. If you did not stop all your projects before upgrading, then the first time you start an application you will see an error page requesting that you restart the application.
4. Restart the application to complete the upgrade.
5. If you still see old applications or icons after restart, reload the page to reset the browser cache.

## Uninstalling AEN

Each AEN node must be uninstalled separately.

- *Uninstalling a server node*
- *Uninstalling a gateway node*
- *Uninstalling a compute node*
- *OPTIONAL: Removing projects from compute nodes*

Begin by setting the AEN Functional ID (NFI). The NFI is the username of the AEN Service Account which is used to run all AEN services and is also the username of the AEN Admin account. The NFI may be any name. The default NFI is `wakari`. The NFI is also often set to `aen_admin`. The NFI (and AEN Functional Group or NFG) are described in *the installation instructions*.

Set the NFI with this command:

```
export AEN_SRVC_ACCT="aen_admin"
```

Replace the name `aen_admin` with the NFI that was set in your installation of Anaconda Enterprise Notebooks.

## Uninstalling a server node

To remove a server node, run the following commands as root or sudo on the server node's host system:

1. Stop the server processes:

```
service wakari-server stop
```

2. Stop MongoDB:

```
service mongod stop
```

3. Remove AEN server software, AEN database files and NGINX configuration:

```
rm -Rf /opt/wakari/wakari-server
rm -Rf /opt/wakari/miniconda
rm -Rf /var/lib/mongo/wakari*
rm -Rf /etc/nginx/conf.d/www.enterprise.conf
```

NOTE: Remove `/etc/nginx/conf.d/www.enterprise.https.conf` if SSL is enabled on the Server node.

4. Restart MongoDB and NGINX:

```
service mongod restart
service nginx restart
```

5. Check for any outstanding server processes and stop them:

```
ps -ef | grep -e wakari-server -e wk-server
```

6. Remove the AEN Service Account:

```
userdel $AEN_SRVC_ACCT
```

7. Check for and remove any references to “aen” or “wakari” from the root user’s `.condarc` file:

```
grep -i aen ~/.condarc
grep -i wakari ~/.condarc
```

## Uninstalling a gateway node

To uninstall a gateway node, run the following commands as root or sudo on the gateway host system:

1. Stop the gateway processes:

```
service wakari-gateway stop
```

2. Remove gateway software:

```
rm -Rf /opt/wakari/wakari-gateway
```

3. Check for any outstanding gateway processes and stop them:

```
ps -ef | grep -e wakari-gateway -e wk-gateway
```

4. Remove the AEN Service Account:

```
userdel $AEN_SRVC_ACCT
```

5. Check for and remove any references to “aen” or “wakari” from the root user’s `.condarc` file:

```
grep -i aen ~/.condarc
grep -i wakari ~/.condarc
```



## Uninstalling a compute node

To remove a compute node, run the following commands as root or sudo on each compute node host system:

1. Stop the compute processes:

```
service wakari-compute stop
```

2. Remove the compute software:

```
rm -Rf /opt/wakari/wakari-compute
rm -Rf /opt/wakari/miniconda
rm -Rf /opt/wakari/anaconda
```

3. Check for any outstanding compute processes and stop them:

```
ps -ef | grep -e wakari-compute -e wk-compute
```

4. Remove the AEN Service Account:

```
userdel $AEN_SRVC_ACCT
```

5. Check for and remove any references to “aen” or “wakari” from the root user’s `.condarc` file:

```
grep -i aen ~/.condarc
grep -i wakari ~/.condarc
```

## OPTIONAL: Removing projects from compute nodes

**CAUTION:** This is an extreme measure and is not necessary in most instances. We recommend you create and verify a backup before doing this or any other file removal.

To remove all AEN projects from all of your compute nodes:

```
rm -Rf /projects
```

This is a step-by-step guide to installing an Anaconda Enterprise Notebooks system comprised of a front-end server, a gateway and compute machines.

If you have any questions about these instructions or you encounter any issues while installing AEN, please contact your sales representative or Priority Support team.

When you have completed the installation process, review the [optional configuration tasks](#) to see if any are appropriate for your system.

## Distributed install

In a distributed install the server and gateway run on separate hosts.

## Single-box install

In a single-box install, both the server and the gateway need separate external ports since they are independent services that are running on the same host in the single-box installation.

Both port 80 and port 8089 must be open on the firewall for a single-box install.

The compute node only receives connections from the gateway and server nodes and typically runs on port 80 or port 443.

### User management

#### Adding or removing an administrative user

An administrator can make any other user an administrator—or remove their administrator permissions—by using administrator commands in the Terminal application.

A user can also be designated as a superuser or as staff, giving them greater administrative privileges within the system.

#### Designating a user as an administrator/superuser

To designate a user as an administrator and superuser:

```
/opt/wakari/wakari-server/bin/wk-server-admin superuser --add <username>
```

NOTE: Replace <username> with the actual username.

EXAMPLE: To give administrative privileges to the user named “jsmith” and set them as a superuser, run:

```
/opt/wakari/wakari-server/bin/wk-server-admin superuser --add jsmith
```

#### Removing an administrator/superuser

To remove a user’s administrative privileges:

```
/opt/wakari/wakari-server/bin/wk-server-admin superuser --remove <username>
```

NOTE: Replace <username> with the actual username.

#### Allowing and restricting new user registration

When Open Registration is enabled, anyone who has access to the URL of your AEN server can create their own account.

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select Accounts.
3. To open user registration, select the Open Registration checkbox. To close registration, clear the checkbox.
4. Click the Update button.

**Staff**

- Daily Report
- Password Reset
- Notification
- Exceptions

**Cloud Registration**

☒ Open Registration  
Allow new user signups

Update

**Site Admin**

- General
- Accounts

## Resetting a user password

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Staff** menu, select Password Reset:

Anaconda Enterprise Notebooks settings accessible only by the system administrator.

**Staff**

- Daily Report
- Password Reset
- Notification
- Exceptions

**Password Reset**

Generate URL

3. Enter the username of the user whose password needs to be reset.
4. Click the Generate URL button.

A password reset link is generated that you can email to the user.

Alternatively you may use the command line interface:

1. Use ssh to log into the server as root.
2. Run:

```
/opt/wakari/wakari-server/bin/wk-server-admin reset-password -u SOME_USER -p SOME_
↪PASSWORD
```

NOTE: Replace SOME\_USER with the username and SOME\_PASSWORD with the password.

3. Log into AEN as the user.

### Managing permissions

This page explains the admin commands used to manage user permissions.

#### Checking file ownership

To verify that all files in the `/opt/wakari/anaconda` directory are owned by the `wakari` user or group:

```
root@server # find /opt/wakari/anaconda \! -user wakari -print
root@server # find /opt/wakari/anaconda \! -group wakari -print
```

#### Fixing file ownership settings

To fix the ownership settings of any files that are listed in the output:

```
chown -R wakari:wakari /opt/wakari/anaconda
```

#### Setting a file owner and permissions

To set a file owner and set its permissions:

```
chown wakari:wakari /opt/wakari/wakari-server/bin/wk-*
chmod 700 /opt/wakari/wakari-server/bin/wk-*
```

#### Verifying that POSIX ACLs are enabled

The `acl` option must be enabled on the file system that contains the project root directory.

NOTE: By default, the project root directory is `/projects`.

To determine the project root directory where a custom `projectRoot` is configured:

```
root@compute # grep projectRoot /opt/wakari/wakari-compute/etc/wakari/config.json
```

The `mount` options or default options listed by `tune2fs` should indicate that the `acl` option is enabled.

EXAMPLE:

```
root@compute # fs=`df /projects | tail -1 | cut -d " " -f 1`
root@compute # mount | grep $fs
/dev/vda on / type ext4 (rw)
root@compute # tune2fs -l $fs | grep options
Default mount options:    user_xattr acl
```

## Viewing a list of users

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select Users:

The screenshot shows the AEN Admin Settings page. On the left, there are two sidebars. The top sidebar, titled 'Staff', contains links for 'Daily Report', 'Password Reset', 'Notification', and 'Exceptions'. The bottom sidebar, titled 'Site Admin', contains links for 'General', 'Accounts', and 'Users' (which is highlighted in blue). To the right of these sidebars is a table titled 'Users'. The table has three columns: 'Username', 'Projects', and 'Last Seen'. There is one row of data with the username 'aen\_admin', 6 projects, and a last seen time of 'Sep 25, 2017 10:05:58 CDT'.

Users		
Username	Projects	Last Seen
aen_admin	6	Sep 25, 2017 10:05:58 CDT

The Users section lists the all users who are signed up, the number of projects they have created and the last time they logged on to AEN.

## Viewing a list of currently active users


In the AEN navigation bar, click Users.

Click a username to open the user's profile page.


## Viewing a user profile




A user's profile page includes a summary of the projects created by that user and a list of projects on which the user is a team member.

1. In the AEN navigation bar, click Users to see a list of users who are currently logged into the system.
2. On the Users page, click the username of the user whose profile page you want to view.

 ANACONDA

[Admin](#) [Users](#)

 anaconda


  

[Help](#)


# Users




List of currently active users in the system.

 anaconda
 andrew
 bokeh
 christine
 guest
 hubert
 ivan
 paula
 simon
 tanya
 wakari

 ANACONDA

[Admin](#) [Users](#)

 anaconda

[Help](#)

# Users

List of currently active users in the system.

 anaconda
 andrew
 bokeh
 christine
 guest
 hubert
 ivan
 paula
 simon
 tanya
 wakari

## Sending a system message

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Staff** menu, select Notification:

The screenshot shows the Admin Settings page. On the left, there are three main menu sections: **Staff**, **Site Admin**, and **Providers**. The **Staff** section is active, and within it, the **Notification** link is selected. The main content area is titled **Notification Settings**. It contains three radio buttons: **Off** (which is selected), **SES - Amazon Simple Email Service**, and **SMTP Email Server**. Below the radio buttons, the **SMTP Settings** section is expanded, showing four input fields: **SMTP Hostname**, **SMTP Username (optional)**, **SMTP Password (optional)**, and **SMTP From Address (optional)**. At the bottom of the SMTP Settings section is a green **Update** button.

The Notification Settings section allows you to create a system message that can be relayed to users.

By default, notifications are off.

3. To turn on email notifications, select the radio button for the type of email service to use:
  - SES to use Amazon Simple Email Service (SES).
  - SMTP Email Server.
4. If you select SMTP Email Server, complete the SMTP Settings.

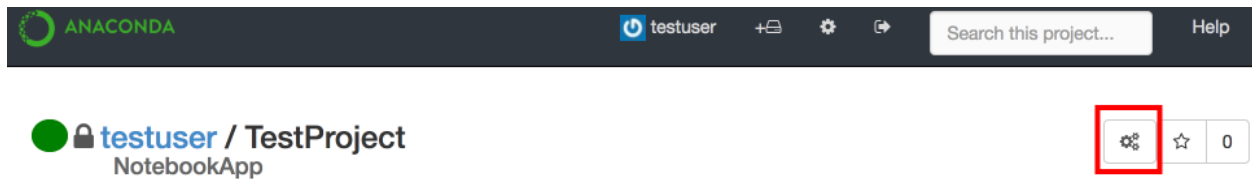
NOTE: If you get an error message after changing the SMTP settings, you may need to restart the server.



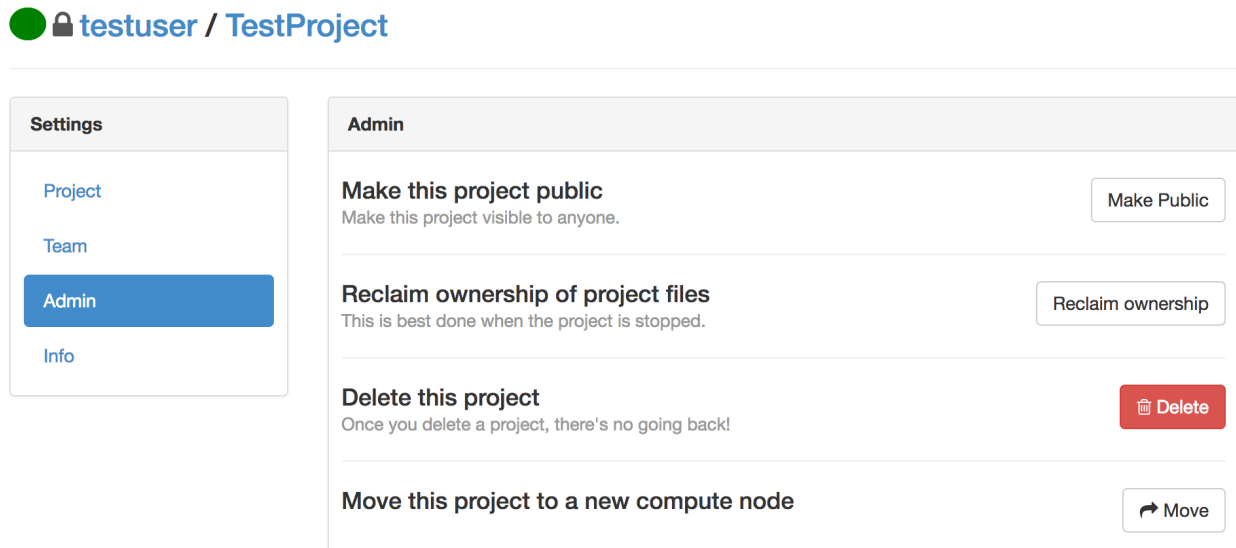
## Moving a project to another compute node

If you have multiple compute nodes available and want to move a project from one to another, the project must exist on both nodes.

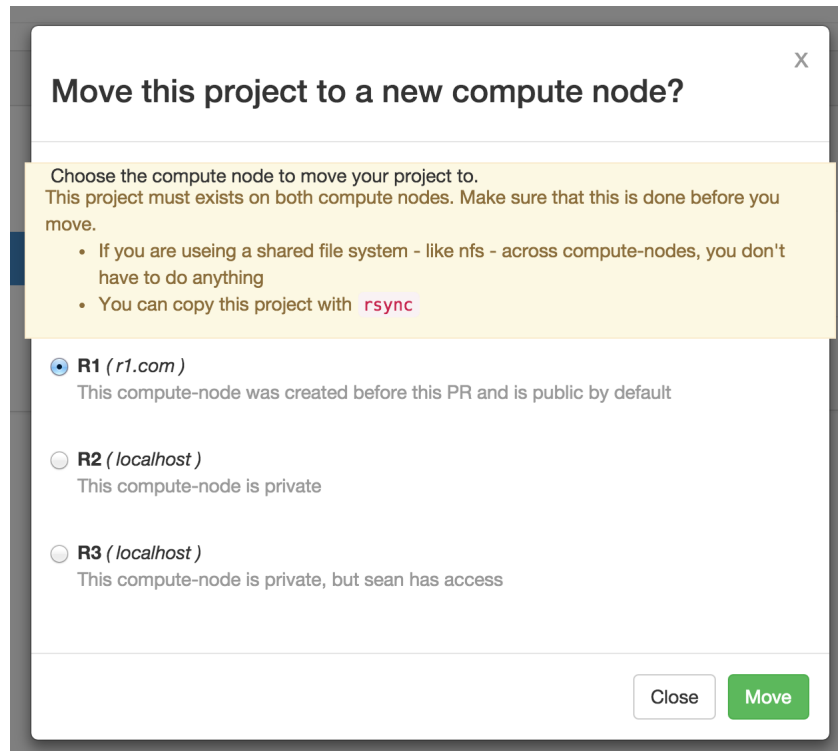
1. Verify that the project has been created on both compute nodes. You can use `rsync` for this job unless you have a shared file system like `nfs`.
2. On the project home page, click the Project Settings icon to open the Project Settings page.



3. In the **Settings** menu, select Admin.



4. Click the Move button.
5. In the move dialog box, click to choose the compute node destination, and click the Move button.



## Deleting a user

To remove a user from the AEN database:

```
/opt/wakari/wakari-server/bin/wk-server-admin remove-user <username>
```

NOTE: Replace `<username>` with the actual username.

NOTE: Changing the owner of a project requires that both the previous owner and the new owner are still AEN users. Before deleting a user, *change the owner* of that user's projects.

## Deleting a project

To remove a project from the AEN database:

```
/opt/wakari/wakari-server/bin/wk-server-admin remove-project <username> <projectname>
```


NOTE: Replace `<username>` with the actual username and `<projectname>` with the actual project name you are removing.

## System management


### Opening the Admin dashboard


If you have administrator privileges, you see two additional links in the AEN navigation bar—Admin and Users:


To open the Admin dashboard, click the Admin link.


 ANACONDA

AdminUsers

 aen\_admin







Search...

Help

# Admin Settings

Anaconda Enterprise Notebooks settings accessible only by the system administrator.

Staff

[Daily Report](#)

[Password Reset](#)

[Notification](#)

[Exceptions](#)

Site Admin

[General](#)

[Accounts](#)

[Users](#)

[Monitor](#)

[Security Log](#)

## Backing up and restoring AEN

- *Document purpose*
- *Important notes*
- *Server component steps*
  - *Backup*
    - \* *Mongo database*
    - \* *AEN Server config files (including License file)*
    - \* *Nginx config (if needed)*
    - \* *SSL certificates (if needed)*
  - *Restore*
    - \* *Reinstall AEN-Server*
    - \* *Restore Mongo database*
    - \* *AEN Server config files (including License file)*
    - \* *Nginx config (if needed)*
    - \* *SSL certificates (if needed)*
    - \* *Restart server*
- *Gateway component steps*
  - *Backup*
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    - \* *Custom .condarc file (if needed)*
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    - \* *Config files*
    - \* *Custom .condarc file (if needed)*
    - \* *SSL certificates (if needed)*
    - \* *Restart gateway*
- *Compute component steps*
  - *Backup*
    - \* *Config files*
    - \* *Custom Changes (rare)*
    - \* *Create user list*

- \* *Project files*
- \* *Full Anaconda (option 1)*
- \* *Partial Anaconda (option 2)*
- *Restore*
  - \* *Reinstall AEN-Compute*
  - \* *Config files*
  - \* *Custom changes (rare)*
  - \* *Create users*
  - \* *Project files*
  - \* *Full Anaconda (option 1)*
  - \* *Partial Anaconda (option 2)*
  - \* *Custom environments (if needed)*
  - \* *Restart compute node*

## Document purpose

This document lays out the steps to backup and restore Anaconda Enterprise Notebooks (AEN) for Disaster Recovery. It is not intended to provide High Availability. Each of the components (Server, Gateway and Compute) has its own instructions and each may be done individually as needed. The steps primarily involve creating tar files of important configuration files and data.

This document is written for a system administrator who is comfortable with basic Linux command line navigation and usage.

To migrate to a new cluster, use these backup and restore instructions to back up the system from the old cluster and restore it to the new cluster.

## Important notes

Review the [Concepts](#) page to become familiar with the different components and how they work together.

Root or sudo access is required for some commands.

**CAUTION:** All commands **MUST** be run by \$AEN\_SRVC\_ACCT (the account used to run AEN) except for those commands explicitly indicated to run as root or sudo. If the commands are not run by the correct user, the installation will not work, and a full uninstallation and reinstallation will be required!

These instructions assume that the fully qualified domain name (FQDN) has not changed for any of the component nodes. If any of the FQDNs are not the same, additional steps will be needed.

## Server component steps

### Backup

### Mongo database

This will create a single tar file called `aen_mongo_backup.tar` that includes only the database named “wakari” that is used by AEN. It also generates a log of the database backup.

NOTE: These commands must be run by `$AEN_SRVC_ACCT`.

```
mongodump -db wakari -o aen_main >> mongo_backup.log
tar -cvf aen_mongo_backup.tar aen_main
```

### AEN Server config files (including License file)

Create a tar file of all of the configuration files, including any license files.

NOTE: This command must be run by `$AEN_SRVC_ACCT`.

```
tar -cvf aen_server_config.tar -C /opt/wakari/ wakari-server/etc/wakari/
```

### Nginx config (if needed)

Make a copy of the nginx configuration file if it has been customized. The default configuration for the AEN server is a symlink.

NOTE: This command must be run by `$AEN_SRVC_ACCT`.

```
/etc/nginx/conf.d/www.enterprise.conf -> /opt/wakari/wakari-server/etc/nginx/conf.d/
↪ www.enterprise.conf
```

### SSL certificates (if needed)

Make a copy of the SSL certificates files (certfiles) for the server, including the key file, and a copy of the certfile for the gateway, which is needed for verification if using self-signed or private CA signed certs.

## Restore

### Reinstall AEN-Server

See *the instructions for installing the current version of AEN-Server*.

It is not necessary to upload the license, because it will be restored with the config files.

NOTE: The new installation will generate a new password for the local `$AEN_SRVC_ACCT` account.

### Restore Mongo database

This assumes that mongo was reinstalled as part of the reinstallation of the server component. Untar the mongo database and restore it.

NOTE: These commands must be run by `$AEN_SRVC_ACCT`.

```
tar -xvf aen_mongo_backup.tar
mongorestore --drop aen_main
```

NOTE: The `--drop` option resets the `$AEN_SRVC_ACCT` user password and restores the database to the exact state it was in at the time of backup. Please see the [MongoDB documentation](#) for more information about mongorestore options for Mongo 2.6.

NOTE: AEN uses Mongo 2.6 by default. If you are using a different version, consult the documentation for your version.

### AEN Server config files (including License file)

Untar the tar file of all of the configuration files, including any license files.

NOTE: This command must be run by `$AEN_SRVC_ACCT`.

```
tar -xvf aen_server_config.tar -C /opt/wakari/
```

Make sure the files are in `/opt/wakari/wakari-server/etc/wakari/` and are owned by the `$AEN_SRVC_ACCT`.

### Nginx config (if needed)

Make sure any modifications to the nginx configuration are either in `/etc/nginx/conf.d` or in `/opt/wakari/wakari-server/etc/nginx/conf.d/` with a proper symlink.

NOTE: This command must be run by `$AEN_SRVC_ACCT`.

```
/etc/nginx/conf.d/www.enterprise.conf -> /opt/wakari/wakari-server/etc/nginx/conf.d/
↪www.enterprise.conf
```

### SSL certificates (if needed)

Move any SSL certificate files to the locations indicated in the config files.

### Restart server

Restart the server application.

NOTE: This command must be run as root or with `sudo`.

```
service wakari-server restart
```

## Gateway component steps

### Backup

### Config files

Create a tar file of all of the configuration files.

NOTE: This command must be run by \$AEN\_SRVC\_ACCT.

```
tar -cvf aen_gateway_config.tar -C /opt/wakari/ wakari-gateway/etc/wakari/
```

### Custom .condarc file (if needed)

Make a copy of any /opt/wakari/miniconda/.condarc if it has been modified.

### SSL certificates (if needed)

Make a copy of SSL certificate files for the gateway (including the key file) and the certfile for the server (needed for verification if using self-signed or private CA signed certs).

### Restore

### Reinstall AEN-Gateway

### Setting variables and changing permissions

NOTE: These commands must be run by \$AEN\_SRVC\_ACCT.

Run:

```
export AEN_SERVER=<FQDN HOSTNAME OR IP ADDRESS> # Use the real FQDN
export AEN_GATEWAY_PORT=8089
export AEN_GATEWAY=<FQDN HOSTNAME OR IP ADDRESS> # will be needed shortly
chmod a+x aen-*.sh # Set installer to be executable
```

NOTE: Change <FQDN HOSTNAME OR IP ADDRESS> to the actual fully qualified domain hostname or IP address.

NOTE: You must perform the entire procedure before closing the terminal to ensure the variable export persists. If the terminal is closed before successful installation, export the variables to continue with the installation.

### Running the AEN gateway installer

Run:

```
sudo -E ./aen-gateway-4.3.2-Linux-x86_64.sh -w $AEN_SERVER
<license text>
...
...

PREFIX=/opt/wakari/wakari-gateway
Logging to /tmp/wakari_gateway.log
...
...
Checking server name
Please restart the Gateway after running the following command
to connect this Gateway to the AEN Server
...
```



## Config files

Untar the configuration files.

NOTE: This command must be run by \$AEN\_SRVC\_ACCT.

```
tar -xvf aen_gateway_config.tar -C /opt/wakari
```

Verify that the files are in `/opt/wakari/wakari-gateway/etc/wakari/` and are owned by the \$AEN\_SRVC\_ACCT.

## Custom .condarc file (if needed)

Move the custom .condarc file to `/opt/wakari/miniconda/.condarc`.

## SSL certificates (if needed)

Move any SSL certificate files to the locations indicated in the config files.

## Restart gateway

Restart the gateway application.

NOTE: This command must be run as root or with sudo.

```
service wakari-gateway restart
```

## Compute component steps

### Backup

### Config files

Create a tar file of all of the configuration files.

NOTE: This command must be run by \$AEN\_SRVC\_ACCT.

```
tar -cvf aen_compute_config.tar -C /opt/wakari/ wakari-compute/etc/wakari
```

## Custom Changes (rare)

Manually backup any custom changes that were applied to the code. One change might be additional files in the skeleton folder:

```
/opt/wakari/wakari-compute/lib/node_modules/wakari-compute-launcher/skeleton
```

### Create user list

AEN uses POSIX access control lists (ACLs) for project sharing, so the backup must preserve the ACL information. This is done with a script that creates a file named `users.lst` containing a list of all users that have access to projects on a given compute node. Download and run the script.

NOTE: These commands must be run by `$AEN_SRVC_ACCT`.

```
wget https://s3.amazonaws.com/continuum-airgap/misc/wk-compute-get-acl-users.py
chmod 755 wk-compute-get-acl-users.py
./wk-compute-get-acl-users.py
```

### Project files

Create a tar of the projects directory with ACLs enabled. The default projects base location is `/projects`.

NOTE: This command must be run as root or with `sudo`.

```
tar --acls -cpvf projects.tar -C <projects base location>/*
```

### Full Anaconda (option 1)

If any changes have been made to the default Anaconda installation (additional packages installed or packages removed), it is necessary to backup the entire Anaconda installation.

NOTE: This command must be run by `$AEN_SRVC_ACCT`.

```
tar -cvf aen_anaconda.tar -C /opt/wakari/anaconda/*
```

If no changes have been made to the default installation of Anaconda, you may just backup the `.condarc` file and any custom environments.

### Partial Anaconda (option 2)

#### Custom `.condarc` file

Make a copy of `/opt/wakari/anaconda/.condarc`.

#### Custom environments (if needed)

Create a tar file of any custom shared environments.

NOTE: This command must be run by `$AEN_SRVC_ACCT`.

```
tar -cvf aen_compute_envs.tar -C /opt/wakari/ anaconda/envs
```

NOTE: If no custom shared environments have been created, the `envs` folder will not be present.

## Restore

### Reinstall AEN-Compute

#### Setting variables and changing permissions

NOTE: These commands must be run by \$AEN\_SRVC\_ACCT.

Run:

```
export AEN_SERVER=<FQDN HOSTNAME OR IP ADDRESS> # Use the real FQDN
chmod a+x aen-*.sh # Set installer to be executable
```

NOTE: Change <FQDN HOSTNAME OR IP ADDRESS> to the actual fully qualified domain hostname or IP address.

NOTE: You must perform the entire procedure before closing the terminal to ensure the variable export persists.

#### Running the AEN compute installer

Run:

```
sudo -E ./aen-compute-4.3.2-Linux-x86_64.sh -w $AEN_SERVER
...
...
PREFIX=/opt/wakari/wakari-compute
Logging to /tmp/wakari_compute.log
Checking server name
...
...
Initial clone of root environment...
Starting Wakari daemons...
installation finished.
Do you wish the installer to prepend the wakari-compute install location
to PATH in your /root/.bashrc ? [yes|no]
[no] >>> yes
```

#### Config files

Untar the config files.

NOTE: This command must be run by \$AEN\_SRVC\_ACCT.

```
tar -xvf aen_compute_config.tar -C /opt/wakari
```

NOTE: Verify that they are located in /opt/wakari/wakari-compute/etc/wakari and are owned by the \$AEN\_SRVC\_ACCT.

#### Custom changes (rare)

Manually restore any custom changes you saved in the backup section. If there are changes in the skeleton directory, these files must be world readable or projects will refuse to start.

### Create users

NOTE: Only create users with these instructions if your Linux machine is not bound to LDAP.

In order for the ACLs to be set properly on restore, all users that have permissions to the files must be available on the machine. Ask your system administrator for the proper way to do this for your system, such as using the “useradd” tool. A list of users that are needed was created in the backup process as a file named `users.lst`.

A process similar to the following `useradd` example will be suitable for most Linux systems.

NOTE: This command must be run by `$AEN_SRVC_ACCT`.

```
xargs -0 -n 1 useradd --user-group < users.lst
```

### Project files

Create the `projects` directory in the location specified in `projectRoot` in `wk-compute-launcher-config.json`.

NOTE: By default this directory is `/projects`.

Then untar the `projects` directory with ACLs.

NOTE: This command must be run as root or with `sudo`:

```
tar --acls -xpvf projects.tar -C <projects base location>
```

### Full Anaconda (option 1)

If you did a full backup of the full Anaconda installation, untar this file to `/opt/wakari/anaconda`.

NOTE: This command must be run by `$AEN_SRVC_ACCT`.

```
tar -xvf aen_anaconda.tar -C /opt/wakari
```

### Partial Anaconda (option 2)

Restore the custom `.condarc` file.

If you did a partial backup of the Anaconda installation, move the copy of the `.condarc` file to `/opt/wakari/anaconda/.condarc`.

### Custom environments (if needed)

Untar any custom environments that were created to `/opt/wakari/anaconda/envs`.

NOTE: This command must be run by `$AEN_SRVC_ACCT`.

```
tar -xvf aen_compute_envs.tar -C /opt/wakari
```

## Restart compute node

Restart the compute-launcher application.

NOTE: This command must be run as root or with sudo.

```
service wakari-compute restart
```

## Viewing a list of admin commands

A user who is promoted to administrator can access administrator commands to perform advanced administrator tasks.

NOTE: Utility files are owned by, and should only be executed by, the AEN user who owns the files.

To display a list of all administrator commands:

```
ls -al /opt/wakari/wakari-server/bin/wk-*
```

## Viewing help for admin commands

To view help information for command, run the command followed by `-h` or `--help`.

EXAMPLE: To view help for the `remove-user` command:

```
/opt/wakari/wakari-server/bin/wk-server-admin remove-user -h  
/opt/wakari/wakari-server/bin/wk-server-admin remove-project -h
```

## Running daily reports

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Staff** menu, select Daily Report:

The Report section displays the following:

- Users—The number of users and projects.
- New User Emails—If *open registration is enabled*, the user names and emails for new users.
- Actions—The actions—projects created, projects updated, user authentications and added users—that have occurred in during the selected time frame—today, yesterday, this week, or this month.

## Viewing system errors

When an error occurs, a red dot is displayed in the AEN navigation bar next to the Admin link. The red dot is removed when all exceptions are marked as “read.”

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Staff** menu, select Exceptions:

Staff

Daily Report

Password Reset

Notification

Exceptions

Site Admin

General

Accounts

Users

Monitor

Security Log

Data Centers

Task Queue

License

Providers

Enterprise Resources

Report

Today

Yesterday

This Week

This Month

From:

Sun Sep 24 15:09:03 2017

Until:

Mon Sep 25 15:09:03 2017

Date Range

1 day, 0:00:00

Users

	New	Total
Users	0	1
Projects	0	6

New User Emails

Username	Email
----------	-------

Actions

Count	Action
82	<a href="#">oauth.authenticate</a>

Staff

Daily Report

Password Reset

Notification

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License

Providers

Enterprise Resources

Exceptions

Mark all as read

☒ `jinja2.exceptions.UnDEFINEDError: 'wk_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'`

☐ `jinja2.exceptions.UnDEFINEDError: 'wk_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'`

☐ `jinja2.exceptions.UnDEFINEDError: 'wk_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'`

☐ `jinja2.exceptions.UnDEFINEDError: 'wk_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'`

☐ `jinja2.exceptions.UnDEFINEDError: 'wk_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'`

☐ `jinja2.exceptions.UnDEFINEDError: 'wk_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'`

☐ `jinja2.exceptions.UnDEFINEDError: 'wk_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'`

☐ `jinja2.exceptions.UnDEFINEDError: 'wk_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'`

☐ `elasticsearch.exceptions.ConnectionError:`

☐ `elasticsearch.exceptions.ConnectionError:`

☐ `elasticsearch.exceptions.ConnectionError:`

☐ `elasticsearch.exceptions.ConnectionError:`

The Exceptions section lists all errors that have occurred while AEN is running.

3. To see the details of an error, click the radio button next to the error. This also marks the error as “read.”
4. To mark all errors as read without reviewing each one, click the Mark all as read button.

## Viewing security errors

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select Security Log:

Staff

Daily Report

Password Reset

Notification

Exceptions

Site Admin

General

Accounts

Users

Monitor

Security Log

Security Log

View	Actor	Action	Date
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 25, 2017 09:46:09 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 25, 2017 09:39:17 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 25, 2017 09:22:04 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 25, 2017 09:10:31 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 25, 2017 08:45:50 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 25, 2017 08:43:12 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 25, 2017 08:10:30 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 25, 2017 08:09:38 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 24, 2017 23:52:06 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 24, 2017 23:51:58 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 24, 2017 23:51:58 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 24, 2017 23:51:58 CDT

The Security Log section lists all errors that have occurred that could potentially affect AEN security.

3. To view a user’s profile page, click their username in the Actor column.
4. To see the details of an error, click the Eye icon next to the error.

The error details are displayed:

5. To close the error details, click the Back link.



Public Profile

Account Settings

Security Log

Applications

oauth.authenticate

_id	59c907f03f94c30fe45ffb9e
action	oauth.authenticate
actor_id	59c069b1ae55d1b3fe9fa45e
actor_username	aen_admin
client_id	59c119cd3f94c30fe45ff5db
remote_addr	None
time	2017-09-25 13:43:12.479000+00:00
token_id	59c907f03f94c30fe45ffb9d

[← Back](#)

Managing data centers

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select Data Centers:

Staff

[Daily Report](#)

[Password Reset](#)

[Notification](#)

[Exceptions](#)

Site Admin

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[Security Log](#)

[Data Centers](#)

Data Centers

[Gateway](#) (ec2-52-90-133-17.compute-1.amazonaws.com:8089)

[+ Add DataCenter](#)

The Data Centers section displays current data center information.

## Adding a data center

1. Click the Add DataCenter button to display the the Register a datacenter form.
2. In the Name box, type a Name for the new data center:

**Data Centers / Register a datacenter**

**Name**

☐ Subdomain Routing  
☐ Https

**Base Domain Name**

**summary**

**Provider**

3. Select the Subdomain Routing and/or Https checkboxes.
4. In the Base Domain Name box, type the base domain name.
5. In the Summary box, type a description of the data center.
6. In the Provider list, select a provider.
7. Click the Submit button.

## Managing enterprise resources

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Providers** menu, select Enterprise Resources:

Staff

[Daily Report](#)  
[Password Reset](#)  
[Notification](#)  
[Exceptions](#)

Site Admin

[General](#)  
[Accounts](#)  
[Users](#)  
[Monitor](#)  
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[Data Centers](#)  
[Task Queue](#)  
[License](#)

Providers

[Enterprise Resources](#)

Resources

Add Resource

Gateway

[ec2-54-210-232-251.compute-1.amazonaws.com](#)

remove

The Resources section lists your existing cloud and local resources.

### Adding a resource

1. Click the Add Resource button to open the new resource form.
2. Complete the form:

**Resources / new**

**Data Center**  
Gateway 59c119cd3f94c30fe45ff5db

**Name**  
Compute Node1

**URL**  
http://ec2-54-210-232-251.compute-1.amazonaws.com:5002

**Description**  
Configuring Compute Node

☒ **Public**  
Uncheck this if you want to control exactly who has access to this compute node

Add Resource

3. Click the Add Resource button.

### Viewing or changing the resource details

1. Click a resource name to open the Local Resource form.
2. If necessary, change the resource details:

**Data Center**

Gateway 59c119cd3f94c30fe45ff5db

**Name**

ec2-54-210-232-251.compute-1.amazonaws.com

**URL**

http://ec2-54-210-232-251.compute-1.amazonaws.com:5002

**Description**☒ **Public**

Uncheck this if you want to control exactly who has access to this compute node

**Update****status**

```
{"status": "ok", "messages": []}
```

3. Click the Update button.

### Making a node public or private

1. Click the resource name to open the Local Resource form.
2. Select or clear the Public checkbox:

**Data Center**  
Gateway 59c119cd3f94c30fe45ff5db

**Name**  
ec2-54-210-232-251.compute-1.amazonaws.com

**URL**  
http://ec2-54-210-232-251.compute-1.amazonaws.com:5002

**Description**

☒ **Public**  
Uncheck this if you want to control exactly who has access to this compute node

Update

**status**  

```
{"status": "ok", "messages": []}
```

3. Click the Update button.

## Removing a resource

Click the Remove button next to the resource you want to remove.

NOTE: When you remove a resource assigned to a project, the project becomes orphaned. To fix an orphaned project, *move the project to a valid Compute Resource*.

## Managing services

The tasks on this page assume that the 3 AEN nodes are installed in the following locations:

- Server—`/opt/wakari/wakari-server/`.
- Gateway—`/opt/wakari/wakari-gateway/`.
- Compute-Launcher—`/opt/wakari/wakari-compute/`.

- *Checking the status of server node processes*
- *Checking the status of gateway node processes*
- *Checking the status of compute node processes*
- *Starting AEN services*
- *Verifying that AEN services are set to start with the system*
- *Stopping AEN services*
- *Restarting AEN services*
- *Identifying extraneous processes*
- *Removing extraneous processes*

## Checking the status of server node processes

1. Run:

```
# service wakari-server status
wk-server          RUNNING      pid 20758, uptime 5 days, 0:30:23
worker            RUNNING      pid 20757, uptime 5 days, 0:30:23
```

OR

```
root@server # ps -Hu wakari
  PID TTY          TIME CMD
 20756 ?           00:02:26 .supervisord
 20757 ?           00:05:58 mtq-worker
 20758 ?           00:00:08 wk-server
```

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```
20765 ?      00:02:00    wk-server
20766 ?      00:01:55    wk-server
20767 ?      00:02:20    wk-server
20770 ?      00:02:02    wk-server
```

## 2. Run:

```
root@server # service nginx status
nginx (pid 26303) is running...
```

For more information on server processes, see *Server processes*.

## Checking the status of gateway node processes

### Run:

```
# service wakari-gateway status
wk-gateway          RUNNING      pid 1137, uptime 5 days, 1:59:28
```

### OR

```
root@gateway # ps -Hu wakari
  PID TTY          TIME CMD
 1136 ?            00:01:59 .supervisord
 1137 ?            00:00:02  wk-gateway
```

For more information on gateway processes, see *Gateway processes*.

## Checking the status of compute node processes

### Run:

```
# service wakari-compute status
wk-compute          RUNNING      pid 22050, uptime 3 days, 1:03:19
```

### OR

```
root@compute # ps -Hu wakari
  PID TTY          TIME CMD
 1150 ?            00:02:01 .supervisord
 1152 ?            00:00:01  wk-compute
```

For more information on compute node processes, see *Compute processes*.

## Starting AEN services

Services should start automatically both when they are first installed and at any point when the system is restarted.

If you need to manually start an AEN service, you must start each node independently, because they may be running on separate machines.

NOTE: The process is basically the same for each node, but the path to the correct commands vary.

To manually start a service:



- On the server node, run:

```
service wakari-server start
```

- On the gateway node, run:

```
service wakari-gateway start
```

- On a compute node, run:

```
service wakari-compute start
```

## Verifying that AEN services are set to start with the system

To verify that AEN services are set up to start automatically:

1. Run the following command on each node:

```
chkconfig --list | grep wakari
```

2. If services are missing, add them:

```
chkconfig --add [wakari-server|wakari-gateway|wakari-compute]
```

3. *Restart the services.*

## Stopping AEN services

CAUTION: Do not stop or kill supervisord without first stopping wk-compute and any other processes that use it.

You must stop services on each node independently, because they may be running on separate machines.

To stop an AEN service:

- On the server node, run:

```
service wakari-server stop
```

- On the gateway node, run:

```
service wakari-gateway stop
```

- On a compute node, run:

```
service wakari-compute stop
```

Compute nodes may have running processes that are not automatically stopped. To stop them, run:

```
sudo /opt/wakari/wakari-compute/bin/wk-compute-apps kill-all
```

## Restarting AEN services

- On the server node, run:

```
service wakari-server restart
```

- On the gateway node, run:

```
service wakari-gateway restart
```

- On a compute node, run:

```
service wakari-compute restart
```

## Identifying extraneous processes

To get a complete list of the processes running under the wakari user account, run `ps -Hu wakari`.

EXAMPLE:

```
root@server # ps -Hu wakari
  PID TTY          TIME CMD
 20756 ?            00:02:26 .supervisord
 20757 ?            00:05:58 mtq-worker
 20758 ?            00:00:08 wk-server
 20765 ?            00:02:00 wk-server
 20766 ?            00:01:55 wk-server
 20767 ?            00:02:20 wk-server
 20770 ?            00:02:02 wk-server

root@server # ps -f -C nginx
UID      PID  PPID  C  STIME TTY          TIME CMD
root    26303    1   0  12:18 ?        00:00:00 nginx: master process /usr/sbin/nginx -c /
→etc/nginx/nginx.conf
nginx   26305 26303   0  12:18 ?        00:00:00 nginx: worker process

root@gateway # ps -Hu wakari
  PID TTY          TIME CMD
 1136 ?            00:01:59 .supervisord
 1137 ?            00:00:02 wk-gateway

root@compute # ps -Hu wakari
  PID TTY          TIME CMD
 1150 ?            00:02:01 .supervisord
 1152 ?            00:00:01 wk-compute
```

- wk-server, wk-gateway and wk-compute should have PIDs reported by supervisorctl.
- The nginx master process should have a PID reported by service nginx status.
- If you have installed more than one AEN node on a single machine, the processes from all of the installed nodes should be displayed for that machine.
- On compute node(s), any AEN applications currently being run by users will be present.

EXAMPLE:

```
root@compute # ps -Hu wakari
  PID TTY          TIME CMD
 1150 ?            00:00:00 .supervisord
 1152 ?            00:00:00 wk-compute
```

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```
1340 ?      00:00:00 bash
1341 ?      00:00:00 notebookwrapper
```

## Removing extraneous processes

If extra `wk-server`, `wk-gateway`, `wk-compute`, or `supervisord` processes are present, use the `kill` command to remove them to prevent issues with AEN.

You can safely *restart* any process that you remove in error.

## Making sure NGINX and MongoDB are running

In order for AEN to run, the dependencies `mongodb` and `nginx` must be up and running. If either of these fail to start, AEN will not be served on port 80.

Check if `nginx` and `mongod` are both running (RHEL 6x):

```
$ sudo service nginx status
nginx (pid 25956) is running...

$ sudo service mongod status
mongod (pid 25928) is running...
```

If either of these failed to start, tail the log files. The default location of log files is:

```
$ tail -n 50 /var/log/mongodb/mongod.log

# nginx errors reported in error.log
$ tail -n 50 /var/log/nginx/error.log
```

## Viewing, terminating, and relaunching applications

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select Monitor:

The Monitor menu lists started applications by user and project.

The list includes columns for the application name, current running status, running node and last seen date.

3. Use the buttons to terminate or relaunch an application.
4. To view an application's logs, click the Logs button with the document icon.

## Viewing the task queue

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select Task Queue:

Staff

[Daily Report](#)  
[Password Reset](#)  
[Notification](#)  
[Exceptions](#)

Site Admin

[General](#)  
[Accounts](#)  
[Users](#)  
[Monitor](#)

Running Apps								
User	Project	Application	Status	Node	Last Seen	Terminate	Relaunch	Logs
aen_admin	asd	notebook	running	localhost	Jul 24, 2017 15:15:24 CDT	<a href="#">Terminate</a>	<a href="#">Relaunch</a>	<a href="#">Logs</a>
aen_admin	Test	notebook	running	localhost	Jul 25, 2017 11:54:05 CDT	<a href="#">Terminate</a>	<a href="#">Relaunch</a>	<a href="#">Logs</a>

Staff

[Daily Report](#)  
[Password Reset](#)  
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Site Admin

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[Monitor](#)  
[Security Log](#)  
[Data Centers](#)  
[Task Queue](#)

## Task Queue

Workers

ip-172-31-10-196.4053 | [high](#) [default](#) [low](#)

Queues

[high](#)  
Backlog: 0  
Failed: 1

[default](#)  
Backlog: 0  
Failed: 3

The Workers section lists the workers in the task queue and whether each worker is set at high, default or low priority.

The Queues section provides information on the default and high priority queues.

3. To view all the tasks in a particular queue, in the Queues section, click the queue name.

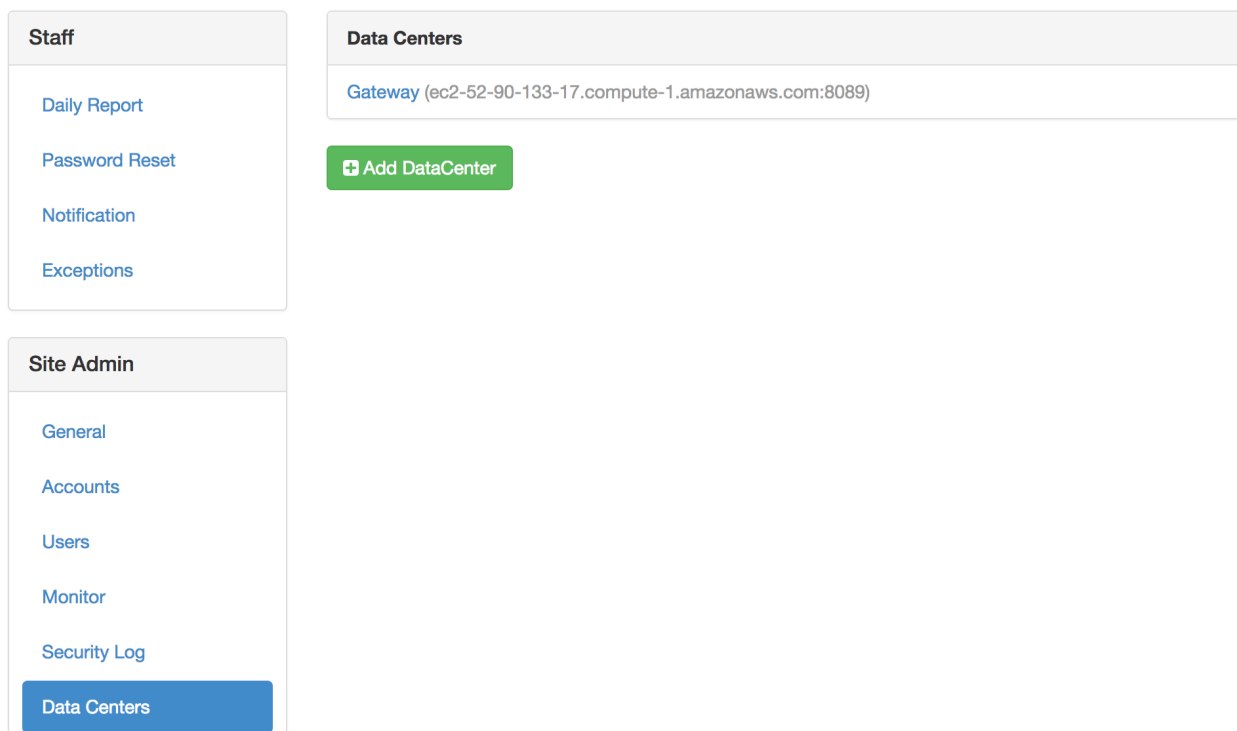
## Checking node connections

When the AEN nodes cannot communicate with each other as intended, it can cause issues with you AEN platform installation.

- *Verifying server to gateway connectivity*
- *Verifying gateway to compute node connectivity*
- *Verifying gateway to server connectivity*

## Verifying server to gateway connectivity

1. On the server, in the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select Data Centers:



3. For each data center in the list, check connectivity from the server to that gateway.

EXAMPLE: The gateway in this example is `http://gateway.example.com:8089`:

```
root@server # curl --connect-timeout 5 http://gateway.example.com:8089 > /dev/null
```

## Verifying gateway to compute node connectivity

1. On the server, in the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Providers** menu, select Enterprise Resources:

The screenshot displays the Anaconda Cloud Admin Settings interface. On the left, there is a navigation sidebar with three main sections: 'Staff', 'Site Admin', and 'Providers'. The 'Providers' section at the bottom has a button labeled 'Enterprise Resources'. The main content area on the right is titled 'Resources' and includes a green '+ Add Resource' button. Below this, there is a 'Gateway' section containing a table with one entry: 'ec2-54-210-232-251.compute-1.amazonaws.com', which has a 'remove' button next to it. The 'Staff' section on the left lists 'Daily Report', 'Password Reset', 'Notification', and 'Exceptions'. The 'Site Admin' section lists 'General', 'Accounts', 'Users', 'Monitor', 'Security Log', 'Data Centers', 'Task Queue', and 'License'.

3. Open each compute node in the Resources section.
4. Verify that the contents of the URL field begin with either `http` or `https`.

**Data Center**

Gateway 59c119cd3f94c30fe45ff5db

**Name**

ec2-54-210-232-251.compute-1.amazonaws.com

**URL**

http://ec2-54-210-232-251.compute-1.amazonaws.com:5002

**Description****Public**

Uncheck this if you want to control exactly who has access to this compute node

**Update****status**

```
{"status": "ok", "messages": []}
```

5. Check connectivity to that URL from the corresponding gateway.

EXAMPLE: The gateway in this example is `http://gateway.example.com:8089`:

```
root@gateway # curl --connect-timeout 5 http://compute.example.com:5002 > /dev/
↪null
```

## Verifying gateway to server connectivity

The gateway-to-server path is used by the gateway configuration command `wk-gateway-configure`.

1. Verify that the gateway is linked to the correct server in the configuration file.
2. Verify that the full server URL is specified.
3. Check connectivity to the server:

```
root@gateway # grep WAKARI_SERVER /opt/wakari/wakari-gateway/etc/wakari/wk-
↪gateway-config.json
"WAKARI_SERVER": "http://wakari.example.com",

root@gateway # curl --connect-timeout 5 http://wakari.example.com > /dev/null
root@gateway # curl --connect-timeout 5 http://error.example.com > /dev/null
curl: (7) Failed to connect to error.example.com port 80: Connection refused
```

4. If a connection fails:
  1. Ensure that gateways (data centers) and compute nodes (Enterprise Resources) are correctly configured on the server.
  2. Verify that processes are listening on the configured ports:

```
$ sudo netstat -nplt
Active Internet connections (only servers)
Proto Recv-Q Send-Q Local Address   Foreign Address State  PID/Program
tcp        0      0 *:80            :::*           LISTEN 26409/nginx
tcp        0      0 *:22            :::*           LISTEN 986/sshd
tcp        0      0 127.0.0.1:25    :::*           LISTEN 1063/master
tcp        0      0 *:5000          :::*           LISTEN 26192/python
tcp        0      0 127.0.0.1:27017 :::*           LISTEN 29261/mongod
tcp        0      0 *:22            :::*           LISTEN 986/sshd
tcp        0      0 127.0.0.1:25    :::*           LISTEN 1063/master
```

3. Check the firewall setting and logs on both hosts to ensure that packets are not being blocked or discarded.

## Verifying and tuning search indexing

For search indexing to work correctly, a compute node must be able to communicate with the server. To verify this:

1. Run:

```
curl -m 5 $AEN_SERVER > /dev/null
```

2. Verify that there are sufficient inotify watches available for the number of subdirectories within the project root file system:



```
cat /proc/sys/fs/inotify/max_user_watches
```

NOTE: Some Linux distributions default to a low number of watches, which may prevent the search indexer from monitoring project directories for changes.

3. If necessary, increase the number of watches:

```
echo fs.inotify.max_user_watches=100000 | sudo tee -a /etc/sysctl.conf && sudo  
→ sysctl -p
```

4. Verify that there are sufficient inotify user instances available—at least one per project:

```
cat /proc/sys/fs/inotify/max_user_instances
```

5. If necessary, increase the number of inotify user instances:

```
echo fs.inotify.max_user_instances=1000 | sudo tee -a /etc/sysctl.conf && sudo  
→ sysctl -p
```

## Changing the AEN server URL

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select General:
3. In the Wakari Server box, type the main URL where the site can be viewed.
4. Click the Update button.

## Changing the static URL for JavaScript files

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select General:
3. In the Static URL box, type the static URL where JavaScript files can be accessed.
4. Click the Update button.

## Changing the AEN account type

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select General:

Staff	General Admin Settings
<a href="#">Daily Report</a>	<b>Wakari Server</b> Set the main URL where this site will be accessed <input type="text" value="http://anaconda-enterprise.trl"/>
<a href="#">Password Reset</a>	<b>Static URL</b> Set static URL where the js can be accessed <input type="text" value="http://anaconda-enterprise.trl/static/"/>
<a href="#">Notification</a>	<b>Default Project Access</b> This will be the default when a user creates a project  <input type="radio"/> <b>Public</b> Anyone can see this project. Collaborators have write access <input checked="" type="radio"/> <b>Private</b> No one can see this project except collaborators.
<a href="#">Exceptions</a>	<b>Account Type</b> <input type="text" value="wk_server.plugins.accounts.cloud"/>
	<input type="button" value="Update"/>
Site Admin	Config Files
<a href="#">General</a>	
<a href="#">Accounts</a>	
<a href="#">Users</a>	
<a href="#">Monitor</a>	
<a href="#">Security Log</a>	
<a href="#">Data Centers</a>	
<a href="#">Task Queue</a>	
<a href="#">License</a>	
Providers	

Staff	General Admin Settings
<a href="#">Daily Report</a>	<b>Wakari Server</b> Set the main URL where this site will be accessed <input type="text" value="http://anaconda-enterprise.trl"/>
<a href="#">Password Reset</a>	<b>Static URL</b> Set static URL where the js can be accessed <input type="text" value="http://anaconda-enterprise.trl/static/"/>
<a href="#">Notification</a>	<b>Default Project Access</b> This will be the default when a user creates a project  <input type="radio"/> <b>Public</b> Anyone can see this project. Collaborators have write access <input checked="" type="radio"/> <b>Private</b> No one can see this project except collaborators.
<a href="#">Exceptions</a>	<b>Account Type</b> <input type="text" value="wk_server.plugins.accounts.cloud"/>
	<input type="button" value="Update"/>
Site Admin	Config Files
<a href="#">General</a>	
<a href="#">Accounts</a>	
<a href="#">Users</a>	
<a href="#">Monitor</a>	
<a href="#">Security Log</a>	
<a href="#">Data Centers</a>	
<a href="#">Task Queue</a>	
<a href="#">License</a>	
Providers	

Staff	General Admin Settings
<a href="#">Daily Report</a>	<b>Wakari Server</b> Set the main URL where this site will be accessed
<a href="#">Password Reset</a>	<input type="text" value="http://anaconda-enterprise.trl"/>
<a href="#">Notification</a>	<b>Static URL</b> Set static URL where the js can be accessed
<a href="#">Exceptions</a>	<input type="text" value="http://anaconda-enterprise.trl/static/"/>
<b>Site Admin</b>	<b>Default Project Access</b> This will be the default when a user creates a project
<b>General</b>	<input type="radio"/> <b>Public</b> Anyone can see this project. Collaborators have write access
<a href="#">Accounts</a>	<input checked="" type="radio"/> <b>Private</b> No one can see this project except collaborators.
<a href="#">Users</a>	<b>Account Type</b>
<a href="#">Monitor</a>	<input type="text" value="wk_server.plugins.accounts.cloud"/>
<a href="#">Security Log</a>	<input type="button" value="Update"/>
<a href="#">Data Centers</a>	
<a href="#">Task Queue</a>	
<a href="#">License</a>	
<b>Providers</b>	<b>Config Files</b>

3. In the Account Type box, select the account type—cloud or LDAP.
4. Click the Update button.

### Changing the default for project access

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select General:

<b>Staff</b> <a href="#">Daily Report</a> <a href="#">Password Reset</a> <a href="#">Notification</a> <a href="#">Exceptions</a>	<b>General Admin Settings</b>  <b>Wakari Server</b> Set the main URL where this site will be accessed <input type="text" value="http://anaconda-enterprise.trl"/>  <b>Static URL</b> Set static URL where the js can be accessed <input data-bbox="521 898 1409 947" type="text" value="http://anaconda-enterprise.trl/static/"/>  <b>Default Project Access</b> This will be the default when a user creates a project  <input type="radio"/> <b>Public</b> Anyone can see this project. Collaborators have write access  <input checked="" type="radio"/> <b>Private</b> No one can see this project except collaborators.  <b>Account Type</b> <input data-bbox="521 1283 1409 1331" type="text" value="wk_server.plugins.accounts.cloud"/>  <input type="button" value="Update"/>
<b>Site Admin</b> <b>General</b> <a href="#">Accounts</a> <a href="#">Users</a> <a href="#">Monitor</a> <a href="#">Security Log</a> <a href="#">Data Centers</a> <a href="#">Task Queue</a> <a href="#">License</a>	<b>Providers</b> <b>Config Files</b>

3. Under Default Project Access, select the default access type for new projects: Public or Private.
4. Click the Update button.

## Changing the owner of a project

To change the owner of a project:

1. Collect the project name, the user name of the previous owner, and the user name of the new owner.
2. Run the `wakari-server` executable command `wk-server-admin`:

```
/opt/wakari/wakari-server/bin/wk-server-admin project-owner --project PROJECT --  
↪old OLD_OWNER --new NEW_OWNER --delete --keep-owner
```

- **PROJECT**: The project name.
- **OLD\_OWNER**: The user name of the previous owner.
- **NEW\_OWNER**: The user name of the new owner.
- **--delete**: An optional flag that deletes the old project directory in the `projects` directory of **OLD\_OWNER**. If this flag is not used, the old project directory is preserved but no longer used.
- **--keep-owner**: An optional flag that makes **OLD\_OWNER** a collaborator of the project after it is transferred to **NEW\_OWNER**. If this flag is not used, **OLD\_OWNER** will no longer have collaborator access to the project.

**NOTE:** The **OLD\_OWNER** user must still exist when the project's owner is changed. Before deleting any user, be sure to change the owner of the user's projects.

## Editing configuration files

1. In the AEN navigation bar, click **Admin** to open the Admin Settings page.
2. In the **Site Admin** menu, select **General**.
3. In the **Config Files** section, change the configuration settings for your AEN installation. For more information on configuration files, see [Using configuration files](#).
4. Click the **Update** button.

## Managing your AEN license

1. In the AEN navigation bar, click **Admin** to open the Admin Settings page.
2. In the **Site Admin** menu, select **License**:

The **Current License** section displays information regarding your AEN license, including the name of the product, vendor, license holder's name, end and issued dates, company name, license type, and contact email.

<b>Staff</b>	<b>General Admin Settings</b>
<a href="#">Daily Report</a>	<b>Wakari Server</b> Set the main URL where this site will be accessed
<a href="#">Password Reset</a>	<input type="text" value="http://anaconda-enterprise.trl"/>
<a href="#">Notification</a>	
<a href="#">Exceptions</a>	<b>Static URL</b> Set static URL where the js can be accessed
	<input type="text" value="http://anaconda-enterprise.trl/static/"/>
<b>Site Admin</b>	<b>Default Project Access</b> This will be the default when a user creates a project
<b>General</b>	<input type="radio"/> <b>Public</b> Anyone can see this project. Collaborators have write access
<a href="#">Accounts</a>	<input checked="" type="radio"/> <b>Private</b> No one can see this project except collaborators.
<a href="#">Users</a>	
<a href="#">Monitor</a>	<b>Account Type</b>
<a href="#">Security Log</a>	<input type="text" value="wk_server.plugins.accounts.cloud"/>
<a href="#">Data Centers</a>	
<a href="#">Task Queue</a>	<input type="button" value="Update"/>
<a href="#">License</a>	
<b>Providers</b>	<b>Config Files</b>

Staff

[Daily Report](#)
[Password Reset](#)
[Notification](#)
[Exceptions](#)

Site Admin

[General](#)
[Accounts](#)
[Users](#)
[Monitor](#)
[Security Log](#)
[Data Centers](#)
[Task Queue](#)
[License](#)

Current License

You have **166 days** remaining on your current license.

Renew your license

<b>product</b>	Anaconda Enterprise Notebooks
<b>vendor</b>	Continuum Analytics, Inc.
<b>name</b>	Continuum Development
<b>end_date</b>	2018-03-10
<b>issued</b>	2017-03-10
<b>company</b>	Continuum Analytics
<b>type</b>	undefined
<b>email</b>	dev@continuum.io

Upload New License

License File

Choose File

No file chosen

Update

## Renewing your AEN license

1. Click the Renew your license button.
2. In the Upload New License section, click the Choose File button.
3. Select the new license file.
4. Click the Open button.
5. Click the Update button.

Your renewed license information is displayed.

## Cheat sheet

The Admin dashboard includes three menus in the left column: **Staff**, **Site Admin** and **Providers**.

### Staff menu

- Daily Report—See the number of users and projects.
- Password Reset—Reset a user password.
- Notification—Send system messages to users via SES or SMTP.



- Exceptions—If errors are raised while AEN is running, a red dot appears in the AEN navigation bar. Review errors and mark them as read.

## Site Admin menu

- General—Change the configuration settings for your AE Notebook server installation.
- Accounts—Turns on or off Open Registration.
- Users—View usernames, number of projects and last logins.
- Monitor—View status of applications with related data, terminate or restart.
- Security Log—View errors that could affect security.
- Data Centers—View current data centers and add a new data center.
- Task Queue—View workers in the task queue and priority.
- License—View current AEN license or upload a new license.

## Providers menu

Enterprise Resources—View, add or remove local or cloud services, and designate public or private to control access to a compute node.

## Troubleshooting

This troubleshooting guide provides you with ways to deal with issues that may occur with your AEN installation.

- *General troubleshooting steps*
- *Browser error: too many redirects*
- *Browser error: too many redirects when starting project apps*
- *Exception: exceptions.TypeError: 'NoneType' object has no attribute '\_\_getitem\_\_'*
- *Error: unix:///opt/wakari/wakari-server/etc/supervisor.sock no such file*
- *Error: “Data Center Not Found” when deleting a project*
- *Forgotten administrator password*
- *Log files being deleted*
- *Error: This socket is closed*
- *Service error 502: Cannot connect to the application manager*
- *502 communication error on Amazon web services (AWS)*
- *Invalid username*
- *Notebook Error: Cannot download notebook as PDF via LaTeX*
- *Unresponsive wk-server thread without error messages*
- *Unresponsive wk-gateway thread without error messages*

- *Error starting projects*
- *Changes in .condarc file are ignored*

### General troubleshooting steps

1. Clear browser cookies. When you change the AEN configuration or upgrade AEN, cookies remaining in the browser can cause issues. Clearing cookies and logging in again can help to resolve problems.
2. *Make sure NGINX and MongoDB are running.*
3. Make sure that AEN services are *set to start at boot*, on all nodes.
4. *Make sure that services are running* as expected. If any services are not running or are missing, *restart them*.
5. *Check for and remove extraneous processes.*
6. *Check the connectivity between nodes.*
7. *Check the configuration file syntax.*
8. *Check file ownership.*
9. *Verify that POSIX ACLs are enabled.*

### Browser error: too many redirects

#### Cause

Browser cookies are out of date.

#### Solution

1. Log out.
2. Clear the browser's cookies.
3. Clear the browser cache.
4. Log in.

### Browser error: too many redirects when starting project apps

Browser shows “Too many redirects” when the user tries to start an application.

#### Cause

The project's Compute Resource is invalid or was deleted.

#### Solution

*Move the project to a valid Compute Resource.*

**Exception: exceptions.TypeError: ‘NoneType’ object has no attribute ‘\_\_getitem\_\_’**

This exception appears on the Admin > Exceptions page when a project does not have a Compute Resource assigned.

**Cause**

The project’s Compute Resource is invalid or was deleted.

**Solution**

*Move the project to a valid Compute Resource.*

**Error: unix:///opt/wakari/wakari-server/etc/supervisor.sock no such file**

This is a supervisorctl error.

**Cause**

supervisord is not running on the Server.

**Solution**

Ensure that supervisord is included in the crontab. Then restart supervisord manually.

**Error: “Data Center Not Found” when deleting a project****Cause**

The data center has been removed.

**Solution**

As root, run:

```
/opt/wakari/wakari-server/bin/wk-server-admin remove-project --db-only <user>  
↪<project>
```

**Forgotten administrator password**

1. Use ssh to log into the server as root.
2. Run:

```
/opt/wakari/wakari-server/bin/wk-server-admin reset-password -u SOME_USER -p SOME_  
↪PASSWORD
```

NOTE: Replace SOME\_USER with the administrator username and SOME\_PASSWORD with the password.

3. Log into AEN as the administrator user with the new password.

Alternatively you may add an administrator user:

1. Use ssh to log into the server as root.
2. Run:

```
/opt/wakari/wakari-server/bin/wk-server-admin add-user SOME_USER --admin -p SOME_
↵PASSWORD -e YOUR_EMAIL
```

NOTE: Replace SOME\_USER with the username, replace SOME\_PASSWORD with the password, and replace YOUR\_EMAIL with your email address.

3. Log into AEN as the administrator user with the new password.

### Log files being deleted

Log files are being deleted.

NOTE: Locations of AEN log files for each process and application are shown in the node sections in [Concepts](#).

### Cause

AEN installers log into `/tmp/wakari\_server, gateway, compute}.log`. If the log files grow too large, they might be deleted.

### Solution

To set the logs to be more or less verbose, Jupyter Notebooks uses `Application.log_level`.

To make the logs less verbose than the default, but still informative, set `Application.log_level` to `ERROR`.

### Error: This socket is closed

You receive the “This socket is closed” error message when you try to start an application.

### Cause

When the `supervisord` process is killed, information sent to the standard output `stdout` and the standard error `stderr` is held in a pipe that will eventually fill up.

Once full, attempting to start any application will cause the “This socket is closed” error.

### Solution

To prevent this issue:

- Follow the instructions in [Managing services](#) to stop and restart processes.
- Do not stop or kill `supervisord` without first stopping `wk-compute` and any other processes that use it.

To resolve the “This socket is closed” error:

1. Stop wk-compute by running `sudo kill -9`.
2. Restart the supervisord and wk-compute processes:

```
sudo /etc/init.d/wakari-compute stop
sudo /etc/init.d/wakari-compute start
```

## Service error 502: Cannot connect to the application manager

Gateway node displays “Service Error 502: Can not connect to the application manager.”

### Cause

A compute node is not responding because the wk-compute process has stopped.

### Solution

Stop and then restart the supervisord and wk-compute processes:

```
sudo /etc/init.d/wakari-compute stop
sudo /etc/init.d/wakari-compute start
```

## 502 communication error on Amazon web services (AWS)

You receive the “502 Communication Error: This gateway could not communicate with the Wakari server” error message.

### Cause

An AEN gateway cannot communicate with the Wakari server on AWS. There may be an issue with the IP address of the Wakari server.

### Solution

Configure your AEN gateway to use the DNS hostname of the server. On AWS this is the DNS hostname of the Amazon Elastic Compute Cloud (EC2) instance.

## Invalid username

### Cause

The username does not follow 1 or more of these rules:

- Must be at least 3 characters and no more than 25 characters.
- The first character must be a letter (A-Z) or a digit (0-9).

- Other characters can be a letter, digit, period (.), underscore (\_) or hyphen (-).
- The [POSIX standard](#) specifies that these characters are the portable filename character set, and that portable usernames have the same character set.

### Solution

Follow the above rules for usernames.

### Notebook Error: Cannot download notebook as PDF via LaTeX

#### Cause

LaTeX is not properly installed.

#### CentOS/6 Solution

1. Install TeXLive from the [TUG site](#). Follow the described steps. The installation may take some time.
2. Add the installation to the PATH in the file `/etc/profile.d/latex.sh`. Add the following, replacing the year and architecture as needed:

```
PATH=/usr/local/texlive/2017/bin/x86_64-linux:$PATH
```

3. Restart the compute node.

#### CentOS/7 Solution

1. Install the missing packages running the command:

```
yum install texlive texlive-xetex texlive-xetexconfig texlive-xetex-def texlive-  
↪adjustbox texlive-upquote texlive-ulem
```

### Unresponsive `wk-server` thread without error messages

#### Cause

Two things can cause the `wk-server` thread to freeze without error messages:

- LDAP freezing
- MongoDB freezing

If LDAP or MongoDB are configured with a long timeout, Gunicorn can time out first and kill the LDAP or MongoDB process. Then the LDAP or MongoDB process dies without logging a timeout error.

### Solution

1. Check for frozen LDAP or MongoDB server processes.
2. You may also wish to configure the Gunicorn timeout to more than 30 seconds.

## Unresponsive `wk-gateway` thread without error messages

### Cause

If TLS is configured with a passphrase protected private key, `wk-gateway` will freeze without any error messages.

### Solution

Update the TLS configuration so that it does not use a passphrase protected private key.

## Error starting projects

Project's status page shows "There was an error starting this project".

### Cause

Lack of disk space in compute nodes prevents projects from starting.

### Solution

1. Verify that the project node meets the *system requirements*.
2. Check if there is enough free space on the compute node's partition where `/projects` lives:

```
df -h /projects
```

3. Free up some disk space to meet the system requirements.
4. Restart the project.

## Changes in `.condarc` file are ignored

Changes applied to `.condarc` are ignored by conda.

### Cause

Conda loads its configuration by merging multiple files together.

### Solution

Check if you are applying the changes to the correct file.

To show the merged state that conda is currently using:

```
conda config --show
```

To show all config files that conda is currently reading:

```
conda config --show-sources
```

### Frequently asked questions

- *What is AEN?*
- *Can notebooks be shared with anyone?*
- *Can I disable the option, “publish your notebook to anaconda.org”?*
- *How can I check the version number of my AEN server?*
- *Can I use AEN to access CSV or Amazon S3 data?*
- *Can I install other Python packages?*
- *Can I create a Python environment from the command line?*
- *Can I connect to GitHub with AEN?*
- *Can I print or print preview my Jupyter Notebooks?*
- *Is there a set amount of storage on AEN?*
- *How do I get help, give feedback, suggest features or report a bug?*

### What is AEN?

For information on AEN, see *Anaconda Enterprise 4 Notebooks*.

### Can notebooks be shared with anyone?

Yes. When you share a Jupyter Notebook through AEN, it can be viewed and run without the need to install anything special, regardless of what libraries were used to create the notebook. Each notebook also includes the python environment that it needs to run in.

AEN allows users to clone a shared Jupyter Notebook into their AEN account to make whatever changes or modifications they want. The notebook’s Python environment is also cloned, so it runs in the same environment as the shared Jupyter Notebook unless it is changed.

### Can I disable the option, “publish your notebook to anaconda.org”?

Yes. The upload button in the notebook app executes the option “publish your notebook to anaconda.org”. To disable it, log in as the AEN\_SRVC\_ACCT and run these commands:

```
source activate /opt/wakari/wakari-compute
jupyter-nbextension disable nb_anacondacloud --py --sys-prefix
jupyter-serverextension disable nb_anacondacloud --py --sys-prefix
```



## How can I check the version number of my AEN server?

Go to this URL in a browser: `http://$AEN_SERVER/admin/list`

NOTE: Replace `$AEN_SERVER` with the domain name or the domain name and port number of your AEN server.

## Can I use AEN to access CSV or Amazon S3 data?

Yes. If your data is in CSV files, upload the CSV files to your AEN account using the upload controls in the File Browser of the Workbench Application or the File Transfer Application.

To access data stored on Amazon S3, use the Boto interface from AEN. See the public data files in AEN for examples of how to use Boto to pull your data from Amazon S3 into AEN. For more information, see [Boto documentation](#).

You can also use IOPro to simplify and optimize the conversion of your data into Python arrays.

## Can I install other Python packages?

Yes, by creating a custom environment for your packages within your project.

For more information, see [Using the NBConda extension](#).

## Can I create a Python environment from the command line?

Yes, you can use the `conda create` command to create custom Python environments with whatever packages you choose. All AEN environments are shared with all the team members of a project.

EXAMPLE: In this example, `myenv` is a new environment containing the NumPy package.

```
conda create -n myenv numpy
```

NOTE: Python, Jupyter Notebooks and PIP are installed by default in all new AEN environments.

To use your new environment, activate it by running `source activate myenv`.

## Can I connect to GitHub with AEN?

Yes, you have full access to GitHub through an AEN Terminal application.

To generate an SSH key from your AEN account and add it to your GitHub account:

1. [Generate a GitHub SSH key](#).
2. Copy your key by running `cat ~/.ssh/id_rsa.pub`.
3. Select and copy the contents of the `id_rsa.pub` file to the clipboard.
4. Follow [GitHub's instructions](#) to go to your GitHub account and paste it from your clipboard into the appropriate box in your GitHub settings.

## Can I print or print preview my Jupyter Notebooks?

Yes, you can print your notebooks using your browser's regular printing capabilities.

You can also preview the printed page by clicking the **File** menu and selecting Print Preview.

### Is there a set amount of storage on AEN?

No, there is no set limit for storage in AEN. You are limited only by the size of the disk where AEN is installed.

If you need more storage, contact your system administrator.

### How do I get help, give feedback, suggest features or report a bug?

See *Help and support*.

### Help and support

Priority support is included with the purchase of an Anaconda subscription.

Contact your administrator first if you are having problems. Your administrator has a service level agreement where your issue will be responded to within a specific response time, depending on type and severity.

### Training and consulting

Training and consulting is available for AEN and any other Anaconda product.

For more information, please contact your account representative or [email the sales team](#).

### Providing feedback

Your feedback is very important to us!

Please, send us any [product feedback](#) while you are thinking about it.

TIP: Be sure to select AEN as the Platform Component Name.

### Submitting feature requests

We'd love to hear your ideas for consideration in future releases!

Your ideas help us build a better product. Your administrator can submit a support ticket for you.

NOTE: You can also request new features by using the [product feedback](#) form.

### Reporting a bug

If you think you have found a bug, please contact your administrator immediately. They will open a support ticket for your issue.

### Additional resources

The following resources are useful for getting started with Jupyter Notebooks:

- [Jupyter Notebook quick start guide](#)
- [Jupyter Notebook user documentation](#)

- [GitHub](#) shows the most popular Jupyter notebooks of the [month](#), [week](#), and [day](#).

## Release notes

### v4.3.2 May 29, 2019

#### Internal Fixes:

- Update Bootstrap to version 4.3.1
- Update jQuery to version 3.3.1
- Update jQuery UI to version 1.12.1
- Update notebook to version 5.7.8
- Update ipywidgets to version 7.4.2
- Update ipyparallel to version 6.2.3
- Set Secure flag on `xsrftoken`, `access_token`, and `refresh_token` cookies

### v4.3.1 March 25, 2019

#### Administrator-facing changes:

- Add option for server-side session management
- Add option to terminate terminal sessions on logout

#### Internal Fixes:

- Set Secure and HTTPOnly flag on session cookies
- Fix XSS vulnerability

### v4.3.0 October 24, 2018

#### Administrator-facing changes:

- Fix bug where compute logging wasn't respecting the `logMaxFiles` key
- Log and display a descriptive error message when there is a problem creating the users index
- Log and display a descriptive error message when there is a problem creating a new user with a duplicated e-mail address when the `uniqueEmail` setting is enabled
- Add footer server pages with server host data (IP, AEN version and server version)
- Fix admin script to change the status of private projects
- Fix validation error when updating/editing an existing resource
- Docs: Add KB article about using MongoDB to update old projects with new Data Center information
- Docs: Add restarting service step to SSO documentation
- Docs: Add support for newer versions of MongoDB
- Docs: Add documentation on `uniqueEmail`
- Docs: Add `projDirsAsHome` key to config docs

- Docs: Rewrite the “Using project directories as home directories” section
- Docs: Add full path to admin commands
- Docs: Warn about upgrading away from tested pkgs
- Docs: Add missing steps to “Authenticating with LDAP” section
- Docs: Add troubleshooting documentation about orphaned projects
- Docs: Warn about not using IP address when you connect to AEN
- Docs: Add an entry about ‘Error starting projects’ in the troubleshooting page
- Docs: Rewrite “Group and user permissions for NFS” section and description of the `identicalGID` key in the config pages
- Docs: Add a new section about using MRO packages in AEN
- Docs: Preserve username capitalization when using LDAP/AD
- Docs: Add umask 0022 to security requirements
- Docs: Add new section about changing install location
- Docs: Add note about how to manually break out Root CA for the gateway
- Docs: Add note about upgrading custom environments
- Docs: Add notes about how to find conda config files inside AEN
- Docs: Add note about using `USE_SERVER_BASED_SESSIONS: false` when configuring SSO between AEN and versions 2.33.3 through 2.33.10 of the Repository

User-facing changes:

- Increase Workbench file upload limit
- Fix Bokeh examples
- Extend `nb_locker` to detect a server disconnection and generate an alert if it occurs
- Docs: Update the notebook app to correctly point to AEN docs
- Docs: Emphasize that permissions are not applied recursively in the workbench

Internal fixes:

- Update Nginx version to v1.12.2
- Remove unused server config file during the compute upgrade process
- Remove already defined compute default settings from the post-script step
- Pin `widgetsnbextension` version to prevent version mismatch issue (ipywidgets)
- Remove `--offline` flag from the conda clone operations
- Support MongoDB 3.4.14 and update pymongo to version 3.2.2
- Fix LDAP username case sensitivity
- Security fixes and enhancements

**v4.2.2 March 1, 2018**

## Administrator-facing changes:

- Add admin command to change project owner
- Server: Add ability to disable public projects
- Gateway: Add support for SSL private key passphrase
- Docs: Add backup and restore runbook to the docs
- Docs: Emphasize backups before upgrading process
- Docs: Recommend putting AEN and projects folder on the same filesystem
- Docs: Add RHEL version 7.4 to supported versions
- Docs: Add troubleshooting instructions to fix problems when downloading notebook as PDF via LaTeX

## User-facing changes:

- Upgrade bokeh to version 0.12.7
- Upgrade holoviews to version 1.8.3
- Upgrade numba to version 0.35.0
- Upgrade scikit-learn to version 0.19.0

## Internal fixes:

- Fix bug in init scripts when requiretty is enabled
- Fix bugs related to AEN\_SUDO\_SSH option
- Fix bug in fix\_ownership function when directories contain spaces
- Docs: Fix error in Active Directory configuration example
- Server: Fix bug when updating user/group in supervisor configuration files in post-install for server and gateway
- Server: Fix bug Admin reports on user totals are inconsistent
- Server: Fix error in login screen when open registration and LDAP are enabled
- Server: Fix bug in Last seen date
- Server: Fix bug Monitor Report blank
- Server: Load JS files from local CDN
- Server: Fix error when terminating or relaunching an application from Monitor
- Server: Fix error creating projects when using Internet Explorer 11
- Compute: Fix 404 errors when using pivottablesjs
- Remove Wakari Cloud leftovers

**v4.2.1 December 18, 2017**

## Administrator-facing changes:

- None

## User-facing changes:

- None

Internal fixes:

- Fix undetected “ca” key when using self-signed certificates signed by a private CA
- Fix login redirects when using SSL
- Add verify gateway SSL certificate for get and post requests

### v4.2.0 November 22, 2017

Administrator-facing changes:

- Feature/allow remote MongoDB
- Allow for configuration for login timeout and set default
- Add verbose option to conda create clone
- Avoid duplicate name for resources / compute-nodes
- Allow renaming main and message queue databases
- PAM-based authentication module
- Change wakari logos to Anaconda logos
- Replace ‘wakari’ wording
- New config option to move the user’s home directory into the user’s project directory
- Make logging less verbose in AEN
- Documentation for PySpark kernel installation
- Improve SSL documentation

User-facing changes:

- New config option to move the user’s home directory into the user’s project directory
- Package cache was moved from user’s home directory into the user’s project directory
- Change wakari logos to Anaconda logos
- Fix error for deleting tags to work
- Define shell prompt in `.projectrc` template
- Replace ‘wakari’ wording

Internal fixes:

- Move server unix socket from `/tmp` to `/opt/wakari/wakari-server/var/run`
- Make project deletion synchronous for consistency
- Avoid storing `csrf` token in the user profile
- Expire gateway session when server logs out
- Allow log rotation in the three components
- Fix permissions on static files
- Change log level to debug in gateway
- Do not log private keys in gateway

- Save request remote address when logging action
- Unify logs formatting and timezone in compute nodes with Winston
- Several fixes and documentation improvements

#### **v4.1.3 August 16, 2017**

- Upgrade conda to version 4.3.24
- Upgrade anaconda to version 4.4.0
- Admin application monitor
- Block access to package list view
- Add placeholders in password reset form
- Change static content location
- Fix error when checking for package updates in notebook application
- Replace slashes in project tags
- Fix submit errors in password reset form
- Replace/remove “wakari” word from multiple places
- Fix missing commands missing sudo in start-project
- Improve gateway and compute node validators
- Check if bzip2 is installed during server setup process
- Include port number in host header
- Forbid creation of empty tags
- Repair “Create Account” link in login page
- Use UTC for server logs
- Mark datacenters as trusted by default
- Disable heart beating
- Compute resource: Show full path to log file
- Improve init scripts
- Allow deleting all projects
- mtq: Implement exponential backoff on connection error to mongodb
- In the general admin display, do not show the bind password for LDAP
- The accelerate package has been removed from the installation
- Other minor bugfixes

#### **v4.1.2 March 29, 2017**

This is mainly a maintenance release improving internal machinery and upgrading the root packages.

- Upgrade conda to version 4.3.14

- Upgrade Anaconda to 4.3.1
- Upgrade r-base to 3.2.2
- Fixed AEN nb\_conda to be compatible with conda 4.3.x series
- Several documentation fixes
- Other minor bugfixes

### **v4.1.1 December 15, 2016**

- Added CentOS 7 support
- Support dots in usernames
- More usernames validation
- Fixed creation (through nb\_conda) of single letter environment names
- Environment names (through nb\_conda) validation
- Fixed uploading of notebook using nb\_anacondacloud
- Fixed attaching of environments in published notebooks through nb\_anacondacloud
- Several documentation fixes
- Other bugfixes

### **v4.1.0 October 21, 2016**

- Added JupyterLab application
- Removed GateOne terminal application
- Included additional notebook extensions (nbpresent and nb\_anaconda\_theme)
- Updated to conda 4.2.9 in default project environments
- Added HTTP timeout setting for gateway and compute launcher
- Changed default gateway port to 8089
- Added support for all-numeric usernames
- Add R channel to default conda configuration file
- Other bugfixes

### **v4.0.0 June 30, 2016**

- Customized installation with:
  - AEN Functional ID and Group
  - AEN (installation and run) sudo commands
  - Removal of root access from the AEN service account
  - Configurable sudo command
  - Restriction of sudo access to all the processes



- Upgrade Jupyter to 4.2
- Upgrade the anaconda-nb-extensions to the latest versions
- Upgrade Anaconda to 4.0
- Deprecate wakari-publisher
- Security enhancements
- SSL configuration documented between all AEN Server components
- Several bugfixes
- Overall documentation revision and general improvement

### **v0.10.0 February 2, 2016**

- New projects dashboard
- Capability to star and tag a project
- Sticky searches
- New Jupyter Notebook extensions
- Updates to all packages. Highlights: bokeh 0.11, ipython/jupyter 4.1.

### **v0.9.1 October 19, 2015**

- New Search capability to find projects and files within a project.
- Added “Related Projects” list to the project view, based on code similarity.
- New UI for fine-grained access control of project files in the Workbench app
- Viewer app now renders plain text files correctly
- Updated LDAP configuration docs
- Updates to all packages. Highlights: bokeh 0.10, ipython/jupyter 4.0.

**Note** Elasticsearch, and an Oracle JRE, must be installed on the server in order to use the new search features. Indexing of project files will begin when the project is started (or paused and re-started). If search features are not desired, set `"SEARCH_ENABLED": false` in the server configuration file to avoid errors.

### **v0.8.0 August 21, 2015**

#### **New Features**

- Updated packages based on Anaconda 2.3, and removed older packages no longer in Anaconda.
- Updated IPython to version 3.2.1
- Documentation is now installed with the server (use the Help link in the top navigation bar)
- Added the ability for the administrator to define a customized default project environment.
- The server has been updated to use python 2.7.10.
- Init scripts are now provided for each Anaconda Enterprise Notebooks service.

- Added relevant links to some error pages

### Problems Resolved in this Release

- Project status indicators (e.g. starting, pausing) now automatically update.
- If an access is unauthorized, the server now returns a 403 (Unauthorized) status code and prompts the user to log in.
- Modified nginx configuration to support running the server on non-standard ports.
- The server installation no longer uses a default password for the wakari user. A random password is generated and displayed during installation.
- Prevent double-click from attempting to create a project twice
- Removed an obsolete script reference that was causes a 404 error to be logged in the browser console when opening the Terminal app.
- The installer scripts no longer fail if the database already contains the 'wakari' user.
- Updated example notebooks to work with latest Bokeh release.
- Fixed terminal app key bindings to allow Mac command key to work normally
- Installers now indicate where the installation logs are stored
- LDAP user attributes containing binary data are now ignored.

### Documentation Updates

- Updated and consolidated Troubleshooting guide.
- Simplified some steps in the installation procedure.
- Updated notebooks in the Examples directory for use with the latest IPython Notebook and Bokeh.
- Added a section on project permissions to the Troubleshooting guide.
- Added notes on how to remove a project if the datacenter has already been removed.

### v0.7.0 June 12, 2015

#### New Features

- Updated Bokeh to v0.9
- Ability to list packages installed on the server
- Administrators now have full access to all projects.
- Added automated checking and display of connection status between server, data centers, and compute resources.
- When creating a new project, an environment for the project is automatically created as a clone of the root Anaconda environment.

## Problems Resolved in this Release

- Problem with checking in files with revision control extension
- Revision control extension can't handle notebook names with spaces
- Problem moving files from one compute node to another if configured for LDAP
- Should default to UTF-8 encoding and warn user if no locale is detected
- Adding a compute resource via the command line admin tool does not work
- The installer now sets `umask 0022` to ensure correct file permissions

## Documentation Updates

- Added a *Troubleshooting* section to the documentation.
- Added notes on how to configure crontab to start the Anaconda Enterprise Notebooks services at startup
- Example SSL config file now has correct log paths
- Added instructions on how to ensure that POSIX ACL support is enabled on the projects directory.
- Fixed syntax problem in sample LDAP config.json
- Added section on how to use self-signed or private CA certificates

## v0.6.3 March 27, 2015

- Updated LDAP module
- LDAP user filtering
- Added Notebook locking
- Added Notebook integrated revision control system
- Move projects between compute nodes
- User-specific binding to compute nodes (private compute nodes)
- Improved installation process and dependency checking
- Incorporated support for SSL for Server and Gateway nodes
- Improved Gateway error handling
- Fixed package dependencies for update process
- Documentation updates

## Previous versions

Documentation for previous versions is provided for users who have not yet upgraded to the current version of AEN.

### Anaconda Enterprise 4 Notebooks

*Empower the Data Science Team with cross-collaboration*

AEN is a browser-based Python data analysis environment and visualization tool from Anaconda®. AEN is a ready-to-use, powerful, fully-configured data analytics environment all in a secure, governed environment.

AEN allows data science team members to create and share private notebooks, manage access, control notebook revisions, compare and identify differences across notebook versions, search notebooks for keywords and packages, use enhanced collaborative notebook features—including revision control and locking—and to access an on-premises and/or cloud collaborative notebook server.

The current version of AEN is 4.3.1, released March 25, 2019.

#### User guide

AEN's browser-based management of private packages, notebooks, and environments allows data science team members to:

- Create, share and manage private notebooks.
- Control notebook revisions.
- Compare and identify differences across notebook versions.
- Search notebooks for keywords and packages.
- Use enhanced collaborative notebook features including revision control and locking.
- Access on-premises and/or cloud-based collaborative notebook servers.
- Utilize multiple language kernels like Python and R language in the same notebook.
- Create new notebook environments on the fly without leaving the notebook or entering commands in a prompt.
- Publish results to business stakeholders as interactive visualizations and presentations.

To quickly get up and running with AEN, see [Getting started](#).

Download the [Cheat sheet](#) for easy reference.

#### Concepts

- [Projects](#)
- [Team collaboration](#)
- [Access control](#)
- [Sharing projects](#)
- [Project tags](#)

#### Projects

AEN users interact with the system predominantly through projects.

A project is a set of conda environments, Jupyter Notebooks, and other files.

Each project has a project drive that all team members can access. The size of the drive is not limited by AEN. Contact your system administrator if you find you do not have sufficient space.

Each project has a separate project directory on the project drive.

The project directory is a directory for project files and data that is separate from the project owner's and team members' home directories, so that team members can share and have equal access.

The path to your project directory is `/projects/<project_owner>/<project_name>`.

For administrative information about projects, directories, and permissions, see [Projects and permissions](#).

## Team collaboration

Teams collaborate in AEN using projects. Projects allow a team to easily come together by sharing the resources, applications, and environments that are necessary to collaborate effectively.

The AEN project owner and any team members connected to their project will have access to the same:

- Shared files and home directories.
- Shared Python and R environments.
- Shared nodes and hardware.
- Common applications.
- Web user interface.

For more information, see [Working with projects](#).

## Access control

AEN access controls allow you to:

- Add and remove project access for new team members.
- Limit the access to specific folders and files to members of your project team.
- Use permissions to extend execute access to team members. By default, all of the team members on a project have read and write access to all project assets.

Access control is performed from each project's Workbench application.

For more information, see [Controlling access to your project](#).

## Sharing projects

AEN supports both public and private sharing.

A project can be “public,” which means that anyone with access to the system can view the project assets.

Any content placed in the `public` folder in a project is publicly accessible using its URL.

A project can be “private,” which means that only the project owner and team members can view the project assets.

You can also [limit who can access specific files](#).

### Sharing Jupyter Notebooks

In addition to general project sharing capabilities, you can also publish Jupyter Notebooks to Anaconda Repository. This automatically versions the notebook and allows you to define who can view the notebook.

### Project tags

Tags are used to:

- Group similar or related projects.
- Identify your project so that it is easier to find.
- Let others know about your project.

You can *add and remove tags* for any project that you have access to.

### Getting started

This section contains information and tasks for first-time AEN users.

In this getting started guide, you will:

- *1. Download the AEN cheat sheet*
- *2. Access your user home page*
- *3. Create a new project*
- *4. Add collaborators*
- *5a. Open an example notebook, OR*
- *5b. Create a new environment and notebook*
- *6. Create checkpoints for version control*
- *7. Share your notebook and environment with others*
- *8. See what to do next*

#### 1. Download the AEN cheat sheet

Before you start, download and print the *AEN cheat sheet* for easy reference.

#### 2. Access your user home page

After your administrator has set up your server and new Anaconda account, you will receive a welcome email.

1. Click the link in the email to open the AEN login page.

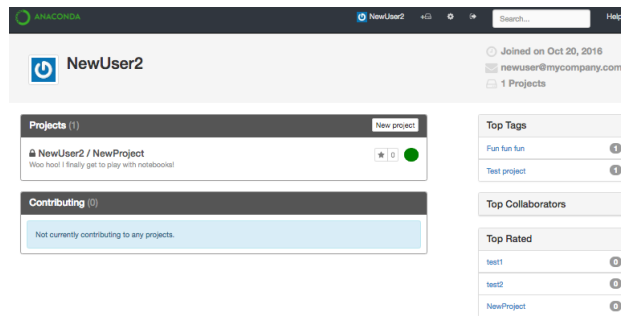
NOTE: Use the domain name and not the IP address when you connect to AEN. Using the IP address can cause TLS and security certificate errors.

2. Enter your AEN account username and password.

NOTE: Some administrators allow you to create your own account. If your administrator has allowed this, in the create a new account section, create your own username and password.

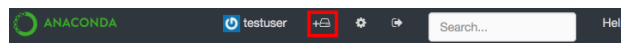
3. Click the Login button.

Your user home page, where all good things happen, is displayed:

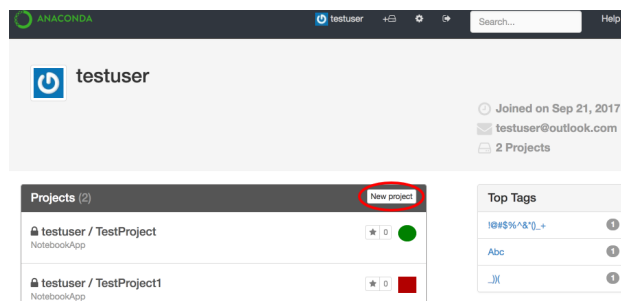


### 3. Create a new project

1. There are 2 ways to create a new project in AEN:
  - On the right side of the AEN task bar, click on the New Project icon:



- On your home page, click the New project button:



2. On the Project page that is displayed, type a name for your project, such as “Testing.”

**New Project**  
Create your project here!

Project Name

Project names must start with a letter and contain only alphanumeric characters.

Summary

☐ Public  
 Anyone can see this project. Collaborators have write access.

☒ Private  
 No one can see this project except collaborators.

Next

3. Type a summary of the project so you can recognize it later.
4. Select whether your project will be public or private.
5. Verify that the default data center is selected.

TIP: You can update the project summary and description at any time from the **Project** menu in the Project Settings. To return to your project at any time, click the project name.

6. Click the Next button.

Your new project's home page is displayed:

**testuser / TestProject1**  
NotebookApp

workbench viewer jupyterlab terminal notebook Compute Resource Config

**Description**  
We recommend that each repository have a description. Treat it like a README of your project for the new developer.

**Public Folder**  
This project does not have contents in its public folder yet!

7. To change the project settings, click the Project Settings icon on at the top right.

**testuser / TestProject**  
NotebookApp

Project Settings icon highlighted

8. Modify the summary or add a description of the project.



TIP: A project description is recommended, and may be written in Markdown syntax (plain text valid Markdown).

To see how Markdown will be displayed, in the description area, click the **Preview** tab.

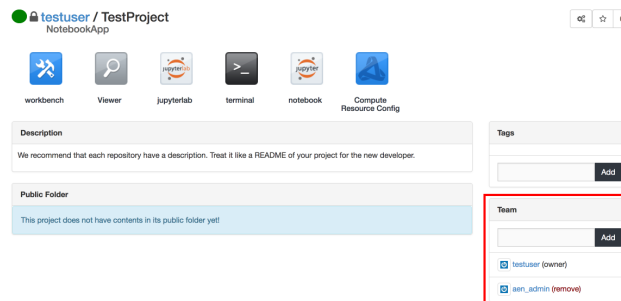
## 4. Add collaborators

You can add team members to your project as collaborators. Adding team members to your projects makes collaboration easy because they have full access to the project's applications, files and services.

When you add team members, their home directory is mounted in the project. There is no need to download and email data or scripts—team members can work on the same files in the same environment in which you are working.

To add collaborators to your project:

1. From your project home page, in the Team box, begin typing a teammate's username.
2. In the list that is displayed, select the teammate's username.
3. Click the Add button.

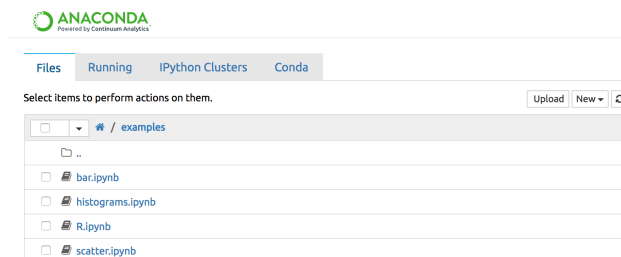


1. Repeat these steps for each team member you want to add as a collaborator.

TIP: You can add or remove team members any time from the **Team** menu in Project Settings. You can also modify a team member's read, write or execute permissions at any time from the [Using Workbench](#).

## 5a. Open an example notebook, OR

1. From your project home page, click the Jupyter Notebooks icon.
2. On the File View page, click the Examples folder.



1. Select any of the example notebooks.

2. To see the default results of the formulas used in the displayed notebook, in the **Cell** menu, select Run All.
3. To experiment with changing the notebook, edit any of the formulas in the notebook.
4. In the **Cell** menu, select Run All.

Any differences resulting from your edits are displayed.

## 5b. Create a new environment and notebook

If you are already familiar with creating notebooks, you can easily set up a new environment with the programs you need—like SciPy and NumPy—then open a new notebook and make your edits.

To create a new environment:

1. From your project home page, click the Jupyter Notebooks icon.
2. On the File View page, click the **Conda** tab.
3. To add a new conda environment, on the top right of the **Conda** tab, click the + icon.
4. Type a name for your environment.
5. Select Python 2, Python 3 or R language kernel.
6. Click the Create button.
7. To activate your new environment, click its name.

The packages that are available and installed in your new environment are displayed.

## Adding SciPy and Numpy packages

1. In the available packages section, search for the package name `numpy`—all lower case.
2. In the results section, next to `numpy`, select the checkbox.

The screenshot shows the Anaconda Cloud interface. At the top, there's a navigation bar with tabs: Files, Running, IPython Clusters, and Conda. Below this, there's a section titled '3 Conda environments' with a table listing environments: 'root', 'default', and 'myenv'. The 'default' environment is marked as the default. Below this, there's a search bar with 'numpy' entered. To the left of the search bar, it says '2 available packages'. To the right, it says '39 installed packages in environment "myenv"'. Below the search bar, there are two tables. The first table lists available packages: 'numpy' (version 1.13.1, channel defaults) and 'numpydoc' (version 0.7.0, channel defaults). The second table lists installed packages in the 'myenv' environment, including 'anaconda-client', 'certifi', 'clyent', 'decorator', 'ipykernel', and 'ipython'.

Action	Name	Default?	Directory
	root		/opt/wakari/anaconda
	default	✓	/projects/aen_admin/TestProject/envs/default
	myenv		/projects/aen_admin/TestProject/envs/myenv

Name	Version	Channel
<input checked="" type="checkbox"/> numpy	1.13.1	defaults
<input type="checkbox"/> numpydoc	0.7.0	defaults

Name	Version	Build	Available
<input type="checkbox"/> anaconda-client	1.6.3	py36_0	
<input type="checkbox"/> certifi	2016.2.28	py36_0	
<input type="checkbox"/> clyent	1.2.2	py36_0	
<input type="checkbox"/> decorator	4.1.2	py36_0	
<input type="checkbox"/> ipykernel	4.6.1	py36_0	
<input type="checkbox"/> ipython	6.1.0	py36_0	

1. Click the Install icon.

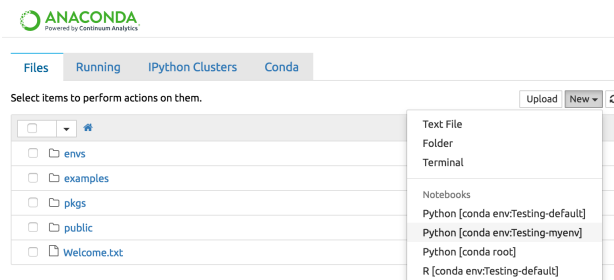
2. To confirm your installation, click the Install button.

Numpy is displayed in the installed packages section—if not, click the Refresh button. Repeat these steps to install the Scipy package—searching for `scipy` in step 1.

TIP: You can return to this screen at any time to add additional packages to this environment.

## Creating a new notebook in your environment

1. From the AEN homepage, click the **Files** tab.
2. On the top right of the **Files** tab, click the New button.
3. Under Notebooks, select the Python environment with the name you entered while *creating a new environment*.



NOTE: If you do not see your new environment listed under Notebooks, next to the New button, click the Refresh button.

A new locked notebook is displayed. Paste or write some code to execute when you are ready.

## 6. Create checkpoints for version control

Whether you are exploring an existing notebook, or creating a new one, you can easily create checkpoints, return to an earlier version, compare two different versions and save them for reference.

To create a checkpoint, in the **File** menu, select Save and Checkpoint:

To revert your notebook to a previous checkpoint, in the **File** menu, select Revert to Checkpoint.

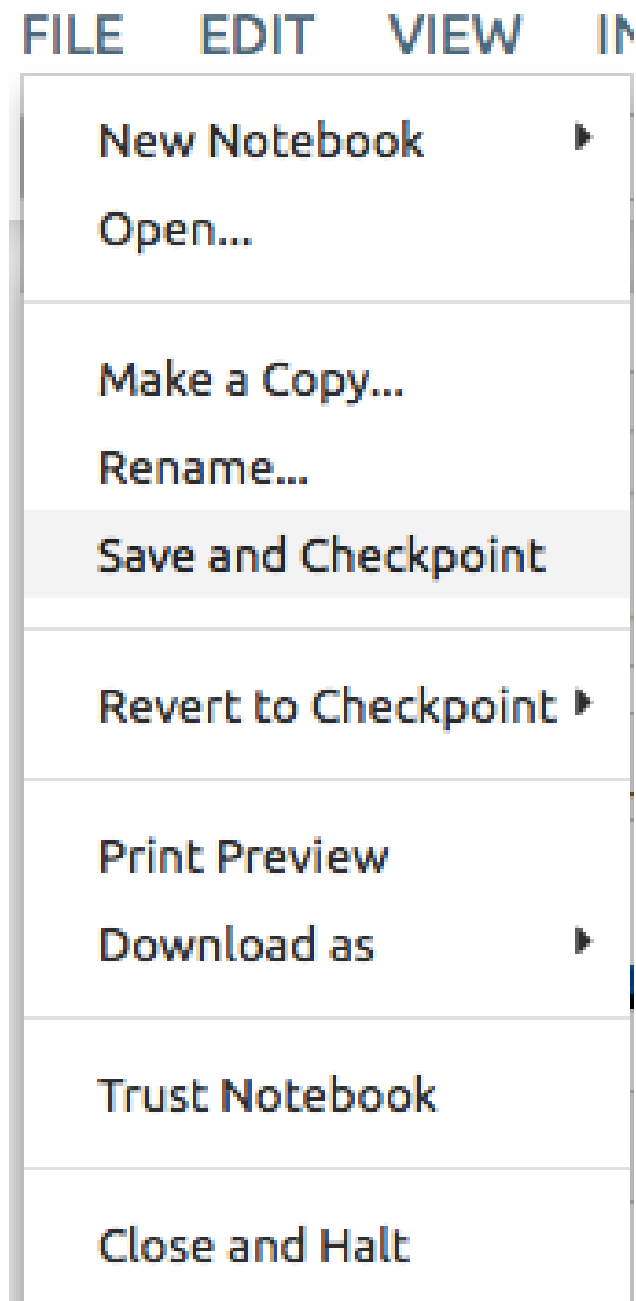
NOTE: For more information about revision control features, including creating commits and comparing differences, see *Using the Revision Control Mechanism extension*.

## 7. Share your notebook and environment with others

See *Sharing projects and notebooks*.

## 8. See what to do next

Now that you have completed the Getting Started guide, you are ready to move on to *basic tasks* and *advanced tasks*.



## Basic tasks

This section contains information and tasks that use the web browser to manage projects and is best-suited for any beginning AEN user:

### Working with projects

Almost everything in AEN starts by opening an existing project or creating a new one.

After that, you can set up a special environment with the packages you want, set their access permissions and modify your project settings.

### Searching for a project or file

- *Types of files searched*
- *Search indexing*
- *Using search constructs*
- *Searching metadata fields*
- *Searching a project*
- *Saving a search*
- *Removing a saved search*

To search for projects and files, use the Search box in the AEN navigation bar. The search provides different results depending on which page you search from:

- On a project home page, search results include any files that match your search criteria within the current project.
- On any other AEN page, search results include any files that match your search criteria within all projects.

**TIP:** Your search results include only files and projects that you can view: public projects, and private projects to which you have a minimum of view access.

### Types of files searched

The following types of files are included in search results:

- `.py`—Python source files.
- `.ipynb`—IPython/Jupyter notebooks.
- `.txt`—plain text files.
- `.md`—Markdown files.

### Search indexing

Files that are modified while a project is running are automatically re-indexed shortly after the files are modified. If you create or update a large number of files—such as cloning a git repository or copying a directory—search results may take several minutes to update.

Files that are modified while the project is not running are re-indexed only after the project is started.

## Using search constructs

You can use the following search constructs:

- Ordinary words will match the full-text contents of any file.
- Wildcards are permitted.

EXAMPLE: `John*` will match John and Johnny. These are glob patterns and are similar to their usage in the command line.

- Combine queries using AND or OR, and group them using parentheses `()`.

Regular expression patterns can be embedded in the query string by wrapping them in forward-slashes `/`:

```
name:/joh?n(ath[oa]n)/
```

The supported regular expression syntax is explained in [the Elasticsearch reference](#).

NOTE: Wildcards apply inside a regular expression. A query string such as `/.*n/` would force the search to visit every term in the index.

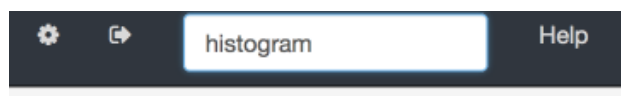
## Searching metadata fields

You can search in specific metadata fields:

- `imports:name`—matches files that import the module name.
- `uses:name`—matches files that reference the identifier name. Referenced names include any functions and globals imported from other modules, as well as the names of any methods invoked on any object.
- `defines:name`—matches files that define the identifier name. Defined names include functions defined at global scope, class names, and method names within classes.
- `acl:user`—matches files in which the named user has read access or higher.

## Searching a project

1. In the Search box, type a string of text:

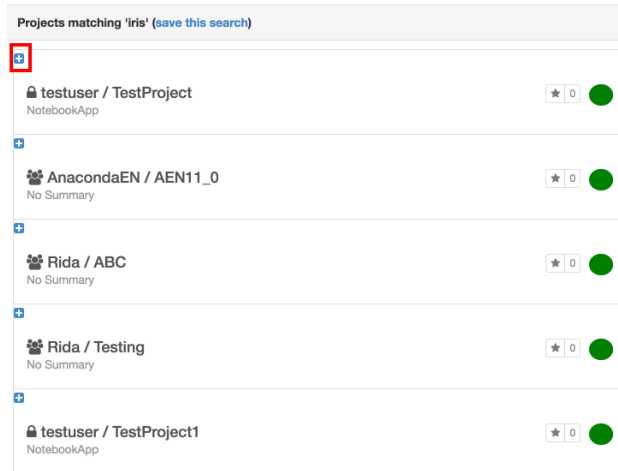


TIP: Search by glob patterns, which are similar to file matching in the command line.

EXAMPLE: To find projects in the test family that are numbered from 00 to 99, search for `Test-??`. To find all projects whose name ends with “Stats,” search for `*Stats`.

2. Press Enter.

3. In the search results, click the plus + icon above a project name to show a list of matching files in the selected project:



TIP: Click the project name to open the project's home page.

4. To view a file, click its file name in the matching files list:

Found 1 files matching 'histogram' in user02/Public_project. (save this search)	
File	Relevance
<a href="#">/examples/histograms.ipynb</a>	42

## Saving a search

1. At the top of the search results, click Save this search:

The “save this search” text changes to “stored” and your search is saved. Your saved searches are listed on your home page.

## Removing a saved search

On your home page, in the Saved searches section, click X next the saved search that you want to remove:

Projects matching 'iris' **Stored**

+

testuser / TestProject

NotebookApp

★ 0

+

AnacondaEN / AEN11\_0

No Summary

★ 0

+

Rida / ABC

No Summary

★ 0

+

Rida / Testing

No Summary

★ 0

+

testuser / TestProject1

NotebookApp

★ 0

Projects (2) 

New project

testuser / TestProject

NotebookApp

★ 0

testuser / TestProject1

NotebookApp

★ 0

Contributing (0)

Not currently contributing to any projects.

Top Tags

l@#%\$%^&\*0\_+ 1

Abc 1

\_)({ 1

Top Collaborators

aan\_admin 1

Top Rated

Project 1

Testing 0

AEN11\_0 0

ABC 0

TestProject 0

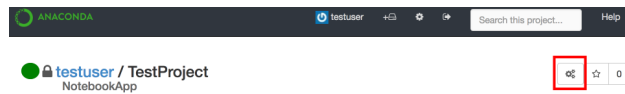
Saved searches

iris x

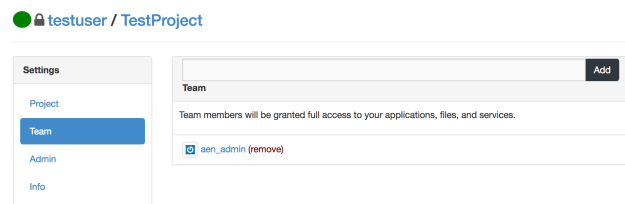


## Adding and removing team members on a project

1. On the project home page, click the Project Settings icon to open the Project Settings page.



2. In the **Settings** menu, select Team.



## Adding a team member

1. In the username box, type in the first few letters of the username for the team member you want to add to the project.
2. In the list of usernames that displays, click the user to add.
3. Click the Add button.

## Removing a team member

Click the red Remove link next to the name of the user you want to remove from the project.

## Controlling access to your project

- *Controlling team member access*
- *Controlling non-team member access*

## Controlling team member access

By default, all of the team members on a project have read and write access permissions for all project assets.

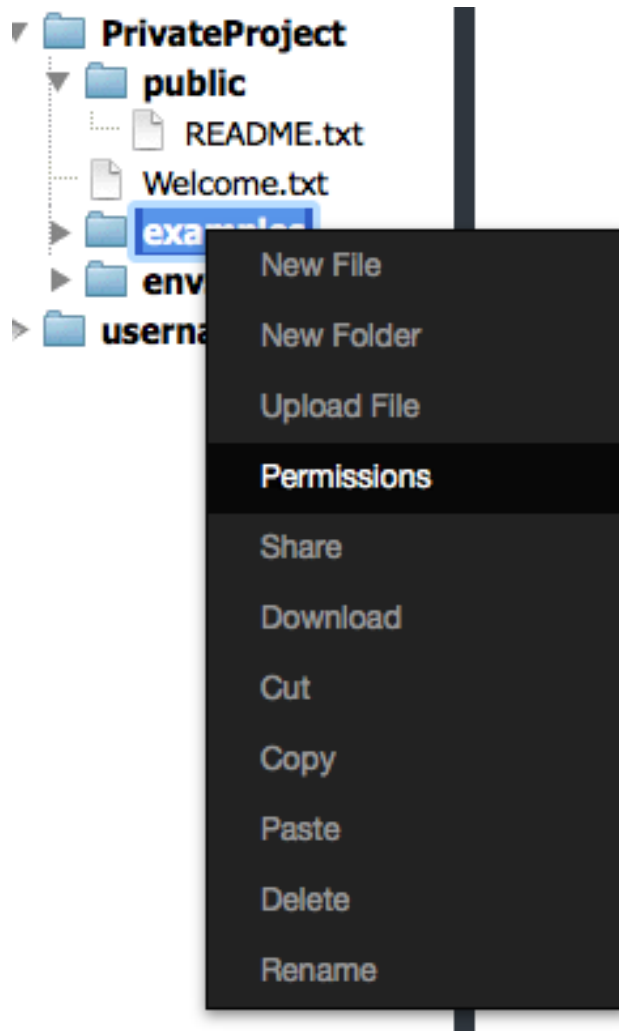
The available permissions are read, write and execute. If you remove all individual or group permissions for a project asset, team members will not be able to access that asset.

To change a project's permissions:

1. Open the project's home page.
2. Click the Workbench icon.
3. In the Workbench app, right-click the file or folder you want to limit access to.

NOTE: When you change a folder's permissions, the permissions of files and folders inside it do not change. You may change the permissions of those files and folders manually.

4. In the menu that displays, select Permissions:



A list of owners and team members who have access to your project is displayed.

- Find the team member you want to change access for:

Permissions for examples

Owner:  Group:

Who	Type	Read	Write	Execute
owner		<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
group		<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
others		<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>
Mask		true	true	true
<input type="text" value="username"/>	User	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input type="text" value="username"/>	Group	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input type="text" value="username2"/>	User	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>
<input type="text" value="username2"/>	Group	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
<input type="text" value="username3"/>	User	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
<input type="text" value="username3"/>	Group	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

- Next to the team member's name, select or deselect the permissions for that user.

NOTE: You can add a team member and set their access at the same time by typing their name in a username box, setting their permissions, and then clicking the Add button.

- Click the Submit button.

The selected permissions are added, and the deselected permissions are removed.

NOTE: If a team member is in the Workbench application when you give them access, they must refresh their browser window to see their current permissions.

## Controlling non-team member access

You can choose to grant file or folder access to someone who is not part of the project team, as long as that person has an AEN account.

Sharing with individuals outside the team is a four step process:

- Copy or move the file or folder to your home directory.*
- Give the user read and execute access to your home directory.*
- Add the user to the file's permissions.*
- Have the user add your directory to their workbench.*

## Copying a file or folder to your home directory

Your home directory is displayed at the bottom of the File Manager pane in the Workbench.

To protect the other files and folders in your home directory—those you are not providing permissions to a user to access—we recommended that you:

1. Create a sub-folder.
2. Rename the folder with the name of the user you are granting access to.
3. Copy or move the file you want to grant permissions for to the renamed folder.

The file is copied or moved to the new location and is ready for you to update the file permissions.

### Granting file access

You must select read and execute access for a user to be able to view, but not edit, the files or folders.

1. Right-click the name of the file or folder you are granting access to.
2. In the menu that is displayed, select Permissions.
3. Click the Add button.
4. Type the username of the user to whom you are granting file access and press Enter.

**TIP:** If you grant access to a folder instead of a specific file, you only have to set permissions the first time you share the folder with each user, unless you need to update the permissions.

### Adding file permissions for a user

Once a user is included in your Permissions list, you must *add the correct permissions* for the user, in the same way as you would for a team member.

Once complete, depending on the access granted, the user will be able to view, read, change, and execute the file.

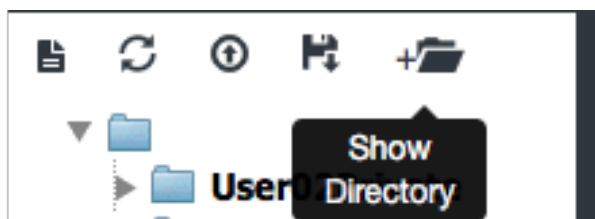
**NOTE:** If you change permissions for a folder instead of a file, the user will be able to see and access any files within that folder.

### Adding a directory to a user's workbench

The user can now add your home directory to their Workbench File Manager.

To add your home directory to another user's workbench, have the other user follow these steps:

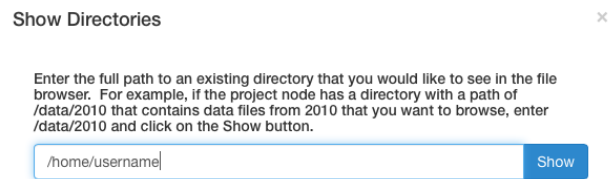
1. Click the Show Directory button at the top of the Workbench File Manager:



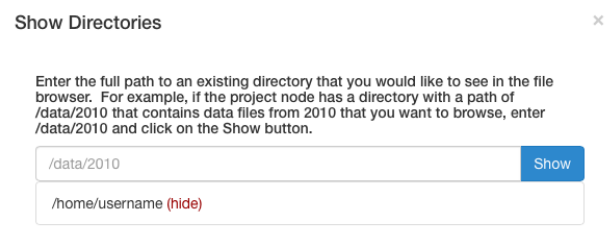
The Show Directories dialog box displays.

2. In the text box, type `/home/[yourusername]`.

NOTE: Replace `[yourusername]` with your AEN username.

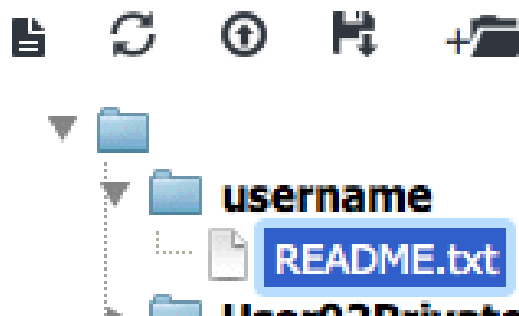


3. Click the Show button.
4. Verify that the folder is now displayed below the text box:



5. Close the Show Directories dialog box by clicking the X in the upper-right corner or by clicking anywhere outside the box.
6. Click the Refresh button.

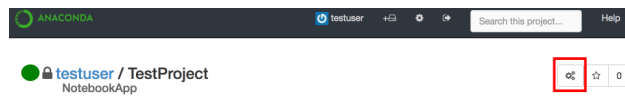
The shared file is displayed in the File Manager:



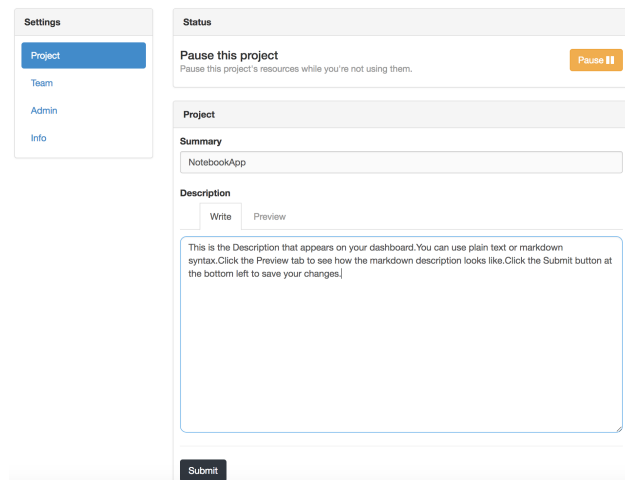
## Starting and stopping a project

TIP: Stopping a project stops all the applications launched for that project that use resources when running, such as memory and compute cycles. It is best to stop projects when they are not in use.

1. On the project home page, click the Project Settings icon to open the Project Settings page.



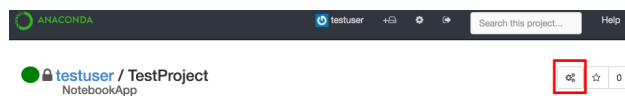
2. In the **Settings** menu, select Project.



3. In the Status section, click the Start or Stop button to toggle between manually starting and stopping your project.

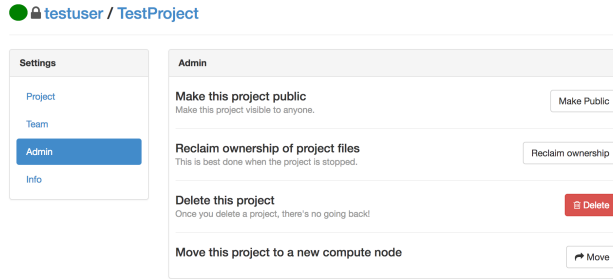
## Making a project public or private

1. On the project home page, click the Project Settings icon to open the Project Settings page.



2. In the **Settings** menu, select Admin.

3. Click the Make Public button.



4. If the project is already public and you want to make it private, click the Make Private button.

## Tagging a project

Existing tags assigned to a project are listed in the Tags section on the project's home page.

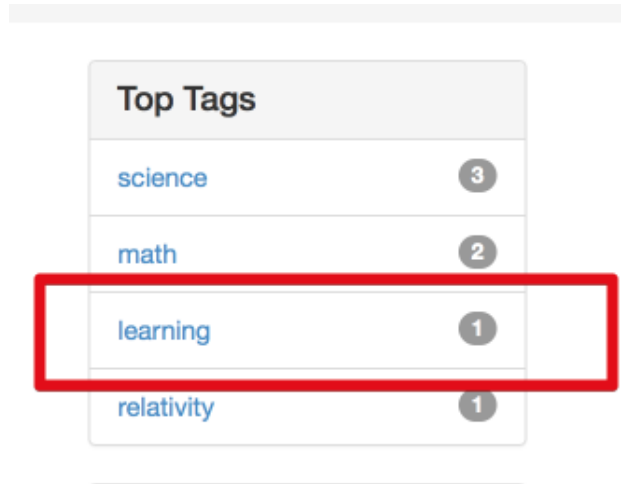
## Adding a tag

1. In the Tags box, type the name of the tag you want to add:

2. Click the Add button.

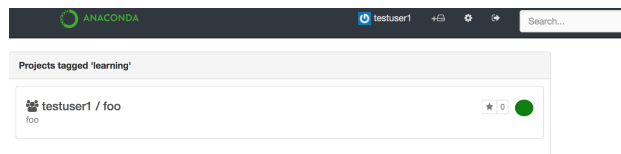
The new tag is added to the Tags list:

If the tag was not already in the Top Tags list on your user home page, it is added. If the tag was already listed because another project used it, the number next to the tag is incremented:



## Removing a tag

1. On your user home page, in the Top Tags list, click the tag name.



1. In the Tags list, click the X button next to tag name.

## Starring a project (rating)

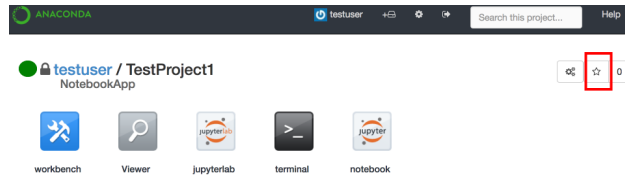
Starring a project makes it appear on your user home page in the Top Rated list.

Adding or removing stars for a project does not affect the stars added by other users.

1. Open the project that you want to star.
2. On the project home page, click the Star icon at the upper right:

3. To unstar a project, click the Star icon again.

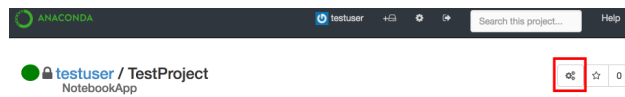




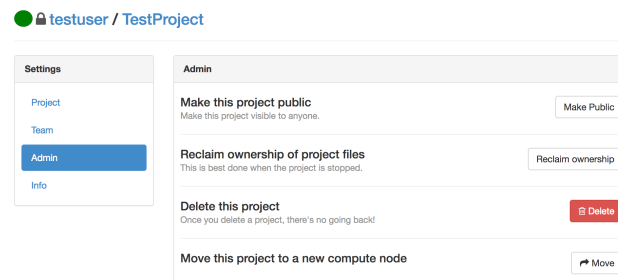
## Claim ownership of a project

When you claim ownership of a project, ownership of all files and folders created by the team members on the project is transferred to you. Project files and folders are copied and renamed.

1. *Stop the project* to prevent team members from making changes while you are changing ownership.
2. On the project home page, click the Project Settings icon to open the Project Settings page.



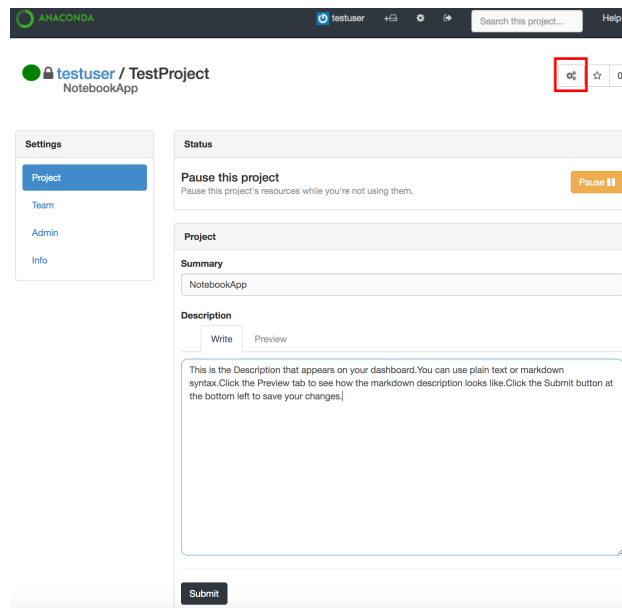
3. In the **Settings** menu, select Admin.



4. Click the Reclaim ownership button.

## Changing a project's summary or description

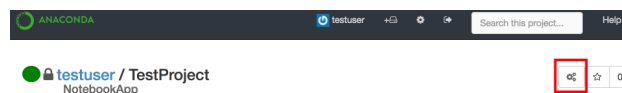
1. On the project home page, click the Project Settings icon to open the Project Settings page.
2. In the **Settings** menu, select Project.



3. Update your project's summary using plain text or its description using Markdown syntax.
4. Click the **Preview** tab to see a preview of the Markdown description.
5. Click the Submit button.

## Viewing a project's status

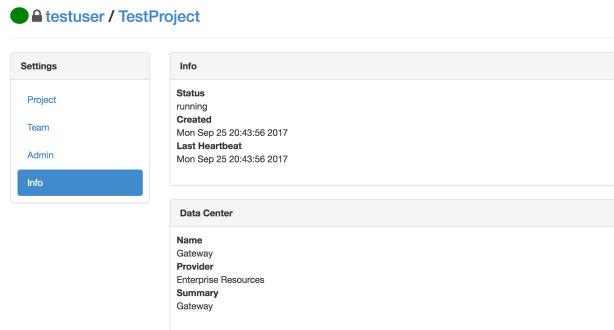
1. On the project home page, click the Project Settings icon to open the Project Settings page.



2. In the **Settings** menu, select Info.

On the Info page, you can see:

- Whether the project is currently running or stopped.
- When the project was created.
- When the project was last accessed.



- The data center in which the project is running.

## Viewing related projects

Related projects are listed on a project's home page.

These are projects that contain fields that are most similar to the current project.

**TIP:** You will only see projects to which you have been granted access: public projects, and private projects on which you are a team member.

## How related projects are identified

To determine which projects should be listed in Related Projects:

1. The recommendation engine scans the current project's files and weights the terms found to determine which of them to use for the likeness search.
2. The engine performs a search, with extra weight given to the "uses" and "imports" keywords.
3. The engine finds the files and projects that are most similar to the current project and scores the results.
4. The top-scoring matches are displayed in Related Projects. Only public projects and private projects to which you have access are included.

## Viewing top-rated projects

Top-rated projects are listed on your home page:

The number next to a project represents the number of stars that have been given to that project.

Click a project name to view the project's home page.

Team

Add

user02 (owner)

user01 (remove)

Related Projects

user01 / TestProject2

No Summary

user02 / User02Private

No Summary

user01 / TestProject

No Summary

Top Rated	
einstein	2
euler	1
laplace	1
plank	1
Public_project	1

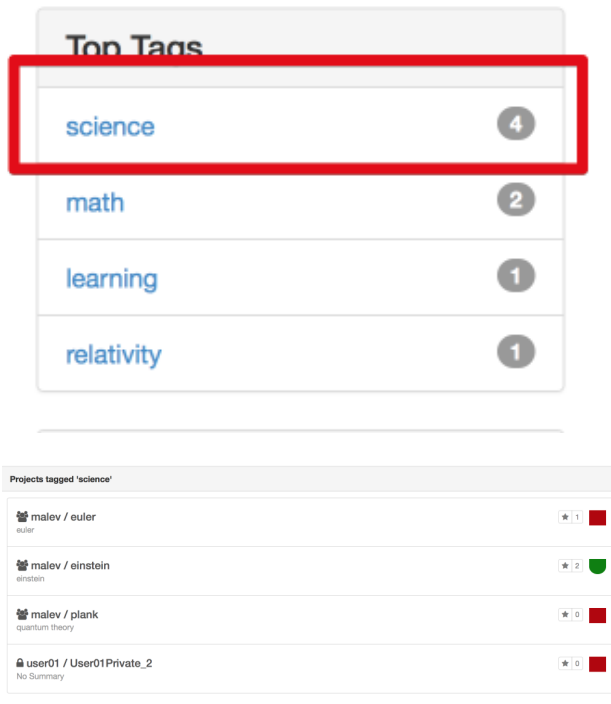
## Using tags to find a project

The top tags used on your projects are listed on your home page:

The screenshot shows the Anaconda user interface for a user named 'NewUser2'. The user's profile information is displayed at the top right, including their join date (Oct 20, 2016) and email (newuser@mycompany.com). The main content area is divided into two columns. The left column contains a 'Projects' section with one project listed: 'NewProject' by 'NewUser2', with a description 'Woo hoo! I finally get to play with notebooks!'. Below this is a 'Contributing' section stating 'Not currently contributing to any projects.' The right column contains three sections: 'Top Tags' with 'Fun fun fun' and 'Test project', 'Top Collaborators', and 'Top Rated' with 'test1', 'test2', and 'NewProject'.

To list all projects that share a specific tag, click the tag name:

A list of projects with the selected tag is displayed:



**TIP:** The list includes only projects that you have access to: public projects, and private projects on which you are a team member.

Click a project name to open the project's home page.

### Viewing your top collaborators

Your top collaborators are listed on your home page:



These are the team members who have the most projects in common with you.

To view a collaborator's home page—where you can see all public projects and the private projects they have shared with you—click the collaborator's name.

## Sharing projects and notebooks

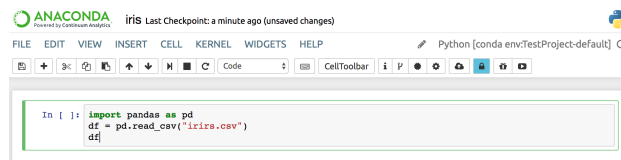
For information on sharing projects via the project settings and access control, see [Sharing projects](#).

To upload a Jupyter Notebook to Anaconda Repository:

1. Log in to Repository by running the `anaconda login` command or by using the login user interface provided by the [nbextension](#).

CAUTION: If you are not using a secure connection, we strongly recommended that you use the command line to log in.

2. To share your notebook environment, select the Attach conda environment checkbox. This ensures that your team members will have the right environment for your notebook.
3. Click the Upload button to upload your notebook to your local Repository or to [Anaconda.org](#), depending on how your administrator has set up AEN:



NOTE: If you have not yet logged into Repository or Anaconda Cloud, or have not created an account, you will be asked to do so.

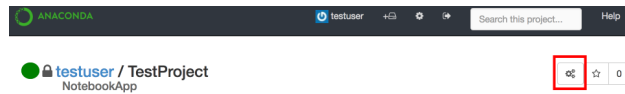
## Other ways to share a notebook

- Print—In the **File** menu, select Print.
- Download and share—In the **File** menu, select one of the following options:
  - Download as Notebook.
  - Download as Python.
  - Download as HTML.
  - Download as Markdown.
  - Download as ReStructured Text.
  - Download as PDF.
- Share and control team members' direct access to read, write and/or execute your notebook file or folder. For more information, see [Controlling access to your project](#).
- Share and control non-team members' file or folder access. For more information, see [Controlling access to your project](#).
- Create a presentation with [NBPresent 4.1](#).

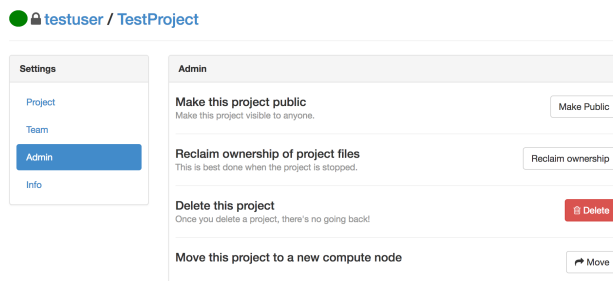
## Deleting a project

CAUTION: Deleting a project deletes all project files and information! There is no undo option.

1. Download a copy of any project files that you need to save.
2. On the project home page, click the Project Settings icon to open the Project Settings page.



3. In the **Settings** menu, select Admin.



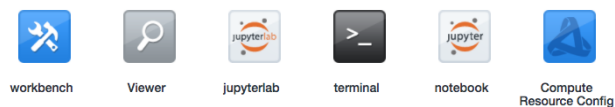
4. Click the Delete button.

## Using AEN applications

The applications in your project make it easy for you to interact with your files and data, manage your project's resources and to customize your AEN experience.

To use applications, log into AEN, then select the project you want to work on or create a new project and open it.

On the project home page, the following application icons are displayed:



TIP: Each application opens in a new browser tab. You can run multiple applications at the same time in your project. For more information on each AEN application, see:



- *Using Workbench*—File viewer and manager, including permissions settings.
- *Using Viewer*—View-only versions of notebooks and other text files.
- *Using JupyterLab*—Alpha preview of the next generation notebook.
- *Using Terminal*—Basic bash shell Terminal.
- *Using Jupyter Notebook*—Jupyter Notebooks with extensions.
- *Using Compute Resource Configuration*—Project information, view and manage applications.

## Using Workbench

- *Opening Workbench*
- *Using File Manager*
- *Opening the Workbench terminal*

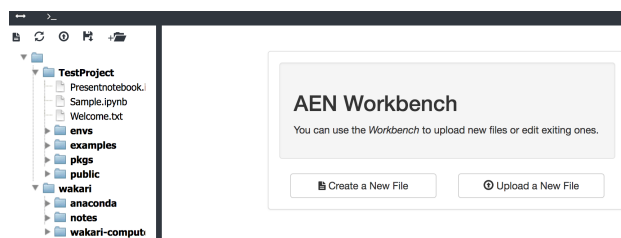
Workbench is a file viewer and manager that includes a file editor and file permissions manager.

You can use Workbench to:

- Upload and download files using the *File Manager*.
- Create new files and folders using the *File Manager*.
- Copy and move files to new locations using the *File Manager*.
- Rename files and/or folders using the *File Manager*.
- Manage the *access permissions* of team members.
- Grant or revoke *access to non-team members*.

Workbench also includes a simple Terminal application, which is convenient because the File Manager is always visible, making navigation simple.

When you first open Workbench, the File Manager is displayed in the left pane, and the Create a New File and Upload a New File buttons are in the right pane:



When you open a file or Workbench Terminal, it is displayed in the right pane. To make the Create or Upload a file options re-appear, refresh your browser window.

Two small icons are displayed in the black navigation bar at the top of the Workbench page. Hovering over them displays tool tips that describe their use:

- The Toggle icon displays or hides the File Manager.
- The Terminal icon opens a simple terminal window.

### Opening Workbench

To open Workbench:

1. Log in to AEN.
2. Select the project you want to work on, or create a new project and open it.
3. On the project home page, click the Workbench icon:



Workbench opens in a new browser window.

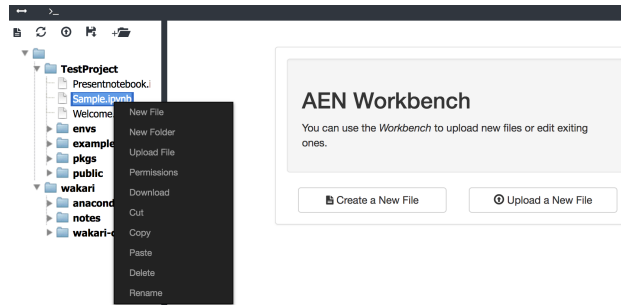
### Using File Manager

The File Manager is an intuitive way to interact with your files and folders.

### Using the options drop-down menu

To perform any of the actions described below:

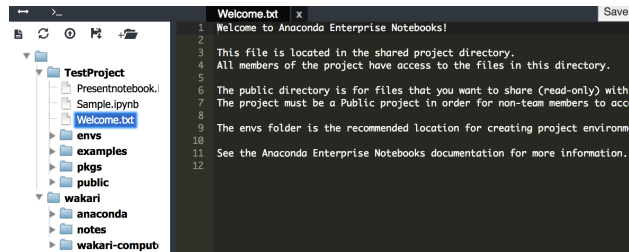
1. Right-click on any folder to display the options drop-down menu.
2. Select one of the following options:
  - New File—Create and edit a new file.
  - New Folder—Create a new folder.
  - Upload File—Upload a file to the selected folder. You can also drag a file to the folder.
  - Permissions—*Control access to files and folders.*
  - Cut—Cut the selected file or folder.
  - Copy—Copy the selected file or folder.
  - Paste—Paste a previously cut or copied file or folder.
  - Delete—Delete the highlighted file or folder.
  - Rename—Rename the highlighted file or folder.



## Editing files using the File Editor

1. Double-click any text file in the File Manager.

The File Editor opens in the right pane:

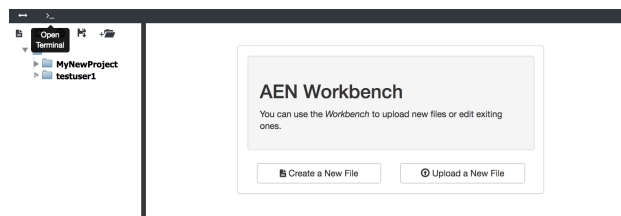


2. When you finish editing the file, click the Save button.

NOTE: To close the file without saving, click the X at the top of the page under the file name.

## Opening the Workbench terminal

In the navigation bar, click the Open terminal icon:



A Terminal—bash shell—is displayed in the right pane.

**TIP:** You can open additional terminals by clicking the Open terminal icon again, or by clicking the Plus + icon at the top of an open terminal.

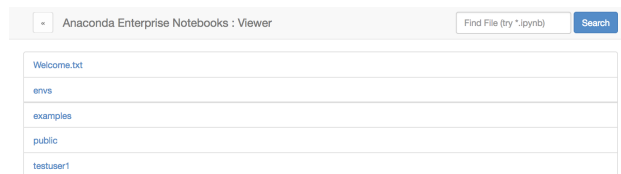
To move between terminal windows, click the **Terminal** tab in the navigation bar, then select the number of the terminal window you want to work in.

### Using Viewer

The Viewer application displays a static, view-only version of your notebooks and other text files by rendering the text files directly and using the NBConvert tool to convert notebooks to static HTML.

1. Log in to AEN.
2. Select the project you want to work on, or create a new project and open it.
3. On the project home page, click the Viewer icon.

Viewer opens in a new browser window:



4. Click any folder to view its contents, or click any filename to view the file.
5. To search for a file or folder name, type text in the Find File box, then press the Enter key. This is not a full-text search, but wildcards are permitted.

### Using JupyterLab

JupyterLab is an early alpha-preview of the next generation of the Jupyter Notebook. It is included so that you can take a tour and play with its capabilities.

**CAUTION:** JupyterLab is experimental. It is not yet intended for production work.

JupyterLab does not include any of the notebook extensions that are available in the *Jupyter Notebook app*.

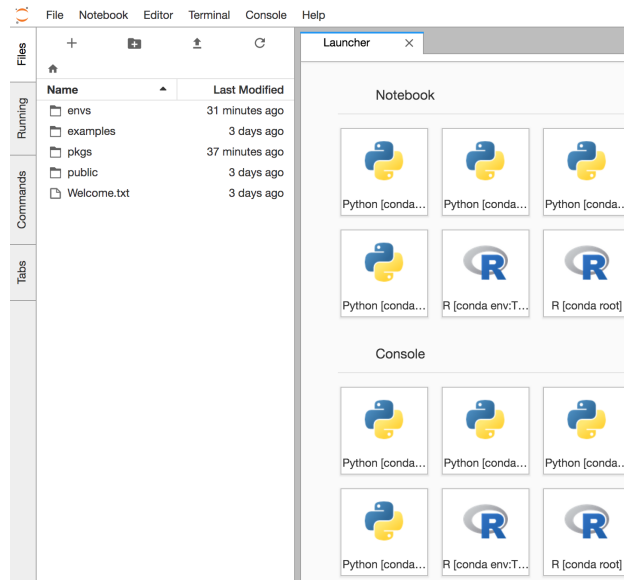
For more information about JupyterLab, see the [documentation](#).

You can also download and print a `Jupyter cheat sheet` on using Jupyter Notebook and the new JupyterLab.

To open JupyterLab:

1. Log in to AEN.
2. Select the project you want to work on, or create a new project and open it.
3. On the project home page, click on the JupyterLab icon.

JupyterLab opens in a new browser window:



Experiment with the application on your own, using the **Notebook**, **Editor**, **Terminal** and **Console** menus.

To review a guided tour of all of the features JupyterLab will contain when it is ready for production, click the Take a tour link in the right pane.

## Using Terminal

The Terminal application is a simple bash shell terminal that runs in your browser:

```

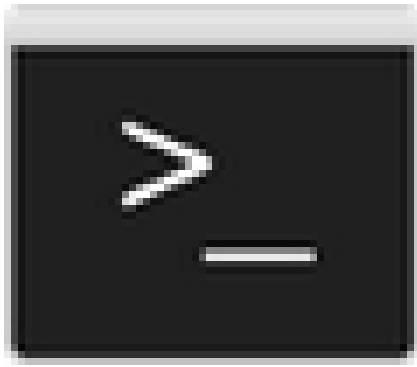
+ 1 bash
(/projects/aen_admin/TestProject/envs/default) ls
envs  examples  pkgs  Presentnotebook.ipynb  public  Sample.ipynb  Welcome
(/projects/aen_admin/TestProject/envs/default)

```

Using Terminal, you can:

- Access your home directory and your project drive.
- Open multiple shells within one instance of Terminal.
- Open multiple instances of Terminal in the same browser window.

1. Log in to AEN.
2. Select a project you want to work on, or create a new project and open it.
3. On the project home page, click the Terminal icon:



## Terminal

Terminal opens the project directory in a new browser window.

By default, the project directory is `/projects/username/project-name`.

EXAMPLE: `/projects/TestUser/MyFirstNotebook`

4. To see the physical path of your directory, run the Print Working Directory command `pwd -P`.

TIP: The physical path `-P` is important because project attaches data to the beginning of your virtual path to keep your project files together.

5. To navigate out of your project directory to your home directory, run the command `cd`.
6. To return to your project directory, run the command `cd/projects/username/project-name`.

TIP: If you are new to navigating in a terminal, you may want to use *the Workbench terminal*, which includes a visual navigation tree in the File Manager.

### Using multiple Terminals

You can open as many terminals as you want.

To open another shell in the terminal, in the upper left of the pane, click the plus `+` icon.



A corresponding number appears after the plus + icon and 1.

To move to another Terminal, click the corresponding number.

The color of the number tab changes to show which terminal is currently selected.

## Using Jupyter Notebook

- *Opening the Jupyter Notebook application*
- *Using example notebooks*
- *Creating a new Jupyter Notebook*

The Jupyter Notebook application allows you to create and edit documents that display the input and output of a Python or R language script. Once saved, you can share these files with others.

NOTE: Python and R language are included by default, but with customization, Notebook can run several other kernel environments.

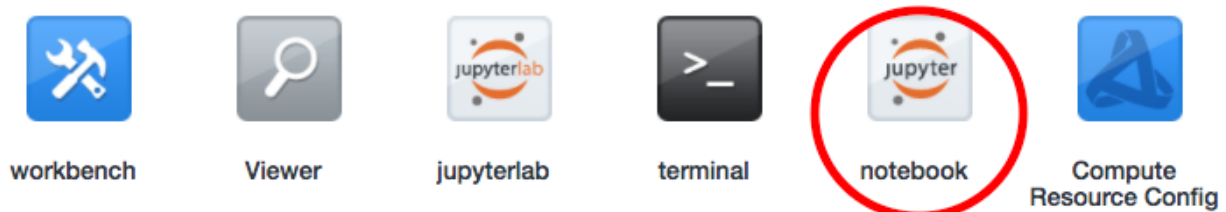
This page provides a brief introduction to Jupyter Notebooks for AEN users.

For the official Jupyter Notebook user instructions, see [Jupyter documentation](#).

For information on the notebook extensions available in AEN, see [Using Jupyter Notebook extensions](#).

## Opening the Jupyter Notebook application

1. Log in to AEN.
2. Select the project you want to work on, or create a new project and open it.
3. On the project home page, click the Jupyter Notebook icon:



Jupyter Notebook opens in a new browser window:

TIP: You can see the same *File Manager* in the Terminal, Workbench, and Viewer applications.



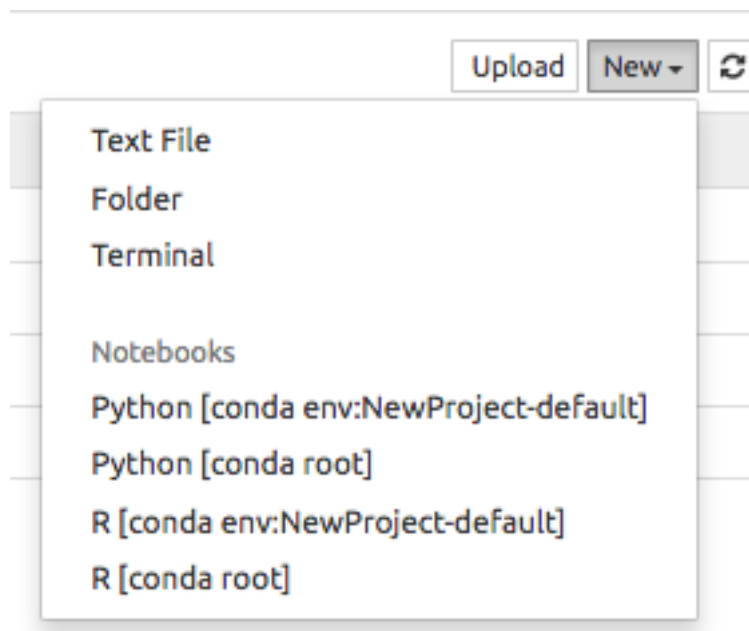
## Using example notebooks

The `Examples` folder in Jupyter Notebook contains several types of Notebook examples created in Python—and one with R language—kernel environments.

Open any example notebook to experiment and see how it works.

## Creating a new Jupyter Notebook

1. At the top right of the **Files** tab, click the **New** button.





2. Select the kernel environment to create your new notebook in.

NOTE: Customizable Python and R Language kernel environments are automatically created for you during project creation.

- Your project's default conda env kernels are a cloned copy of the root environment. You can customize them and install and delete additional packages.
- Root environment is managed by your Administrator. You cannot make or save any changes to it.
- You can switch between Python, R language and any other custom kernels in the notebook as you work in your notebook. For more information, see [Using the Synchronize Environments extension](#).

The new notebook is saved in the related project directory and displayed.

## Using Jupyter Notebook extensions

The following extensions are available for use with AEN's Jupyter Notebook application:

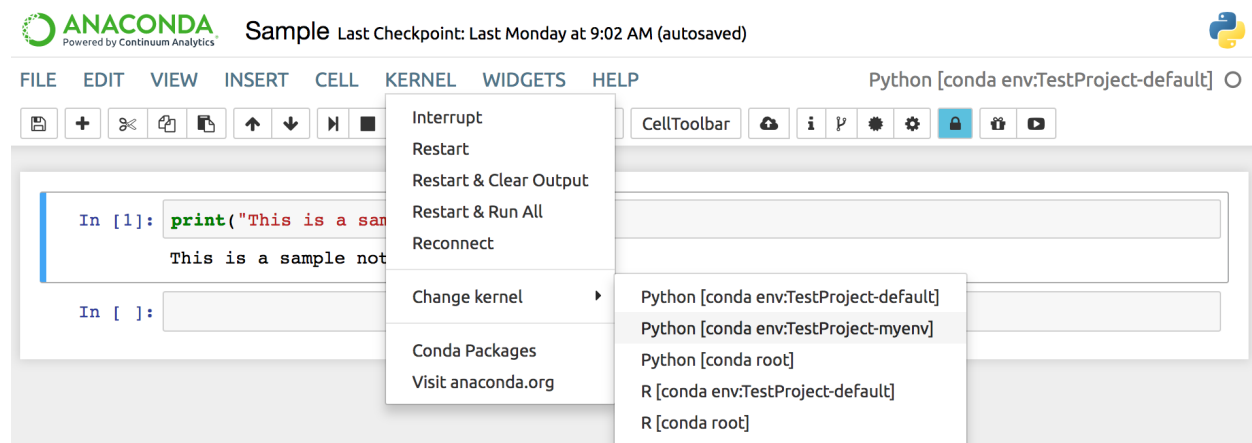
- [Synchronize Environments](#) with Jupyter from the **Kernel** menu.
- [Locking](#) adds multi-user capability from the Lock button.
- [Revision Control Mechanism \(RCM\)](#) adds Status, Checkout and Commit buttons.
- [Conda environment and package management](#) tab.
- [Conda notebook](#) adds conda management inside Notebook from the Kernel > Conda Packages menu option.
- [Anaconda Cloud integration](#) from the Publish to cloud button.
- [Notebook Present](#) turns your notebook into a PowerPoint-style presentation.

## Using the Synchronize Environments extension

The Synchronize Environments extension allows you to apply a Python, R language or any other custom environment inside your current notebook session, without needing to start up several Notebook instances using each of the selected environments.

To change environments:

1. Open the **Kernel** menu.



2. Click the Change kernel option.
3. From the list, select the environment to use.

NOTE: In AEN 4.1+ the default kernel for projects is `default`. In versions prior to 4.0, the default kernel for projects is `root Python`.

## Using the Locking extension

Multi-user capabilities are engaged in AEN when multiple users work in the same notebook file.

The Locking extension allows you to lock a notebook to prevent multiple team members from making changes at the same time. Notebooks are automatically locked when you open them.

If team members open a notebook and make changes while it is locked, their save capability is disabled, and they cannot overwrite the notebook.

To override the lock, they must actively take control of the locked file by clicking the Lock icon in the Notebook menu bar:



NOTE: This is a soft locking model. Team members can choose to override your lock to save their work. If you give team members write access to your files, confirm that they understand that they should never unlock your file unless they are making meaningful, non-destructive team contributions.

## Using the Revision Control Mechanism extension

The Revision Control Mechanism (RCM) Jupyter Notebook extension provides simple version control for notebook files. It uses the internal Jupyter functionality to perform tasks.

On the surface, RCM uses a simple linear model, but beneath that is a more complex git-based branching model. To prevent merge conflicts, this model uses a “latest wins” policy as its main merging strategy.

The RCM Jupyter Notebook extension adds four buttons:



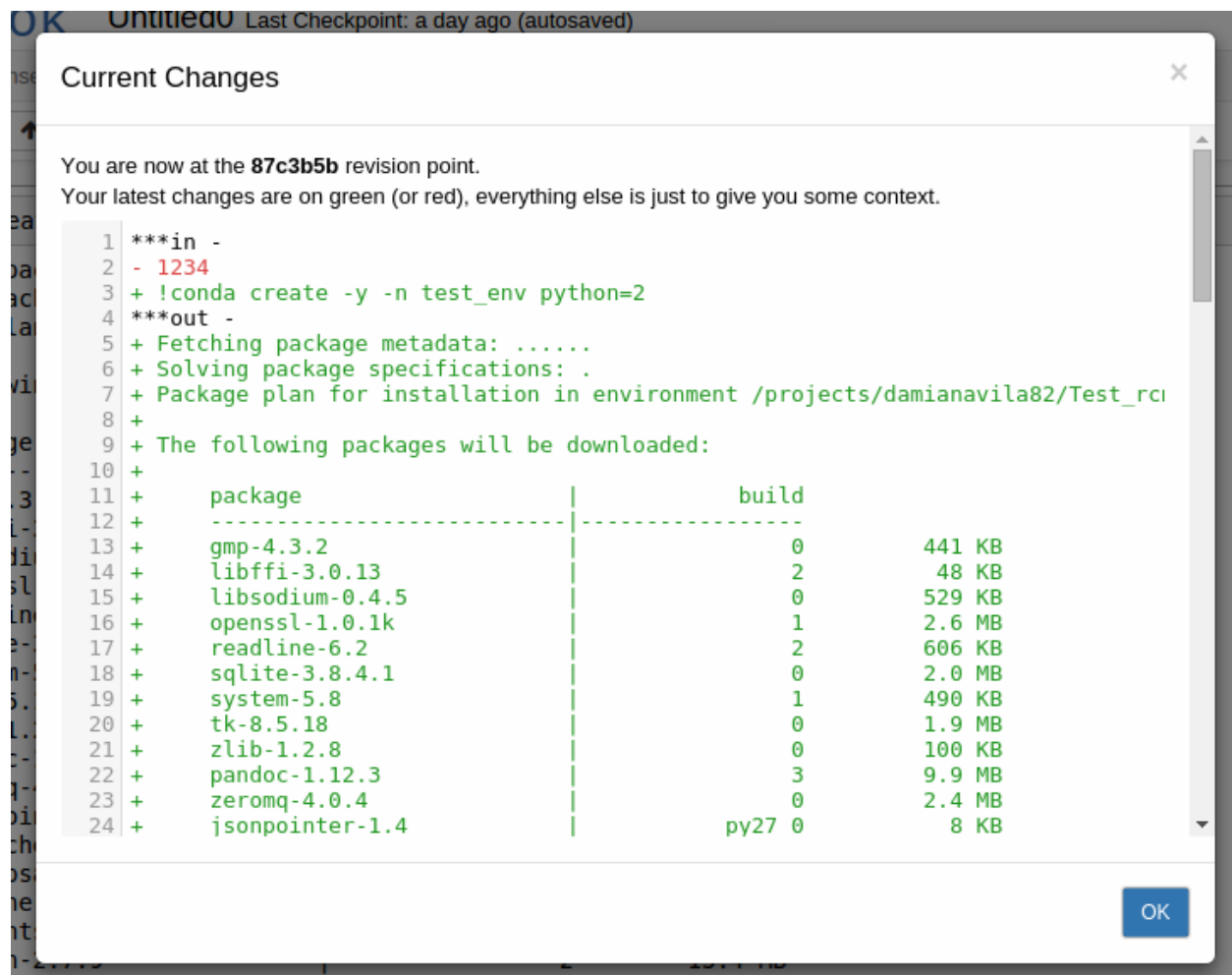
- *Status.*
- *Checkout.*
- *Commit.*
- *Configure git.*

TIP: If you do not see the RCM buttons, see *Setting up RCM for the first time.*

## Using the Status button

The Status button allows you to see what revision you are on.

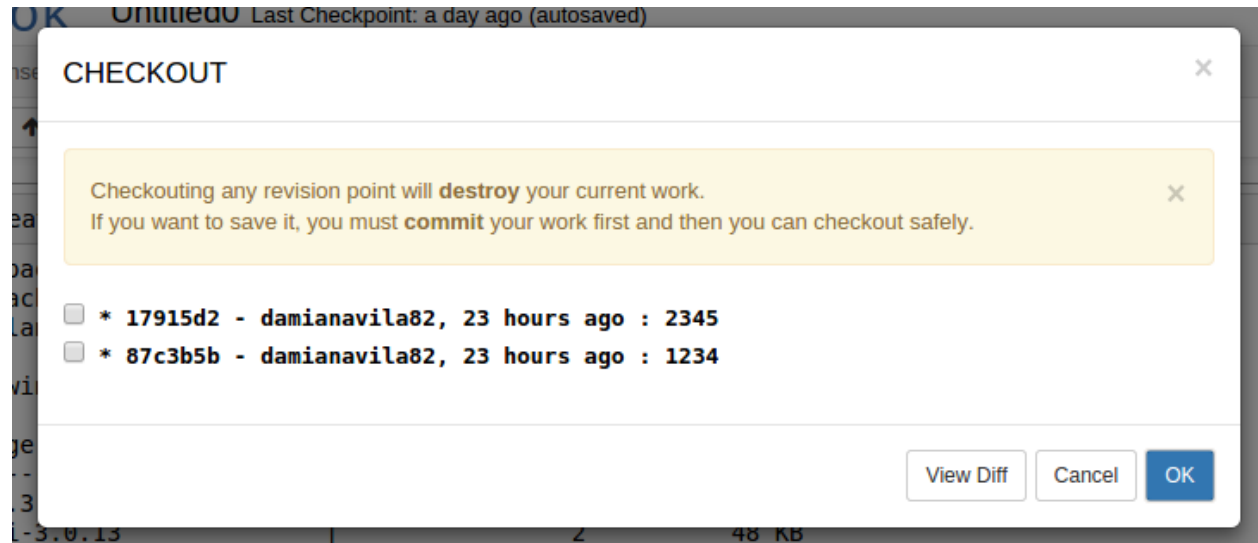
Clicking the Status button displays:



## Using the Checkout button

The Checkout button allows you to view a list of the previous revision points, check out a previous revision or compare differences between revisions.

Clicking the Checkout button displays:



## Checking out a previous revision

To checkout a notebook at an earlier revision point:

1. Select the checkbox next to the desired revision point.
2. Click the OK button.

A copy of the notebook at the selected revision point is displayed.

NOTE: If you have not saved the work in your current project window, checking out a previous revision destroys it. If in doubt, click the Cancel button and save your work before reverting to a previous revision point.

## Comparing revisions

To compare 2 previous revision points:

1. Select the checkboxes of the revision points to compare.
2. Click the View Diff button.

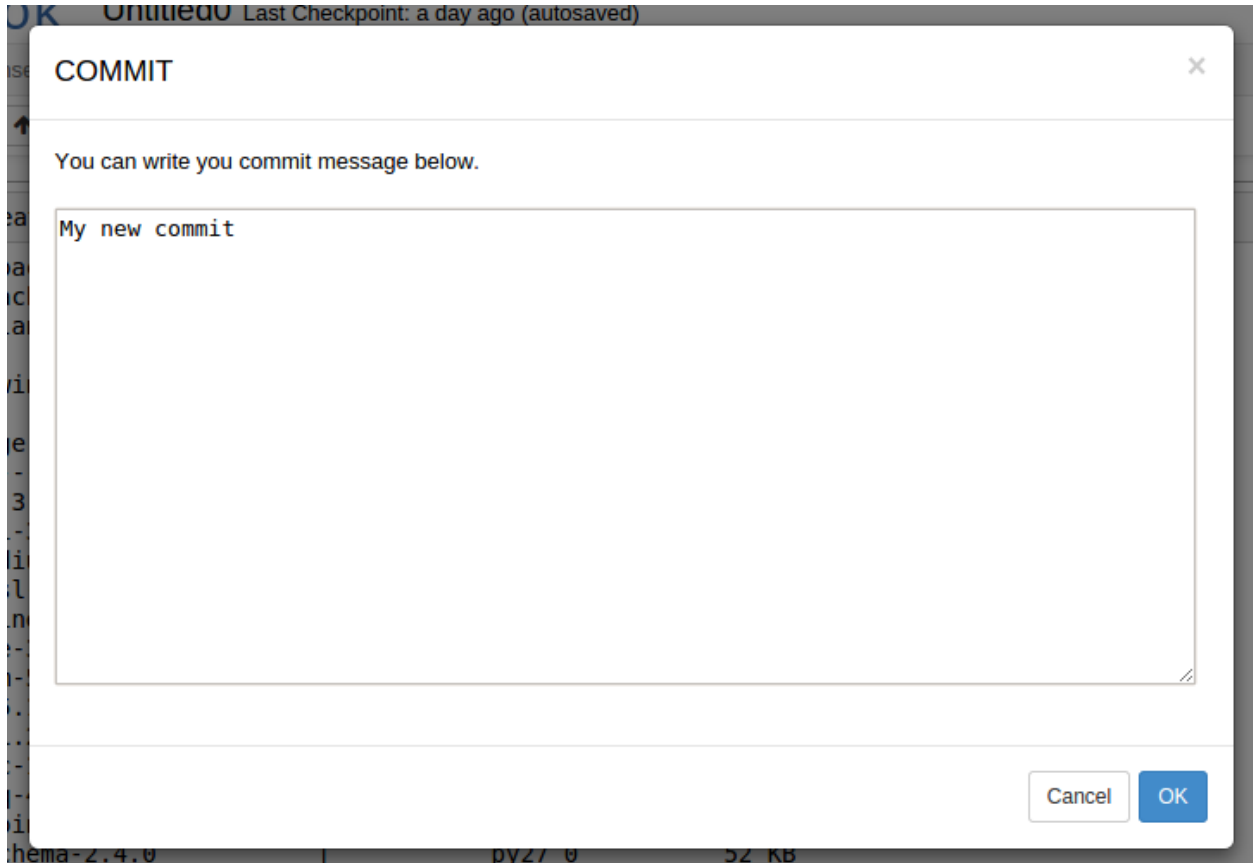
A side-by-side comparison is displayed.

Click the Cancel button to close the differences window.

## Using the Commit button

The Commit button allows you to save or persist the current changes, keeping a permanent record of any changes that are introduced, so that you do not have to worry about losing important data.

Clicking the Commit button displays:



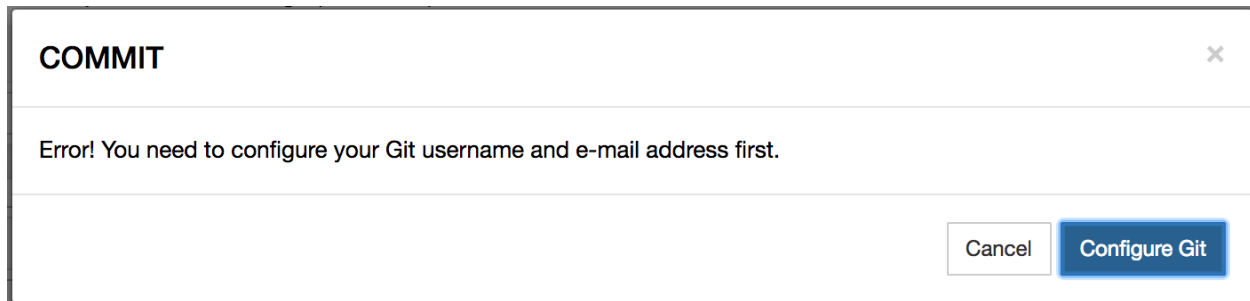
1. Enter a description of the changes in the commit as a reminder in case you need to revert back to it later.
2. Click the OK button.

Your changes are committed and a revision point is created.

If Git user name and user email are not set, the following window appears:

Configure Git and then try to commit again.

TIP: You can roll back committed changes by *checking out a previous version*.



### Using the Configure git button

The Configure git button allows you to configure Git user name and email values.

After clicking the Configure Git button, the following window appears:

A dialog box titled 'Git Configuration' with a close button (X) in the top right corner. It contains two input fields. The first is labeled 'Username' and has the text 'John Doe' entered. The second is labeled 'Email' and has the text 'johndoe@example.com' entered. At the bottom right, there are two buttons: 'Cancel' and 'Save'.

Enter user name and e-mail address. Click the OK button when finished.

### Setting up RCM for the first time

If you do not see the RCM buttons in your notebook:

1. Go to the project home page.
2. Open the Terminal application.
3. In the terminal window, run:

```
git config --global user.email "you@example.com"  
git config --global user.name "Your Name"
```

NOTE: Change `you@example.com` to your email address, and `Your Name` to your actual name.

4. Open Jupyter Notebook and refresh the page.

## Using the NBConda extension

The NBConda extension adds a Conda tab to your notebook for easy environment and package management from within the notebook.



FilesRunningIPython ClustersConda

2 Conda environments

Action	Name	Default?	Directory
	root		/opt/wakari/anaconda
	default	✓	/projects/aen_admin/TestProject/envs/default

1143 available packages

Search...

→

376 installed packages in environment "default"

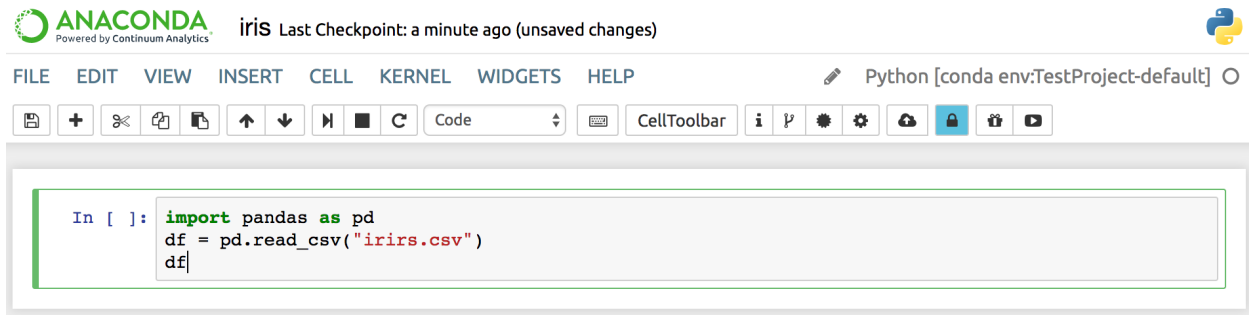
Name	Version	Channel
<input type="checkbox"/> _license	1.1	defaults
<input type="checkbox"/> _nb_ext_conf	0.4.0	defaults
<input type="checkbox"/> abstract-rendering	0.5.1	defaults
<input type="checkbox"/> accelerate	2.3.1	defaults
<input type="checkbox"/> accelerate_cudalib	2.0	defaults
<input type="checkbox"/> aen-app-jupyterlab	0.4.0	wakari

Name	Version	Build	Available
<input type="checkbox"/> _license	1.1	py27_1	
<input type="checkbox"/> alabaster	0.7.10	py27_0	
<input type="checkbox"/> anaconda	custom	py27_0	
<input type="checkbox"/> anaconda-client	1.5.1	py27_0	
<input type="checkbox"/> anaconda-project	0.6.0	py27_0	
<input type="checkbox"/> asn1crypto	0.22.0	py27_0	

Click the Conda tab in a notebook to display:

- Conda environments list—export, clone or delete an environment in the action column, or create a new environment by clicking the plus + icon. Switch to an environment by clicking it; packages for that environment are displayed below in the installed packages list.
- Conda available packages list—for the selected environment in currently configured channels, search for packages and click a package name to install it.
- Installed packages list—in the selected environment, check for updates, update or delete selected packages.

**TIP:** While you are in any notebook, you can jump to the NBConda extension for that environment by clicking the **Kernel** menu and selecting Conda Packages:



## Using the Conda Notebook extension

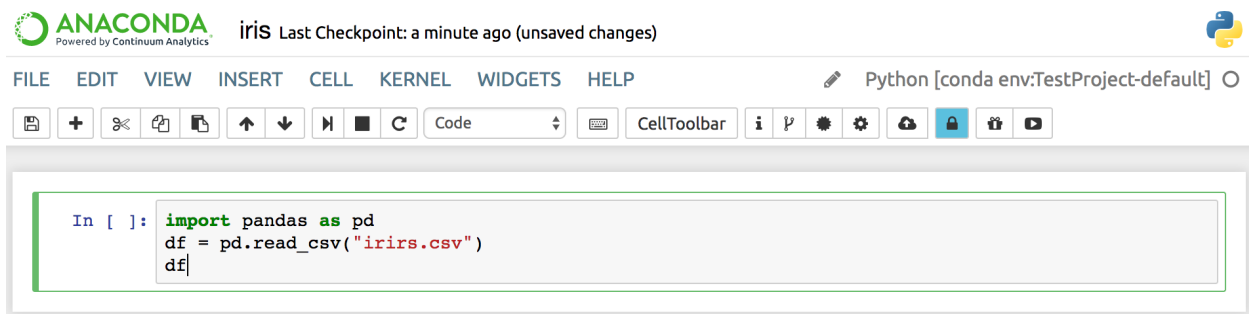
The Conda Notebook extension adds the Conda Packages option to the **Kernel** menu.

Select the Conda Packages option to display a list of all of the Conda packages that are currently used in the environment associated with the running kernel, as well as any available packages.

From the Conda Packages option, you can perform all of the tasks available in the *Conda tab*, but they will only apply to the current environment.

## Using the Anaconda Cloud extension

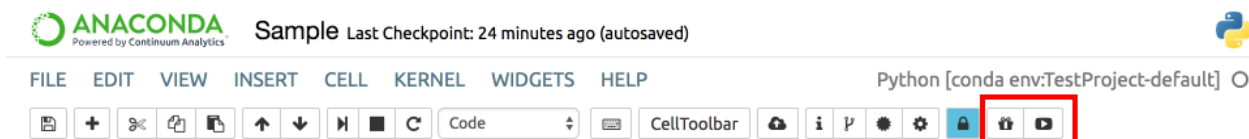
The Anaconda Cloud extension adds the Cloud button to your notebook, allowing you to easily upload your notebook to Cloud:



## Using the Notebook Present extension

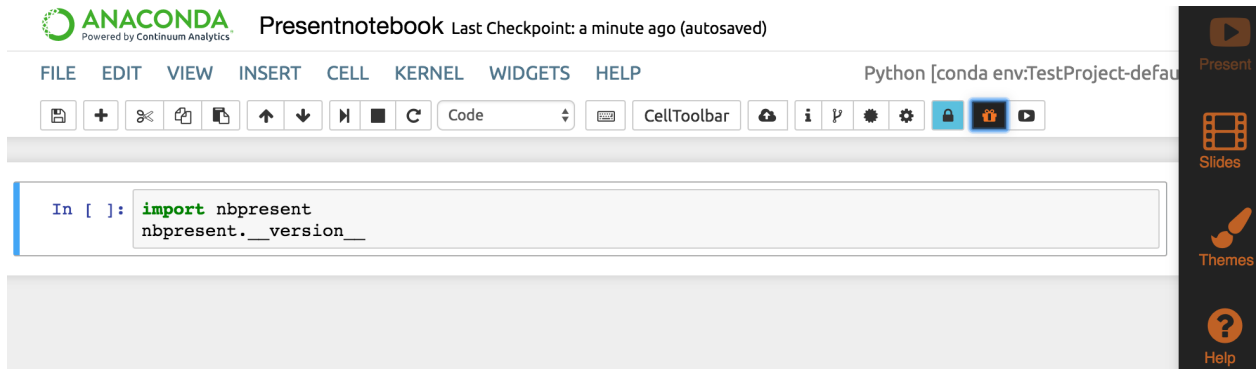
The AEN Notebook Present extension turns your notebook into a Microsoft PowerPoint-style presentation.

The Present extension adds 2 buttons to Notebook's menu bar—Edit Presentation and Show Presentation:





To begin using Notebook Present, click the Edit Presentation button.

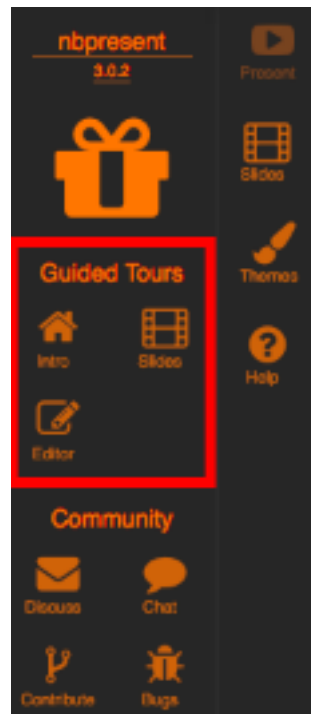


The Notebook Present sidebar is displayed on the right side of your browser:

Clicking each icon changes the menu and layout of your notebook.

Clicking the Help icon displays 3 tours—demonstrations—of the main features of Present:

- *Intro tour.*
- *Slides tour.*
- *Editor tour.*



Select one of the tours to view a short presentation regarding the specifics of that feature.

### Intro tour

The Intro tour is a 2-minute presentation that explains how to use the main features of Present, including a description of each button's purpose.

NOTE: At any time, you can pause, go back to the previous or move forward to the next slide.

The following information is covered in the Intro tour:

- **App Bar**—When Authoring, this allows you control the content and style of your presentation. It also can be used to activate several keyboard shortcuts for editing:
- **Stop Authoring**—Clicking the Edit Presentation button again stops Authoring, and removes all keyboard shortcuts.
- **Show Presentation**—If you just want to run your presentation without using any Authoring tools, just click the Show Presentation button.
- **Presenting/Authoring**—Once you've made some slides, start Presenting, where you can use most Notebook functions with the Theme we have defined, as well as customize slides on the fly.
- **Slides button**—Slides, made of Regions linked to Cell Parts are the bread and butter of any presentation, and can be imported, created, linked, reordered, and edited here.
- **Theming**—Theming lets you select from existing colors, typography, and backgrounds to make distinctive presentations. The first theme you select will become the default, while you can choose custom themes for a particular slide, like a title.
- **Saving**—Whenever you save your Notebook, all your presentation data will be stored right in the Notebook .ipynb file.
- **Downloading**—After you've made a presentation, you can download it as an HTML page by choosing Download → Download As: Presentation (.html) in the menu.
- **Help**—Activate Help at any time to try other tours, connect with the Present developers and community, and other information.

## Keyboard shortcuts



The Jupyter Notebook has two different keyboard input modes. **Edit mode** allows you to type code/text into a cell and is indicated by a green cell border. **Command mode** binds the keyboard to notebook level actions and is indicated by a grey cell border with a blue left margin.

Mac OS X modifier keys:

: Command

: Control

: Option

: Shift

: Return

: Space

: Tab

### Command Mode (press to enable)

: find and replace

: previous slide

: next slide

: next slide

: enter edit mode

: open the command palette

: run cell, select below

: run selected cells

: run cell, insert below

: to code

: to markdown

: extend selected cells above

: extend selected cells above

: extend selected cells below

: extend selected cells below

: insert cell above

: insert cell below

: cut selected cells

: copy selected cells

: paste cells above

: paste cells below

: undo cell deletion

Close

The screenshot shows the Anaconda Presentnotebook interface. At the top, the Anaconda logo is on the left, and the title "Presentnotebook" is followed by "Last Checkpoint: 4 minutes ago (autosaved)". Below the title is a menu bar with "FILE", "EDIT", "VIEW", "INSERT", "CELL", "KERNEL", "WIDGETS", and "HELP". To the right of the menu bar, it says "Python [conda env:TestProject-defa". Below the menu bar is a toolbar with various icons for file operations, navigation, and execution. The main area contains a code cell with the following code:

```
In [ ]: import nbpresent
        nbpresent.__version__
```

Below the code cell, there is a large gray area with the text "No Slides... yet!" and "You can create an empty slide by pressing **+** or by importing slides:". To the right of this text is a button labeled "Basic" with a slide icon and "1 Slides". At the bottom left, it says "Your Slides". On the right side, there is a vertical sidebar with icons for "Present", "Slides", "Themes", "Help", and a "+ Slide" button at the bottom.

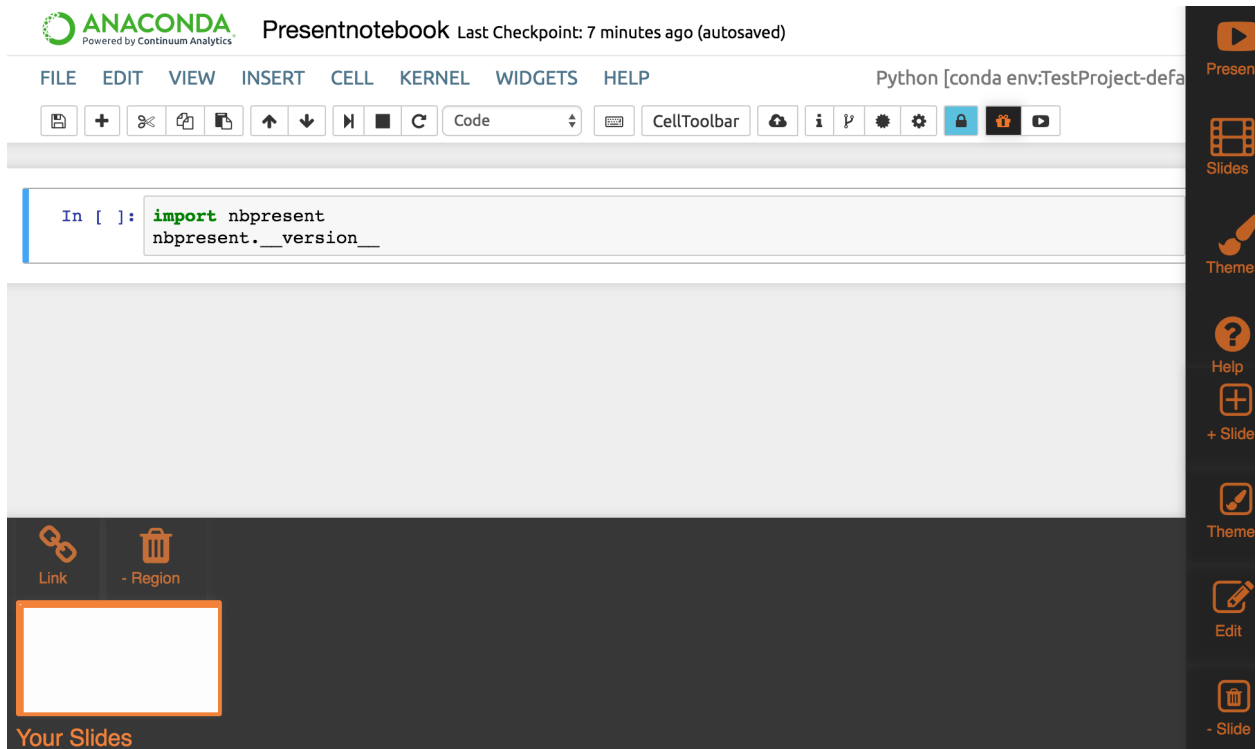
The screenshot shows the Anaconda Presentnotebook interface with a slide titled "Hello, *nbpresent!*". The slide content includes a code cell with the following code:

```
In [ ]: import nbpresent
        nbpresent.__version__
```

Below the code cell, there is another code cell with the prompt "In [ ]:". On the right side, there is a vertical sidebar with icons for "Present", "Slides", "Themes", "Help", and a "+ Slide" button at the bottom. The sidebar also shows a list of themes: "li 5", "h1 5.25", "h4 3", "h6", "h3 3.75", "h1 7", and "h4 3".

## Slides tour

Slides make up a presentation. Clicking Slides toggles the sorter view and the Slide Toolbar on and off:



The Slides tour explains how to create and manage slides, including the following information:

- Slide Toolbar—Create a new slide. Clicking + Slide will offer some choices for creating your new slide.
- Import—The quickest way to create a presentation is to import each cell as a slide. If you’ve already created slides with the official slideshow cell toolbar or RISE, you can import most of that content.
- Template Library—You can create a presentation from an existing template.
  - Reuse Slide as Template—You can create a presentation based on an existing slide.
  - Simple Template—A common template is the Quad Chart, with four pieces of content arranged in a grid.
- Region—The Quad Chart has four Regions. To select a region, click it.
  - Link a Region to a Cell Part—Each Region can be linked to a single Cell Part using the Link Overlay, which shows all of the parts available.
    - \* Cell Part: Source (blue)—Source, such as code and Markdown text.
    - \* Cell Part: Outputs (red)—Outputs, such as rich figures and script results.
    - \* Cell Part: Widgets (purple)—Jupyter widgets, interactive widgets that provide both visualization and user input.

- \* Cell Part: Whole (orange)—Finally, a Whole Cell, including its Source, Widgets and Outputs can be linked to a single region.
- Unlink a region from a Cell Part—Unlinking removes the connection between a region and a cell part, without deleting either one.
- Region: Trashing—Trashing a Region permanently deletes it, without affecting any linked Cell Part.
- Part Thumbnail—We'll try to draw a part thumbnail. It can only be reliably updated when a linked Cell Part is on-screen when you mouse over it, but you should usually be able to get an idea of what you're seeing. The colors of the regions correspond to the cell types.
- Presenting—Clicking the Present button while editing brings up the Presenter with editing mode still enabled:
  - Linked inputs and widgets are still interactive.
  - Go forward—Click to go to the next slide
  - Go back—Click to go back to the previous slide
  - Go back to the beginning—Click to go back to the first slide
  - My work is done here—Click to go back to the Notebook.

### Editor tour

Once you've made a few slides, you'll likely want to customize them. The Editor tour explains how to edit your notebook, including the following information:

- Editing Slides—Activate the Slide Editor by double-clicking it, or by clicking Edit Slide.
- Region Editor—Click to drag Regions around and resize them.
- Region Tree—Reorder Regions and see the details of how Regions will show their linked Parts.
- Add Region—Add new regions.
- Attribute Editor—Edit the properties of a region.
- Data Layouts—In addition to manually moving regions, you can apply these layouts to automatically fill your slides.
- More Regions—Add more regions—with a weight of 1.
- Tree Weight—Make a Region bigger or smaller, based on its relative weight.
- 12 Grid—A compromise between the Free and Treemap layouts, the 12 Grid option rounds all of the values in a layout to a factor of 12.

### Using Compute Resource Configuration

The Compute Resource Configuration (CRC) application displays information about the current project and allows you to set a custom project environment and view and manage your other AEN applications, including stopping, starting, restarting and viewing the logs of each.

The CRC application screen contains 3 sections:

- *Info.*
- *Conda environment.*
- *Running apps.*

The screenshot shows the Anaconda AEN interface with three main sections:

- Info:** Displays system information including Hostname (davila-aen-test), Project Home (/projects/testuser1/demo), and Project RC file (/projects/testuser1/demo/.projectrc).
- Conda Environment:** Shows the current default environment path (/projects/testuser1/demo/envs/default). A yellow warning box states: "Setting the default environment for this project will affect all users by modifying the .projectrc file. All running apps will be shutdown. Make sure No one working on this project has any unsaved documents!". A green "Set Project Environment" button is at the bottom.
- Running Apps:** A table listing active applications.

User	Application	Status	Last Seen	Terminate	Relaunch	Logs
testuser1	terminal	running	1 hours ago	<a href="#">Terminate</a>	<a href="#">Relaunch</a>	<a href="#">Logs</a>

## Info

The Info section displays:

- Hostname—IP address of the host computer.
- Project Home—File path to the project home.
- Project RC file—File path to the project runtime configuration file `.projectrc`. This file is sourced when a user opens any AEN application. It sets several AEN internal environment variables, sets up the project environment and sets additional user environment variables for the project.

## Conda environment

This section displays the path to the default conda environment.

**CAUTION:** Changing the default environment will affect all users. Be sure that no team members have any unsaved documents before changing the project environment.

To change the default conda environment location:

1. Edit the path to point to your preferred conda environment.
2. Click the Set Project Environment button.

Your `.projectrc` file is modified.

## Running apps

The Running Apps section displays a list of users and the applications that are in use, as well as when the app was last modified.

To terminate any individual application, click the Terminate button.

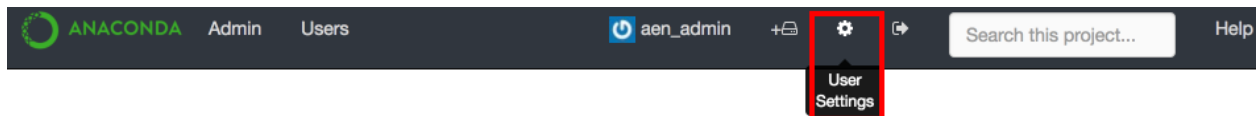
To stop and re-launch any individual application, click the Relaunch button.

To review the run logs of any active application, which may be useful for troubleshooting, click the Logs button.

### Managing your account

- *Updating your public profile*
- *Changing your password*
- *Deleting your AEN account*
- *Viewing account operations*
- *Registering an application*

To access your account information, click the User Settings icon in the AEN navigation bar:



### Updating your public profile

Your public profile is made up of a name, a personal URL, your company and location.

1. In the left navigation pane, click the **Public Profile** tab.
2. To update your profile picture, create a [Gravatar](#) that is associated with the email address you used to create your AEN account. The gravatar will automatically appear.

### Changing your password

1. In the left navigation pane, click the **Account Settings** tab.

### Deleting your AEN account

1. In the left navigation pane, click the **Account Settings** tab.

### Viewing account operations

1. In the left navigation pane, click the **Security Log** tab to view a list of operations performed on your account.



# Settings

Change your account and profile settings.

Public Profile

Account Settings

Security Log

Applications

Security Log

	aen_admin	oauth.authenticate	2017-09-25 04:52:06.713000+00:00
	aen_admin	oauth.authenticate	2017-09-25 04:51:58.954000+00:00
	aen_admin	oauth.authenticate	2017-09-25 04:51:58.720000+00:00
	aen_admin	oauth.authenticate	2017-09-25 04:51:58.490000+00:00
	aen_admin	oauth.authenticate	2017-09-25 04:51:58.259000+00:00
	aen_admin	oauth.authenticate	2017-09-25 04:51:58.033000+00:00
	aen_admin	oauth.authenticate	2017-09-25 04:51:57.802000+00:00

- 2. For more information about an operation, click the Eye icon to the left of the the operation name.

## Registering an application

If you want to create an application for AEN or have already done so, you must register your application.

- 1. In the left navigation pane, click the **Applications** tab.

# Settings

Change your account and profile settings.

Public Profile

Account Settings

Security Log

Applications

Developer Applications

Register New Application

These are applications you have registered to use the Anaconda Enterprise Notebooks API.

Gateway ()

Authorized applications

Gateway ()

revoke

- 2. Click the Register New Application button to open a form for registering your application.

## Advanced tasks

Advanced tasks are best-suited for users who are comfortable working in a Terminal.

## Working with environments

AEN runs on conda, a package management system and environment management system for installing multiple versions of software packages and their dependencies and switching easily between them.

A conda environment usually includes 1 version of Python or R language and some packages.

The ability to have a custom project environment is one of the most powerful features of AEN. Your project environment is integrated so that all of your project applications recognize it and all of your team members have access to it.

This section contains information about:

- *Creating a default conda environment using the Jupyter Notebook application*
- *Creating a default conda environment using the Jupyter Notebook application*
- *Using your conda environment in a notebook*
- *Customizing your conda environment*
- *Installing a conda package using Terminal*
- *Installing a conda package using Notebook*
- *Uninstalling a conda package*

NOTE: This conda environments guide is specific to AEN. For full conda documentation—including cheat sheets, a conda test drive, and command reference—see the [conda documentation](#).

## Creating a default conda environment using the Jupyter Notebook application

You can create, activate, and install packages and deactivate environments from within the Notebook menu bar.

To install from the Notebook menu bar:

1. Click the **Conda** tab and select the plus sign icon.
2. Search for `numpy` in the package search box.
3. Select `numpy` from the search results.

The screenshot shows the Anaconda Cloud interface with the 'Conda' tab selected. It displays a list of 3 conda environments: 'root', 'default' (which is the default environment, indicated by a checkmark), and 'myenv'. Below this, there is a search bar with 'numpy' entered, showing 2 available packages: 'numpy' (version 1.13.1, channel defaults) and 'numpydoc' (version 0.7.0, channel defaults). To the right, there is a list of 39 installed packages in the 'myenv' environment, including 'anaconda-client', 'certifi', 'clyent', 'decorator', 'ipykernel', and 'ipython'.

Name	Version	Channel
<input checked="" type="checkbox"/> numpy	1.13.1	defaults
<input type="checkbox"/> numpydoc	0.7.0	defaults

Name	Version	Build	Available
<input type="checkbox"/> anaconda-client	1.6.3	py36_0	
<input type="checkbox"/> certifi	2016.2.28	py36_0	
<input type="checkbox"/> clyent	1.2.2	py36_0	
<input type="checkbox"/> decorator	4.1.2	py36_0	
<input type="checkbox"/> ipykernel	4.6.1	py36_0	
<input type="checkbox"/> ipython	6.1.0	py36_0	

1. Click the Install button.

The environment is added to the project's `env` directory.

## Creating a default conda environment using Terminal

In AEN, all new environments created with conda automatically include Python, Jupyter Notebooks and pip. You can specify any other packages you want included in your new environment.

**TIP:** By default, conda creates a new environment in your project's `env` directory—so that all team members have access to the environment. For information about limiting your team member's read, write or execute permissions, see [Workbench](#).

To create a new environment within your AEN account, run the command `conda` in a [Terminal](#) application.

**EXAMPLE:** To create a new environment named `WeatherModel` that contains Python, NumPy, pip and Jupyter Notebooks in your project's `env` directory:

1. Log in to AEN.
2. Open a project.
3. On the project home page, click the Terminal application icon to open a Terminal.
4. Create the environment:

```
conda create -n WeatherModel numpy
```

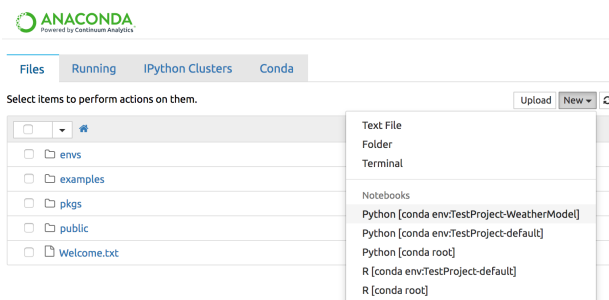
**TIP:** Python, pip and Jupyter Notebooks are automatically installed in each new environment. You only need to specify NumPy in this command.

5. Make the new environment your default:

```
source activate WeatherModel
```

6. To use your new environment with Jupyter Notebooks, open the Notebook application.
7. Click the New button to open a new notebook. In the drop-down menu under Notebooks, the environment you just created is displayed.
8. To activate that environment, select it.

The environment is added to the project's `env` directory.



NOTE: You can deactivate the new environment when you are finished with your notebook by opening the Terminal application and running the command `source deactivate`.

### Using your conda environment in a notebook

Whether you have created an environment using conda in a terminal, or from the **Conda** tab in a notebook, you can use the conda environment in the same way.

When working in a notebook, to select the environment you have created and want to use with that notebook, in the **Kernel** menu, select Change Kernel.

EXAMPLE: If you have an environment named `my_env` in a project named `test1` that includes NumPy and SciPy and you want to use that environment in your notebook, in the **Kernel** menu, select Python [conda env:test1-my\_env].

The notebook code will run in that environment and can import NumPy and SciPy functions.

### Customizing your conda environment

If you need a Python package that AEN doesn't include by default, you can install additional packages into your AEN environment.

TIP: You cannot install packages into the default Anaconda environment. You must create your own environment before installing a new package into that environment.

AEN is built on Anaconda, so you can install additional Python packages using conda or pip—both of which are included with Anaconda.

### Installing a conda package using Terminal

To install a conda package using the Terminal application:

1. Create and activate the environment using the steps in *Creating a default conda environment using the Jupyter Notebook application*.
2. In your Terminal application, run the command `conda install <packagename>`.

NOTE: Be sure to specify the Python version you want when using conda to create the environment, or it will use the same version as root.

EXAMPLE:

```
conda create -n mpy3 python=3 numpy scipy
```

A conda environment named `mpy3`, running on Python 3 and containing NumPy and SciPy is created. All subsequent packages added to this environment will be the Python 3 compatible versions.

### Installing a conda package using Notebook

You can also install the package within your notebook without using the terminal app:

1. From the Notebook application, click the **Conda** tab.
2. Select the environment you wish to use.

3. Search for the package you want to add.
4. Click the Install button.

## Uninstalling a conda package

To uninstall a package using this method, run the command `conda remove <packagename>`.

NOTE: Replace `<packagename>` with the name of the package you are uninstalling.

## Using visualization packages

AEN supports multiple visualization packages for Python and R language.

For Python, the default environment has *Matplotlib* and *Bokeh* installed.

For R language, the default environment has *r-ggplot2* and *r-bokeh* installed.

## Matplotlib

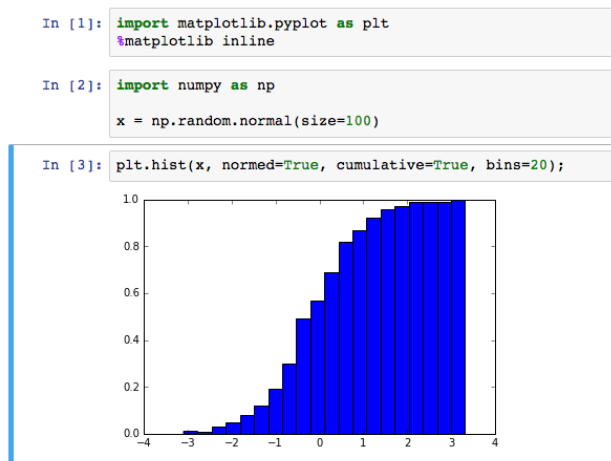
Matplotlib is a Python 2D and 3D plotting and visualization library that produces publication-quality figures in a variety of hardcopy formats and interactive environments across platforms.

To display Matplotlib figures in the output cells of a notebook running the default environment, run:

```
import matplotlib.pyplot as plt
%matplotlib inline
```

Any Matplotlib figures in the notebook are displayed in its output cells.

EXAMPLE: The following screenshot is of a cumulative density function (CDF) plot using values taken from a normal distribution:



For more information, including a [gallery](#), [examples](#), [documentation](#) and a [list of plotting commands](#), see the [Matplotlib website](#).

## Bokeh

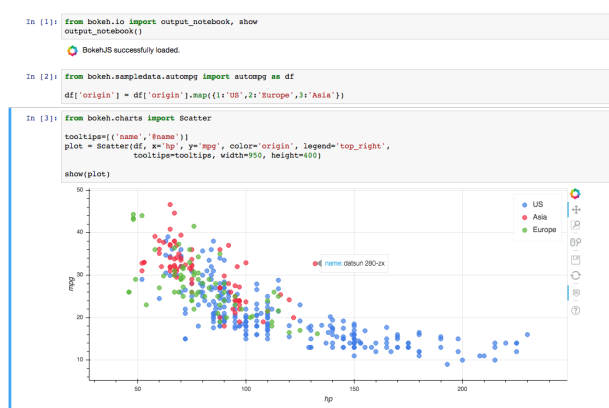
**Bokeh** is an interactive visualization library that targets modern web browsers to provide elegant, concise construction of novel graphics.

To display Bokeh figures in the output cells of a notebook running the default environment, run:

```
from bokeh.io import output_notebook, show
output_notebook()
```

Any Bokeh figures in the notebook are displayed in its output cells.

The following screenshot is of a scatter plot of miles-per-gallon vs. horsepower for 392 automobiles using the `autompg` sample dataset:



## ggplot2

**Ggplot2** is a plotting system for R language which is based on the grammar of graphics. Ggplot2 tries to take only the good parts of base and lattice graphics and none of the bad parts.

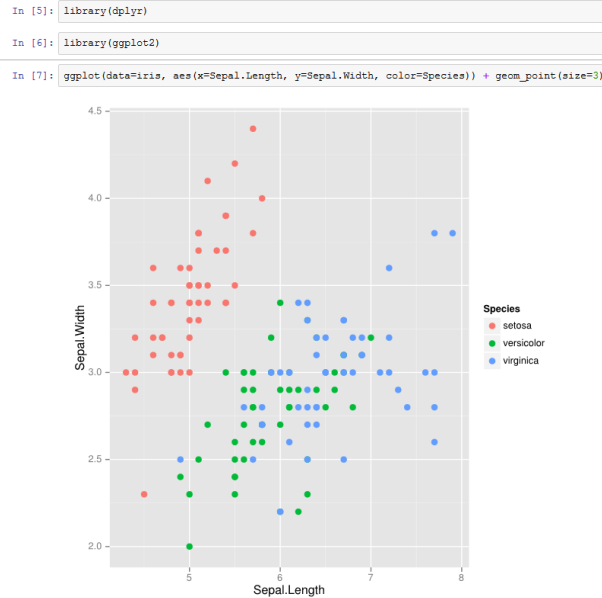
To use ggplot2 with AEN:

1. Open a new Notebook using the R kernel.
2. Load the ggplot2 library with the following code:

```
library(ggplot2)
```

The ggplot2 library is loaded and ready for use in AEN.

The following screenshot is of a scatter plot of sepal width vs sepal length using the `iris` dataset provided by the `dplyr` library:



## Using environment variables

Some Python packages depend on environment variables for correct operation.

EXAMPLE: Theano requires that the directory containing the CUDA compiler is included in the \$PATH environment variable in order for GPU acceleration to be enabled.

To change environment variables for all AEN applications, modify the project runtime configuration file `.projectrc`. For more information, see [Using Compute Resource Configuration](#).

`.projectrc` sets several AEN internal environment variables, sets up the project environment and can set additional user environment variables for that project. This file is sourced when a user opens any AEN application—including Jupyter Notebook—and Jupyter kernels will be able to read the included environment variables.

## Cheat sheet

See the [Anaconda Enterprise Notebooks cheat sheet PDF \(232 KB\)](#) for a single-page summary of the most important information about using AEN.

## Troubleshooting

This troubleshooting guide provides you with ways to deal with issues that may occur with your AEN installation.

### AEN application not working properly

An AEN application is not working as expected.

#### Cause

There are several reasons an application may not work as expected.

## Solution

Most AEN application issues can be resolved by following these steps:

1. Refresh the page.
2. If the issue is not resolved, close and open the application.
3. If the issue is not resolved, *stop and restart your project*.
4. If the issue is not resolved, check that you are using the latest version of your web browser—Chrome, Safari, Edge, or Firefox.
5. Log out of AEN.
6. Restart your browser, and log back in.

If you continue to have issues, then please contact your administrator or enterprise support representative.

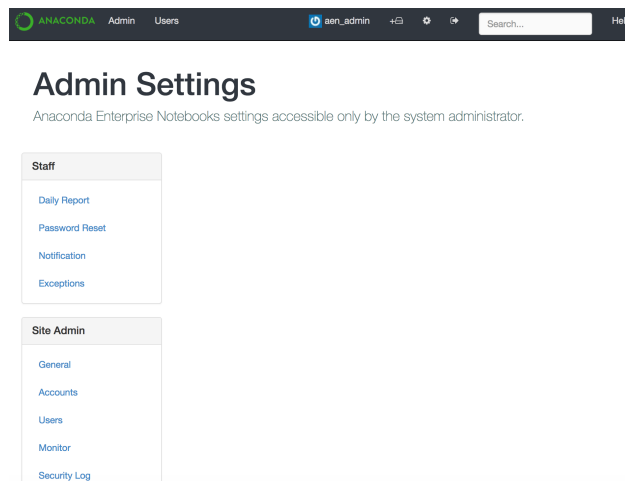
## Admin guide

This administrator guide provides information about the administration of an AEN installation.

Most AEN system management is done from the administrative user interface (admin UI). Some advanced tasks are done *using the command line*.

Any AEN user account can be *upgraded to an administrator account* to have both user and administrator privileges.

Administrators see two additional links in the AEN Navigation bar—Admin and Users:



All of the other navigation bar items are the same as for a user account.

## Concepts



- *System overview*
- *Server node*
- *Gateway node*
- *Compute node(s)*
- *Supervisor and supervisor d*
- *Service Account*
- *Anaconda environments*
- *Projects and permissions*

## System overview

The Anaconda Enterprise Notebooks platform consists of 3 main service groups: AEN server, AEN gateway and AEN compute, which are called “nodes”:

- *Server node*—The administrative front-end to the system where users login, user accounts are stored, and administrators manage the system.
- *Gateway node(s)*—A reverse proxy that authenticates users and directs them to the proper compute node for their project. Users will not notice this node after installation as it automatically routes them.
- *Compute nodes*—Where projects are stored and run.

These services can be run on a single machine or distributed across multiple servers.

Organizationally, each AEN installation has exactly 1 server instance and 1 or more gateway instances. Each compute node can only be connected to a single gateway. The collection of compute nodes served by a single gateway is called a **data center**. You can add data centers to the AEN installation at any time.

EXAMPLE: An AEN deployment with 2 data centers, where 1 gateway has a cluster of 20 physical computers, and the second gateway has 30 virtual machines, must have the following services installed and running:

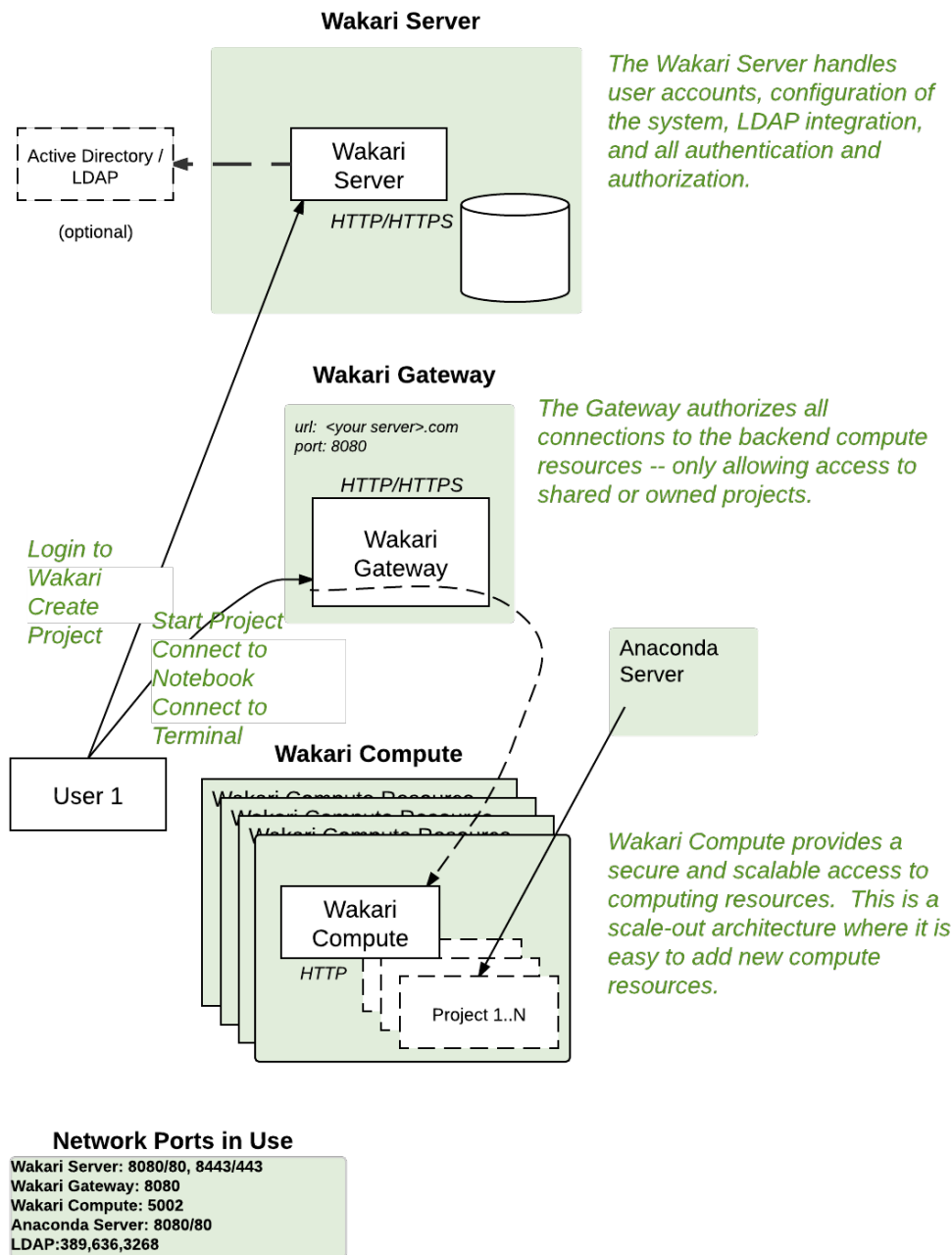
- 1 AEN server instance
- 2 AEN gateway instances
- 50 AEN compute instances (20 + 30)

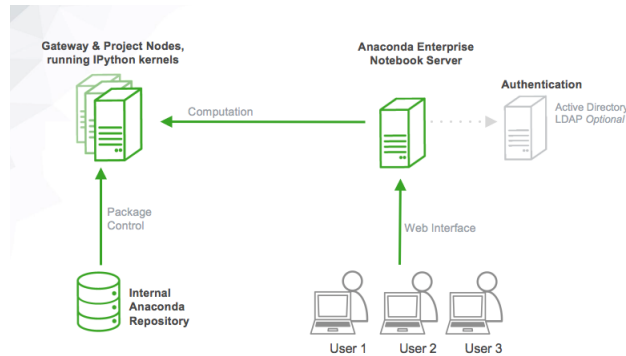
Nodes must be configured and maintained separately.

## Server node

The server node controls login, accounts, admin, project creation and management as well as interfacing with the database. It is the main entry point to AEN for all users. The server node handles project setup and ensures that users

## Anaconda Enterprise Notebooks





are sent to the correct project data center.

Since AEN is web-based, it uses the standard HTTP port 80 or HTTPS port 443 on the server.

AEN uses MongoDB for its internal data persistency. It is typically run on the same host as the server but can also be *installed* on a separate host.

Server nodes use NGINX to handle the user-facing AEN web interface. NGINX acts as a request proxy for the actual server web-process which runs on a high numbered port that only listens on localhost. NGINX is also responsible for static content.

Server is installed in the `/opt/wakari/wakari-server` directory.

## Server processes

When you *view the status of server processes*, you may see the processes explained below.

supervisord	details
description	Manage wakari-worker, multiple processes of wk-server.
user	wakari
configuration	/opt/wakari/wakari-server/etc/supervisord.conf
log	/opt/wakari/wakari-server/var/log/supervisord.log
control	service wakari-server
ports	none

wk-server	details
description	Handles user interaction and passing jobs on to the wakari gateway. Access to it is managed by NGINX.
user	wakari
command	/opt/wakari/wakari-server/bin/wk-server
configuration	/opt/wakari/wakari-server/etc/wakari/
control	service wakari-server
logs	/opt/wakari/wakari-server/var/log/wakari/server.log
ports	Not used in versions after 4.1.2 *

\* AEN 4.1.2 and earlier use port 5000. This port is used only on localhost. Later versions of AEN use Unix sockets instead. The Unix socket path is: `unix:/opt/wakari/wakari-server/var/run/wakari-server.sock`

wakari-worker	details
description	Asynchronously executes tasks from <code>wk-server</code> .
user	wakari
logs	<code>/opt/wakari/wakari-server/var/log/wakari/worker.log</code>
control	<code>service wakari-server</code>

nginx	details
description	Serves static files and acts as proxy for all other requests passed to <code>wk-server</code> process. *
user	nginx
configuration	<code>/etc/nginx/nginx.conf</code> <code>/opt/wakari/wakari-server/etc/conf.d/www.enterprise.conf</code>
logs	<code>/var/log/nginx/woc.log</code> <code>/var/log/nginx/woc-error.log</code>
control	<code>service nginx status</code>
port	80

\* In AEN 4.1.2 and earlier the `wk-server` process runs on port 5000 on localhost only. In later versions of AEN the `wk-server` process uses the Unix socket path `unix:/opt/wakari/wakari-server/var/run/wakari-server.sock`.

NGINX runs at least two processes:

- Master process running as root user.
- Worker processes running as nginx user.

## Gateway node

The gateway node serves as an access point for a given group of compute nodes. It acts as a proxy service and manages the authorization and mapping of URLs and ports to services that are running on those nodes. The gateway nodes provide a consistent uniform interface for the user.

NOTE: The gateway may also be referred to as a data center because it serves as the proxy for a collection of compute nodes.

You can put a gateway in each data center in a tiered scale-out fashion.

AEN gateway is installed in the `/opt/wakari/wakari-gateway` directory.

## Gateway processes

When you *view the status of server processes*, you may see the processes explained below.

supervisord	details
description	Manages the <code>wk-gateway</code> process.
user	wakari
configuration	<code>/opt/wakari/wakari-gateway/etc/supervisord.conf</code>
log	<code>/opt/wakari/wakari-gateway/var/log/supervisord.log</code>
control	<code>service wakari-gateway</code>
ports	none

wakari-gateway	details
description	Passes requests from the AEN Server to the Compute nodes.
user	wakari
configuration	/opt/wakari/wakari-gateway/etc/wakari/wk-gateway-config.json
logs	/opt/wakari/wakari-gateway/var/log/wakari/gateway.application.log /opt/wakari/wakari-gateway/var/log/wakari/gateway.log
working dir	/ (root)
port	8089 (webcache)

## Compute node(s)

Compute nodes are where applications such as Jupyter Notebook and Workbench actually run. They are also the hosts that a user sees when using the Terminal app or when using SSH to access a node. Compute nodes contain all user-visible programs.

Compute nodes only need to communicate with a gateway, so they can be completely isolated by a firewall.

Each project is associated with one or more compute nodes that are part of a single data center.

AEN compute nodes are installed in the /opt/wakari/wakari-compute directory.

Each compute node in the AEN system requires a compute launcher service to mediate access to the server and gateway.

## Compute processes

When you *view the status of server processes*, you may see the processes explained below.

supervisord	details
description	Manages the wk-compute process.
user	wakari
configuration	/opt/wakari/wakari-compute/etc/supervisord.conf
log	/opt/wakari/wakari-compute/var/log/supervisord.log
control	service wakari-compute
working dir	/opt/wakari/wakari-compute/etc
ports	none

wk-compute	details
de-scrip-tion	Launches compute processes.
user	wakari
con-figura-tion	/opt/wakari/wakari-compute/etc/wakari/wk-compute-launcher-config.json /opt/wakari/wakari-compute/etc/wakari/scripts/config.json
logs	/opt/wakari/wakari-compute/var/log/wakari/compute-launcher. application.log /opt/wakari/wakari-compute/var/log/wakari/ compute-launcher.log
work-ing dir	/ (root)
con-trol	service wakari-compute
port	5002 (rfe)

Wk-compute loads each of the following configuration files, in this order:

- /etc/wakari/config.json.
- /etc/wakari/compute-launcher-config.json.
- ./compute-launcher-config.json.
- Any configuration file specified by the `-c` option.

If an option is specified in multiple files, the last one encountered takes precedence.

## Supervisor and supervisord

AEN uses a process control system called “Supervisor” to run its services. Supervisor is run by the AEN Service Account user, usually wakari or aen\_admin.

The Supervisor daemon process is called “supervisord”. It runs in the background and should rarely need to be restarted.

## Service Account

AEN must be installed and executed by a Linux account called the AEN Service Account. The username of the AEN Service Account is called the AEN Functional ID (NFI). The AEN Service Account is created during AEN installation—if it does not exist—and is used to run all AEN services.

The default NFI username is wakari. Another popular choice is aen\_admin.

**WARNING:** The Service Account should only be used for administrative tasks, and should not be used for operating AEN the way an ordinary user would. If the Service Account creates or starts projects, the permissions on the AEN package cache will be reset to match the Service Account, which will interfere with the normal operation of AEN for all other users.

## Anaconda environments

Each project has an associated conda environment containing the packages needed for that project. When a project is first started, AEN clones a default environment with the name “default” into the project directory.

Each release of AEN 4 includes specific tested versions of conda and the conda packages included with AEN. These tested conda packages include Python, R, and other packages, and these tested conda packages include all of the packages in Anaconda.

If you upgrade or install different versions of conda or different versions of any of these conda packages, the new packages will not have been tested as part of the AEN 4 release.

These different packages will usually work, especially if they are newer versions, but they are not tested or guaranteed to work, and in some cases they may break product functionality.

You can use a new conda environment to test a new version of a package before installing it in your existing environments.

If using conda to change the version of a package breaks product functionality, you can use conda to change the version of the package back to the version known to work.

For more information about environments, see [Working with environments](#).

## Projects and permissions

AEN users interact with the system predominantly through [projects](#).

Projects are associated with a single data center within the AEN environment. The team of users includes one owner, which is the user that created the project.

Projects live in the `projectRoot` folder on the compute node—by default, `/projects`.

The project directory is created the first time a project is started. The `start-project` script clones it from `/opt/wakari/wakari-compute/lib/node_modules/wakari-compute-launcher/skeleton`.

Project directory permissions are:

```
owner: rwx, user who created the project
group: rwx, group of the owner
other: --x, to allow access to the Public folder
ACL: rwx for any other team members
```

Files and subdirectories within the project directory have the same permissions as the project directory, except:

- The public folder and everything in it are open to anyone.
- Any files hardlinked into the root anaconda environment—`/opt/wakari/anaconda`—are owned by the root or wakari users.

Project file and directory permissions are maintained by the `start-project` script. All files and directories in the project will have their permissions set when the project is started, except for files owned by root or the AEN\_SRVC\_ACCT user—by default, wakari or aen\_admin.

The permissions set for files owned by root or the AEN\_SRVC\_ACCT user are not changed to avoid changing the permissions settings of any linked files in the `/opt/wakari/anaconda` directory.

**CAUTION:** Do not start a project as the AEN\_SRVC\_ACCT user. The permissions system does not correctly manage project files owned by this user.

## Installation

### Installation requirements

- *Hardware requirements*
- *Software requirements*
- *Security requirements*
- *Network requirements*
- *Other requirements*
- *What's next*

### Hardware requirements

AEN server—At least:

- 2+GB RAM.
- 2+CPU cores.
- 20GB storage.

AEN gateway—At least:

- 2 GB RAM.
- 2 CPU cores.

AEN compute (N-machines)—Configured to meet the needs of the projects. At least:

- 2GB RAM.
- 2 CPU cores.
- 20 GB.

NOTE: We recommend putting `/opt/wakari` and `/projects` on the same filesystem. If the project and conda env directories are on separate filesystems then more disk space will be required on compute nodes and performance will be worse.

### Software requirements

- RHEL/CentOS on all nodes. Versions from 6.5 through 7.4 are supported. Other operating systems are supported. However, this document assumes RHEL or CentOS.
- Linux home directories—Jupyter looks in `$HOME` for profiles and extensions.
- Ability to install in AEN directory `/opt/wakari` with at least 10 GB of storage.
- Ability to install in Projects directory `/projects` with at least 20 GB of storage. Size depends on number and size of projects.

NOTE: To install AEN in a different location see *Installing AEN in a custom location*.



## Linux system accounts

Some Linux system accounts (UIDs) are added to the system during installation.

If your organization requires special actions, the following list is available:

- mongod (RHEL) or mongodb (Ubuntu/Debian)—created by the RPM or deb package.
- elasticsearch—created by RPM or deb package.
- nginx—created by RPM or deb package.
- AEN\_SRVC\_ACCT—created during installation of AEN, and defaults to wakari.
- ANON\_USER—An account such as “public” or “anonymous” on the compute node.

NOTE: If ANON\_USER is not found, AEN\_SRVC\_ACCT will attempt to create it. If it fails, the project(s) will fail to start.

- ACL directories need the filesystem mounted with Posix ACL support (Posix.1e).

NOTE: You can verify ACL from the command line by running `mount` and `tune2fs -l /path/to/filesystem | grep options`.

## Software prerequisites

- AEN server:
  - Mongo—Equal to or higher than version 2.6.8 and lower than version 3.0.
  - NGINX—Equal to or higher than version 1.6.2.
  - Elasticsearch—Equal to or higher than version 1.7.2.
  - Oracle JRE version 7 or 8.
  - bzip2.
- AEN Gateway:
  - bzip2.
- AEN compute:
  - git
  - bzip2
  - bash or zsh
  - X Window System

NOTE: If you don’t want to install the whole X Window System, you must install the following packages to have R plotting support:

```
sudo yum install -y libXrender libXext libXdmc6 libSM libICE libXt \
dejavu-sans-fonts dejavu-serif-fonts dejavu-fonts-common \
fontpackages-filesystem
```

## Security requirements

- Root or sudo access.
- File permissions: `umask 0022` is required during the installation.
- SELinux in permissive or disabled mode.

Edit the following file using either root or sudo access:

```
/etc/sysconfig/selinux
```

Edit the following:

```
# This file controls the state of SELinux on the system.
# SELINUX= can take one of these three values:
#   enforcing - SELinux security policy is enforced.
#   permissive - SELinux prints warnings instead of enforcing.
#   disabled - No SELinux policy is loaded.

SELINUX=enforcing

# SELINUXTYPE= can take one of these two values:
#   targeted - Targeted processes are protected,
#   mls - Multi Level Security protection.

SELINUXTYPE=targeted
```

NOTE: You must reboot for the changes to take effect.

Verify changes with `getenforce`.

## Network requirements

TCP Ports:

Direction	Type	Default Port	Protocol	Optional	Configurable	Comments
Inbound	TCP	80	HTTP or HTTPS	No	Yes	Server
Inbound	TCP	8089	HTTP or HTTPS	No	Yes	Gateway
Inbound	TCP	5002	HTTP	No	Yes	Compute

## Other requirements

As long as the above requirements are met, there are no additional dependencies for AEN.

See also system requirements for Anaconda Repository and Anaconda Scale.

## What's next

*Prepare for installation.*

## Preparing for installation

- *Downloading AEN installers*
- *Gathering IP addresses or FQDNs*
- *Set up variables*
- *What's next*

## Downloading AEN installers

Download the installers and copy them to the corresponding servers.

```
RPM_CDN="https://820451f3d8380952ce65-4cc6343b423784e82fd202bb87cf87cf.ssl.cf1.
↪rackcdn.com"
curl -O $RPM_CDN/aen-server-4.3.1-Linux-x86_64.sh
curl -O $RPM_CDN/aen-gateway-4.3.1-Linux-x86_64.sh
curl -O $RPM_CDN/aen-compute-4.3.1-Linux-x86_64.sh
```

NOTE: The current \$RPM\_CDN server will be confirmed in an email provided by your sales rep.

NOTE: These instructions use *curl* or *wget* to download packages, but you may use other means to move the necessary files into the installation directory.

## Gathering IP addresses or FQDNs

AEN is very sensitive to the IP address or domain name used to connect to the server and gateway nodes. If users will be using the domain name, you should install the nodes using the domain name instead of the IP addresses. The authentication system requires the proper hostnames when authenticating users between the services.

Print this page and fill in the domain names or IP addresses of the nodes below and record the user name and auto-generated password for the administrative user account in the box below after installing the AEN server node:

Node   Name or IP address	Port Number	Username   Password	
AEN server			
AEN gateway			
AEN compute			

NOTE: The values of these IP entries or DNS entries are referred to as <AEN\_SERVER\_IP> or <AEN\_SERVER\_FQDN>, particularly in examples of shell commands. Consider actually assigning those values to environment variables with similar names.

## Set up variables

Certain variables need to have values assigned to them before you start the installation.

### AEN server address

To define an environment variable for the AEN server address—FQDN or IP:

```
export AEN_SERVER=<AEN_SERVER_IP> # <from table above>
```

NOTE: The address—FQDN or IP—specified for the AEN server must be resolvable by your intended AEN users' web clients.

To verify your hostname, run `echo $AEN_SERVER`.

### AEN functional ID

AEN must be installed and executed by a Linux account called the AEN Service Account. The username of the AEN Service Account is called the AEN Functional ID (NFI). The AEN Service Account is created during AEN installation—if it does not exist—and is used to run all AEN services.

The default NFI username is `wakari`. Another popular choice is `aen_admin`.

To set the environment variable `AEN_SRVC_ACCT` to `wakari` or your chosen name before installation, run `export AEN_SRVC_ACCT="aen_admin"`.

This name is now the username of the AEN Service Account and of the AEN administrator account.

When upgrading AEN, set the NFI to the NFI of the current installation.

WARNING: The Service Account should only be used for administrative tasks, and should not be used for operating AEN the way an ordinary user would. If the Service Account creates or starts projects, the permissions on the AEN package cache will be reset to match the Service Account, which will interfere with the normal operation of AEN for all other users.

### AEN functional group

The AEN Functional Group (NFG) may be given any name. Most often, it is set to `aen_admin` or `wakari`. This Linux group includes the AEN service account, so all files and directories that have the owner NFI also have the group NFG.

When upgrading AEN, set the NFG to the NFG of the current installation.

To set the NFG before installation, run:

```
export AEN_SRVC_GRP="<NFG>"
```

NOTE: Replace `<NFG>` with your NFG name.

### AEN install sudo command

During AEN installation the installers perform various operations that require root level privileges. By default, the installers use the `sudo` command to perform these operations.

Before installation, set the `AEN_SUDO_CMD_INSTALL` environment variable to perform root level operations. You can also set it to no command at all if the user running the installer(s) has root privileges and the `sudo` command is not needed or is not available.

EXAMPLES:

```
export AEN_SUDO_CMD_INSTALL=""
export AEN_SUDO_CMD_INSTALL="sudo2"
```

## AEN sudo command

By default the AEN services uses `sudo -u` to perform operations on behalf of other users—including `mkdir`, `chmod`, `cp` and `mv`.

To override the default `sudo` command when `sudo` is not available on the system, before installing, set the `AEN_SUDO_CMD` environment variable.

AEN must have the ability to perform operations on behalf of other users. Therefore, this environment variable cannot be set to an empty string or to `null`.

**CAUTION:** Any command that replaces `AEN_SUDO_CMD` must support the `-u` command line parameter—similarly to the `sudo` command.

**EXAMPLE:**

```
export AEN_SUDO_CMD="sudo2"
```

The optional environmental variable `AEN_SUDO_SH` is another way to customize AEN `sudo` operations. When AEN executes any `sudo` command, it will include the value of `AEN_SUDO_SH`, if it is set.

**EXAMPLE:** If your username is “jsmith” and the values are set as:

```
AEN_SUDO_CMD=sudo
OWNER=jsmith
AEN_SUDO_SH=sudologger
PROJECT_HOME=/projects/jsmith/myproj
```

Then AEN will resolve:

```
$AEN_SUDO_CMD -u ${OWNER} $AEN_SUDO_SH rm -rf $PROJECT_HOME
```

As:

```
sudo -u jsmith sudologger rm -rf /projects/jsmith/myproj
```

In this case the `sudologger` utility could be a pass-through utility that logs all `sudo` usage and then executes the remaining parameters.

## Post-installation Sudo configuration

While `root/sudo` privileges are required during installation, `root/sudo` privileges are not required during normal operations after install, if user accounts are managed outside the software. However `root/sudo` privileges are required to start the services, thus in the service config files there may still need to be an `AEN_SUDO_CMD` entry.

For more information, see [Configuring sudo customizations](#).

## AEN remote database settings

By default AEN server uses a local database. To override the default database location, see [Install AEN connected to a remote Mongo DB instance](#).

### What's next

*Install the AEN server.*

### Installing the AEN server

- *Installing the bzip2 package*
- *Downloading prerequisite RPMs*
- *Installing prerequisite RPMs*
- *Setting variables and changing permissions*
- *Running the AEN server installer*
- *Starting NGINX and Elasticsearch*
- *Testing AEN server installation*
- *Updating your license*
- *What's next*

The AEN server is the administrative front end to the system. This is where users log in to the system, where user accounts are stored, and where admins can manage the system.

Server is installed in the `/opt/wakari/wakari-server` directory.

### Installing the bzip2 package

Be sure you have the *bzip2* package installed. If this package is not installed on your system, install it:

```
sudo yum install bzip2
```

### Downloading prerequisite RPMs

To install AEN on a CentOS 6 server:

```
RPM_CDN="https://820451f3d8380952ce65-4cc6343b423784e82fd202bb87cf87cf.ssl.cf1.
↪rackcdn.com"
curl -O $RPM_CDN/nginx-1.6.2-1.el6ngx.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-tools-2.6.8-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-shell-2.6.8-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-server-2.6.8-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-mongos-2.6.8-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-2.6.8-1.x86_64.rpm
curl -O $RPM_CDN/elasticsearch-1.7.2.noarch.rpm
curl -O $RPM_CDN/jre-8u65-linux-x64.rpm
```

To install AEN on a CentOS 7 server:

```
RPM_CDN="https://820451f3d8380952ce65-4cc6343b423784e82fd202bb87cf87cf.ssl.cf1.
↳rackcdn.com"
curl -O $RPM_CDN/nginx-1.10.2-1.el7ngx.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-tools-2.6.12-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-shell-2.6.12-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-server-2.6.12-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-mongos-2.6.12-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-2.6.12-1.x86_64.rpm
curl -O $RPM_CDN/jre-8u112-linux-x64.rpm
curl -O $RPM_CDN/elasticsearch-1.7.6.noarch.rpm
```

## Installing prerequisite RPMs

Run:

```
sudo yum install -y *.rpm
sudo service mongod start
sudo chkconfig --add elasticsearch
```

## Setting variables and changing permissions

Run:

```
export AEN_SERVER=<FQDN HOSTNAME OR IP ADDRESS> # Use the real FQDN
chmod a+x aen-*.sh # Set installer to be executable
```

NOTE: Change <FQDN HOSTNAME OR IP ADDRESS> to the actual fully qualified domain hostname or IP address.

## Running the AEN server installer

Run:

```
sudo -E ./aen-server-4.3.1-Linux-x86_64.sh -w $AEN_SERVER
<license text>
...
...
PREFIX=/opt/wakari/wakari-server
Logging to /tmp/wakari_server.log
Checking server name
Ready for pre-install steps
Installing miniconda
...
...
Checking server name
Loading config from /opt/wakari/wakari-server/etc/wakari/config.json
Loading config from /opt/wakari/wakari-server/etc/wakari/wk-server-config.json

=====

Created password '<RANDOM_PASSWORD>' for user 'aen_admin'
```

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```
=====

Starting Wakari daemons...
installation finished.
```

After successfully completing the installation script, the installer creates the administrator account—AEN\_SRVC\_ACCT user—and assigns it a password.

EXAMPLE:

```
Created password '<RANDOM_PASSWORD>' for user 'aen_admin'
```

**TIP:** Record this password. It will be needed in the following steps. It is also available in the installation log file `/tmp/wakari_server.log`.

## Starting NGINX and Elasticsearch

When SELinux is enabled, it blocks NGINX from connecting to the socket created by Gunicorn. If you have SELinux enabled, run these commands to correct these permissions and allow connections between NGINX and Gunicorn:

```
sudo semanage fcontext -a -t httpd_var_run_t "/opt/wakari/wakari-server/var/run/
↪wakari-server.sock"
sudo restorecon -r /opt/wakari/wakari-server/var/run
```

To start NGINX and Elasticsearch to read the new config file:

```
sudo service nginx start
sudo service elasticsearch start
```

**TIP:** If the AEN web page shows an NGINX 404 error, restart NGINX:

```
sudo nginx -s stop
sudo nginx
```

## Testing AEN server installation

Visit [http://\protect\TI\textdollarAEN\\_SERVER](http://\protect\TI\textdollarAEN_SERVER).

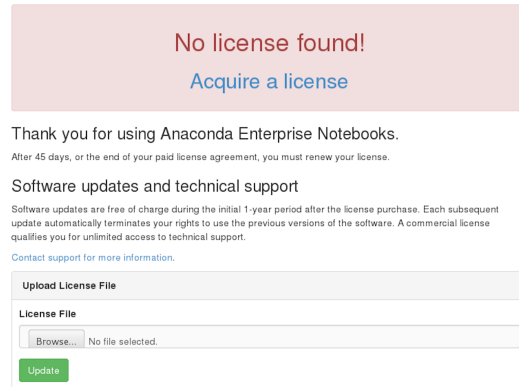
The License expired page is displayed.

## Updating your license

From the License expired page, follow the onscreen instructions to upload your license file.

After your license is submitted, you will see this page:





**No license found!**  
[Acquire a license](#)

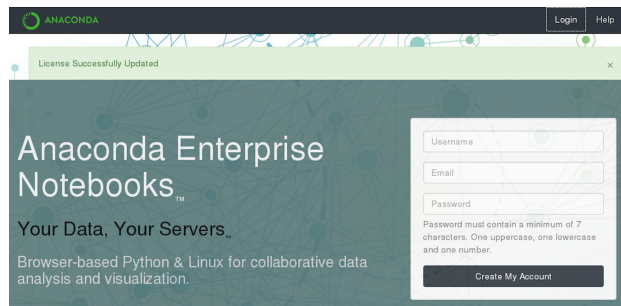
Thank you for using Anaconda Enterprise Notebooks.  
After 45 days, or the end of your paid license agreement, you must renew your license.

**Software updates and technical support**  
Software updates are free of charge during the initial 1-year period after the license purchase. Each subsequent update automatically terminates your rights to use the previous versions of the software. A commercial license qualifies you for unlimited access to technical support.  
[Contact support for more information.](#)

**Upload License File**

License File  
Browse... No file selected.

Update



## What's next

*Install the AEN gateway.*

## Installing the AEN gateway

- *Setting variables and changing permissions*
- *Running the AEN gateway installer*
- *Registering your gateway*
- *What's next*

The gateway is a reverse proxy that authenticates users and automatically directs them to the proper AEN compute node for their project. Users will not notice this node as it automatically routes them.

Gateway is installed in the `/opt/wakari/wakari-gateway` directory.

## Setting variables and changing permissions

Run:

```
export AEN_SERVER=<FQDN HOSTNAME OR IP ADDRESS> # Use the real FQDN
export AEN_GATEWAY_PORT=8089
```

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(continued from previous page)

```
export AEN_GATEWAY=<FQDN HOSTNAME OR IP ADDRESS> # will be needed shortly
chmod a+x aen-*.sh # Set installer to be executable
```

NOTE: Change <FQDN HOSTNAME OR IP ADDRESS> to the actual fully qualified domain hostname or IP address.

NOTE: You must perform the entire procedure before closing the terminal to ensure the variable export persists. If the terminal is closed before successful installation, export the variables to continue with the installation.

## Running the AEN gateway installer

Run:

```
sudo -E ./aen-gateway-4.3.1-Linux-x86_64.sh -w $AEN_SERVER
<license text>
...
...

PREFIX=/opt/wakari/wakari-gateway
Logging to /tmp/wakari_gateway.log
...
...
Checking server name
Please restart the Gateway after running the following command
to connect this Gateway to the AEN Server
...
```

## Registering your gateway

The gateway needs to register with the AEN server.

This needs to be authenticated, so the NFI user's credentials created during the AEN server install must be used.

To write the configuration file `/opt/wakari/wakari-gateway/etc/wakari/wk-gateway-config.json`, run the following as `sudo` or `root`:

```
sudo /opt/wakari/wakari-gateway/bin/wk-gateway-configure \
--server http://$AEN_SERVER --host $AEN_GATEWAY \
--port $AEN_GATEWAY_PORT --name Gateway --protocol http \
--summary Gateway --username $AEN_SRVC_ACCT \
--password '<NFI USER PASSWORD>'
```

NOTE: replace <NFI USER PASSWORD> with the password of the NFI user that was generated during *server installation*.

## Setting permissions

Run:

```
sudo chown $AEN_SRVC_ACCT /opt/wakari/wakari-gateway/etc/wakari/wk-gateway-config.json
```

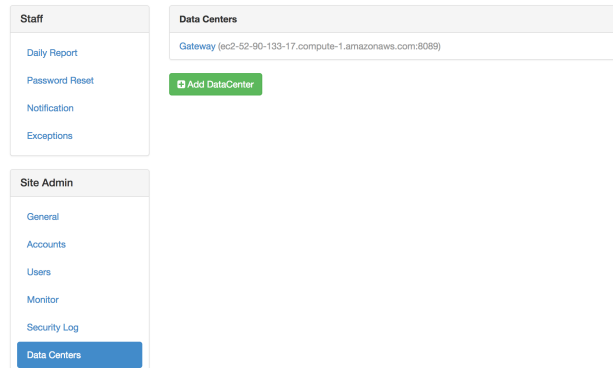
## Starting the gateway

Run:

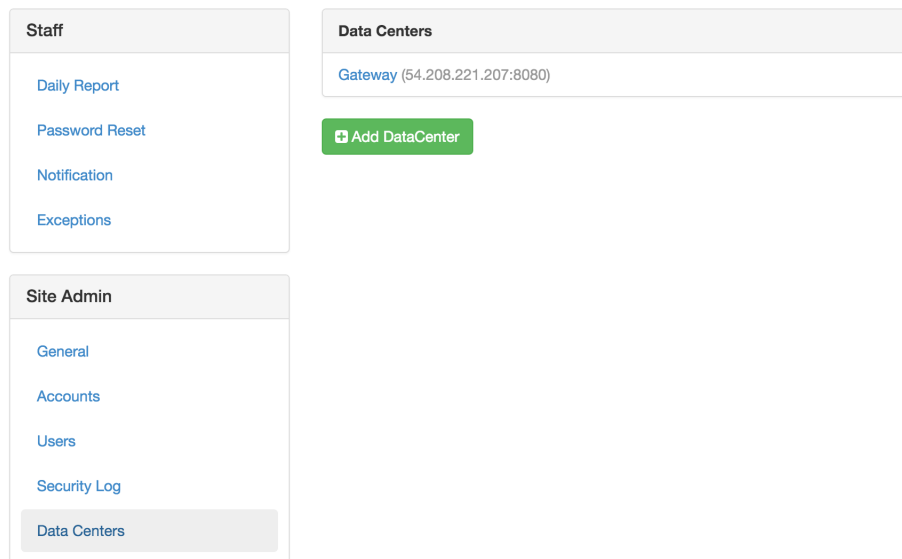
```
sudo service wakari-gateway start
```

## Verifying your gateway registration

1. Log into the AEN server using the Chrome or Firefox browser and the AEN\_SRVC\_ACCT user.
2. In the AEN navigation bar, click Admin to open the Admin Settings page.
3. In the **Site Admin** menu, select Data Centers:



4. Click your data center:



5. Verify that your data center is registered and the status is {"status": "ok", "messages": []}:

Staff

[Daily Report](#)
[Password Reset](#)
[Notification](#)
[Exceptions](#)

Site Admin

[General](#)
[Accounts](#)
[Users](#)
[Monitor](#)
[Security Log](#)
[Data Centers](#)
[Task Queue](#)

Datacenter Gateway

Provider

wk\_server.plugins.providers.enterprise

Client ID

59c119cd3f94c30fe45ff5db

Client Secret

50cc629d-4e8e-44a5-9a2e-a46fee7c1921

Redirect URIs

http://ec2-52-90-133-17.compute-1.amazonaws.com:8089/login/authorized

wk-gateway-config.json

```
{
  "CDN": "http://ec2-204-236-198-47.compute-1.amazonaws.com/static/",
  "SUBDOMAIN_ROUTING": false,
  "client_id": "59c119cd3f94c30fe45ff5db",
  "client_secret": "50cc629d-4e8e-44a5-9a2e-a46fee7c1921",
  "WAKARI_SERVER": "http://ec2-204-236-198-47.compute-1.amazonaws.com",
  "port": 8089
}
```

status

```
{"status": "ok", "messages": []}
```

Back

Remove

## What's next

*Install the AEN compute node(s).*

## Installing the AEN compute node(s)

- *Setting variables and changing permissions*
- *Running the AEN compute installer*
- *Restart the AEN Server*
- *Configuring your compute node(s)*
- *What's next*

Compute nodes are where projects are stored and run.

Adding multiple AEN compute machines allows you to scale-out horizontally to increase capacity. Projects can be created on individual compute nodes to spread the load.

Repeat this procedure on each compute machine.

## Setting variables and changing permissions

Run:

```
export AEN_SERVER=<FQDN HOSTNAME OR IP ADDRESS> # Use the real FQDN
chmod a+x aen-*.sh # Set installer to be executable
```

NOTE: Change <FQDN HOSTNAME OR IP ADDRESS> to the actual fully qualified domain hostname or IP address.

NOTE: You must perform the entire procedure before closing the terminal to ensure the variable export persists.

## Running the AEN compute installer

Run:

```
sudo -E ./aen-compute-4.3.1-Linux-x86_64.sh -w $AEN_SERVER
...
...
PREFIX=/opt/wakari/wakari-compute
Logging to /tmp/wakari_compute.log
Checking server name
...
...
Initial clone of root environment...
Starting Wakari daemons...
installation finished.
Do you wish the installer to prepend the wakari-compute install location
to PATH in your /root/.bashrc ? [yes|no]
[no] >>> yes
```

## Restart the AEN Server

Once configured, restart the AEN server:

```
sudo service wakari-server restart
```

## Configuring your compute node(s)

Once installed, you must configure the compute launcher on your server:

1. In your browser, go to your AEN server.
2. Log in as the AEN\_SRVC\_ACCT user.
3. In the AEN navigation bar, click Admin to open the Admin Settings page.
4. In the **Providers** menu, select Enterprise Resources:
5. Click the Add Resource button to open the new resource form.
6. Select the data center to associate this compute node with.

**Staff**

- Daily Report
- Password Reset
- Notification
- Exceptions

**Resources** [Add Resource](#)

**Gateway**

ec2-54-210-232-251.compute-1.amazonaws.com [remove](#)

**Site Admin**

- General
- Accounts
- Users
- Monitor
- Security Log
- Data Centers
- Task Queue
- License

**Providers**
[Enterprise Resources](#)

Resources / new

**Data Center**

Gateway 59c119cd3f94c30fe45ff5db

**Name**

Compute Node1

**URL**

http://ec2-54-210-232-251.compute-1.amazonaws.com:5002

**Description**

Configuring Compute Node

☒ **Public**  
Uncheck this if you want to control exactly who has access to this compute node

[Add Resource](#)

7. In the URL box, type: `http://$AEN_COMPUTE:5002`.

NOTE: If the compute launcher is located on the same box as the gateway, we recommended that you type `http://localhost:5002` instead.

8. Type a Name and Description for the compute node.
9. Click the Add Resource button to save the changes.

Your AEN compute node is configured.

## What's next

*Configure conda to use your local on-site AEN repository.*

## Configuring conda to use your local on-site AEN repository

You can configure AEN to use a local on-site Anaconda Repository server instead of Anaconda.org.

To configure AEN to use a local on-site Repository, you must:

1. *Edit condarc on the compute node.*
2. *Configure the Anaconda client.*

## Editing condarc on the compute node

NOTE: If there are channels that you haven't mirrored, you must remove them from the configuration.

Edit the file `.condarc` to match the following:

```
#/opt/wakari/anaconda/.condarc
channels:
  - defaults

create_default_packages:
  - anaconda-client
  - ipykernel

# Default channels is needed for when users override the system .condarc
# with ~/.condarc. This ensures that "defaults" maps to your Anaconda Repository and
↪not
# repo.anaconda.com
default_channels:
  - http://<your Anaconda Repository name>:8080/conda/anaconda
  - http://<your Anaconda Repository name>:8080/conda/wakari
  - http://<your Anaconda Repository name>:8080/conda/r-channel

# Note: You must add the "conda" subdirectory to the end
channel_alias: http://<your Anaconda Repository name>:8080/conda
```

NOTE: Replace `<your Anaconda Repository name>` with the actual name or IP address of your local Anaconda Repository installation.

### Configuring the Anaconda client

Anaconda client lets users work with Repository from the command-line—including searching for packages, logging in, uploading packages, and more.

To set the default configuration of anaconda-client for all users on your compute node:

```
sudo /opt/wakari/anaconda/bin/anaconda config --set url http://<your Anaconda_
↳Repository>:8080/api -s
```

NOTE: Sudo is required because the configuration file is written to the root file system: `/etc/xdg/binstar/config.yaml`.

NOTE: Replace `<your Anaconda Repository>` with the actual name or IP address of your local Anaconda Repository installation.

### What's next

Review the *optional configuration* tasks to see if any apply to your system.

### Optional configuration

#### Using configuration files

- *AEN configuration keys*
- *Checking configuration file syntax*

The default locations for each component's configuration files are:

- Server—`/opt/wakari/wakari-server/etc/wakari/config.json`.
- Gateway—`/opt/wakari/wakari-gateway/etc/wakari/config.json`.
- Compute—`/opt/wakari/wakari-compute/etc/wakari/config.json`.

Additionally, service-specific configuration files may also be present in the following locations:

- Server—`/opt/wakari/wakari-server/etc/wakari/wk-server-config.json`.
- Gateway—`/opt/wakari/wakari-gateway/etc/wakari/wk-gateway-config.json`.
- Compute—`/opt/wakari/wakari-compute/etc/wakari/wk-compute-config.json`.

Each service loads each of the configuration files in the following order and updates the AEN configuration at each step:

1. `/etc/wakari/config.json`.
2. `/etc/wakari/wk-gateway-config.json`.
3. `/opt/wakari/wakari-SERVICE/etc/wakari/config.json`.
4. `/opt/wakari/wakari-SERVICE/etc/wakari/wk-SERVICE-config.json`.
5. `./config.json`.
6. `./wk-gateway-config.json`.



## AEN configuration keys

The following is a list of AEN supported configuration keys:

Table 13: Server Configuration Keys

Key	Default	Description
CDN	\$WAKARI_SERVER/ static/	The location of static assets.
MONGO_DB	wakari	The name of the AEN database in mongodb.
MONGO_URL	mongodb:// localhost/	The URL of your AEN server's mon- godb instance. Format: mongodb:// <username>:<password>@<host>:<port>/
WAKARI_SERVER		The URL of this AEN server.
DEFAULT_PRIVACY	public	The default project privacy setting—can be either public or private.
SESSION_COOKIE_NAME	wk. enterprise. session	The Cookie name used to maintain Anaconda Enterprise Note- books Enterprise login sessions.
PERMANENT_SESSION	true	Sets cookie session to permanent. This will keep the session open after the browser is closed. The session will still expire af- ter the number of minutes set in the SESSION_LIFETIME key.
SESSION_LIFETIME	120	Time in minutes until the session expires. The counter resets with each request.
USE_SES	false	Sets whether AEN will use Amazon SES to send emails.
SMTP		Sets the SMTP email settings.
- host		A SMTP subkey—the SMTP mail server hostname.
- user		SMTP subkey—the username for SMTP server authentication.
- password		SMTP subkey—the password for SMTP server authentication.
- from_addr		SMTP subkey—the From address for emails sent through SMTP.
verify_gateway_certificate	true	A boolean setting that indicates whether your AEN server should verify the gateway SSL certificate.
accounts	wk_server. plugins .accounts.cloud	The account provider class. For LDAP, this should be set to wk_server.plugins.accounts.ldap_accounts.
uniqueEmail	true	A boolean setting that indicates whether unique user email ad- dresses are required. See <a href="#">note below</a> about updating the database when setting uniqueEmail.
has_internet	true	Boolean for retrieving the avatar from the gravatar URL. If false a local default is used instead.
LDAP	389	LDAP configurations.
- SERVER		LDAP subkey—A list of LDAP servers. At least one server name must be listed. The primary server should be listed first. All secondary or fail-over servers should be listed after the pri- mary.
- PORT	389	LDAP subkey—The LDAP port on the LDAP server.
- AUTH_TYPE		LDAP subkey—LDAP Authentication types. simple—no encryption not secure. “TLS”—encrypted secure requires the TLS_CERT to be set.
- TLS_CERT		LDAP subkey—the full path to the TLS certificate file. The cer- tificate file must also be provided by the Enterprise.
- BASEDN		LDAP subkey—the LDAP Base DN value.
- OU		LDAP subkey—a list of Organizational Units. Some Enterprises group users by OUs in their LDAP server records. AEN will loop over the list of OUs when authenticating a user. The OU value is a list of lists to support multiple OUs where each OU is a single name or a hierarchy of names.
ANON_USER	anonymous	Username—such as public or anonymous—assigned users who are not logged in to access projects. To disable public access use the special value disable. For more information, see <a href="#">Configuring sudo customizations</a> .
SEARCH_ENABLED	true	Boolean indicating whether ElasticSearch is enabled
SEARCH_SERVER	'localhost:9200'	IP address or domain name and port of ElasticSearch server

NOTE: If you set `uniqueEmail` to `false`, you must drop the existing index in the database. EXAMPLE: If the index name is `email_1`, run `db.users.dropIndex("email_1")`.

Table 14: Gateway Configuration Keys

Key	Default	Description
WAKARI_SERVER		The URL of the AEN WAKARI_SERVER.
port	8089	The Port number used by the gateway application. Must be a non-privileged port ( $\geq 1024$ ).
client_id		The client ID assigned to this gateway by the server during <code>wk-gateway-configure</code> .
client_secret		The Client secret assigned to this gateway by the server during <code>wk-gateway-configure</code> .
httpTimeout	600	Timeout in seconds. The default is 10 minutes to allow project creation.
logLevel	info	Log verbosity. One of: 'error' 'warn' 'info' 'debug'.
https		Enable SSL encryption. For more information, see <a href="#">Configuring SSL</a> .
- key		A https subkey-Path to gateway key.
- cert		A https subkey-Path to gateway cert.
- ca		A https subkey-Required if cert was signed by a private root CA or signed by an intermediate authority. It must contain separate values for the paths to the CA root, any intermediates and the certificate for the Server.
- passphrase		A https subkey-Passphrase required to decrypt SSL certs.

Table 15: Compute Node Configuration Keys

Key	Default	Description
WAKARI_SERVER		The URL of the AEN WAKARI_SERVER.
MANAGE_ACCOUNTS	true	A boolean setting that indicates whether AEN should manage system user accounts. Set to false for LDAP installations.
identicalGID	false	<b>To make the AEN compute service create groups with the same uid. Set to true</b> /projects folder resides on an NFSv3 volume. For more information, see <i>Group and user permissions for NFS</i> .
port	2227	The port number used by the compute-launcher application. Note that individual applications use dynamic ports.
projectRoot	/projects	The location of project file storage.
logLevel	info	Log verbosity. One of: 'error' 'warn' 'info' 'debug'
logMaxSize	10000000	Max size in bytes of the logfile. Default is 10 MB. If the size is exceeded then a new file is created and a counter will become a suffix of the log file.
logMaxFiles	30	Limit the number of files created when the size of the logfile is exceeded
appIdleTime	172800000 (48 hours)	The amount of idle time before applications will be auto-terminated (in msec).
idleCheckInterval	13600000 (1 hour)	The frequency of idle checks.
numericUsernames	false	A boolean setting that indicates whether numeric usernames are permitted.
httpTimeout	600	The time before a timeout—in seconds. The default is 10 minutes—600 seconds—to allow time for project creation.
ANON_USER	anonymous	Username such as public or anonymous for users who are not logged in to access projects. To disable public access use the special value disabled. For more information, see <i>Configuring sudo customizations</i> .
projDirsAsHome	false	A boolean setting. When false AEN apps use /home/<username> as HOME. When true AEN apps use /projects/<username> as HOME.

Table 16: Server Internal Configuration Keys - Do not change

Key	Default	Description
PROVIDERS	["wk_server. plugins providers. enterprise"]	A list of compute provider classes.
MONGO_ACTION_LOG_SIZE	262144000	The size of the Mongo action log in bytes.
SITE_ADMINS		A list of site administrator email addresses—used for crash notifications and LDAP password reset requests.
FROM_EMAIL_ADDR		The From address for notification emails sent by AEN.
uniqueUserName	true	A boolean setting that indicates whether unique usernames are required.

Table 17: Gateway Internal Configuration Keys - Do not change

Key	Default	Description
CDN	\$WAKARI_SERVER/ static/	The location of static assets.
SUBDOMAIN_ROUTING	false	A boolean that indicates whether subdomains are being used.
refreshTokenExpiration	60000	Idle time in milliseconds before the Gateway session expires.

Table 18: Compute Node Internal Configuration Keys - Do not change

Key	Default	Description
CDN	\$WAKARI_SERVER/ static/	The location of static assets.
USE_SES	false	Sets whether AEN will use Amazon SES to send emails.
multiUser	true	A boolean that indicates whether multi-user support is enabled.
multiProject	true	A boolean that indicates whether multi-project support is enabled.
ANACONDA_ROOT	/opt/wakari/ anaconda	The location of your Anaconda installation.
appLogs	/opt/wakari/ wakari- compute/var/ log/wakari/ compute-launcher-apps	The directory where application logs are stored.
appPIDs	/opt/wakari/ wakari-compute/ var/run/ compute-launcher-apps	The directory where application PID files are stored.
applicationLog	/opt/wakari/ wakari-compute/ var/log/ wakari/ compute-launcher. application. log	The path to the compute launcher log.
accessLog	opt/wakari/ wakari-compute/ var/log/ wakari/ compute-launcher. access.log	Path to compute launcher access log

## Checking configuration file syntax

To verify that the configuration file contains valid JSON, run:

```
root@server # python -m json.tool /opt/wakari/wakari-server/etc/wakari/*.json
root@gateway # python -m json.tool /opt/wakari/wakari-gateway/etc/wakari/*.json
root@compute # python -m json.tool /opt/wakari/wakari-compute/etc/wakari/*.json
```

If the file is correct, the contents are displayed.

If there is a syntax error in the file, a “No JSON object could be decoded” message is displayed instead.

To fix any errors, edit the configuration file and verify that it contains the correct JSON syntax.

## Increasing HTTP timeout between gateway and compute nodes

The default HTTP timeout is 600 seconds (10 minutes).

This setting works for HTTP timeout only, not HTTPS.

To modify the HTTP timeout setting:

1. Open the `/opt/wakari/wakari-compute/etc/wakari/wk-compute-launcher-config.json` file and modify the `httpTimeout` key:

```
"httpTimeout": 600
```

2. Update the gateway node by modifying the `httpTimeout` key in the `/opt/wakari/wakari-gateway/etc/wakari/wk-gateway-config.json` file to match the above settings.
3. Restart the AEN compute service:

```
sudo service wakari-compute restart
```

## Installing AEN in a custom location

To install AEN in a custom location:

1. Make the custom install folder owned by `$AEN_SRVC_ACCT`. **EXAMPLE:** `/data/aen/`.
2. Make a symlink from `/opt/wakari` to `/data/aen`.
3. Run the installers.
4. Move the folder from `/projects` to your chosen custom location. **EXAMPLE:** `/data/aen/projects`.
5. Make a symlink from `/projects` to `/data/aen/projects`.

**NOTE:** We recommend putting `/opt/wakari` and `/projects` on the same filesystem. If the project and conda environment directories are on separate filesystems then more disk space will be required on compute nodes and performance will be worse.

## Changing where projects are stored

**NOTE:** We recommend putting `/opt/wakari` and `/projects` on the same filesystem. If the project and conda env directories are on separate filesystems then more disk space will be required on compute nodes and performance will be worse.

To make `aen-compute` service use a different directory than `/projects` to store your AEN projects:

1. Modify the `/opt/wakari/wakari-compute/etc/wakari/wk-compute-launcher-config.json` file:

```
"projectRoot" : "/nfs/storage/services/wakari/projects",
```

**NOTE:** The directory `/nfs/storage/services/wakari/projects` specified as `projectRoot` must already exist for this command to resolve properly.

2. Restart the AEN compute service:

```
sudo service wakari-compute restart
```

## Group and user permissions for NFS

To install AEN with multiple compute nodes and a `/projects` folder on an NFSv3 volume, manually pre-create both the anonymous user and the `$AEN_SRVC_ACCOUNT` user on all nodes. Each of these users must have the same user identity number (UID) and group identity number (GID) on all nodes.

By default AEN creates local users with a different GID on each node. To make the AEN compute service create groups with the same GID:

1. In the `/opt/wakari/wakari-compute/etc/wakari/wk-compute-launcher-config.json` file, change the `identicalGID` key value to `true`:

```
, "identicalGID": true
```

If you don't see the `identicalGID` key, add it.

NOTE: You must add the comma at the beginning of the line. If you add this line as the last key, you must remove any comma at the end of the line.

2. Restart the AEN compute service:

```
sudo service wakari-compute restart
```

## Using numeric usernames

1. In the `/opt/wakari/wakari-compute/etc/wakari/wk-compute-launcher-config.json` file, change the `numericUsernames` key value to `true`.

```
, "numericUsernames": true
```

If you don't see the `numericUsernames` key, add it.

NOTE: You must add the comma at the beginning of the line. If you add this line as the last key, you must remove any comma at the end of the line.

2. Restart the AEN compute service:

```
sudo service wakari-compute restart
```

## Using project directories as home directories

The `projDirsAsHome` option changes the AEN home directories from the standard `/home/<username>` location to the project directories and the location `/projects/<username>/<project_name>/<username>/`. This ensures that AEN and AEN apps will not be affected by configuration files in a user's home directory, such as `.bashrc` or configuration files in subdirectories such as `.ipython` and `.jupyter`.

## Package cache locations

AEN version 4.1.3 stores the cache of packages in `/home/<username>`, while AEN versions 4.2.0 and higher store the cache of packages in `/projects/<username>/<project_name>/<username>/`. By moving the

package cache to the same filesystem as the project, AEN versions 4.2.0 and higher can use hardlinks and save disk space and time when creating or cloning environments.

These package cache locations are not affected by the `projDirsAsHome` option.

After upgrading from AEN 4.1.3 to AEN 4.2.0 or higher, existing projects will still use the package cache in `/home/<username>`. Do not remove this cache, or the existing projects will break.

When users create new projects or install packages, the newly installed packages will use the new cache location.

If you wish to remove the older package cache in `/home/<username>`:

- Upgrade AEN to 4.2.0 or higher.
- Use `conda remove` to remove every non-default package in every project.
- Use `conda install` to replace them. The replaced packages will link to the new package cache in `/projects/<username>/<project_name>/<username>/`.
- You can now safely remove the older package cache.

### Enabling `projDirsAsHome`

NOTE: The `projDirsAsHome` option should be enabled immediately after performing the installation process and before any users have logged in to AEN. This ensures that users will not have home directories in different places due to some creating their home directories when the option was disabled and others creating their home directories when the option was enabled.

1. In the `/opt/wakari/wakari-compute/etc/wakari/wk-compute-launcher-config.json` file, add the `projDirsAsHome` key value and set it to `true`.

```
, "projDirsAsHome": true
```

NOTE: You must add the comma at the beginning of the line. If you add this line as the last key, you must remove any comma at the end of the line.

2. Restart the AEN compute service:

```
sudo service wakari-compute restart
```

### Setting up a default project environment

AEN includes a full installation of the Anaconda Python distribution—along with several additional packages—located within the root conda environment in `/opt/wakari/anaconda`.

The first time any new AEN project is started, this default project environment is cloned into the new project's workspace.

To configure a different set of packages than the default:

1. Create a new conda environment in the `/opt/wakari/anaconda/envs/default` directory.

EXAMPLE: Using a Python 3.4 base environment, run:

```
sudo -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda \
create -p /opt/wakari/anaconda/envs/default python=3.4
```

2. Use `conda` to install any additional packages into the environment.
3. After the environment is created, clone it to ensure that it works correctly:



```
sudo -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda \
  create -p /opt/wakari/testenv --clone /opt/wakari/anaconda/envs/default
sudo -u $AEN_SRVC_ACCT rm -rf /opt/wakari/testenv
```

For more information and examples about creating a default project environment with Microsoft R Open (MRO), see *Using MRO in AEN*.

## Converting an existing project

1. Run the following command to clone the environment:

```
sudo -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda \
  create -n /projects/owner/project/envs/<ENV_NAME> \
  --clone /opt/wakari/anaconda/envs/default
```

NOTE: Replace `/projects/owner/project/envs/<ENV_NAME>` with the path to the new environment you would like to create within the project.

2. Open the *Compute Resource Configuration application* for your project and set the project environment path there as well.

## Using MRO in AEN

In AEN 4.2.2 and higher, you can choose to create environments with the Microsoft R Open (MRO) interpreter by installing the `mro-base` package, or create environments with the R interpreter by installing the `r-base` package. Unless you request a change, conda will continue to use the existing interpreter in each environment. In AEN `r-base` is the default.

EXAMPLE: To create a custom environment called `mro_env` with MRO and R Essentials:

```
.. code-block:: bash

sudo -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda \
  create -c https://repo.anaconda.com/pkgs/main \
  -n mro_env r-essentials
```

NOTE: Conda 4.4 and higher include the `main` channel by default. Earlier versions of conda do not.

## Making a default project environment with MRO

You can also create an environment with MRO and make this the default AEN project environment.

The first time a new project is started, the default project environment is cloned into the new project's workspace.

1. Create a new conda environment in the `/opt/wakari/anaconda/envs/default` directory.

The command is similar to the one used in the previous example to create a custom environment.

```
sudo -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda \
  create -c https://repo.anaconda.com/pkgs/main \
  -p /opt/wakari/anaconda/envs/default r-essentials
```

2. Use conda to install any additional packages into the environment.
3. After the environment is created, clone it to check that it works correctly, and then clean up the clone.

```
sudo -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda \
    create -p /opt/wakari/testenv --clone /opt/wakari/anaconda/envs/default
sudo -u $AEN_SRVC_ACCT rm -rf /opt/wakari/testenv
```

NOTE: To convert existing projects, see *Converting an existing project*.

## Install AEN connected to a remote Mongo DB instance

To install AEN with a remote database:

1. Connect to the Mongodb instance and create the user for AEN:

```
> user = { user: "<username>",
  pwd: "<super-secure-password>",
  roles: [
    { role: "dbOwner", db: "<db_name>" },
    { role: "dbOwner", db: "<db_name>_mq" }
  ]
}
> db.createUser(user)
Successfully added user: { ... }
```

2. Before installing AEN-server export the database URL and name:

```
$ export MONGO_URL="mongodb://<username>:<password>@<host>:<port>/"
$ export MONGO_DB="<database_name>"
```

3. Continue the installation process: *Install the AEN server*.

## Migrate from local to remote MongoDB

To configure your remote database to work with an already installed AEN server:

1. Stop the server, gateway and compute nodes:

```
sudo service wakari-server stop
sudo service wakari-gateway stop
sudo service wakari-compute stop
```

2. Open the `/opt/wakari/wakari-server/etc/wakari/config.json` file and create the `MONGO_URL` key. For the value parameter, add the database information.

The final file should read:

```
{
  "MONGO_URL": "mongodb://MONGO-USER:MONGO-PASSWORD@MONGO-URL:MONGO-PORT",
  "MONGO_DB": "MONGO-DB-NAME",
  "WAKARI_SERVER": "http://YOUR-IP",
  "USE_SES": false,
  "CDN": "http://YOUR-IP/static/",
  "ANON_USER": "anonymous"
}
```

For more information about configuration keys, see *Using configuration files*.

3. Migrate the data from the former database into the new one. For more information, see the [MongoDB documentation website](#).
4. After migration, restart the nodes:

```
sudo service wakari-server start
sudo service wakari-gateway start
sudo service wakari-compute start
```

## Running SELinux in enforcing mode

To run SELinux in Enforcing mode, a few ports must be set up using the `semanage port` command.

The `semanage` command relies on `polycoreutils-python`. To install `polycoreutils-python`, if needed, run:

```
sudo yum -y install polycoreutils-python
```

Enable ports 9200 and 9300 for Elasticsearch:

```
sudo semanage port -a -t http_port_t -p tcp 9200
sudo semanage port -a -t http_port_t -p tcp 9300
```

## Changing server hostnames

It is possible to change the domain names (hostnames) of the various AEN nodes by updating the configuration files.

NOTE: After the configuration files are updated, the associated nodes need to be restarted.

To edit the information for all of the data centers that you are changing the base domain name for:

1. Go to the Site Admin section of the Admin Settings page.
2. In the Data Centers section, click the Edit button.
3. Make any necessary updates.

NOTE: This must include the service port if it is different from the default—80 for HTTP and 443 for HTTPS.

4. In the Enterprise Resources sub-section of the Providers section, edit each compute node that has a changed domain name.

NOTE: These URLs should include the protocol, hostname and port.

## Authenticating with LDAP

Anaconda Enterprise Notebooks performs local authentication against accounts in the AEN database by default.

To configure AEN to authenticate against accounts in an LDAP (Lightweight Directory Access Protocol) server, follow the instructions below.

## Installing OpenLDAP libraries

The system needs OpenLDAP libraries to be installed and accessible by AEN. AEN uses the OpenLDAP libraries to establish an LDAP connection to your LDAP servers.

To install OpenLDAP on CentOS or Redhat:

```
sudo yum install openldap
```

To install OpenLDAP on Ubuntu or Debian, follow the official [OpenLDAP installation instructions](#).

## Configuring OpenLDAP

1. Open the `/opt/wakari/wakari-server/etc/wakari/wk-server-config.json` file.
2. Add the following LDAP settings:

```
{
  "accounts": "wk_server.plugins.accounts.ldap2",
  "LDAP" : {
    "URI": "ldap://openldap.EXAMPLE.COM",
    "BIND_DN": "cn=Bob Jones,ou=Users,DC=EXAMPLE,DC=COM",
    "BIND_AUTH": "secretpass",
    "USER_SEARCH": { "base": "DC=EXAMPLE,DC=COM",
                     "filter": "(| (& (ou=Payroll)
                                   (uid=%(username)s))
                               (& (ou=Facilities)
                                   (uid=%(username)s)))"
                   },
    "KEY_MAP": { "email": "mail",
                 "name": "cn"
               }
  }
}
```

- **URI**—The IP address or hostname of your OpenLDAP server. For SSL/TLS, use the `ldaps://` prefix and specify a `TLS_CACERT` as described in the SSL/TLS configuration section below.
- **BIND\_DN**—The full directory path of the user you want AEN server to bind as.
- **BIND\_AUTH**—The password of the **BIND\_DN** user.
- **USER\_SEARCH**:
  - **base**—The level at which you want to start the search.
  - **filter**—The default is to search for the `sAMAccountName` attribute, and use its value for the AEN server username field.
- **KEY\_MAP**—Maps user attributes in AEN server to LDAP user attributes.

EXAMPLE: The `mail` attribute in LDAP maps to the `email` attribute in AEN server.

3. Restart AEN server to load new settings.
4. Log in with the admin account. This creates the admin user in the local database.
5. As soon as LDAP is installed, LDAP authentication takes over, so you need to add your admin account again:

```
/opt/wakari/wakari-server/bin/wk-server-admin superuser --add "jsmith"
```

## Configuring Active Directory

Microsoft Active Directory is a server program that provides directory services and uses the open industry standard Lightweight Directory Access Protocol (LDAP).

To enable Active Directory support:

1. Open the `/opt/wakari/wakari-server/etc/wakari/wk-server-config.json` file.
2. Add the following LDAP settings:

```
{
  "accounts": "wk_server.plugins.accounts.ldap2",
  "LDAP" : {
    "URI": "ldap://<ad.EXAMPLE.COM>",
    "BIND_DN": "CN=Bind User,CN=Users,DC=EXAMPLE,DC=COM",
    "BIND_AUTH": "secretpass",
    "USER_SEARCH": { "base": "CN=Users,DC=EXAMPLE,DC=COM",
                     "filter": "sAMAccountName=%(username)s"
                   },
    "KEY_MAP": { "email": "mail",
                 "name": "cn"
               }
  }
}
```

- **URI**—The IP address or hostname of your Active Directory server. Replace `<ad.EXAMPLE.COM>` with the actual URI. For SSL/TLS, use the `ldaps://` prefix and specify a `TLS_CACERT` as described in the SSL/TLS configuration section below.
- **BIND\_DN**—The full directory path of the user you want AEN server to bind as.
- **BIND\_AUTH**—The password of the **BIND\_DN** user.
- **USER\_SEARCH**:
  - **base**—the level at which you want to start the search.
  - **filter**—default is to search for the `sAMAccountName` attribute, and use its value for the AEN server `username` field.
- **KEY\_MAP**—Maps user attributes in AEN server to LDAP user attributes.

EXAMPLE: The `mail` attribute in LDAP maps to the `email` attribute in AEN server.

3. Restart AEN server to load new settings.
4. Log in with the admin account. This creates the admin user in the local database.
5. As soon as LDAP is installed, LDAP authentication takes over, so you need to add your admin account again:

```
/opt/wakari/wakari-server/bin/wk-server-admin superuser --add "jsmith"
```

## Configuring SSL/TLS

AEN uses system-wide LDAP settings, including SSL/TLS support.

- On Redhat/CentOS systems, these settings are located in the `/etc/openldap/ldap.conf` file.
- On Ubuntu/Debian systems, these settings are located in the `/etc/ldap/ldap.conf` file.

Typically, the only configuration necessary is updating the file to read:

```
TLS_CACERT /path/to/CA.cert
```

NOTE: `CA.cert` is the Certificate Authority used to sign the LDAP server's SSL certificate. In the case of a self-signed SSL certificate, this is the path to the SSL certificate itself.

### Testing LDAP configuration

Test your LDAP configuration using `flask-ldap-login-check`:

```
/opt/wakari/wakari-server/bin/flask-ldap-login-check \
wk_server.wsgi:app \
-u [username] \
-p [password]
```

NOTE: `username` is the username of a valid user and `password` is that user's `BIND_AUTH` password.

### Configuring sudo customizations

If your organization's IT security policy does not allow root access or has restrictions on the use of `sudo`, after AEN installation, you may customize AEN to meet their requirements.

Your organization may choose to implement any or all of the following:

- *Remove root access* for AEN service account (Note: this restricts AEN from managing user accounts).
- *Configurable sudo command*.
- *Restrict sudo access to all processes*.

These customizations must be done in a terminal window after copying the files to the server node.

### Removing all root access from the service account

Because root access is required for `useradd`, the following process restricts AEN from managing user accounts.

1. Modify the `/etc/sudoers.d/wakari_sudo` file to read:

```
Defaults:wakari !requiretty, visiblepw
Runas_Alias    OP = ALL,!root
wakari ALL=(OP) NOPASSWD: ALL
```

NOTE: If you used a service account name other than `wakari`, enter that name instead of `wakari`.

2. Modify the `/opt/wakari/wakari-compute/etc/wakari/config.json` file to read:

```
"MANAGE_ACCOUNTS": false,
```

Using this option means that your IT department must create and manage all user accounts at the OS level.

After an OS-level account exists, you may create on the main AEN web page an AEN account using the same name. The password you choose is not linked in any way to the OS-level password for the account.

Alternatively, you can configure the system to *use LDAP for authenticating users*.

## Allowing public users to have access to your AEN projects

A public account is visible to anyone who can access the AEN server. The name of this account can be configured to any name you wish. For example, `public` or `anonymous`. To disable this feature use the special value `disabled`.

1. In the `/opt/wakari/wakari-compute/etc/wakari/wk-compute-launcher-config.json` file, modify the `ANON_USER` line to read:

```
"ANON_USER": "public"
```

2. Restart AEN compute node:

```
sudo service wakari-compute restart
```

3. In the `/opt/wakari/wakari-server/etc/wakari/wk-server-config.json` file, modify the `ANON_USER` line to read:

```
"ANON_USER": "public"
```

4. Restart AEN server:

```
sudo service wakari-server restart
```

For more information about configuration keys, see [Using configuration files](#).

## Using a sudo alternative

You can use a sudo alternative as long as it supports the same execution semantics as the original sudo. The alternative must be configured to give the service account permission to run commands on behalf of AEN users.

1. In your terminal window, open the `/opt/wakari/wakari-compute/etc/wakari/config.json` file.
2. Modify the `AEN_SUDO_CMD` line to read:

```
"AEN_SUDO_CMD": "/path/to/alternative/sudo",
```

NOTE: If the alternate sudo command is available on `PATH`, then the full path is not required.

## Restricting sudo access to a single gatekeeper

By default, `sudoers` is configured to allow AEN to run any command as a particular user which allows the platform to initiate processes as the logged-in end user. If more restrictive control is required, it should be implemented using a suitable `sudoers` policy. If that is not possible or practical, it is also possible to route all AEN ID-changing operations through a single gatekeeper.

This gatekeeper wraps the desired executable and provides an alternate way to log, monitor, or control which processes can be initiated by AEN on behalf of a user.

CAUTION: Gatekeeper is a special case configuration and should only be used if required.

To configure an AEN gatekeeper:

1. Modify the `/etc/sudoers.d/wakari_sudo` file to contain:

```
Defaults:wakari !requiretty, visiblepw
Runas_Alias    OP = ALL,!root
wakari ALL=(OP) NOPASSWD: /path/to/gatekeeper
```

2. In the `/opt/wakari/wakari-compute/etc/wakari/config.json` file, modify the `AEN_SUDO_SH` line to read:

```
"AEN_SUDO_SH": "/path/to/gatekeeper"
```

EXAMPLE: The gatekeeper can be as simple as a script with contents such as:

```
#!/bin/bash
first_cmd=$1
if [ 'bash' == $1 ]; then
    shift
    export HOME=~
    export SHELL=/bin/bash
    export PATH=$PATH:/opt/wakari/anaconda/bin
    bash "$@"
else
    exec $@
fi
```

## Configuring SSL

The server node uses NGINX to proxy all incoming http(s) requests to the server running on a local port, and uses NGINX for SSL termination. The default setup uses http—non-SSL—since cert files are required to configure SSL and each enterprise will have their own cert files.

The `www.enterprise.conf` file is the default `nginx.conf` file used for AEN. It is copied to the `/etc/nginx/conf.d` directory during server installation.

NOTE: This section describes setting up SSL after your gateway node has been installed and registered with the server node.

## Copying the required files

To configure SSL on AEN, you will need the following files:

- Server certificate and key
- Server CA bundle
- Gateway certificate and key
- Gateway CA bundle

Configure SSL on AEN:

1. Copy the Gateway certificate and key to `/opt/wakari/wakari-gateway/etc/` on the Gateway as `gateway.crt` and `gateway.key`.
2. Copy the Gateway CA bundle to `/opt/wakari/wakari-server/etc/` on the Server.
3. Copy the Server certificate and key to `/etc/nginx` on the Server as `server.crt` and `server.key`.
4. Copy the Server CA bundle to `/opt/wakari/wakari-gateway/etc/` on the Gateway.

If you have a certificate that was signed by a private root CA and/or an intermediate authority:



- The Gateway CA bundle must contain the full chain: root CA, any intermediate authority and the certificate.

```
cat gateway.crt intermediate.crt root.crt >> gateway-crt-int-root.crt
```

- The Server CA bundle must be separated into individual files for the root CA, any intermediate and the certificate.

## Configuring SSL on the server node

The `www.enterprise.https.conf` is an NGINX configuration file for SSL. It is set up to use the `server.crt` and `server.key` cert files.

**CAUTION:** You must change these values to point to the signed cert files for your domain.

**NOTE:** Self-signed certs or those signed by a private root CA require additional configuration.

Perform the following steps as root:

1. Stop NGINX:

```
service nginx stop
```

2. Move the `/etc/nginx/conf.d/www.enterprise.conf` file to a backup directory.
3. Copy the `/opt/wakari/wakari-server/etc/nginx/conf.d/www.enterprise.https.conf` file to `/etc/nginx/conf.d`.  
**NOTE:** `/etc/nginx/conf.d` may have `www.enterprise.conf` or `www.enterprise.https.conf` but it may not have both.
4. Edit the `/etc/nginx/conf.d/www.enterprise.https.conf` file and change the `server.crt` and `server.key` values to the names of the real cert and key files if they are different.
5. Restart NGINX by running:

```
service nginx start
```

6. Update the `WAKARI_SERVER` and `CDN` settings to use `https` instead of `http` in the following configuration files:

```
/opt/wakari/wakari-server/etc/wakari/config.json
/opt/wakari/wakari-gateway/etc/wakari/wk-gateway-config.json
/opt/wakari/wakari-compute/etc/wakari/config.json
```

7. Copy the gateway certificate, `gateway.crt` to `/opt/wakari/wakari-server/etc/`.
8. In an editor, open `/opt/wakari/wakari-server/etc/wakari/wk-server-config.json` and add:

```
"verify_gateway_certificate": "/opt/wakari/wakari-server/etc/gateway.crt"
```

9. Restart AEN services on the server by running:

```
service wakari-server restart
```

**NOTE:** This step may return an error since the gateway has not yet been configured for SSL.

10. In AEN, verify that the browser uses `https`. On the Admin Settings page, under Data Centers, click Gateway, then select `https`:

# Admin Settings

Anaconda Enterprise Notebooks settings accessible only by the administrator

The screenshot shows two side-by-side panels. The left panel, titled 'Staff', contains three links: 'Daily Report', 'Password Reset', and 'Notification'. The right panel, titled 'Data Centers / Register a datacenter', contains a 'Name' field with the value 'Gateway 1', a checkbox for 'Subdomain Routing' which is unchecked, and a checkbox for 'Https' which is checked.

## Configuring SSL on the gateway

1. For all types of SSL certificates, in `/opt/wakari/wakari-gateway/etc/wakari/wk-gateway-config.json`, add:

```
{
  EXISTING_CONFIGURATION,
  "https": {
    "key": "/opt/wakari/wakari-gateway/etc/gateway.key",
    "cert": "/opt/wakari/wakari-gateway/etc/gateway.crt"
  }
}
```

2. For a server certificate signed by a private root CA or signed by an intermediate authority, add:

```
{
  EXISTING_CONFIGURATION,
  "https": {
    "key": "/opt/wakari/wakari-gateway/etc/gateway.key",
    "cert": "/opt/wakari/wakari-gateway/etc/gateway.crt",
    "ca": ["/opt/wakari/wakari-gateway/etc/server.crt"]
  }
}
```

**NOTE:** When the certificate chain has more than one intermediate cert signed by a higher root CA authority, you must manually break up the certs in the chain into individual files, and enumerate them in the `ca` key:

```
{
  EXISTING_CONFIGURATION,
  "https": {
```

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```

    "key": "/opt/wakari/wakari-gateway/etc/gateway.key",
    "cert": "/opt/wakari/wakari-gateway/etc/gateway.crt",
    "ca": ["/opt/wakari/wakari-gateway/etc/server1.crt",
           "/opt/wakari/wakari-gateway/etc/server2.crt",
           "/opt/wakari/wakari-gateway/etc/server3.crt"]
  }
}

```

3. For a gateway certificate that is encrypted using a passphrase, add:

```

{
  EXISTING_CONFIGURATION,
  "https": {
    "key": "/opt/wakari/wakari-gateway/etc/gateway.key",
    "cert": "/opt/wakari/wakari-gateway/etc/gateway.crt",
    "passphrase": "mysecretpassphrase"
  }
}

```

NOTE: Alternatively, the passphrase can be passed using an environment variable or entered when the wakari-gateway service is manually started.

#### EXAMPLES:

```

# using an environment variable
AEN_GATEWAY_SSL_PASSPHRASE='mysecretpassphrase' wk-gateway

```

```

# starting wakari-gateway manually
sudo service wakari-gateway start --ask-for-passphrase
Passphrase?

```

4. Restart the gateway:

```

sudo service wakari-gateway restart

```

## Configuring SSL on compute nodes

Anaconda Enterprise does not support direct SSL on Compute Nodes. If you need SSL on Compute Nodes, you must install each Compute Node on the same server as a Gateway using `http://localhost:5002` for the URL value while adding it as a resource, and you must use a Gateway for each and every Compute Node.

## Security reminder

The permissions on the cert files must be set correctly to prevent them from being read by others. Since NGINX is run by the root user, only the root user needs read access to the cert files.

EXAMPLE: If the cert files are called `server.crt` and `server.key`, then use the root account to set permissions:

```

chmod 600 server.key
chmod 600 server.crt

```

## Enabling or disabling the Strict-Transport-Security header

By default, Strict-Transport-Security (STS) is enabled in the `www.enterprise.https.conf` file:

```
add_header Strict-Transport-Security max-age=31536000;
```

It can remain enabled if either of the following is true:

- The gateway is running on a different host than the server.
- or
- SSL has been enabled for the gateway.

You must comment out this line if both of the following are true:

- The gateway is running on the same host as the server.
- and
- SSL has not been enabled for the gateway.

Leaving STS enabled when these conditions are true will cause a mismatch in protocols between the server and gateway, causing your apps to fail to launch correctly.

## Configuring single sign-on

AEN's single sign-on (SSO) capability creates a new authentication provider that defers to your Anaconda Repository for login and authentication cookies.

To enable SSO:

1. Deploy AEN and Repository on the same machine.
2. In the `/opt/wakari/wakari-server/etc/wakari/config.json` file, add:

```
{
  EXISTING_CONFIGURATION,
  "SECRET_KEY": "<repo signing secret>",
  "REPO_LOGIN_URL":
    "http://example_repo.com:8080/account/login?next=http://example_repo.com/"
}
```

3. Copy the `SECRET_KEY` from the Repository configuration file.
4. In the `/opt/wakari/wakari-server/etc/wakari/wk-server-config.json` file, modify:

```
{
  EXISTING_CONFIGURATION,
  "accounts": "wk_server.plugins.accounts.repo",
}
```

5. If you are using Repository version 2.33.3 through 2.33.10, set `USE_SERVER_BASED_SESSIONS: false` in the Repository configuration.

This setting affects the network security properties of AEN and Repository. Specifically, if `USE_SERVER_BASED_SESSIONS` is set to false, and if a new cross-site scripting (XSS) vulnerability is discovered, it could expose an additional server fixation vulnerability. Please discuss this with your Anaconda representative and be sure the feature is compatible with your network requirements before setting `USE_SERVER_BASED_SESSIONS: false`.

6. To activate the changes restart `wakari-server`:

```
sudo service wakari-server restart
```

SSO is enabled.

## Adding a third-party extension

Anaconda officially supports and tests functionality of the default environment(s) only for those extensions that ship with AEN.

It is possible to add third-party and custom extensions from `conda-forge` or `pip`, but doing so may cause instability in your default project environments or kernels.

CAUTION: Anaconda does not officially support third-party extensions. This section is informational only.

## Installing unofficial Jupyter Notebook extensions for AEN

TIP: Always back up and verify your complete system before installing extensions.

The `jupyter-contrib-nbextensions` extensions are installed on a compute node.

The default `conda` executable directory for AEN is `/opt/wakari/anaconda/bin/conda`. If you are installing a Jupyter extension, it must be installed in the `wakari-compute` directory.

EXAMPLE: Run:

```
/opt/wakari/anaconda/bin/conda install -p /opt/wakari/wakari-compute/ -c conda-forge_
↪ jupyter_contrib_nbextension
```

For more information, see [Unofficial Jupyter Notebook Extensions](#).

## Configure search indexing

For search indexing to work correctly, verify that the AEN Compute node can communicate with the AEN Server.

```
curl -m 5 $AEN_SERVER > /dev/null
```

There must be at least one `inotify` watch available for the number of subdirectories within the project root filesystem. Some Linux distributions default to a low number of watches, which can prevent the search indexer from monitoring project directories for changes.

```
cat /proc/sys/fs/inotify/max_user_watches
```

If necessary, increase the number of max user watches with the following command:

```
echo fs.inotify.max_user_watches=100000 | sudo tee -a /etc/sysctl.conf && sudo sysctl_
↪ -p
```

There must be at least one `inotify` user instance available per project.

```
cat /proc/sys/fs/inotify/max_user_instances
```

If necessary, this can be increased with the following command:

```
echo fs.inotify.max_user_instances=1000 | sudo tee -a /etc/sysctl.conf && sudo sysctl_
↪-p
```

### Create custom Jupyter kernel for Pyspark

These instructions add a custom Jupyter Notebook option to allow users to select PySpark as the kernel.

### Install Spark

The easiest way to install Spark is with [Cloudera CDH](#).

You will use YARN as a resource manager. After installing Cloudera CDH, [install Spark](#). Spark comes with a PySpark shell.

### Create a notebook kernel for PySpark

You may create the kernel as an administrator or as a regular user. Read the instructions below to help you choose which method to use.

#### 1. As an administrator

Create a new kernel and point it to the root env in each project. To do so create a directory 'pyspark' in */opt/wakari/wakari-compute/share/jupyter/kernels/*.

Create the following kernel.json file:

```
{ "argv": [ "/opt/wakari/anaconda/bin/python",
  "-m", "ipykernel", "-f", "connection_file", "--profile", "pyspark"],
  "display_name": "PySpark", "language": "python" }
```

You may choose any name for the 'display\_name'.

This configuration is pointing to the python executable in the root environment. Since that environment is under admin control, users cannot add new packages to the environment. They will need an admin to help update the environment.

#### 2. As an administrator without IPython profile

To have an admin level PySpark kernel without the user .ipython space:

```
{ "argv":
  [ "/opt/wakari/wakari-compute/etc/ipython/pyspark.sh", "-f", "{connection_file}" ],
  "display_name": "PySpark", "language": "python" }
```

NOTE: The pyspark.sh script is defined in *Without IPython profile* section below.

#### 3. As a regular user

Create a new directory in the user's home directory: *.local/share/jupyter/kernels/pyspark/*. This way the user will be using the default environment and able to upgrade or install new packages.

Create the following kernel.json file:

```
{ "argv": [ "/projects/<username>/<project_name>/envs/default/bin/python",
  "-m", "ipykernel", "-f", "connection_file", "--profile", "pyspark"],
  "display_name": "PySpark", "language": "python" }
```

NOTE: Replace “<username>” with the correct user name and “<project\_name>” with the correct project name.

You may choose any name for the ‘display\_name’.

## Create an IPython profile

The above profile call from the kernel requires that we define a particular PySpark profile. This profile should be created for each user that logs in to AEN to use the PySpark kernel.

In the user’s home, create the directory and file ~/.ipython/profile\_pyspark/startup/00-pyspark-setup.py with the file contents:

```
import os
import sys

# The place where CDH installed spark, if the user installed Spark locally it can be
↪ changed here.
# Optionally we can check if the variable can be retrieved from environment.

os.environ["SPARK_HOME"] = "/usr/lib/spark"

os.environ["PYSPARK_PYTHON"] = "/opt/wakari/anaconda/bin/python"

# And Python path
os.environ["PYLIB"] = os.environ["SPARK_HOME"] + "/python/lib"
sys.path.insert(0, os.environ["PYLIB"] + "/py4j-0.9-src.zip") #10.4-src.zip")
sys.path.insert(0, os.environ["PYLIB"] + "/pyspark.zip")

os.environ["PYSPARK_SUBMIT_ARGS"] = "--name yarn pyspark-shell"
```

Now log in using the user account that has the PySpark profile.

## Without IPython profile

If it is necessary to avoid creating a local profile for the users, a script can be made to be called from the kernel. Create a bash script that will load the environment variables:

```
sudo -u $AEN_SRVC_ACCT mkdir /opt/wakari/wakari-compute/etc/ipython
sudo -u $AEN_SRVC_ACCT touch /opt/wakari/wakari-compute/etc/ipython/pyspark.sh
sudo -u $AEN_SRVC_ACCT chmod a+x /opt/wakari/wakari-compute/etc/ipython/pyspark.sh
```

The contents of the file should look like:

```
#!/usr/bin/env bash
# setup environment variable, etc.

export PYSPARK_PYTHON="/opt/wakari/anaconda/bin/python"
export SPARK_HOME="/usr/lib/spark"
```

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```
# And Python path
export PYLIB=$SPARK_HOME:/python/lib
export PYTHONPATH=$PYTHONPATH:$PYLIB:/py4j-0.9-src.zip
export PYTHONPATH=$PYTHONPATH:$PYLIB:/pyspark.zip

export PYSARK_SUBMIT_ARGS="--name yarn pyspark-shell"

# run the ipykernel
exec /opt/wakari/anaconda/bin/python -m ipykernel $@
```

## Using PySpark

When creating a new notebook in a project, now there will be the option to select PySpark as the kernel. When creating such a notebook you'll be able to import pyspark and start using it:

```
from pyspark import SparkConf
from pyspark import SparkContext
```

NOTE: You can always add those lines and any other command you may use frequently in the PySpark setup file 00-pyspark-setup.py as shown above.

## Enabling server-side session management

By default, AEN uses client-side session management which is vulnerable to session replay attacks if an attacker manages to steal a valid session ID of a user.

To enable server-side session management:

1. Modify the /opt/wakari/wakari-server/etc/wakari/wk-server-config.json file:

```
"USE_SERVER_BASED_SESSIONS": true,
```

2. Restart the AEN server service:

```
sudo service wakari-server restart
```

## Terminate terminal sessions on logout

By default, when a user logs out, their open terminal sessions will remain active.

To disable this behavior:

1. Modify the /opt/wakari/wakari-server/etc/wakari/wk-server-config.json file:

```
"TERMINATE_TERMINALS_ON_LOGOUT": true,
```

2. Modify the /opt/wakari/wakari-gateway/etc/wakari/wk-gateway-config.json file:

```
"TERMINATE_TERMINALS_ON_LOGOUT": true,
```

3. Restart the AEN server service:



```
sudo service wakari-server restart
```

4. Restart the AEN gateway service:

```
sudo service wakari-gateway restart
```

## Upgrading AEN

- *Before you upgrade*
- *Upgrading the AEN server node*
- *Upgrading the AEN gateway node*
- *Upgrading AEN compute nodes*
- *After upgrading*

CAUTION: These instructions are for upgrading AEN to the current version 4.3.1 from 4.3.0 ONLY. Each version must be upgraded iteratively from the previous version. Do not skip versions.

Upgrade instructions for previous versions:

- *AEN 4.3.0 upgrade instructions*
- *AEN 4.2.2 upgrade instructions*
- *AEN 4.2.1 upgrade instructions*
- *AEN 4.2.0 upgrade instructions*
- *AEN 4.1.3 upgrade instructions*
- *AEN 4.1.2 upgrade instructions*
- *AEN 4.1.1 upgrade instructions.*
- *AEN 4.1.0 upgrade instructions.*
- *AEN 4.0.0 upgrade instructions.*

For upgrades from versions before those listed above, please contact your enterprise support representative.

NOTE: Named Service Account functionality is available with AEN 4.0.0+ for new installations only. It is not available for upgraded installations. Contact your enterprise support representative for more information.

An AEN platform update requires that each instance of the 3 node types be upgraded individually:

- AEN Server
- AEN Gateway
- AEN Compute

The upgrade process requires that all AEN service instances be stopped, upgraded, and then restarted.

NOTE: Any commands that call for the root user can also be done using sudo.

If you encounter any difficulty during the upgrade process, see [Troubleshooting](#) which provides guidance on:

- processes
- configuration files

- log files
- ports

If you are unable to resolve an installation or upgrade problem, please contact your enterprise support representative.

### Before you upgrade

**CAUTION:** Make a tested backup of your installation before starting the upgrade. Upgrading to a higher version of AEN is not reversible. Any errors during the upgrade procedure may result in partial or complete data loss and require restoring data from backups.

**CAUTION:** Terminate all AEN applications and stop all projects before starting the upgrade process.

Before upgrading each service on each host:

1. Suspend the services on each of the nodes:

```
sudo service wakari-server stop
sudo service wakari-gateway stop
sudo service wakari-compute stop
```

2. Set the AEN Functional ID (“NFI”) and AEN Functional Group (“NFG”) to the NFI and NFG of the current installation:

```
export AEN_SRVC_ACCT="wakari"
export AEN_SRVC_GRP="wakari"
```

**NOTE:** The default NFI is wakari, but aen\_admin or any other name may be used instead.

For more information on NFI and NFG, see the *installation instructions*.

3. Install wget:

```
yum install wget
```

### Upgrading the AEN server node

**NOTE:** If you are using LDAP-based authentication, back up the /opt/wakari/wakari-server/etc/wakari/wk-server-config.json configuration file. After the server has been upgraded, copy that file back into the same location as before the upgrade.

Complete the following steps on the server host:

1. Stop the Elasticsearch service:

```
sudo service elasticsearch stop
```

2. Remove any previous index:

```
sudo rm -rf /var/lib/elasticsearch/*
```

**NOTE:** You can choose to keep the old index, but if you detect any issues with the search capabilities after the upgrade, you will need to run the following to start with a clean index:

```
sudo service wakari-server stop
sudo service elasticsearch stop
sudo rm -rf /var/lib/elasticsearch/*
sudo service elasticsearch start
sudo service wakari-server start
```

### 3. Upgrade the server:

```
pushd /tmp
wget http://j.mp/aen-server-update-4_3_1

sudo -E -u $AEN_SRVC_ACCT /opt/wakari/miniconda/bin/conda install \
    -p /opt/wakari/wakari-server \
    --file aen-server-update-4_3_1

sudo -E -u $AEN_SRVC_ACCT /opt/wakari/miniconda/bin/conda install \
    -p /opt/wakari/wakari-server \
    --no-deps \
    wakari-enterprise-server-conf-update=2.0.11

popd
```

### 4. Start Elasticsearch:

```
sudo service elasticsearch start
```

Or, if you do not want to use the search features, edit your server's `/opt/wakari/wakari-server/etc/wakari/config.json` file by adding the line `"SEARCH_ENABLED": false`.

### 5. Restart the NGINX server:

AEN server version  $\geq 4.1.3$  uses Unix sockets for communication with NGINX. Restart NGINX to load this new configuration:

```
sudo service nginx restart
```

Alternatively, you can restart NGINX with:

```
sudo nginx -s stop
sudo nginx
```

### 6. Start the server:

```
sudo service wakari-server start
```

### 7. Check that the server is running properly:

```
sudo service wakari-server status
```

8. If you see NGINX errors, please check the configuration at `/opt/wakari/wakari-server/etc/nginx/conf.d/www.enterprise.conf:18`.
9. Connect to AEN server using your web browser with the correct protocol (http or https), hostname and port number.

## Upgrading the AEN gateway node

Complete the following steps on each gateway host:

## 1. Upgrade the gateway:

```
pushd /tmp
wget http://j.mp/aen-gateway-update-4_3_1

sudo -E -u $AEN_SRVC_ACCT /opt/wakari/miniconda/bin/conda install \
    -p /opt/wakari/wakari-gateway \
    --file aen-gateway-update-4_3_1

sudo -E -u $AEN_SRVC_ACCT /opt/wakari/miniconda/bin/conda install \
    -p /opt/wakari/wakari-gateway \
    --no-deps \
    wakari-enterprise-gateway-conf-update=2.0.11

popd
```

## 2. Start the gateway:

```
sudo service wakari-gateway start
```

## 3. Check that the gateway is running properly:

```
sudo service wakari-gateway status
```

## 4. Connect to the gateway using your web browser with the correct http/https, hostname and port number.

## Upgrading AEN compute nodes

Complete the following steps on each host where an AEN compute service is running:

## 1. Check for any wakari-indexer processes running:

```
ps aux | grep wakari-indexer
```

NOTE: If you stopped all the projects, you will not see any wakari-indexer processes running.

Terminate any remaining wakari-indexer processes:

```
sudo killall wakari-indexer
```

NOTE: The processes killed with killall are run by the \$AEN\_SRVC\_ACCT user, so they can be killed as root with sudo killall or killed as the \$AEN\_SRVC\_ACCT user with sudo -u \$AEN\_SRVC\_ACCT killall. Example commands show the sudo killall option.

## 2. Check for any AEN applications processes running—Workbench, Viewer, Terminal or Notebook:

```
ps aux | grep wk-app-gateone
ps aux | grep wk-app-workbench
ps aux | grep wk-app-viewer
ps aux | grep wk-app-terminal
ps aux | grep jupyter-notebook
```

NOTE: If you stopped all the projects, you will not see any AEN app processes running.

Terminate any remaining AEN application processes by running one or more of the following:

```
sudo killall wk-app-gateone
sudo killall wk-app-workbench
```

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```
sudo killall wk-app-viewer
sudo killall wk-app-terminal
sudo killall jupyter-notebook
```

3. Verify the contents of `/opt/wakari/anaconda/.condarc`. Modify it to contain the following entries, and possibly others if you customized the `.condarc` file.

NOTE: Modify the file as the `AEN_SRVC_ACCT` user (or be sure to keep the same ownership).

```
channels:
- https://conda.anaconda.org/t/<TOKEN>/anaconda-nb-extensions
- r
- https://conda.anaconda.org/wakari
- defaults

create_default_packages:
- anaconda-client
- ipykernel
```

NOTE: Contact your enterprise support representative to get your token for the Anaconda channel referenced above. Replace `<TOKEN>` with the actual token from your enterprise support representative.

4. Upgrade each compute service:

```
pushd /tmp
wget http://j.mp/aen-compute-update-4_3_1

sudo -E -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda install \
    -p /opt/wakari/wakari-compute \
    --file aen-compute-update-4_3_1

sudo -E -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda install \
    --no-deps \
    -p /opt/wakari/wakari-compute \
    wakari-enterprise-compute-conf-update=2.0.15

popd
```

NOTE: When upgrading the wakari-compute environment, you may see `ImportError` warnings with some nbextensions. As long as the Validating message is OK, the `ImportError` warnings are harmless—a consequence of the post-link presence on those packages.

5. Initialize the root environment to prime the package cache:

```
sudo -E -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda create \
    -p /opt/wakari/testenv \
    --clone root
```

6. Test the offline cloning step:

```
sudo -E -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda create \
    -p /opt/wakari/testenvoffline \
    --clone root --offline
```

7. Remove the test environments:

```
sudo rm -rf /opt/wakari/testenv
sudo rm -rf /opt/wakari/testenvoffline
```

8. Install necessary dependencies:

NOTE: Skip this step if you already have these dependencies installed from previous installations.

```
sudo yum groupinstall "X Window System" -y
sudo yum install git -y
```

NOTE: If you don't want to install the whole X Window System, you must install the following packages to have R plotting support:

```
sudo yum install -y libXrender libXext libXdmp libSM libICE libXt \
dejavu-sans-fonts dejavu-serif-fonts dejavu-fonts-common \
fontpackages-filesystem
```

9. Start the compute service:

```
sudo service wakari-compute start
```

10. Verify the compute service is running properly:

```
sudo service wakari-compute status
```

11. Restart the AEN Server with:

```
sudo service wakari-server restart
```

12. Repeat this upgrade procedure for all compute nodes in your Data Center.

### After upgrading

1. Restart the projects and start using AEN applications.
2. If you have a *customized default environment*, you may choose to upgrade it depending on the needs of your users.

Upgrade the customized default environment at `/opt/wakari/anaconda/envs/default` with the `$AEN_SRVC_ACCT` user:

```
pushd /tmp
wget http://j.mp/aen-anaconda-update-4_3_1

sudo -E -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda install \
-p /opt/wakari/anaconda/envs/default \
--file aen-anaconda-update-4_3_1
popd
```

To upgrade the customized default environments for every user and every project at `/projects/<USER>/<PROJECT>/envs/default`, run these commands for **every** user as that user:

```
pushd /tmp
wget http://j.mp/aen-anaconda-update-4_3_1

sudo -E -u <USER> /opt/wakari/anaconda/bin/conda install \
-p /projects/<USER>/<PROJECT>/envs/default \
--file aen-anaconda-update-4_3_1
popd
```

NOTE: Replace <USER> with the user's name. Replace <PROJECT> with the project name.

NOTE: Upgrading the default environment at `/opt/wakari/anaconda/envs/default` does NOT automatically upgrade the default environment in the users pre-existing projects. For pre-existing projects, the upgrade, if requested, should be done on a per-user basis.

NOTE: These commands update packages listed in `aen-anaconda-update-4_3_1` and do not update any other package.

3. If you did not stop all your projects before upgrading, then the first time you start an application you will see an error page requesting that you restart the application.
4. Restart the application to complete the upgrade.
5. If you still see old applications or icons after restart, reload the page to reset the browser cache.

## Uninstalling AEN

Each AEN node must be uninstalled separately.

- *Uninstalling a server node*
- *Uninstalling a gateway node*
- *Uninstalling a compute node*
- *OPTIONAL: Removing projects from compute nodes*

Begin by setting the AEN Functional ID (NFI). The NFI is the username of the AEN Service Account which is used to run all AEN services and is also the username of the AEN Admin account. The NFI may be any name. The default NFI is `wakari`. The NFI is also often set to `aen_admin`. The NFI (and AEN Functional Group or NFG) are described in *the installation instructions*.

Set the NFI with this command:

```
export AEN_SRVC_ACCT="aen_admin"
```

Replace the name `aen_admin` with the NFI that was set in your installation of Anaconda Enterprise Notebooks.

## Uninstalling a server node

To remove a server node, run the following commands as root or sudo on the server node's host system:

1. Stop the server processes:

```
service wakari-server stop
```

2. Stop MongoDB:

```
service mongod stop
```

3. Remove AEN server software, AEN database files and NGINX configuration:

```
rm -Rf /opt/wakari/wakari-server
rm -Rf /opt/wakari/miniconda
rm -Rf /var/lib/mongo/wakari*
rm -Rf /etc/nginx/conf.d/www.enterprise.conf
```

NOTE: Remove `/etc/nginx/conf.d/www.enterprise.https.conf` if SSL is enabled on the Server node.

4. Restart MongoDB and NGINX:

```
service mongod restart
service nginx restart
```

5. Check for any outstanding server processes and stop them:

```
ps -ef | grep -e wakari-server -e wk-server
```

6. Remove the AEN Service Account:

```
userdel $AEN_SRVC_ACCT
```

7. Check for and remove any references to “aen” or “wakari” from the root user’s `.condarc` file:

```
grep -i aen ~/.condarc
grep -i wakari ~/.condarc
```

## Uninstalling a gateway node

To uninstall a gateway node, run the following commands as root or sudo on the gateway host system:

1. Stop the gateway processes:

```
service wakari-gateway stop
```

2. Remove gateway software:

```
rm -Rf /opt/wakari/wakari-gateway
```

3. Check for any outstanding gateway processes and stop them:

```
ps -ef | grep -e wakari-gateway -e wk-gateway
```

4. Remove the AEN Service Account:

```
userdel $AEN_SRVC_ACCT
```

5. Check for and remove any references to “aen” or “wakari” from the root user’s `.condarc` file:

```
grep -i aen ~/.condarc
grep -i wakari ~/.condarc
```

## Uninstalling a compute node

To remove a compute node, run the following commands as root or sudo on each compute node host system:

1. Stop the compute processes:

```
service wakari-compute stop
```

2. Remove the compute software:



```
rm -Rf /opt/wakari/wakari-compute
rm -Rf /opt/wakari/miniconda
rm -Rf /opt/wakari/anaconda
```

3. Check for any outstanding compute processes and stop them:

```
ps -ef | grep -e wakari-compute -e wk-compute
```

4. Remove the AEN Service Account:

```
userdel $AEN_SRVC_ACCT
```

5. Check for and remove any references to “aen” or “wakari” from the root user’s `.condarc` file:

```
grep -i aen ~/.condarc
grep -i wakari ~/.condarc
```

## OPTIONAL: Removing projects from compute nodes

**CAUTION:** This is an extreme measure and is not necessary in most instances. We recommend you create and verify a backup before doing this or any other file removal.

To remove all AEN projects from all of your compute nodes:

```
rm -Rf /projects
```

This is a step-by-step guide to installing an Anaconda Enterprise Notebooks system comprised of a front-end server, a gateway and compute machines.

If you have any questions about these instructions or you encounter any issues while installing AEN, please contact your sales representative or Priority Support team.

When you have completed the installation process, review the [optional configuration tasks](#) to see if any are appropriate for your system.

## Distributed install

In a distributed install the server and gateway run on separate hosts.

## Single-box install

In a single-box install, both the server and the gateway need separate external ports since they are independent services that are running on the same host in the single-box installation.

Both port 80 and port 8089 must be open on the firewall for a single-box install.

The compute node only receives connections from the gateway and server nodes and typically runs on port 80 or port 443.

## User management

## Adding or removing an administrative user

An administrator can make any other user an administrator—or remove their administrator permissions—by using administrator commands in the Terminal application.

A user can also be designated as a superuser or as staff, giving them greater administrative privileges within the system.

## Designating a user as an administrator/superuser

To designate a user as an administrator and superuser:

```
/opt/wakari/wakari-server/bin/wk-server-admin superuser --add <username>
```

NOTE: Replace <username> with the actual username.

EXAMPLE: To give administrative privileges to the user named “jsmith” and set them as a superuser, run:

```
/opt/wakari/wakari-server/bin/wk-server-admin superuser --add jsmith
```

## Removing an administrator/superuser

To remove a user’s administrative privileges:

```
/opt/wakari/wakari-server/bin/wk-server-admin superuser --remove <username>
```

NOTE: Replace <username> with the actual username.

## Allowing and restricting new user registration

When Open Registration is enabled, anyone who has access to the URL of your AEN server can create their own account.

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select Accounts.

The screenshot shows the Admin Settings page. On the left, there is a navigation menu with two main sections: 'Staff' and 'Site Admin'. The 'Staff' section includes links for 'Daily Report', 'Password Reset', 'Notification', and 'Exceptions'. The 'Site Admin' section includes links for 'General' and 'Accounts'. The 'Accounts' link is highlighted. On the right, the 'Cloud Registration' settings are displayed. It features a checkbox labeled 'Open Registration' which is checked, with the text 'Allow new user signups' below it. A green 'Update' button is located at the bottom of the settings box.

3. To open user registration, select the Open Registration checkbox. To close registration, clear the checkbox.
4. Click the Update button.

## Resetting a user password

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Staff** menu, select Password Reset:

Anaconda Enterprise Notebooks settings accessible only by the system administrator.

3. Enter the username of the user whose password needs to be reset.
4. Click the Generate URL button.

A password reset link is generated that you can email to the user.

Alternatively you may use the command line interface:

1. Use ssh to log into the server as root.
2. Run:

```
/opt/wakari/wakari-server/bin/wk-server-admin reset-password -u SOME_USER -p SOME_
↵PASSWORD
```

NOTE: Replace SOME\_USER with the username and SOME\_PASSWORD with the password.

3. Log into AEN as the user.

## Managing permissions

This page explains the admin commands used to manage user permissions.

### Checking file ownership

To verify that all files in the `/opt/wakari/anaconda` directory are owned by the `wakari` user or group:

```
root@server # find /opt/wakari/anaconda \! -user wakari -print
root@server # find /opt/wakari/anaconda \! -group wakari -print
```

### Fixing file ownership settings

To fix the ownership settings of any files that are listed in the output:

```
chown -R wakari:wakari /opt/wakari/anaconda
```

### Setting a file owner and permissions

To set a file owner and set its permissions:

```
chown wakari:wakari /opt/wakari/wakari-server/bin/wk-*
chmod 700 /opt/wakari/wakari-server/bin/wk-*
```

### Verifying that POSIX ACLs are enabled

The `acl` option must be enabled on the file system that contains the project root directory.

NOTE: By default, the project root directory is `/projects`.

To determine the project root directory where a custom `projectRoot` is configured:

```
root@compute # grep projectRoot /opt/wakari/wakari-compute/etc/wakari/config.json
```

The `mount` options or default options listed by `tune2fs` should indicate that the `acl` option is enabled.

EXAMPLE:

```
root@compute # fs=`df /projects | tail -1 | cut -d " " -f 1`
root@compute # mount | grep $fs
/dev/vda on / type ext4 (rw)
root@compute # tune2fs -l $fs | grep options
Default mount options:    user_xattr acl
```

### Viewing a list of users

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select Users:

The Users section lists the all users who are signed up, the number of projects they have created and the last time they logged on to AEN.

The screenshot displays the AEN interface. On the left, there are two vertical navigation menus. The top menu, titled 'Staff', contains links for 'Daily Report', 'Password Reset', 'Notification', and 'Exceptions'. The bottom menu, titled 'Site Admin', contains links for 'General', 'Accounts', and 'Users' (which is highlighted in blue). To the right of these menus is a table titled 'Users'. The table has three columns: 'Username', 'Projects', and 'Last Seen'. It contains one row with the username 'aen\_admin', 6 projects, and a last seen time of 'Sep 25, 2017 10:05:58 CDT'.

Users		
Username	Projects	Last Seen
aen_admin	6	Sep 25, 2017 10:05:58 CDT

## Viewing a list of currently active users

In the AEN navigation bar, click Users.

Click a username to open the user's profile page.

## Viewing a user profile


A user's profile page includes a summary of the projects created by that user and a list of projects on which the user is a team member.

1. In the AEN navigation bar, click Users to see a list of users who are currently logged into the system.
2. On the Users page, click the username of the user whose profile page you want to view.


## Sending a system message




1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Staff** menu, select Notification:

The Notification Settings section allows you to create a system message that can be relayed to users.

 ANACONDA

[Admin](#) [Users](#)

 anaconda


  

[Help](#)


# Users




List of currently active users in the system.

 anaconda
 andrew
 bokeh
 christine
 guest
 hubert
 ivan
 paula
 simon
 tanya
 wakari

 ANACONDA

[Admin](#) [Users](#)

 anaconda

[Help](#)

# Users

List of currently active users in the system.

 anaconda
 andrew
 bokeh
 christine
 guest
 hubert
 ivan
 paula
 simon
 tanya
 wakari

Staff

[Daily Report](#)  
[Password Reset](#)  
[Notification](#)  
[Exceptions](#)

Site Admin

[General](#)  
[Accounts](#)  
[Users](#)  
[Security Log](#)  
[Data Centers](#)  
[Task Queue](#)  
[License](#)

Providers

[Enterprise Resources](#)

Notification Settings

☒ **Off**  
No email notification will be sent

☐ **SES - Amazon Simple Email Service**  
This requires a .boto file in the wakari home dir

☐ **SMTP Email Server**

SMTP Settings

SMTP Hostname

SMTP Username *(optional)*

SMTP Password *(optional)*

SMTP From Address *(optional)*

Update



By default, notifications are off.

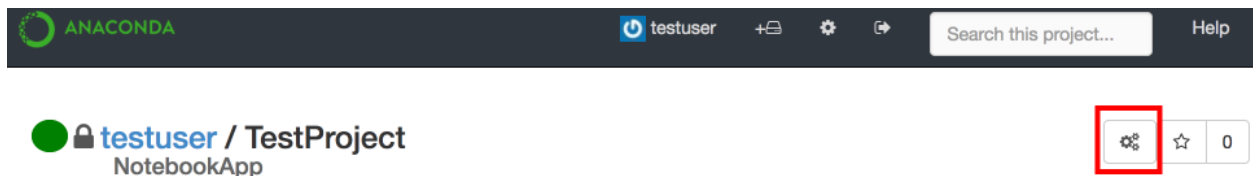
3. To turn on email notifications, select the radio button for the type of email service to use:
  - SES to use Amazon Simple Email Service (SES).
  - SMTP Email Server.
4. If you select SMTP Email Server, complete the SMTP Settings.

NOTE: If you get an error message after changing the SMTP settings, you may need to restart the server.

## Moving a project to another compute node

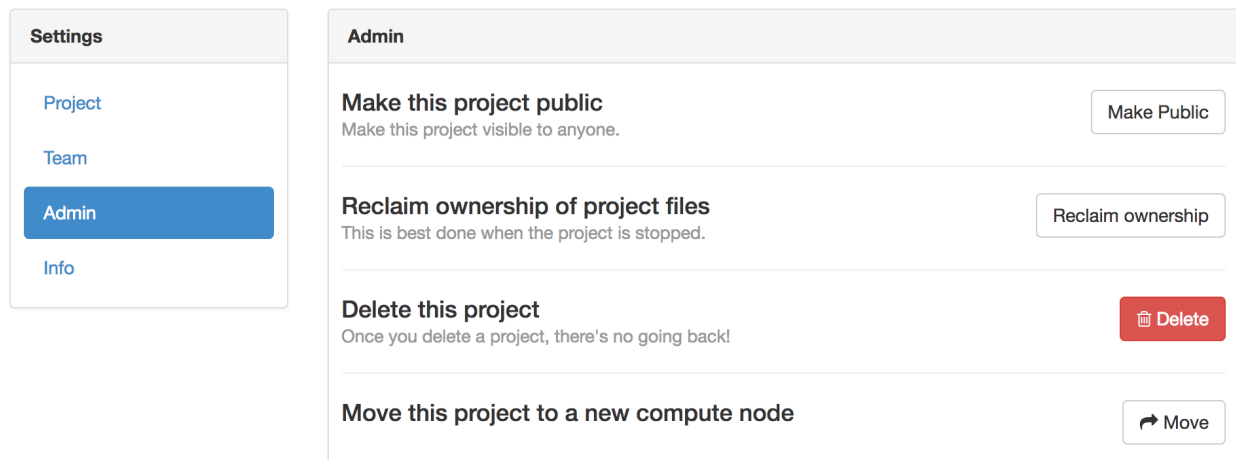
If you have multiple compute nodes available and want to move a project from one to another, the project must exist on both nodes.

1. Verify that the project has been created on both compute nodes. You can use `rsync` for this job unless you have a shared file system like `nfs`.
2. On the project home page, click the Project Settings icon to open the Project Settings page.

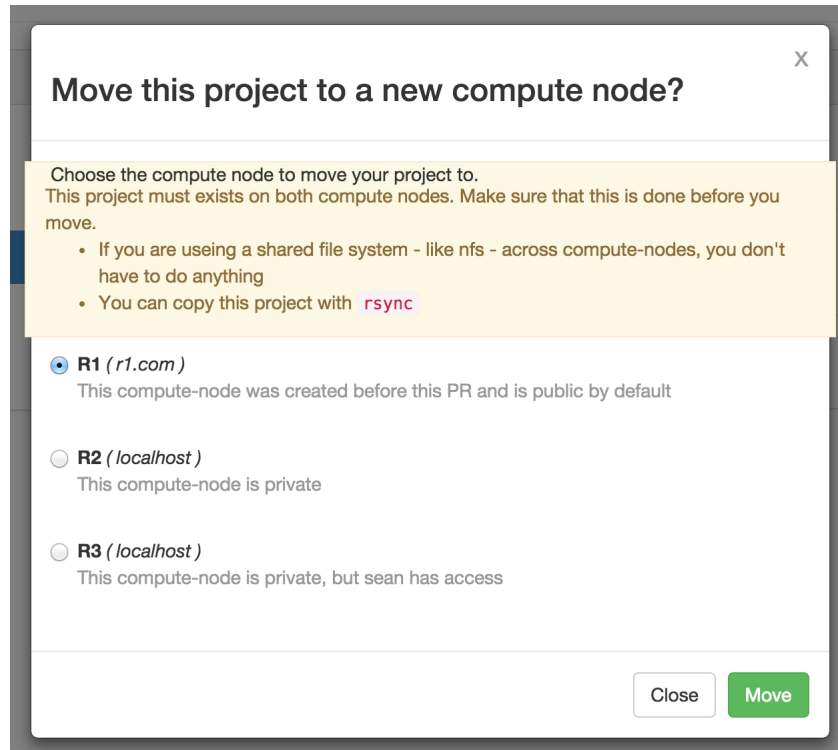


3. In the **Settings** menu, select Admin.

testuser / TestProject



4. Click the Move button.
5. In the move dialog box, click to choose the compute node destination, and click the Move button.



## Deleting a user

To remove a user from the AEN database:

```
/opt/wakari/wakari-server/bin/wk-server-admin remove-user <username>
```

NOTE: Replace <username> with the actual username.

NOTE: Changing the owner of a project requires that both the previous owner and the new owner are still AEN users. Before deleting a user, *change the owner* of that user's projects.

## Deleting a project

To remove a project from the AEN database:

```
/opt/wakari/wakari-server/bin/wk-server-admin remove-project <username> <projectname>
```

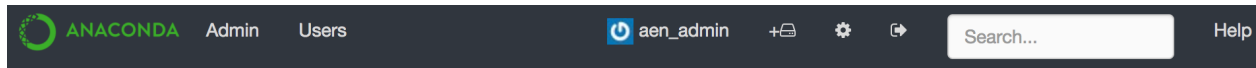
NOTE: Replace <username> with the actual username and <projectname> with the actual project name you are removing.

## System management

### Opening the Admin dashboard

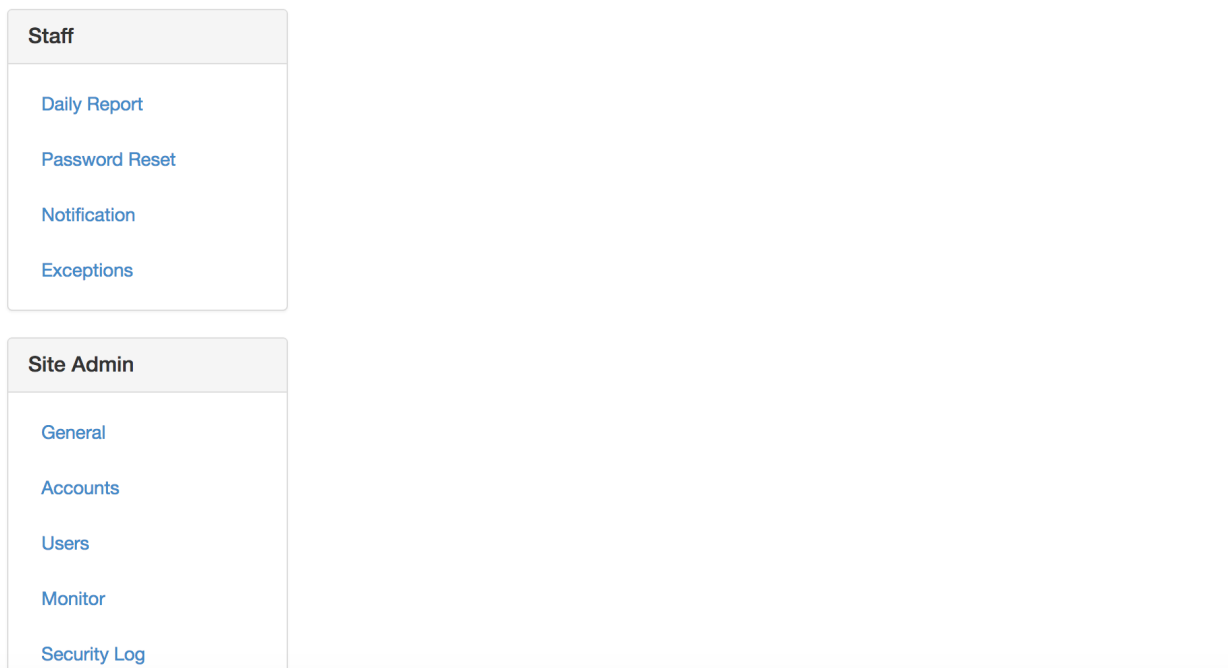
If you have administrator privileges, you see two additional links in the AEN navigation bar—Admin and Users:

To open the Admin dashboard, click the Admin link.



# Admin Settings

Anaconda Enterprise Notebooks settings accessible only by the system administrator.



## Backing up and restoring AEN

- *Document purpose*
- *Important notes*
- *Server component steps*
  - *Backup*

- \* *Mongo database*
- \* *AEN Server config files (including License file)*
- \* *Nginx config (if needed)*
- \* *SSL certificates (if needed)*
- *Restore*
  - \* *Reinstall AEN-Server*
  - \* *Restore Mongo database*
  - \* *AEN Server config files (including License file)*
  - \* *Nginx config (if needed)*
  - \* *SSL certificates (if needed)*
  - \* *Restart server*
- *Gateway component steps*
  - *Backup*
    - \* *Config files*
    - \* *Custom .condarc file (if needed)*
    - \* *SSL certificates (if needed)*
  - *Restore*
    - \* *Reinstall AEN-Gateway*
    - \* *Config files*
    - \* *Custom .condarc file (if needed)*
    - \* *SSL certificates (if needed)*
    - \* *Restart gateway*
- *Compute component steps*
  - *Backup*
    - \* *Config files*
    - \* *Custom Changes (rare)*
    - \* *Create user list*
    - \* *Project files*
    - \* *Full Anaconda (option 1)*
    - \* *Partial Anaconda (option 2)*
  - *Restore*
    - \* *Reinstall AEN-Compute*
    - \* *Config files*
    - \* *Custom changes (rare)*
    - \* *Create users*

- \* *Project files*
- \* *Full Anaconda (option 1)*
- \* *Partial Anaconda (option 2)*
- \* *Custom environments (if needed)*
- \* *Restart compute node*

## Document purpose

This document lays out the steps to backup and restore Anaconda Enterprise Notebooks (AEN) for Disaster Recovery. It is not intended to provide High Availability. Each of the components (Server, Gateway and Compute) has its own instructions and each may be done individually as needed. The steps primarily involve creating tar files of important configuration files and data.

This document is written for a system administrator who is comfortable with basic Linux command line navigation and usage.

To migrate to a new cluster, use these backup and restore instructions to back up the system from the old cluster and restore it to the new cluster.

## Important notes

Review the [Concepts](#) page to become familiar with the different components and how they work together.

Root or sudo access is required for some commands.

**CAUTION:** All commands **MUST** be run by \$AEN\_SRVC\_ACCT (the account used to run AEN) except for those commands explicitly indicated to run as root or sudo. If the commands are not run by the correct user, the installation will not work, and a full uninstallation and reinstallation will be required!

These instructions assume that the fully qualified domain name (FQDN) has not changed for any of the component nodes. If any of the FQDNs are not the same, additional steps will be needed.

## Server component steps

### Backup

#### Mongo database

This will create a single tar file called `aen_mongo_backup.tar` that includes only the database named “wakari” that is used by AEN. It also generates a log of the database backup.

NOTE: These commands must be run by \$AEN\_SRVC\_ACCT.

```
mongodump -db wakari -o aen_main >> mongo_backup.log
tar -cvf aen_mongo_backup.tar aen_main
```

#### AEN Server config files (including License file)

Create a tar file of all of the configuration files, including any license files.

NOTE: This command must be run by \$AEN\_SRVC\_ACCT.

```
tar -cvf aen_server_config.tar -C /opt/wakari/ wakari-server/etc/wakari/
```

### Nginx config (if needed)

Make a copy of the nginx configuration file if it has been customized. The default configuration for the AEN server is a symlink.

NOTE: This command must be run by \$AEN\_SRVC\_ACCT.

```
/etc/nginx/conf.d/www.enterprise.conf -> /opt/wakari/wakari-server/etc/nginx/conf.d/  
↪www.enterprise.conf
```

### SSL certificates (if needed)

Make a copy of the SSL certificates files (certfiles) for the server, including the key file, and a copy of the certfile for the gateway, which is needed for verification if using self-signed or private CA signed certs.

## Restore

### Reinstall AEN-Server

See *the instructions for installing the current version of AEN-Server*.

It is not necessary to upload the license, because it will be restored with the config files.

NOTE: The new installation will generate a new password for the local \$AEN\_SRVC\_ACCT account.

### Restore Mongo database

This assumes that mongo was reinstalled as part of the reinstallation of the server component. Untar the mongo database and restore it.

NOTE: These commands must be run by \$AEN\_SRVC\_ACCT.

```
tar -xvf aen_mongo_backup.tar  
mongorestore --drop aen_main
```

NOTE: The --drop option resets the \$AEN\_SRVC\_ACCT user password and restores the database to the exact state it was in at the time of backup. Please see the [MongoDB documentation](#) for more information about mongorestore options for Mongo 2.6.

NOTE: AEN uses Mongo 2.6 by default. If you are using a different version, consult the documentation for your version.

### AEN Server config files (including License file)

Untar the tar file of all of the configuration files, including any license files.

NOTE: This command must be run by \$AEN\_SRVC\_ACCT.

```
tar -xvf aen_server_config.tar -C /opt/wakari/
```

Make sure the files are in `/opt/wakari/wakari-server/etc/wakari/` and are owned by the `$AEN_SRVC_ACCT`.

### Nginx config (if needed)

Make sure any modifications to the nginx configuration are either in `/etc/nginx/conf.d` or in `/opt/wakari/wakari-server/etc/nginx/conf.d/` with a proper symlink.

NOTE: This command must be run by `$AEN_SRVC_ACCT`.

```
/etc/nginx/conf.d/www.enterprise.conf -> /opt/wakari/wakari-server/etc/nginx/conf.d/  
↪www.enterprise.conf
```

### SSL certificates (if needed)

Move any SSL certificate files to the locations indicated in the config files.

### Restart server

Restart the server application.

NOTE: This command must be run as root or with `sudo`.

```
service wakari-server restart
```

## Gateway component steps

### Backup

### Config files

Create a tar file of all of the configuration files.

NOTE: This command must be run by `$AEN_SRVC_ACCT`.

```
tar -cvf aen_gateway_config.tar -C /opt/wakari/ wakari-gateway/etc/wakari/
```

### Custom .condarc file (if needed)

Make a copy of any `/opt/wakari/miniconda/.condarc` if it has been modified.

### SSL certificates (if needed)

Make a copy of SSL certificate files for the gateway (including the key file) and the certfile for the server (needed for verification if using self-signed or private CA signed certs).

### Restore

### Reinstall AEN-Gateway

### Setting variables and changing permissions

NOTE: These commands must be run by \$AEN\_SRVC\_ACCT.

Run:

```
export AEN_SERVER=<FQDN HOSTNAME OR IP ADDRESS> # Use the real FQDN
export AEN_GATEWAY_PORT=8089
export AEN_GATEWAY=<FQDN HOSTNAME OR IP ADDRESS> # will be needed shortly
chmod a+x aen-*.sh # Set installer to be executable
```

NOTE: Change <FQDN HOSTNAME OR IP ADDRESS> to the actual fully qualified domain hostname or IP address.

NOTE: You must perform the entire procedure before closing the terminal to ensure the variable export persists. If the terminal is closed before successful installation, export the variables to continue with the installation.

### Running the AEN gateway installer

Run:

```
sudo -E ./aen-gateway-4.3.1-Linux-x86_64.sh -w $AEN_SERVER
<license text>
...
...

PREFIX=/opt/wakari/wakari-gateway
Logging to /tmp/wakari_gateway.log
...
...
Checking server name
Please restart the Gateway after running the following command
to connect this Gateway to the AEN Server
...
```

### Config files

Untar the configuration files.

NOTE: This command must be run by \$AEN\_SRVC\_ACCT.

```
tar -xvf aen_gateway_config.tar -C /opt/wakari
```

Verify that the files are in /opt/wakari/wakari-gateway/etc/wakari/ and are owned by the \$AEN\_SRVC\_ACCT.

### Custom .condarc file (if needed)

Move the custom .condarc file to /opt/wakari/miniconda/.condarc.



## SSL certificates (if needed)

Move any SSL certificate files to the locations indicated in the config files.

## Restart gateway

Restart the gateway application.

NOTE: This command must be run as root or with sudo.

```
service wakari-gateway restart
```

## Compute component steps

### Backup

### Config files

Create a tar file of all of the configuration files.

NOTE: This command must be run by \$AEN\_SRVC\_ACCT.

```
tar -cvf aen_compute_config.tar -C /opt/wakari/ wakari-compute/etc/wakari
```

## Custom Changes (rare)

Manually backup any custom changes that were applied to the code. One change might be additional files in the skeleton folder:

```
/opt/wakari/wakari-compute/lib/node_modules/wakari-compute-launcher/skeleton
```

## Create user list

AEN uses POSIX access control lists (ACLs) for project sharing, so the backup must preserve the ACL information. This is done with a script that creates a file named `users.lst` containing a list of all users that have access to projects on a given compute node. Download and run the script.

NOTE: These commands must be run by \$AEN\_SRVC\_ACCT.

```
wget https://s3.amazonaws.com/continuum-airgap/misc/wk-compute-get-acl-users.py
chmod 755 wk-compute-get-acl-users.py
./wk-compute-get-acl-users.py
```

## Project files

Create a tar of the projects directory with ACLs enabled. The default projects base location is `/projects`.

NOTE: This command must be run as root or with sudo.

```
tar --acls -cpvf projects.tar -C <projects base location>/*
```

### Full Anaconda (option 1)

If any changes have been made to the default Anaconda installation (additional packages installed or packages removed), it is necessary to backup the entire Anaconda installation.

NOTE: This command must be run by \$AEN\_SRVC\_ACCT.

```
tar -cvf aen_anaconda.tar -C /opt/wakari/anaconda/*
```

If no changes have been made to the default installation of Anaconda, you may just backup the `.condarc` file and any custom environments.

### Partial Anaconda (option 2)

#### Custom `.condarc` file

Make a copy of `/opt/wakari/anaconda/.condarc`.

#### Custom environments (if needed)

Create a tar file of any custom shared environments.

NOTE: This command must be run by \$AEN\_SRVC\_ACCT.

```
tar -cvf aen_compute_envs.tar -C /opt/wakari/ anaconda/envs
```

NOTE: If no custom shared environments have been created, the `envs` folder will not be present.

### Restore

#### Reinstall AEN-Compute

#### Setting variables and changing permissions

NOTE: These commands must be run by \$AEN\_SRVC\_ACCT.

Run:

```
export AEN_SERVER=<FQDN HOSTNAME OR IP ADDRESS> # Use the real FQDN
chmod a+x aen-*.sh                               # Set installer to be executable
```

NOTE: Change `<FQDN HOSTNAME OR IP ADDRESS>` to the actual fully qualified domain hostname or IP address.

NOTE: You must perform the entire procedure before closing the terminal to ensure the variable export persists.

## Running the AEN compute installer

Run:

```
sudo -E ./aen-compute-4.3.1-Linux-x86_64.sh -w $AEN_SERVER
...
...
PREFIX=/opt/wakari/wakari-compute
Logging to /tmp/wakari_compute.log
Checking server name
...
...
Initial clone of root environment...
Starting Wakari daemons...
installation finished.
Do you wish the installer to prepend the wakari-compute install location
to PATH in your /root/.bashrc ? [yes|no]
[no] >>> yes
```

## Config files

Untar the config files.

NOTE: This command must be run by \$AEN\_SRVC\_ACCT.

```
tar -xvf aen_compute_config.tar -C /opt/wakari
```

NOTE: Verify that they are located in /opt/wakari/wakari-compute/etc/wakari and are owned by the \$AEN\_SRVC\_ACCT.

## Custom changes (rare)

Manually restore any custom changes you saved in the backup section. If there are changes in the skeleton directory, these files must be world readable or projects will refuse to start.

## Create users

NOTE: Only create users with these instructions if your Linux machine is not bound to LDAP.

In order for the ACLs to be set properly on restore, all users that have permissions to the files must be available on the machine. Ask your system administrator for the proper way to do this for your system, such as using the “useradd” tool. A list of users that are needed was created in the backup process as a file named `users.lst`.

A process similar to the following `useradd` example will be suitable for most Linux systems.

NOTE: This command must be run by \$AEN\_SRVC\_ACCT.

```
xargs -0 -n 1 useradd --user-group < users.lst
```

## Project files

Create the projects directory in the location specified in `projectRoot` in `wk-compute-launcher-config.json`.

NOTE: By default this directory is `/projects`.

Then untar the projects directory with ACLs.

NOTE: This command must be run as root or with `sudo`:

```
tar --acls -xpvf projects.tar -C <projects base location>
```

### Full Anaconda (option 1)

If you did a full backup of the full Anaconda installation, untar this file to `/opt/wakari/anaconda`.

NOTE: This command must be run by `$AEN_SRVC_ACCT`.

```
tar -xvf aen_anaconda.tar -C /opt/wakari
```

### Partial Anaconda (option 2)

Restore the custom `.condarc` file.

If you did a partial backup of the Anaconda installation, move the copy of the `.condarc` file to `/opt/wakari/anaconda/.condarc`.

### Custom environments (if needed)

Untar any custom environments that were created to `/opt/wakari/anaconda/envs`.

NOTE: This command must be run by `$AEN_SRVC_ACCT`.

```
tar -xvf aen_compute_envs.tar -C /opt/wakari
```

### Restart compute node

Restart the compute-launcher application.

NOTE: This command must be run as root or with `sudo`.

```
service wakari-compute restart
```

### Viewing a list of admin commands

A user who is promoted to administrator can access administrator commands to perform advanced administrator tasks.

NOTE: Utility files are owned by, and should only be executed by, the AEN user who owns the files.

To display a list of all administrator commands:

```
ls -al /opt/wakari/wakari-server/bin/wk-*
```

## Viewing help for admin commands

To view help information for command, run the command followed by `-h` or `--help`.

EXAMPLE: To view help for the `remove-user` command:

```
/opt/wakari/wakari-server/bin/wk-server-admin remove-user -h
/opt/wakari/wakari-server/bin/wk-server-admin remove-project -h
```

## Running daily reports

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Staff** menu, select Daily Report:

Staff

[Daily Report](#)
[Password Reset](#)
[Notification](#)
[Exceptions](#)

Site Admin

[General](#)
[Accounts](#)
[Users](#)
[Monitor](#)
[Security Log](#)
[Data Centers](#)
[Task Queue](#)
[License](#)

Providers

[Enterprise Resources](#)

## Report

Today
Yesterday
This Week
This Month

**From:**  
Sun Sep 24 15:09:03 2017  
**Until:**  
Mon Sep 25 15:09:03 2017  
**Date Range**  
1 day, 0:00:00

### Users

	New	Total
<b>Users</b>	0	1
<b>Projects</b>	0	6

### New User Emails

Username	Email
----------	-------

### Actions

Count	Action
82	<a href="#">oauth.authenticate</a>

The Report section displays the following:

- Users—The number of users and projects.
- New User Emails—If *open registration is enabled*, the user names and emails for new users.
- Actions—The actions—projects created, projects updated, user authentications and added users—that have occurred in during the selected time frame—today, yesterday, this week, or this month.

## Viewing system errors

When an error occurs, a red dot is displayed in the AEN navigation bar next to the Admin link. The red dot is removed when all exceptions are marked as “read.”

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Staff** menu, select Exceptions:

The screenshot shows the Anaconda Cloud Admin interface. On the left, the 'Staff' menu is expanded, showing options: Daily Report, Password Reset, Notification, and Exceptions (which is highlighted). Below 'Staff' is the 'Site Admin' menu with options: General, Accounts, Users, Security Log, Data Centers, Task Queue, and License. At the bottom is the 'Providers' menu with 'Enterprise Resources'. The main content area is titled 'Exceptions' and has a 'Mark all as read' button in the top right corner. The list of exceptions includes several 'jinja2.exceptions.UndefinedError' messages and three 'elasticsearch.exceptions.ConnectionError' messages. The first exception in the list is highlighted with a red box.

Exceptions		Mark all as read
<input checked="" type="radio"/>	jinja2.exceptions.UndefinedError: 'wk_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'	
<input type="radio"/>	jinja2.exceptions.UndefinedError: 'wk_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'	
<input type="radio"/>	jinja2.exceptions.UndefinedError: 'wk_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'	
<input type="radio"/>	jinja2.exceptions.UndefinedError: 'wk_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'	
<input type="radio"/>	jinja2.exceptions.UndefinedError: 'wk_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'	
<input type="radio"/>	jinja2.exceptions.UndefinedError: 'wk_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'	
<input type="radio"/>	jinja2.exceptions.UndefinedError: 'wk_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'	
<input type="radio"/>	jinja2.exceptions.UndefinedError: 'wk_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'	
<input type="radio"/>	elasticsearch.exceptions.ConnectionError:	
<input type="radio"/>	elasticsearch.exceptions.ConnectionError:	
<input type="radio"/>	elasticsearch.exceptions.ConnectionError:	
<input type="radio"/>	elasticsearch.exceptions.ConnectionError:	

The Exceptions section lists all errors that have occurred while AEN is running.

3. To see the details of an error, click the radio button next to the error. This also marks the error as “read.”
4. To mark all errors as read without reviewing each one, click the Mark all as read button.

## Viewing security errors

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select Security Log:

Staff

Daily Report

Password Reset

Notification

Exceptions

Site Admin

General

Accounts

Users

Monitor

Security Log

Security Log

View	Actor	Action	Date
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 25, 2017 09:46:09 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 25, 2017 09:39:17 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 25, 2017 09:22:04 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 25, 2017 09:10:31 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 25, 2017 08:45:50 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 25, 2017 08:43:12 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 25, 2017 08:10:30 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 25, 2017 08:09:38 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 24, 2017 23:52:06 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 24, 2017 23:51:58 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 24, 2017 23:51:58 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 24, 2017 23:51:58 CDT

The Security Log section lists all errors that have occurred that could potentially affect AEN security.

3. To view a user’s profile page, click their username in the Actor column.
4. To see the details of an error, click the Eye icon next to the error.

The error details are displayed:

5. To close the error details, click the Back link.

Public Profile

Account Settings

Security Log

Applications

oauth.authenticate	
_id	59c907f03f94c30fe45ffb9e
action	oauth.authenticate
actor_id	59c069b1ae55d1b3fe9fa45e
actor_username	aen_admin
client_id	59c119cd3f94c30fe45ff5db
remote_addr	None
time	2017-09-25 13:43:12.479000+00:00
token_id	59c907f03f94c30fe45ffb9d

[← Back](#)

Managing data centers

- 1. In the AEN navigation bar, click Admin to open the Admin Settings page.
- 2. In the **Site Admin** menu, select Data Centers:

Staff

Daily Report

Password Reset

Notification

Exceptions

Site Admin

General

Accounts

Users

Monitor

Security Log

Data Centers

Data Centers

Gateway (ec2-52-90-133-17.compute-1.amazonaws.com:8089)

+ Add DataCenter

The Data Centers section displays current data center information.



## Adding a data center

1. Click the Add DataCenter button to display the the Register a datacenter form.
2. In the Name box, type a Name for the new data center:

**Data Centers / Register a datacenter**

**Name**

☐ Subdomain Routing
   
☐ Https

**Base Domain Name**

**summary**

**Provider**

3. Select the Subdomain Routing and/or Https checkboxes.
4. In the Base Domain Name box, type the base domain name.
5. In the Summary box, type a description of the data center.
6. In the Provider list, select a provider.
7. Click the Submit button.

## Managing enterprise resources

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Providers** menu, select Enterprise Resources:

Staff

[Daily Report](#)  
[Password Reset](#)  
[Notification](#)  
[Exceptions](#)

Site Admin

[General](#)  
[Accounts](#)  
[Users](#)  
[Monitor](#)  
[Security Log](#)  
[Data Centers](#)  
[Task Queue](#)  
[License](#)

Providers

[Enterprise Resources](#)

Resources

Add Resource

Gateway

[ec2-54-210-232-251.compute-1.amazonaws.com](#)

remove

The Resources section lists your existing cloud and local resources.

### Adding a resource

1. Click the Add Resource button to open the new resource form.
2. Complete the form:

**Resources / new**

**Data Center**  
Gateway 59c119cd3f94c30fe45ff5db

**Name**  
Compute Node1

**URL**  
http://ec2-54-210-232-251.compute-1.amazonaws.com:5002

**Description**  
Configuring Compute Node

☒ **Public**  
Uncheck this if you want to control exactly who has access to this compute node

Add Resource

3. Click the Add Resource button.

### Viewing or changing the resource details

1. Click a resource name to open the Local Resource form.
2. If necessary, change the resource details:

**Data Center**

Gateway 59c119cd3f94c30fe45ff5db

**Name**

ec2-54-210-232-251.compute-1.amazonaws.com

**URL**

http://ec2-54-210-232-251.compute-1.amazonaws.com:5002

**Description**

☒ **Public**  
Uncheck this if you want to control exactly who has access to this compute node

Update

**status**

{"status": "ok", "messages": []}

3. Click the Update button.

### Making a node public or private

1. Click the resource name to open the Local Resource form.
2. Select or clear the Public checkbox:

**Data Center**  
Gateway 59c119cd3f94c30fe45ff5db

**Name**  
ec2-54-210-232-251.compute-1.amazonaws.com

**URL**  
http://ec2-54-210-232-251.compute-1.amazonaws.com:5002

**Description**

☒ **Public**  
Uncheck this if you want to control exactly who has access to this compute node

**Update**

**status**  
{"status": "ok", "messages": []}

3. Click the Update button.

## Removing a resource

Click the Remove button next to the resource you want to remove.

NOTE: When you remove a resource assigned to a project, the project becomes orphaned. To fix an orphaned project, *move the project to a valid Compute Resource*.

## Managing services

The tasks on this page assume that the 3 AEN nodes are installed in the following locations:

- Server—`/opt/wakari/wakari-server/`.
- Gateway—`/opt/wakari/wakari-gateway/`.
- Compute-Launcher—`/opt/wakari/wakari-compute/`.

- *Checking the status of server node processes*
- *Checking the status of gateway node processes*
- *Checking the status of compute node processes*
- *Starting AEN services*
- *Verifying that AEN services are set to start with the system*
- *Stopping AEN services*
- *Restarting AEN services*
- *Identifying extraneous processes*
- *Removing extraneous processes*

## Checking the status of server node processes

1. Run:

```
# service wakari-server status
wk-server          RUNNING      pid 20758, uptime 5 days, 0:30:23
worker            RUNNING      pid 20757, uptime 5 days, 0:30:23
```

OR

```
root@server # ps -Hu wakari
PID TTY          TIME CMD
20756 ?              00:02:26 .supervisord
20757 ?              00:05:58 mtq-worker
20758 ?              00:00:08 wk-server
```

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```
20765 ?      00:02:00      wk-server
20766 ?      00:01:55      wk-server
20767 ?      00:02:20      wk-server
20770 ?      00:02:02      wk-server
```

**2. Run:**

```
root@server # service nginx status
nginx (pid 26303) is running...
```

For more information on server processes, see *Server processes*.

**Checking the status of gateway node processes****Run:**

```
# service wakari-gateway status
wk-gateway          RUNNING      pid 1137, uptime 5 days, 1:59:28
```

**OR**

```
root@gateway # ps -Hu wakari
  PID TTY          TIME CMD
 1136 ?            00:01:59 .supervisord
 1137 ?            00:00:02  wk-gateway
```

For more information on gateway processes, see *Gateway processes*.

**Checking the status of compute node processes****Run:**

```
# service wakari-compute status
wk-compute          RUNNING      pid 22050, uptime 3 days, 1:03:19
```

**OR**

```
root@compute # ps -Hu wakari
  PID TTY          TIME CMD
 1150 ?            00:02:01 .supervisord
 1152 ?            00:00:01  wk-compute
```

For more information on compute node processes, see *Compute processes*.

**Starting AEN services**

Services should start automatically both when they are first installed and at any point when the system is restarted.

If you need to manually start an AEN service, you must start each node independently, because they may be running on separate machines.

NOTE: The process is basically the same for each node, but the path to the correct commands vary.

To manually start a service:

- On the server node, run:

```
service wakari-server start
```

- On the gateway node, run:

```
service wakari-gateway start
```

- On a compute node, run:

```
service wakari-compute start
```

### Verifying that AEN services are set to start with the system

To verify that AEN services are set up to start automatically:

1. Run the following command on each node:

```
chkconfig --list | grep wakari
```

2. If services are missing, add them:

```
chkconfig --add [wakari-server|wakari-gateway|wakari-compute]
```

3. *Restart the services.*

### Stopping AEN services

**CAUTION:** Do not stop or kill supervisord without first stopping wk-compute and any other processes that use it.

You must stop services on each node independently, because they may be running on separate machines.

To stop an AEN service:

- On the server node, run:

```
service wakari-server stop
```

- On the gateway node, run:

```
service wakari-gateway stop
```

- On a compute node, run:

```
service wakari-compute stop
```

Compute nodes may have running processes that are not automatically stopped. To stop them, run:

```
sudo /opt/wakari/wakari-compute/bin/wk-compute-apps kill-all
```

### Restarting AEN services

- On the server node, run:



```
service wakari-server restart
```

- On the gateway node, run:

```
service wakari-gateway restart
```

- On a compute node, run:

```
service wakari-compute restart
```

## Identifying extraneous processes

To get a complete list of the processes running under the wakari user account, run `ps -Hu wakari`.

EXAMPLE:

```
root@server # ps -Hu wakari
  PID TTY          TIME CMD
 20756 ?            00:02:26 .supervisord
 20757 ?            00:05:58 mtq-worker
 20758 ?            00:00:08 wk-server
 20765 ?            00:02:00 wk-server
 20766 ?            00:01:55 wk-server
 20767 ?            00:02:20 wk-server
 20770 ?            00:02:02 wk-server

root@server # ps -f -C nginx
UID      PID  PPID  C  STIME TTY          TIME CMD
root    26303    1   0  12:18 ?        00:00:00 nginx: master process /usr/sbin/nginx -c /
→etc/nginx/nginx.conf
nginx   26305 26303   0  12:18 ?        00:00:00 nginx: worker process

root@gateway # ps -Hu wakari
  PID TTY          TIME CMD
 1136 ?            00:01:59 .supervisord
 1137 ?            00:00:02 wk-gateway

root@compute # ps -Hu wakari
  PID TTY          TIME CMD
 1150 ?            00:02:01 .supervisord
 1152 ?            00:00:01 wk-compute
```

- wk-server, wk-gateway and wk-compute should have PIDs reported by supervisorctl.
- The nginx master process should have a PID reported by service nginx status.
- If you have installed more than one AEN node on a single machine, the processes from all of the installed nodes should be displayed for that machine.
- On compute node(s), any AEN applications currently being run by users will be present.

EXAMPLE:

```
root@compute # ps -Hu wakari
  PID TTY          TIME CMD
 1150 ?            00:00:00 .supervisord
 1152 ?            00:00:00 wk-compute
```

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```
1340 ?      00:00:00 bash
1341 ?      00:00:00 notebookwrapper
```

## Removing extraneous processes

If extra `wk-server`, `wk-gateway`, `wk-compute`, or `supervisord` processes are present, use the `kill` command to remove them to prevent issues with AEN.

You can safely *restart* any process that you remove in error.

## Making sure NGINX and MongoDB are running

In order for AEN to run, the dependencies `mongodb` and `nginx` must be up and running. If either of these fail to start, AEN will not be served on port 80.

Check if `nginx` and `mongod` are both running (RHEL 6x):

```
$ sudo service nginx status
nginx (pid 25956) is running...

$ sudo service mongod status
mongod (pid 25928) is running...
```

If either of these failed to start, tail the log files. The default location of log files is:

```
$ tail -n 50 /var/log/mongodb/mongod.log

# nginx errors reported in error.log
$ tail -n 50 /var/log/nginx/error.log
```

## Viewing, terminating, and relaunching applications

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select Monitor:

The Monitor menu lists started applications by user and project.

The list includes columns for the application name, current running status, running node and last seen date.

3. Use the buttons to terminate or relaunch an application.
4. To view an application's logs, click the Logs button with the document icon.

## Viewing the task queue

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select Task Queue:

Staff

Daily Report

Password Reset

Notification

Exceptions

Site Admin

General

Accounts

Users

Monitor

Running Apps								
User	Project	Application	Status	Node	Last Seen	Terminate	Relaunch	Logs
aen_admin	asd	notebook	running	localhost	Jul 24, 2017 15:15:24 CDT	<div>⏻ Terminate</div>	<div>🔄 Relaunch</div>	<div>📄</div>
aen_admin	Test	notebook	running	localhost	Jul 25, 2017 11:54:05 CDT	<div>⏻ Terminate</div>	<div>🔄 Relaunch</div>	<div>📄</div>

Staff

Daily Report

Password Reset

Notification

Exceptions

Site Admin

General

Accounts

Users

Monitor

Security Log

Data Centers

Task Queue

## Task Queue

Workers

ip-172-31-10-196.4053 | 

high

default

low

Queues

high

Backlog: 0

Failed: 1

default

Backlog: 0

Failed: 3

The Workers section lists the workers in the task queue and whether each worker is set at high, default or low priority.

The Queues section provides information on the default and high priority queues.

3. To view all the tasks in a particular queue, in the Queues section, click the queue name.

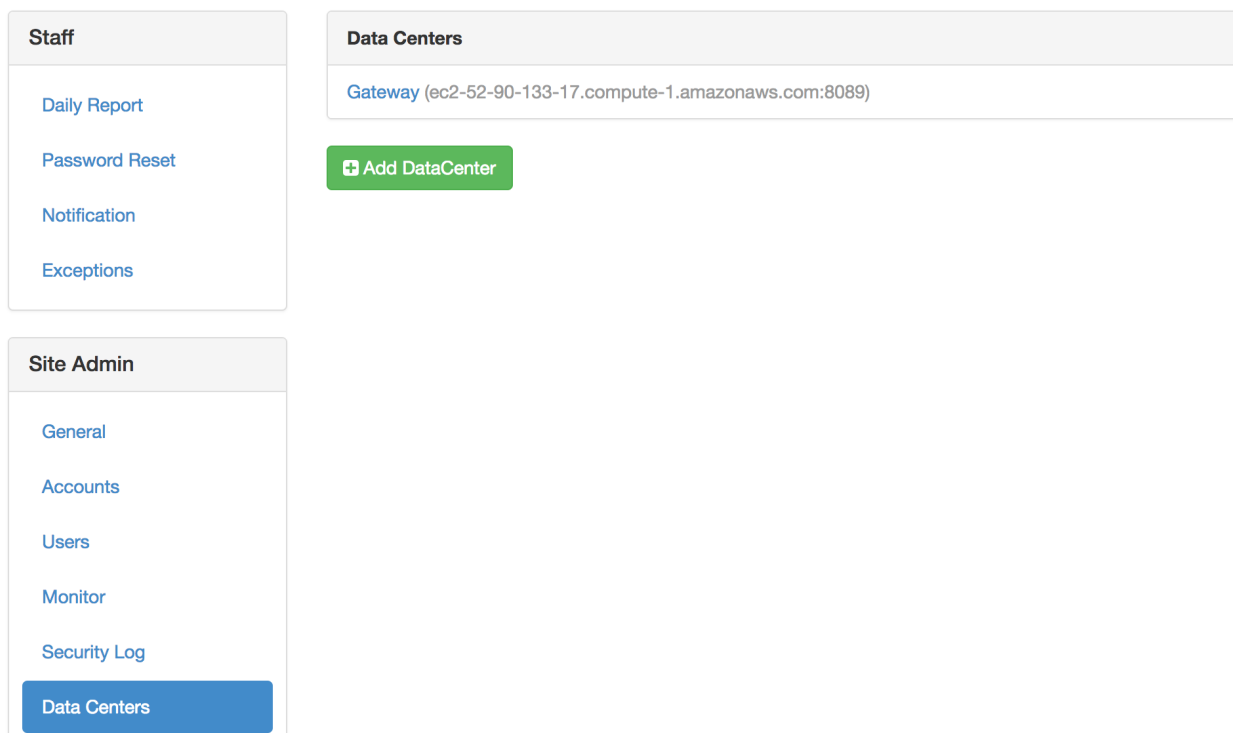
## Checking node connections

When the AEN nodes cannot communicate with each other as intended, it can cause issues with you AEN platform installation.

- *Verifying server to gateway connectivity*
- *Verifying gateway to compute node connectivity*
- *Verifying gateway to server connectivity*

## Verifying server to gateway connectivity

1. On the server, in the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select Data Centers:



- For each data center in the list, check connectivity from the server to that gateway.

EXAMPLE: The gateway in this example is `http://gateway.example.com:8089`:

```
root@server # curl --connect-timeout 5 http://gateway.example.com:8089 > /dev/null
```

## Verifying gateway to compute node connectivity

- On the server, in the AEN navigation bar, click Admin to open the Admin Settings page.
- In the **Providers** menu, select Enterprise Resources:

The screenshot shows the Anaconda Enterprise Admin Settings page. On the left, there is a navigation menu with the following sections:

- Staff**
  - Daily Report
  - Password Reset
  - Notification
  - Exceptions
- Site Admin**
  - General
  - Accounts
  - Users
  - Monitor
  - Security Log
  - Data Centers
  - Task Queue
  - License
- Providers**
  - Enterprise Resources

On the right, the **Resources** section is visible, featuring a green **+ Add Resource** button. Below this, the **Gateway** section contains a table with one entry:

Gateway	
ec2-54-210-232-251.compute-1.amazonaws.com	<a href="#">remove</a>

- Open each compute node in the Resources section.
- Verify that the contents of the URL field begin with either `http` or `https`.

**Data Center**

Gateway 59c119cd3f94c30fe45ff5db

**Name**

ec2-54-210-232-251.compute-1.amazonaws.com

**URL**

http://ec2-54-210-232-251.compute-1.amazonaws.com:5002

**Description**

☒ **Public**  
Uncheck this if you want to control exactly who has access to this compute node

Update

**status**

{"status": "ok", "messages": []}

5. Check connectivity to that URL from the corresponding gateway.

EXAMPLE: The gateway in this example is `http://gateway.example.com:8089`:

```
root@gateway # curl --connect-timeout 5 http://compute.example.com:5002 > /dev/
↪null
```

## Verifying gateway to server connectivity

The gateway-to-server path is used by the gateway configuration command `wk-gateway-configure`.

1. Verify that the gateway is linked to the correct server in the configuration file.
2. Verify that the full server URL is specified.
3. Check connectivity to the server:

```
root@gateway # grep WAKARI_SERVER /opt/wakari/wakari-gateway/etc/wakari/wk-
↪gateway-config.json
"WAKARI_SERVER": "http://wakari.example.com",

root@gateway # curl --connect-timeout 5 http://wakari.example.com > /dev/null
root@gateway # curl --connect-timeout 5 http://error.example.com > /dev/null
curl: (7) Failed to connect to error.example.com port 80: Connection refused
```

4. If a connection fails:
  1. Ensure that gateways (data centers) and compute nodes (Enterprise Resources) are correctly configured on the server.
  2. Verify that processes are listening on the configured ports:

```
$ sudo netstat -nplt
Active Internet connections (only servers)
Proto Recv-Q Send-Q Local Address   Foreign Address State  PID/Program
tcp        0      0 *:80            :::*           LISTEN 26409/nginx
tcp        0      0 *:22            :::*           LISTEN 986/sshd
tcp        0      0 127.0.0.1:25    :::*           LISTEN 1063/master
tcp        0      0 *:5000          :::*           LISTEN 26192/python
tcp        0      0 127.0.0.1:27017 :::*           LISTEN 29261/mongod
tcp        0      0 *:22            :::*           LISTEN 986/sshd
tcp        0      0 127.0.0.1:25    :::*           LISTEN 1063/master
```

3. Check the firewall setting and logs on both hosts to ensure that packets are not being blocked or discarded.

## Verifying and tuning search indexing

For search indexing to work correctly, a compute node must be able to communicate with the server. To verify this:

1. Run:

```
curl -m 5 $AEN_SERVER > /dev/null
```

2. Verify that there are sufficient inotify watches available for the number of subdirectories within the project root file system:

```
cat /proc/sys/fs/inotify/max_user_watches
```

NOTE: Some Linux distributions default to a low number of watches, which may prevent the search indexer from monitoring project directories for changes.

3. If necessary, increase the number of watches:

```
echo fs.inotify.max_user_watches=100000 | sudo tee -a /etc/sysctl.conf && sudo  
→ sysctl -p
```

4. Verify that there are sufficient inotify user instances available—at least one per project:

```
cat /proc/sys/fs/inotify/max_user_instances
```

5. If necessary, increase the number of inotify user instances:

```
echo fs.inotify.max_user_instances=1000 | sudo tee -a /etc/sysctl.conf && sudo  
→ sysctl -p
```

### Changing the AEN server URL

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select General:
3. In the Wakari Server box, type the main URL where the site can be viewed.
4. Click the Update button.

### Changing the static URL for JavaScript files

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select General:
3. In the Static URL box, type the static URL where JavaScript files can be accessed.
4. Click the Update button.

### Changing the AEN account type

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select General:



<b>Staff</b>	<b>General Admin Settings</b>
<a href="#">Daily Report</a>	<b>Wakari Server</b> Set the main URL where this site will be accessed
<a href="#">Password Reset</a>	<input type="text" value="http://anaconda-enterprise.trl"/>
<a href="#">Notification</a>	
<a href="#">Exceptions</a>	<b>Static URL</b> Set static URL where the js can be accessed
	<input type="text" value="http://anaconda-enterprise.trl/static/"/>
<b>Site Admin</b>	
<b>General</b>	<b>Default Project Access</b> This will be the default when a user creates a project
<a href="#">Accounts</a>	<input type="radio"/> <b>Public</b> Anyone can see this project. Collaborators have write access
<a href="#">Users</a>	<input checked="" type="radio"/> <b>Private</b> No one can see this project except collaborators.
<a href="#">Monitor</a>	
<a href="#">Security Log</a>	<b>Account Type</b>
<a href="#">Data Centers</a>	<input type="text" value="wk_server.plugins.accounts.cloud"/>
<a href="#">Task Queue</a>	
<a href="#">License</a>	<input type="button" value="Update"/>
<b>Providers</b>	<b>Config Files</b>

Staff	General Admin Settings
<a href="#">Daily Report</a>	<b>Wakari Server</b> Set the main URL where this site will be accessed <input type="text" value="http://anaconda-enterprise.trl"/>
<a href="#">Password Reset</a>	<b>Static URL</b> Set static URL where the js can be accessed <input type="text" value="http://anaconda-enterprise.trl/static/"/>
<a href="#">Notification</a>	<b>Default Project Access</b> This will be the default when a user creates a project  <input type="radio"/> <b>Public</b> Anyone can see this project. Collaborators have write access <input checked="" type="radio"/> <b>Private</b> No one can see this project except collaborators.
<a href="#">Exceptions</a>	<b>Account Type</b> <input type="text" value="wk_server.plugins.accounts.cloud"/>
	<input type="button" value="Update"/>
Site Admin	Config Files
<a href="#">General</a>	
<a href="#">Accounts</a>	
<a href="#">Users</a>	
<a href="#">Monitor</a>	
<a href="#">Security Log</a>	
<a href="#">Data Centers</a>	
<a href="#">Task Queue</a>	
<a href="#">License</a>	
Providers	

Staff	General Admin Settings
<a href="#">Daily Report</a>	<b>Wakari Server</b> Set the main URL where this site will be accessed <input type="text" value="http://anaconda-enterprise.trl"/>
<a href="#">Password Reset</a>	<b>Static URL</b> Set static URL where the js can be accessed <input type="text" value="http://anaconda-enterprise.trl/static/"/>
<a href="#">Notification</a>	<b>Default Project Access</b> This will be the default when a user creates a project  <input type="radio"/> <b>Public</b> Anyone can see this project. Collaborators have write access <input checked="" type="radio"/> <b>Private</b> No one can see this project except collaborators.
<a href="#">Exceptions</a>	<b>Account Type</b> <input type="text" value="wk_server.plugins.accounts.cloud"/>
	<input type="button" value="Update"/>
<b>Site Admin</b>	
<a href="#">General</a>	
<a href="#">Accounts</a>	
<a href="#">Users</a>	
<a href="#">Monitor</a>	
<a href="#">Security Log</a>	
<a href="#">Data Centers</a>	
<a href="#">Task Queue</a>	
<a href="#">License</a>	
<b>Providers</b>	<b>Config Files</b>

3. In the Account Type box, select the account type—cloud or LDAP.
4. Click the Update button.

### Changing the default for project access

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select General:

<b>Staff</b>	<b>General Admin Settings</b>
<a href="#">Daily Report</a>	<b>Wakari Server</b> Set the main URL where this site will be accessed
<a href="#">Password Reset</a>	<input type="text" value="http://anaconda-enterprise.trl"/>
<a href="#">Notification</a>	<b>Static URL</b> Set static URL where the js can be accessed
<a href="#">Exceptions</a>	<input type="text" value="http://anaconda-enterprise.trl/static/"/>
<b>Site Admin</b>	<b>Default Project Access</b> This will be the default when a user creates a project
<b>General</b>	<input type="radio"/> <b>Public</b> Anyone can see this project. Collaborators have write access
<a href="#">Accounts</a>	<input checked="" type="radio"/> <b>Private</b> No one can see this project except collaborators.
<a href="#">Users</a>	<b>Account Type</b>
<a href="#">Monitor</a>	<input type="text" value="wk_server.plugins.accounts.cloud"/>
<a href="#">Security Log</a>	<input type="button" value="Update"/>
<a href="#">Data Centers</a>	
<a href="#">Task Queue</a>	
<a href="#">License</a>	
<b>Providers</b>	<b>Config Files</b>

3. Under Default Project Access, select the default access type for new projects: Public or Private.
4. Click the Update button.

## Changing the owner of a project

To change the owner of a project:

1. Collect the project name, the user name of the previous owner, and the user name of the new owner.
2. Run the `wakari-server` executable command `wk-server-admin`:

```
/opt/wakari/wakari-server/bin/wk-server-admin project-owner --project PROJECT --  
↪old OLD_OWNER --new NEW_OWNER --delete --keep-owner
```

- **PROJECT**: The project name.
- **OLD\_OWNER**: The user name of the previous owner.
- **NEW\_OWNER**: The user name of the new owner.
- **--delete**: An optional flag that deletes the old project directory in the `projects` directory of **OLD\_OWNER**. If this flag is not used, the old project directory is preserved but no longer used.
- **--keep-owner**: An optional flag that makes **OLD\_OWNER** a collaborator of the project after it is transferred to **NEW\_OWNER**. If this flag is not used, **OLD\_OWNER** will no longer have collaborator access to the project.

**NOTE:** The **OLD\_OWNER** user must still exist when the project's owner is changed. Before deleting any user, be sure to change the owner of the user's projects.

## Editing configuration files

1. In the AEN navigation bar, click **Admin** to open the Admin Settings page.
2. In the **Site Admin** menu, select **General**.
3. In the **Config Files** section, change the configuration settings for your AEN installation. For more information on configuration files, see [Using configuration files](#).
4. Click the **Update** button.

## Managing your AEN license

1. In the AEN navigation bar, click **Admin** to open the Admin Settings page.
2. In the **Site Admin** menu, select **License**:

The **Current License** section displays information regarding your AEN license, including the name of the product, vendor, license holder's name, end and issued dates, company name, license type, and contact email.

Staff	General Admin Settings
<a href="#">Daily Report</a>	<b>Wakari Server</b> Set the main URL where this site will be accessed
<a href="#">Password Reset</a>	<input type="text" value="http://anaconda-enterprise.trl"/>
<a href="#">Notification</a>	<b>Static URL</b> Set static URL where the js can be accessed
<a href="#">Exceptions</a>	<input type="text" value="http://anaconda-enterprise.trl/static/"/>
<b>Site Admin</b>	<b>Default Project Access</b> This will be the default when a user creates a project
<b>General</b>	<input type="radio"/> <b>Public</b> Anyone can see this project. Collaborators have write access
<a href="#">Accounts</a>	<input checked="" type="radio"/> <b>Private</b> No one can see this project except collaborators.
<a href="#">Users</a>	<b>Account Type</b>
<a href="#">Monitor</a>	<input type="text" value="wk_server.plugins.accounts.cloud"/>
<a href="#">Security Log</a>	<input type="button" value="Update"/>
<a href="#">Data Centers</a>	
<a href="#">Task Queue</a>	
<a href="#">License</a>	
<b>Providers</b>	<b>Config Files</b>

Staff

[Daily Report](#)
[Password Reset](#)
[Notification](#)
[Exceptions](#)

Site Admin

[General](#)
[Accounts](#)
[Users](#)
[Monitor](#)
[Security Log](#)
[Data Centers](#)
[Task Queue](#)
[License](#)

Current License

You have **166 days** remaining on your current license.

Renew your license

<b>product</b>	Anaconda Enterprise Notebooks
<b>vendor</b>	Continuum Analytics, Inc.
<b>name</b>	Continuum Development
<b>end_date</b>	2018-03-10
<b>issued</b>	2017-03-10
<b>company</b>	Continuum Analytics
<b>type</b>	undefined
<b>email</b>	dev@continuum.io

Upload New License

License File

Choose File

No file chosen

Update

## Renewing your AEN license

1. Click the Renew your license button.
2. In the Upload New License section, click the Choose File button.
3. Select the new license file.
4. Click the Open button.
5. Click the Update button.

Your renewed license information is displayed.

## Cheat sheet

The Admin dashboard includes three menus in the left column: **Staff**, **Site Admin** and **Providers**.

### Staff menu

- Daily Report—See the number of users and projects.
- Password Reset—Reset a user password.
- Notification—Send system messages to users via SES or SMTP.

- Exceptions—If errors are raised while AEN is running, a red dot appears in the AEN navigation bar. Review errors and mark them as read.

### Site Admin menu

- General—Change the configuration settings for your AE Notebook server installation.
- Accounts—Turns on or off Open Registration.
- Users—View usernames, number of projects and last logins.
- Monitor—View status of applications with related data, terminate or restart
- Security Log—View errors that could affect security.
- Data Centers—View current data centers and add a new data center.
- Task Queue—View workers in the task queue and priority.
- License—View current AEN license or upload a new license.

### Providers menu

Enterprise Resources—View, add or remove local or cloud services and designate public or private to control access to a compute node.

### Troubleshooting

This troubleshooting guide provides you with ways to deal with issues that may occur with your AEN installation.

- *General troubleshooting steps*
- *Browser error: too many redirects*
- *Browser error: too many redirects when starting project apps*
- *Exception: exceptions.TypeError: 'NoneType' object has no attribute '\_\_getitem\_\_'*
- *Error: unix:///opt/wakari/wakari-server/etc/supervisor.sock no such file*
- *Error: “Data Center Not Found” when deleting a project*
- *Forgotten administrator password*
- *Log files being deleted*
- *Error: This socket is closed*
- *Service error 502: Cannot connect to the application manager*
- *502 communication error on Amazon web services (AWS)*
- *Invalid username*
- *Notebook Error: Cannot download notebook as PDF via LaTeX*
- *Unresponsive wk-server thread without error messages*
- *Unresponsive wk-gateway thread without error messages*



- *Error starting projects*
- *Changes in .condarc file are ignored*

## General troubleshooting steps

1. Clear browser cookies. When you change the AEN configuration or upgrade AEN, cookies remaining in the browser can cause issues. Clearing cookies and logging in again can help to resolve problems.
2. *Make sure NGINX and MongoDB are running.*
3. Make sure that AEN services are *set to start at boot*, on all nodes.
4. *Make sure that services are running* as expected. If any services are not running or are missing, *restart them*.
5. *Check for and remove extraneous processes.*
6. *Check the connectivity between nodes.*
7. *Check the configuration file syntax.*
8. *Check file ownership.*
9. *Verify that POSIX ACLs are enabled.*

## Browser error: too many redirects

### Cause

Browser cookies are out of date.

### Solution

1. Log out.
2. Clear the browser's cookies.
3. Clear the browser cache.
4. Log in.

## Browser error: too many redirects when starting project apps

Browser shows “Too many redirects” when the user tries to start an application.

### Cause

The project's Compute Resource is invalid or was deleted.

### Solution

*Move the project to a valid Compute Resource.*

### Exception: `exceptions.TypeError: 'NoneType' object has no attribute '__getitem__'`

This exception appears on the Admin > Exceptions page when a project does not have a Compute Resource assigned.

#### Cause

The project's Compute Resource is invalid or was deleted.

#### Solution

*Move the project to a valid Compute Resource.*

### Error: `unix:///opt/wakari/wakari-server/etc/supervisor.sock no such file`

This is a supervisorctl error.

#### Cause

supervisord is not running on the Server.

#### Solution

Ensure that supervisord is included in the crontab. Then restart supervisord manually.

### Error: “Data Center Not Found” when deleting a project

#### Cause

The data center has been removed.

#### Solution

As root, run:

```
/opt/wakari/wakari-server/bin/wk-server-admin remove-project --db-only <user>  
↪<project>
```

### Forgotten administrator password

1. Use ssh to log into the server as root.
2. Run:

```
/opt/wakari/wakari-server/bin/wk-server-admin reset-password -u SOME_USER -p SOME_  
↪PASSWORD
```

NOTE: Replace SOME\_USER with the administrator username and SOME\_PASSWORD with the password.

3. Log into AEN as the administrator user with the new password.

Alternatively you may add an administrator user:

1. Use ssh to log into the server as root.
2. Run:

```
/opt/wakari/wakari-server/bin/wk-server-admin add-user SOME_USER --admin -p SOME_
-PASSWORD -e YOUR_EMAIL
```

NOTE: Replace SOME\_USER with the username, replace SOME\_PASSWORD with the password, and replace YOUR\_EMAIL with your email address.

3. Log into AEN as the administrator user with the new password.

## Log files being deleted

Log files are being deleted.

NOTE: Locations of AEN log files for each process and application are shown in the node sections in [Concepts](#).

## Cause

AEN installers log into `/tmp/wakari\_server, gateway, compute}.log`. If the log files grow too large, they might be deleted.

## Solution

To set the logs to be more or less verbose, Jupyter Notebooks uses `Application.log_level`.

To make the logs less verbose than the default, but still informative, set `Application.log_level` to `ERROR`.

## Error: This socket is closed

You receive the “This socket is closed” error message when you try to start an application.

## Cause

When the `supervisord` process is killed, information sent to the standard output `stdout` and the standard error `stderr` is held in a pipe that will eventually fill up.

Once full, attempting to start any application will cause the “This socket is closed” error.

## Solution

To prevent this issue:

- Follow the instructions in [Managing services](#) to stop and restart processes.
- Do not stop or kill `supervisord` without first stopping `wk-compute` and any other processes that use it.

To resolve the “This socket is closed” error:

1. Stop wk-compute by running `sudo kill -9`.
2. Restart the supervisord and wk-compute processes:

```
sudo /etc/init.d/wakari-compute stop
sudo /etc/init.d/wakari-compute start
```

### Service error 502: Cannot connect to the application manager

Gateway node displays “Service Error 502: Can not connect to the application manager.”

#### Cause

A compute node is not responding because the wk-compute process has stopped.

#### Solution

Stop and then restart the supervisord and wk-compute processes:

```
sudo /etc/init.d/wakari-compute stop
sudo /etc/init.d/wakari-compute start
```

### 502 communication error on Amazon web services (AWS)

You receive the “502 Communication Error: This gateway could not communicate with the Wakari server” error message.

#### Cause

An AEN gateway cannot communicate with the Wakari server on AWS. There may be an issue with the IP address of the Wakari server.

#### Solution

Configure your AEN gateway to use the DNS hostname of the server. On AWS this is the DNS hostname of the Amazon Elastic Compute Cloud (EC2) instance.

### Invalid username

#### Cause

The username does not follow 1 or more of these rules:

- Must be at least 3 characters and no more than 25 characters.
- The first character must be a letter (A-Z) or a digit (0-9).

- Other characters can be a letter, digit, period (.), underscore (\_) or hyphen (-).
- The [POSIX standard](#) specifies that these characters are the portable filename character set, and that portable usernames have the same character set.

## Solution

Follow the above rules for usernames.

## Notebook Error: Cannot download notebook as PDF via LaTeX

### Cause

LaTeX is not properly installed.

### CentOS/6 Solution

1. Install TeXLive from the [TUG site](#). Follow the described steps. The installation may take some time.
2. Add the installation to the PATH in the file `/etc/profile.d/latex.sh`. Add the following, replacing the year and architecture as needed:

```
PATH=/usr/local/texlive/2017/bin/x86_64-linux:$PATH
```

3. Restart the compute node.

### CentOS/7 Solution

1. Install the missing packages running the command:

```
yum install texlive texlive-xetex texlive-xetexconfig texlive-xetex-def texlive-  
↪adjustbox texlive-upquote texlive-ulem
```

## Unresponsive `wk-server` thread without error messages

### Cause

Two things can cause the `wk-server` thread to freeze without error messages:

- LDAP freezing
- MongoDB freezing

If LDAP or MongoDB are configured with a long timeout, Gunicorn can time out first and kill the LDAP or MongoDB process. Then the LDAP or MongoDB process dies without logging a timeout error.

## Solution

1. Check for frozen LDAP or MongoDB server processes.
2. You may also wish to configure the Gunicorn timeout to more than 30 seconds.

### Unresponsive `wk-gateway` thread without error messages

#### Cause

If TLS is configured with a passphrase protected private key, `wk-gateway` will freeze without any error messages.

#### Solution

Update the TLS configuration so that it does not use a passphrase protected private key.

### Error starting projects

Project's status page shows "There was an error starting this project".

#### Cause

Lack of disk space in compute nodes prevents projects from starting.

#### Solution

1. Verify that the project node meets the *system requirements*.
2. Check if there is enough free space on the compute node's partition where `/projects` lives:

```
df -h /projects
```

3. Free up some disk space to meet the system requirements.
4. Restart the project.

### Changes in `.condarc` file are ignored

Changes applied to `.condarc` are ignored by conda.

#### Cause

Conda loads its configuration by merging multiple files together.

#### Solution

Check if you are applying the changes to the correct file.

To show the merged state that conda is currently using:

```
conda config --show
```

To show all config files that conda is currently reading:

```
conda config --show-sources
```

## Frequently asked questions

- *What is AEN?*
- *Can notebooks be shared with anyone?*
- *Can I disable the option, “publish your notebook to anaconda.org”?*
- *How can I check the version number of my AEN server?*
- *Can I use AEN to access CSV or Amazon S3 data?*
- *Can I install other Python packages?*
- *Can I create a Python environment from the command line?*
- *Can I connect to GitHub with AEN?*
- *Can I print or print preview my Jupyter Notebooks?*
- *Is there a set amount of storage on AEN?*
- *How do I get help, give feedback, suggest features or report a bug?*

## What is AEN?

For information on AEN, see *Anaconda Enterprise 4 Notebooks*.

## Can notebooks be shared with anyone?

Yes. When you share a Jupyter Notebook through AEN, it can be viewed and run without the need to install anything special, regardless of what libraries were used to create the notebook. Each notebook also includes the python environment that it needs to run in.

AEN allows users to clone a shared Jupyter Notebook into their AEN account to make whatever changes or modifications they want. The notebook’s Python environment is also cloned, so it runs in the same environment as the shared Jupyter Notebook unless it is changed.

## Can I disable the option, “publish your notebook to anaconda.org”?

Yes. The upload button in the notebook app executes the option “publish your notebook to anaconda.org”. To disable it, log in as the AEN\_SRVC\_ACCT and run these commands:

```
source activate /opt/wakari/wakari-compute
jupyter-nbextension disable nb_anacondacloud --py --sys-prefix
jupyter-serverextension disable nb_anacondacloud --py --sys-prefix
```

### How can I check the version number of my AEN server?

Go to this URL in a browser: `http://$AEN_SERVER/admin/list`

NOTE: Replace `$AEN_SERVER` with the domain name or the domain name and port number of your AEN server.

### Can I use AEN to access CSV or Amazon S3 data?

Yes. If your data is in CSV files, upload the CSV files to your AEN account using the upload controls in the File Browser of the Workbench Application or the File Transfer Application.

To access data stored on Amazon S3, use the Boto interface from AEN. See the public data files in AEN for examples of how to use Boto to pull your data from Amazon S3 into AEN. For more information, see [Boto documentation](#).

You can also use IOPro to simplify and optimize the conversion of your data into Python arrays.

### Can I install other Python packages?

Yes, by creating a custom environment for your packages within your project.

For more information, see [Using the NBConda extension](#).

### Can I create a Python environment from the command line?

Yes, you can use the `conda create` command to create custom Python environments with whatever packages you choose. All AEN environments are shared with all the team members of a project.

EXAMPLE: In this example, `myenv` is a new environment containing the NumPy package.

```
conda create -n myenv numpy
```

NOTE: Python, Jupyter Notebooks and PIP are installed by default in all new AEN environments.

To use your new environment, activate it by running `source activate myenv`.

### Can I connect to GitHub with AEN?

Yes, you have full access to GitHub through an AEN Terminal application.

To generate an SSH key from your AEN account and add it to your GitHub account:

1. [Generate a GitHub SSH key](#).
2. Copy your key by running `cat ~/.ssh/id_rsa.pub`.
3. Select and copy the contents of the `id_rsa.pub` file to the clipboard.
4. Follow [GitHub's instructions](#) to go to your GitHub account and paste it from your clipboard into the appropriate box in your GitHub settings.

### Can I print or print preview my Jupyter Notebooks?

Yes, you can print your notebooks using your browser's regular printing capabilities.

You can also preview the printed page by clicking the **File** menu and selecting Print Preview.



### Is there a set amount of storage on AEN?

No, there is no set limit for storage in AEN. You are limited only by the size of the disk where AEN is installed.

If you need more storage, contact your system administrator.

### How do I get help, give feedback, suggest features or report a bug?

See *Help and support*.

### Help and support

Priority support is included with the purchase of an Anaconda subscription.

Contact your administrator first if you are having problems. Your administrator has a service level agreement where your issue will be responded to within a specific response time, depending on type and severity.

### Training and consulting

Training and consulting is available for AEN and any other Anaconda product.

For more information, please contact your account representative or [email the sales team](#).

### Providing feedback

Your feedback is very important to us!

Please, send us any [product feedback](#) while you are thinking about it.

TIP: Be sure to select AEN as the Platform Component Name.

### Submitting feature requests

We'd love to hear your ideas for consideration in future releases!

Your ideas help us build a better product. Your administrator can submit a support ticket for you.

NOTE: You can also request new features by using the [product feedback](#) form.

### Reporting a bug

If you think you have found a bug, please contact your administrator immediately. They will open a support ticket for your issue.

### Additional resources

The following resources are useful for getting started with Jupyter Notebooks:

- [Jupyter Notebook quick start guide](#)
- [Jupyter Notebook user documentation](#)

- [GitHub](#) shows the most popular Jupyter notebooks of the [month](#), [week](#), and [day](#).

### Release notes

#### v4.3.1 March 25, 2019

Administrator-facing changes:

- Add option for server-side session management
- Add option to terminate terminal sessions on logout

Internal Fixes: - Set Secure and HTTPOnly flag on session cookies - Fix XSS vulnerability

#### v4.3.0 October 24, 2018

Administrator-facing changes:

- Fix bug where compute logging wasn't respecting the `logMaxFiles` key
- Log and display a descriptive error message when there is a problem creating the users index
- Log and display a descriptive error message when there is a problem creating a new user with a duplicated e-mail address when the `uniqueEmail` setting is enabled
- Add footer server pages with server host data (IP, AEN version and server version)
- Fix admin script to change the status of private projects
- Fix validation error when updating/editing an existing resource
- Docs: Add KB article about using MongoDB to update old projects with new Data Center information
- Docs: Add restarting service step to SSO documentation
- Docs: Add support for newer versions of MongoDB
- Docs: Add documentation on `uniqueEmail`
- Docs: Add `projDirsAsHome` key to config docs
- Docs: Rewrite the "Using project directories as home directories" section
- Docs: Add full path to admin commands
- Docs: Warn about upgrading away from tested pkgs
- Docs: Add missing steps to "Authenticating with LDAP" section
- Docs: Add troubleshooting documentation about orphaned projects
- Docs: Warn about not using IP address when you connect to AEN
- Docs: Add an entry about 'Error starting projects' in the troubleshooting page
- Docs: Rewrite "Group and user permissions for NFS" section and description of the `identicalGID` key in the config pages
- Docs: Add a new section about using MRO packages in AEN
- Docs: Preserve username capitalization when using LDAP/AD
- Docs: Add `umask 0022` to security requirements
- Docs: Add new section about changing install location

- Docs: Add note about how to manually break out Root CA for the gateway
- Docs: Add note about upgrading custom environments
- Docs: Add notes about how to find conda config files inside AEN
- Docs: Add note about using `USE_SERVER_BASED_SESSIONS: false` when configuring SSO between AEN and versions 2.33.3 through 2.33.10 of the Repository

User-facing changes:

- Increase Workbench file upload limit
- Fix Bokeh examples
- Extend `nb_locker` to detect a server disconnection and generate an alert if it occurs
- Docs: Update the notebook app to correctly point to AEN docs
- Docs: Emphasize that permissions are not applied recursively in the workbench

Internal fixes:

- Update Nginx version to v1.12.2
- Remove unused server config file during the compute upgrade process
- Remove already defined compute default settings from the post-script step
- Pin `widgetsnbextension` version to prevent version mismatch issue (ipywidgets)
- Remove `--offline` flag from the conda clone operations
- Support MongoDB 3.4.14 and update pymongo to version 3.2.2
- Fix LDAP username case sensitivity
- Security fixes and enhancements

## **v4.2.2 March 1, 2018**

Administrator-facing changes:

- Add admin command to change project owner
- Server: Add ability to disable public projects
- Gateway: Add support for SSL private key passphrase
- Docs: Add backup and restore runbook to the docs
- Docs: Emphasize backups before upgrading process
- Docs: Recommend putting AEN and projects folder on the same filesystem
- Docs: Add RHEL version 7.4 to supported versions
- Docs: Add troubleshooting instructions to fix problems when downloading notebook as PDF via LaTeX

User-facing changes:

- Upgrade bokeh to version 0.12.7
- Upgrade holoviews to version 1.8.3
- Upgrade numba to version 0.35.0
- Upgrade scikit-learn to version 0.19.0

Internal fixes:

- Fix bug in init scripts when requiretty is enabled
- Fix bugs related to AEN\_SUDO\_SSH option
- Fix bug in fix\_ownership function when directories contain spaces
- Docs: Fix error in Active Directory configuration example
- Server: Fix bug when updating user/group in supervisor configuration files in post-install for server and gateway
- Server: Fix bug Admin reports on user totals are inconsistent
- Server: Fix error in login screen when open registration and LDAP are enabled
- Server: Fix bug in Last seen date
- Server: Fix bug Monitor Report blank
- Server: Load JS files from local CDN
- Server: Fix error when terminating or relaunching an application from Monitor
- Server: Fix error creating projects when using Internet Explorer 11
- Compute: Fix 404 errors when using pivottablesjs
- Remove Wakari Cloud leftovers

### **v4.2.1 December 18, 2017**

Administrator-facing changes:

- None

User-facing changes:

- None

Internal fixes:

- Fix undetected “ca” key when using self-signed certificates signed by a private CA
- Fix login redirects when using SSL
- Add verify gateway SSL certificate for get and post requests

### **v4.2.0 November 22, 2017**

Administrator-facing changes:

- Feature/allow remote MongoDB
- Allow for configuration for login timeout and set default
- Add verbose option to conda create clone
- Avoid duplicate name for resources / compute-nodes
- Allow renaming main and message queue databases
- PAM-based authentication module
- Change wakari logos to Anaconda logos

- Replace ‘wakari’ wording
- New config option to move the user’s home directory into the user’s project directory
- Make logging less verbose in AEN
- Documentation for PySpark kernel installation
- Improve SSL documentation

User-facing changes:

- New config option to move the user’s home directory into the user’s project directory
- Package cache was moved from user’s home directory into the user’s project directory
- Change wakari logos to Anaconda logos
- Fix error for deleting tags to work
- Define shell prompt in `.projectrc` template
- Replace ‘wakari’ wording

Internal fixes:

- Move server unix socket from `/tmp` to `/opt/wakari/wakari-server/var/run`
- Make project deletion synchronous for consistency
- Avoid storing `csrf` token in the user profile
- Expire gateway session when server logs out
- Allow log rotation in the three components
- Fix permissions on static files
- Change log level to debug in gateway
- Do not log private keys in gateway
- Save request remote address when logging action
- Unify logs formatting and timezone in compute nodes with Winston
- Several fixes and documentation improvements

### **v4.1.3 August 16, 2017**

- Upgrade conda to version 4.3.24
- Upgrade anaconda to version 4.4.0
- Admin application monitor
- Block access to package list view
- Add placeholders in password reset form
- Change static content location
- Fix error when checking for package updates in notebook application
- Replace slashes in project tags
- Fix submit errors in password reset form
- Replace/remove “wakari” word from multiple places

- Fix missing commands missing sudo in start-project
- Improve gateway and compute node validators
- Check if bzip2 is installed during server setup process
- Include port number in host header
- Forbid creation of empty tags
- Repair “Create Account” link in login page
- Use UTC for server logs
- Mark datacenters as trusted by default
- Disable heart beating
- Compute resource: Show full path to log file
- Improve init scripts
- Allow deleting all projects
- mtq: Implement exponential backoff on connection error to mongodb
- In the general admin display, do not show the bind password for LDAP
- The accelerate package has been removed from the installation
- Other minor bugfixes

### **v4.1.2 March 29, 2017**

This is mainly a maintenance release improving internal machinery and upgrading the root packages.

- Upgrade conda to version 4.3.14
- Upgrade Anaconda to 4.3.1
- Upgrade r-base to 3.2.2
- Fixed AEN nb\_conda to be compatible with conda 4.3.x series
- Several documentation fixes
- Other minor bugfixes

### **v4.1.1 December 15, 2016**

- Added CentOS 7 support
- Support dots in usernames
- More usernames validation
- Fixed creation (through nb\_conda) of single letter environment names
- Environment names (through nb\_conda) validation
- Fixed uploading of notebook using nb\_anacondacloud
- Fixed attaching of environments in published notebooks through nb\_anacondacloud
- Several documentation fixes

- Other bugfixes

#### **v4.1.0 October 21, 2016**

- Added JupyterLab application
- Removed GateOne terminal application
- Included additional notebook extensions (`nbpresent` and `nb_anaconda_theme`)
- Updated to conda 4.2.9 in default project environments
- Added HTTP timeout setting for gateway and compute launcher
- Changed default gateway port to 8089
- Added support for all-numeric usernames
- Add R channel to default conda configuration file
- Other bugfixes

#### **v4.0.0 June 30, 2016**

- Customized installation with:
  - AEN Functional ID and Group
  - AEN (installation and run) `sudo` commands
  - Removal of root access from the AEN service account
  - Configurable `sudo` command
  - Restriction of `sudo` access to all the processes
- Upgrade Jupyter to 4.2
- Upgrade the `anaconda-nb-extensions` to the latest versions
- Upgrade Anaconda to 4.0
- Deprecate `wakari-publisher`
- Security enhancements
- SSL configuration documented between all AEN Server components
- Several bugfixes
- Overall documentation revision and general improvement

#### **v0.10.0 February 2, 2016**

- New projects dashboard
- Capability to star and tag a project
- Sticky searches
- New Jupyter Notebook extensions
- Updates to all packages. Highlights: `bokeh` 0.11, `ipython/jupyter` 4.1.

### v0.9.1 October 19, 2015

- New Search capability to find projects and files within a project.
- Added “Related Projects” list to the project view, based on code similarity.
- New UI for fine-grained access control of project files in the Workbench app
- Viewer app now renders plain text files correctly
- Updated LDAP configuration docs
- Updates to all packages. Highlights: bokeh 0.10, ipython/jupyter 4.0.

**Note** ElasticSearch, and an Oracle JRE, must be installed on the server in order to use the new search features. Indexing of project files will begin when the project is started (or paused and re-started). If search features are not desired, set `"SEARCH_ENABLED": false` in the server configuration file to avoid errors.

### v0.8.0 August 21, 2015

#### New Features

- Updated packages based on Anaconda 2.3, and removed older packages no longer in Anaconda.
- Updated IPython to version 3.2.1
- Documentation is now installed with the server (use the Help link in the top navigation bar)
- Added the ability for the administrator to define a customized default project environment.
- The server has been updated to use python 2.7.10.
- Init scripts are now provided for each Anaconda Enterprise Notebooks service.
- Added relevant links to some error pages

#### Problems Resolved in this Release

- Project status indicators (e.g. starting, pausing) now automatically update.
- If an access is unauthorized, the server now returns a 403 (Unauthorized) status code and prompts the user to log in.
- Modified nginx configuration to support running the server on non-standard ports.
- The server installation no longer uses a default password for the wakari user. A random password is generated and displayed during installation.
- Prevent double-click from attempting to create a project twice
- Removed an obsolete script reference that was causes a 404 error to be logged in the browser console when opening the Terminal app.
- The installer scripts no longer fail if the database already contains the ‘wakari’ user.
- Updated example notebooks to work with latest Bokeh release.
- Fixed terminal app key bindings to allow Mac command key to work normally
- Installers now indicate where the installation logs are stored
- LDAP user attributes containing binary data are now ignored.



## Documentation Updates

- Updated and consolidated Troubleshooting guide.
- Simplified some steps in the installation procedure.
- Updated notebooks in the Examples directory for use with the latest IPython Notebook and Bokeh.
- Added a section on project permissions to the Troubleshooting guide.
- Added notes on how to remove a project if the datacenter has already been removed.

## v0.7.0 June 12, 2015

### New Features

- Updated Bokeh to v0.9
- Ability to list packages installed on the server
- Administrators now have full access to all projects.
- Added automated checking and display of connection status between server, data centers, and compute resources.
- When creating a new project, an environment for the project is automatically created as a clone of the root Anaconda environment.

### Problems Resolved in this Release

- Problem with checking in files with revision control extension
- Revision control extension can't handle notebook names with spaces
- Problem moving files from one compute node to another if configured for LDAP
- Should default to UTF-8 encoding and warn user if no locale is detected
- Adding a compute resource via the command line admin tool does not work
- The installer now sets `umask 0022` to ensure correct file permissions

## Documentation Updates

- Added a *Troubleshooting* section to the documentation.
- Added notes on how to configure crontab to start the Anaconda Enterprise Notebooks services at startup
- Example SSL config file now has correct log paths
- Added instructions on how to ensure that POSIX ACL support is enabled on the projects directory.
- Fixed syntax problem in sample LDAP config.json
- Added section on how to use self-signed or private CA certificates

### v0.6.3 March 27, 2015

- Updated LDAP module
- LDAP user filtering
- Added Notebook locking
- Added Notebook integrated revision control system
- Move projects between compute nodes
- User-specific binding to compute nodes (private compute nodes)
- Improved installation process and dependency checking
- Incorporated support for SSL for Server and Gateway nodes
- Improved Gateway error handling
- Fixed package dependencies for update process
- Documentation updates

### Previous versions

Previous version documentation is provided for users who have not yet upgraded to the current version of AEN.

### Anaconda Enterprise 4 Notebooks

*Empower the Data Science Team with cross-collaboration*

AEN is a browser-based Python data analysis environment and visualization tool from Anaconda®. AEN is a ready-to-use, powerful, fully-configured data analytics environment all in a secure, governed environment.

AEN allows data science team members to create and share private notebooks, manage access, control notebook revisions, compare and identify differences across notebook versions, search notebooks for keywords and packages, use enhanced collaborative notebook features—including revision control and locking—and to access an on-premises and/or cloud collaborative notebook server.

The current version of AEN is 4.3.0, released October 24th, 2018.

### User guide

AEN's browser-based management of private packages, notebooks, and environments allows data science team members to:

- Create, share and manage private notebooks.
- Control notebook revisions.
- Compare and identify differences across notebook versions.
- Search notebooks for keywords and packages.
- Use enhanced collaborative notebook features including revision control and locking.
- Access on-premises and/or cloud-based collaborative notebook servers.
- Utilize multiple language kernels like Python and R language in the same notebook.

- Create new notebook environments on the fly without leaving the notebook or entering commands in a prompt.
- Publish results to business stakeholders as interactive visualizations and presentations.

To quickly get up and running with AEN, see [Getting started](#).

Download the [Cheat sheet](#) for easy reference.

## Concepts

- [Projects](#)
- [Team collaboration](#)
- [Access control](#)
- [Sharing projects](#)
- [Project tags](#)

## Projects

AEN users interact with the system predominantly through projects.

A project is a set of conda environments, Jupyter Notebooks, and other files.

Each project has a project drive that all team members can access. The size of the drive is not limited by AEN. Contact your system administrator if you find you do not have sufficient space.

Each project has a separate project directory on the project drive.

The project directory is a directory for project files and data that is separate from the project owner's and team members' home directories, so that team members can share and have equal access.

The path to your project directory is `/projects/<project_owner>/<project_name>`.

For administrative information about projects, directories, and permissions, see [Projects and permissions](#).

## Team collaboration

Teams collaborate in AEN using projects. Projects allow a team to easily come together by sharing the resources, applications, and environments that are necessary to collaborate effectively.

The AEN project owner and any team members connected to their project will have access to the same:

- Shared files and home directories.
- Shared Python and R environments.
- Shared nodes and hardware.
- Common applications.
- Web user interface.

For more information, see [Working with projects](#).

### Access control

AEN access controls allow you to:

- Add and remove project access for new team members.
- Limit the access to specific folders and files to members of your project team.
- Use permissions to extend execute access to team members. By default, all of the team members on a project have read and write access to all project assets.

Access control is performed from each project's Workbench application.

For more information, see [Controlling access to your project](#).

### Sharing projects

AEN supports both public and private sharing.

A project can be “public,” which means that anyone with access to the system can view the project assets.

Any content placed in the `public` folder in a project is publicly accessible using its URL.

A project can be “private,” which means that only the project owner and team members can view the project assets.

You can also [limit who can access specific files](#).

### Sharing Jupyter Notebooks

In addition to general project sharing capabilities, you can also publish Jupyter Notebooks to Anaconda Repository. This automatically versions the notebook and allows you to define who can view the notebook.

### Project tags

Tags are used to:

- Group similar or related projects.
- Identify your project so that it is easier to find.
- Let others know about your project.

You can [add and remove tags](#) for any project that you have access to.

### Getting started

This section contains information and tasks for first-time AEN users.

In this getting started guide, you will:

- [1. Download the AEN cheat sheet](#)
- [2. Access your user home page](#)
- [3. Create a new project](#)

- 4. *Add collaborators*
- 5a. *Open an example notebook, OR*
- 5b. *Create a new environment and notebook*
- 6. *Create checkpoints for version control*
- 7. *Share your notebook and environment with others*
- 8. *See what to do next*

## 1. Download the AEN cheat sheet

Before you start, download and print the *AEN cheat sheet* for easy reference.

## 2. Access your user home page

After your administrator has set up your server and new Anaconda account, you will receive a welcome email.

1. Click the link in the email to open the AEN login page.

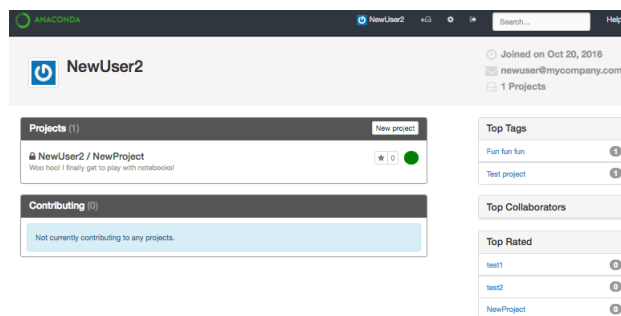
NOTE: Use the domain name and not the IP address when you connect to AEN. Using the IP address can cause TLS and security certificate errors.

2. Enter your AEN account username and password.

NOTE: Some administrators allow you to create your own account. If your administrator has allowed this, in the create a new account section, create your own username and password.

3. Click the Login button.

Your user home page, where all good things happen, is displayed:

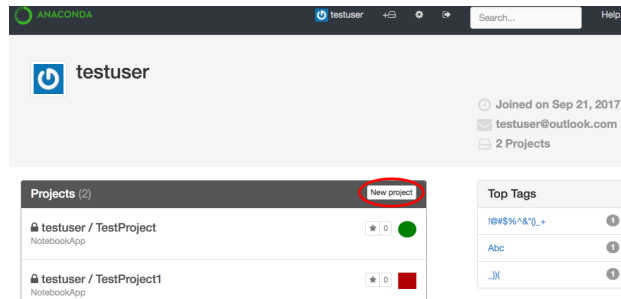


## 3. Create a new project

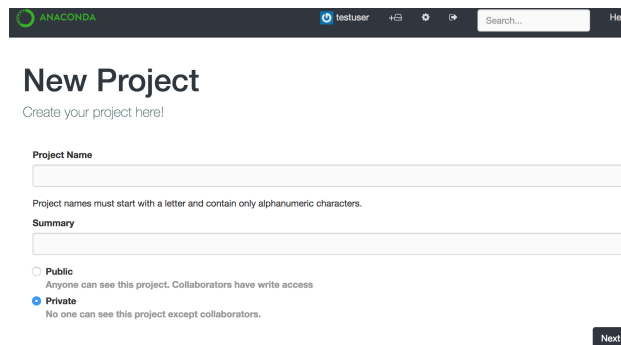
1. There are 2 ways to create a new project in AEN:
  - On the right side of the AEN task bar, click on the New Project icon:



- On your home page, click the New project button:



2. On the Project page that is displayed, type a name for your project, such as “Testing.”



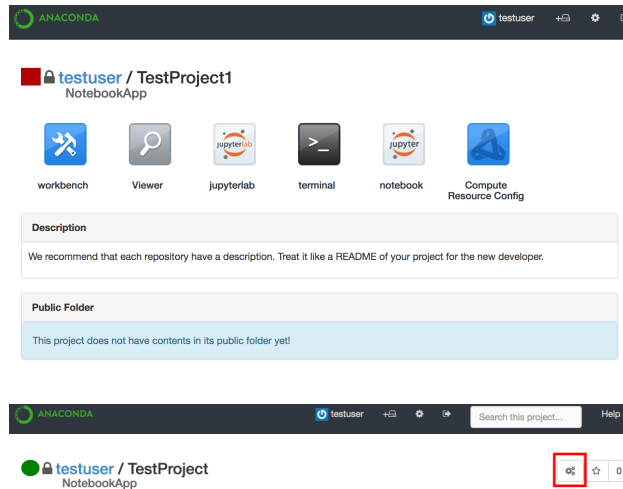
3. Type a summary of the project so you can recognize it later.
4. Select whether your project will be public or private.
5. Verify that the default data center is selected.

TIP: You can update the project summary and description at any time from the **Project** menu in the Project Settings. To return to your project at any time, click the project name.

6. Click the Next button.

Your new project's home page is displayed:

7. To change the project settings, click the Project Settings icon on at the top right.



8. Modify the summary or add a description of the project.

TIP: A project description is recommended, and may be written in Markdown syntax (plain text valid Markdown).

To see how Markdown will be displayed, in the description area, click the **Preview** tab.

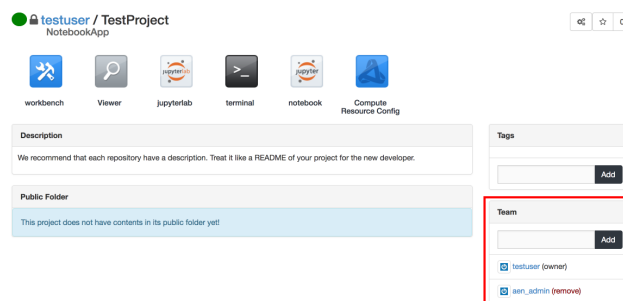
#### 4. Add collaborators

You can add team members to your project as collaborators. Adding team members to your projects makes collaboration easy because they have full access to the project's applications, files and services.

When you add team members, their home directory is mounted in the project. There is no need to download and email data or scripts—team members can work on the same files in the same environment in which you are working.

To add collaborators to your project:

1. From your project home page, in the Team box, begin typing a teammate's username.
2. In the list that is displayed, select the teammate's username.
3. Click the Add button.

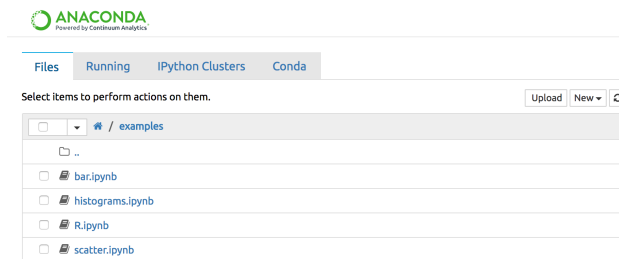


1. Repeat these steps for each team member you want to add as a collaborator.

TIP: You can add or remove team members any time from the **Team** menu in Project Settings. You can also modify a team member's read, write or execute permissions at any time from the *Using Workbench*.

### 5a. Open an example notebook, OR

1. From your project home page, click the Jupyter Notebooks icon.
2. On the File View page, click the Examples folder.



1. Select any of the example notebooks.
2. To see the default results of the formulas used in the displayed notebook, in the **Cell** menu, select Run All.
3. To experiment with changing the notebook, edit any of the formulas in the notebook.
4. In the **Cell** menu, select Run All.

Any differences resulting from your edits are displayed.

### 5b. Create a new environment and notebook

If you are already familiar with creating notebooks, you can easily set up a new environment with the programs you need—like SciPy and NumPy—then open a new notebook and make your edits.

To create a new environment:

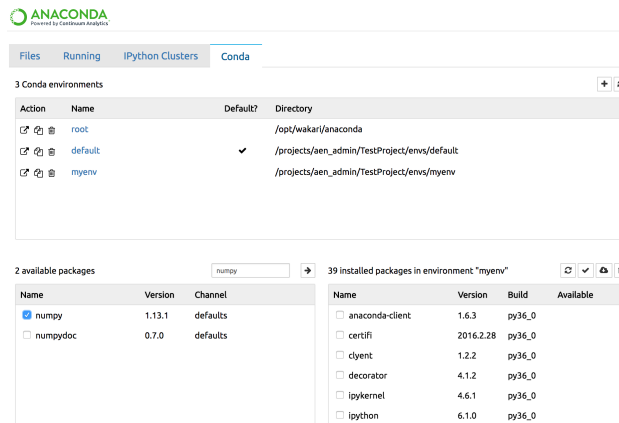
1. From your project home page, click the Jupyter Notebooks icon.
2. On the File View page, click the **Conda** tab.
3. To add a new conda environment, on the top right of the **Conda** tab, click the + icon.
4. Type a name for your environment.
5. Select Python 2, Python 3 or R language kernel.
6. Click the Create button.
7. To activate your new environment, click its name.

The packages that are available and installed in your new environment are displayed.

### Adding SciPy and Numpy packages

1. In the available packages section, search for the package name `numpy`—all lower case.
2. In the results section, next to `numpy`, select the checkbox.





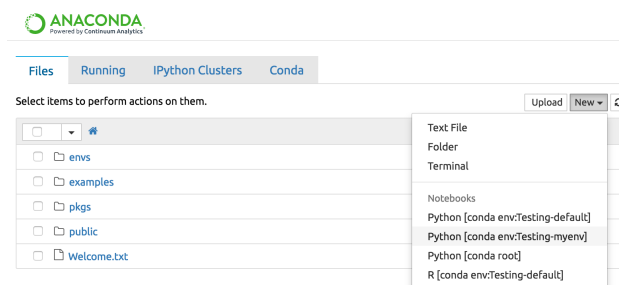
1. Click the Install icon.
2. To confirm your installation, click the Install button.

Numpy is displayed in the installed packages section—if not, click the Refresh button. Repeat these steps to install the Scipy package—searching for `scipy` in step 1.

TIP: You can return to this screen at any time to add additional packages to this environment.

## Creating a new notebook in your environment

1. From the AEN homepage, click the **Files** tab.
2. On the top right of the **Files** tab, click the New button.
3. Under Notebooks, select the Python environment with the name you entered while *creating a new environment*.



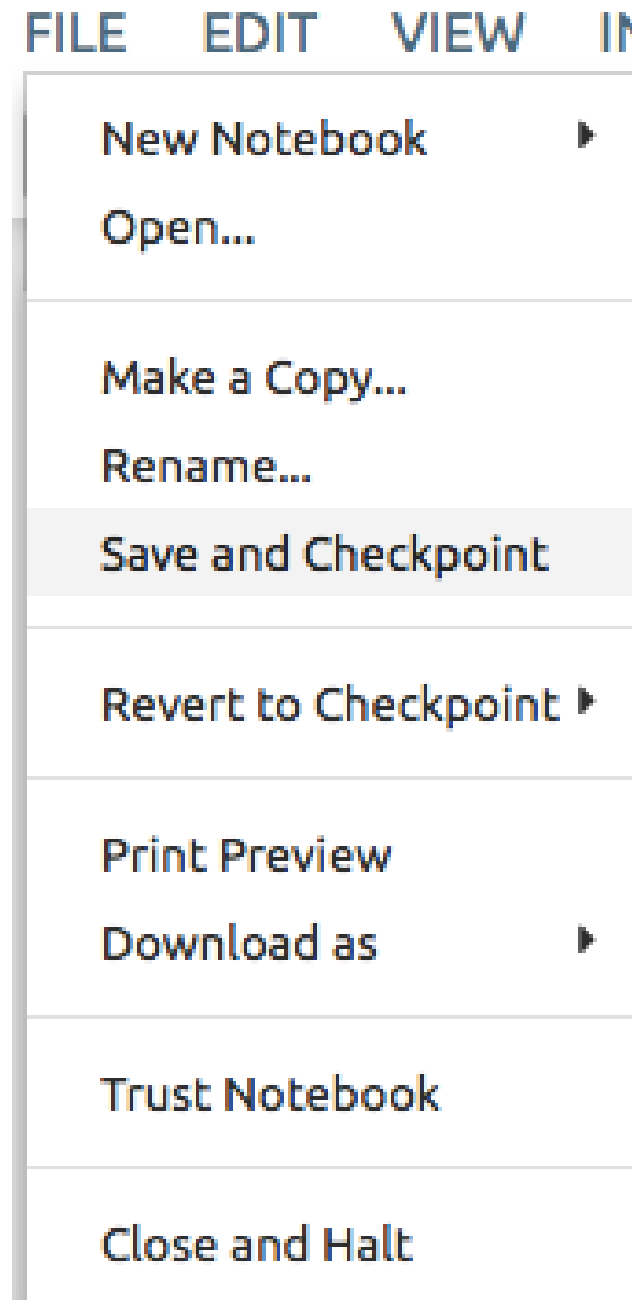
NOTE: If you do not see your new environment listed under Notebooks, next to the New button, click the Refresh button.

A new locked notebook is displayed. Paste or write some code to execute when you are ready.

## 6. Create checkpoints for version control

Whether you are exploring an existing notebook, or creating a new one, you can easily create checkpoints, return to an earlier version, compare two different versions and save them for reference.

To create a checkpoint, in the **File** menu, select Save and Checkpoint:



To revert your notebook to a previous checkpoint, in the **File** menu, select Revert to Checkpoint.

NOTE: For more information about revision control features, including creating commits and comparing differences, see *Using the Revision Control Mechanism extension*.

## 7. Share your notebook and environment with others

See *Sharing projects and notebooks*.

## 8. See what to do next

Now that you have completed the Getting Started guide, you are ready to move on to *basic tasks* and *advanced tasks*.

### Basic tasks

This section contains information and tasks that use the web browser to manage projects and is best-suited for any beginning AEN user:

#### Working with projects

Almost everything in AEN starts by opening an existing project or creating a new one.

After that, you can set up a special environment with the packages you want, set their access permissions and modify your project settings.

#### Searching for a project or file

- *Types of files searched*
- *Search indexing*
- *Using search constructs*
- *Searching metadata fields*
- *Searching a project*
- *Saving a search*
- *Removing a saved search*

To search for projects and files, use the Search box in the AEN navigation bar. The search provides different results depending on which page you search from:

- On a project home page, search results include any files that match your search criteria within the current project.
- On any other AEN page, search results include any files that match your search criteria within all projects.

TIP: Your search results include only files and projects that you can view: public projects, and private projects to which you have a minimum of view access.

## Types of files searched

The following types of files are included in search results:

- `.py`—Python source files.
- `.ipynb`—IPython/Jupyter notebooks.
- `.txt`—plain text files.
- `.md`—Markdown files.

## Search indexing

Files that are modified while a project is running are automatically re-indexed shortly after the files are modified. If you create or update a large number of files—such as cloning a git repository or copying a directory—search results may take several minutes to update.

Files that are modified while the project is not running are re-indexed only after the project is started.

## Using search constructs

You can use the following search constructs:

- Ordinary words will match the full-text contents of any file.
- Wildcards are permitted.

EXAMPLE: `John*` will match John and Johnny. These are glob patterns and are similar to their usage in the command line.

- Combine queries using AND or OR, and group them using parentheses `()`.

Regular expression patterns can be embedded in the query string by wrapping them in forward-slashes `/`:

```
name:/joh?n(ath[oa]n)/
```

The supported regular expression syntax is explained in [the Elasticsearch reference](#).

NOTE: Wildcards apply inside a regular expression. A query string such as `/*.n/` would force the search to visit every term in the index.

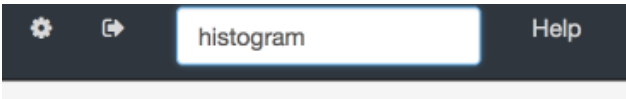
## Searching metadata fields

You can search in specific metadata fields:

- `imports:name`—matches files that import the module name.
- `uses:name`—matches files that reference the identifier name. Referenced names include any functions and globals imported from other modules, as well as the names of any methods invoked on any object.
- `defines:name`—matches files that define the identifier name. Defined names include functions defined at global scope, class names, and method names within classes.
- `acl:user`—matches files in which the named user has read access or higher.

Searching a project

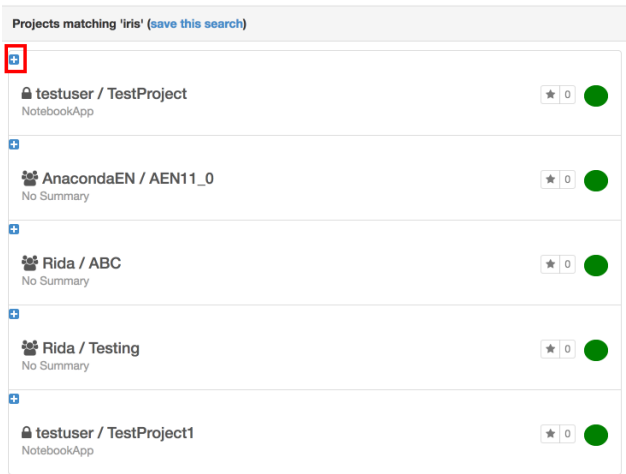
- 1. In the Search box, type a string of text:



TIP: Search by glob patterns, which are similar to file matching in the command line.

EXAMPLE: To find projects in the test family that are numbered from 00 to 99, search for `Test-??`. To find all projects whose name ends with “Stats,” search for `*Stats`.

- 2. Press Enter.
- 3. In the search results, click the plus + icon above a project name to show a list of matching files in the selected project:



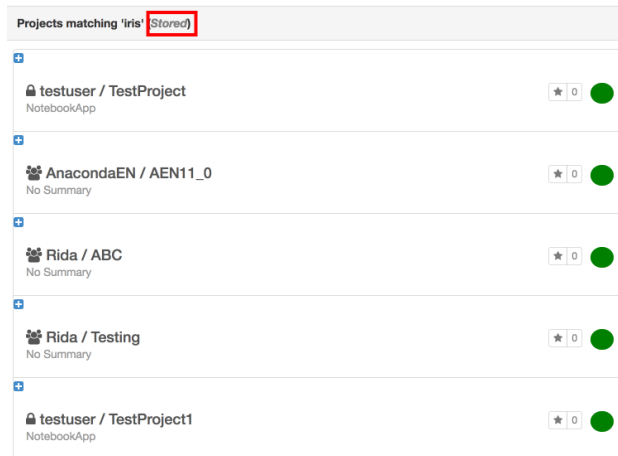
TIP: Click the project name to open the project’s home page.

- 4. To view a file, click its file name in the matching files list:



## Saving a search

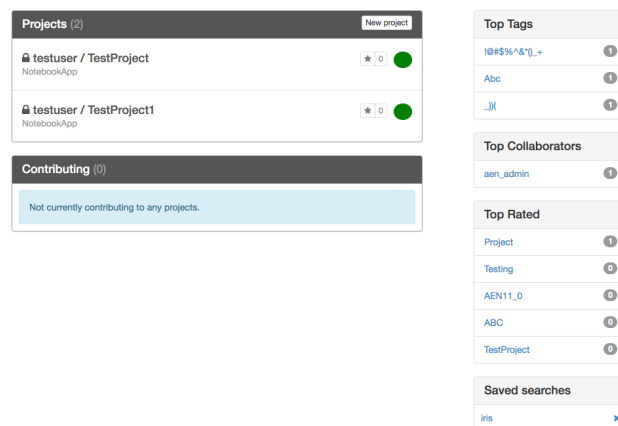
1. At the top of the search results, click Save this search:



The “save this search” text changes to “stored” and your search is saved. Your saved searches are listed on your home page.

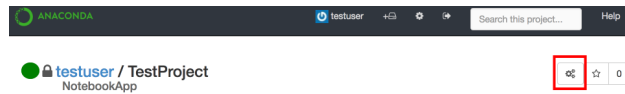
## Removing a saved search

On your home page, in the Saved searches section, click X next the saved search that you want to remove:

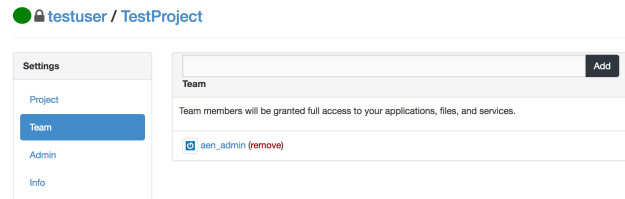


## Adding and removing team members on a project

1. On the project home page, click the Project Settings icon to open the Project Settings page.



2. In the **Settings** menu, select Team.



## Adding a team member

1. In the username box, type in the first few letters of the username for the team member you want to add to the project.
2. In the list of usernames that displays, click the user to add.
3. Click the Add button.

## Removing a team member

Click the red Remove link next to the name of the user you want to remove from the project.

## Controlling access to your project

- *Controlling team member access*
- *Controlling non-team member access*

## Controlling team member access

By default, all of the team members on a project have read and write access permissions for all project assets.

The available permissions are read, write and execute. If you remove all individual or group permissions for a project asset, team members will not be able to access that asset.

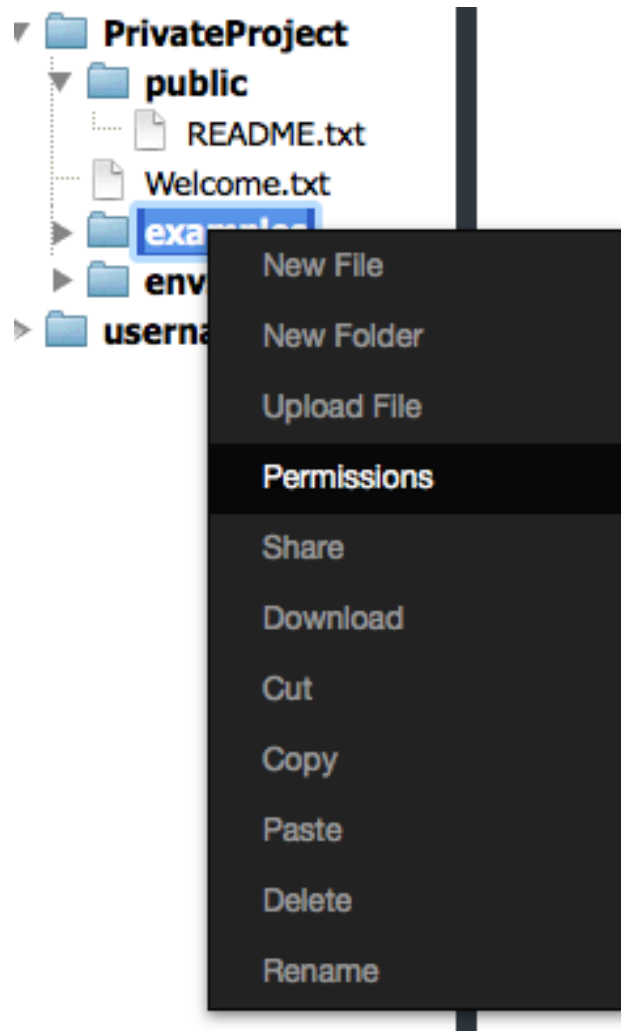
To change a project's permissions:

1. Open the project's home page.

2. Click the Workbench icon.
3. In the Workbench app, right-click the file or folder you want to limit access to.

NOTE: When you change a folder's permissions, the permissions of files and folders inside it do not change. You may change the permissions of those files and folders manually.

4. In the menu that displays, select Permissions:



A list of owners and team members who have access to your project is displayed.

5. Find the team member you want to change access for:
6. Next to the team member's name, select or deselect the permissions for that user.



Permissions for examples

Owner  Group

Who	Type	Read	Write	Execute
owner		<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
group		<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
others		<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>
Mask		Read	Write	Execute
<input type="text" value="username"/>	User	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input type="text" value="username"/>	Group	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input type="text" value="username2"/>	User	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>
<input type="text" value="username2"/>	Group	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
<input type="text" value="username3"/>	User	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
<input type="text" value="username3"/>	Group	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

NOTE: You can add a team member and set their access at the same time by typing their name in a username box, setting their permissions, and then clicking the Add button.

7. Click the Submit button.

The selected permissions are added, and the deselected permissions are removed.

NOTE: If a team member is in the Workbench application when you give them access, they must refresh their browser window to see their current permissions.

## Controlling non-team member access

You can choose to grant file or folder access to someone who is not part of the project team, as long as that person has an AEN account.

Sharing with individuals outside the team is a four step process:

1. *Copy or move the file or folder to your home directory.*
2. *Give the user read and execute access to your home directory.*
3. *Add the user to the file's permissions.*
4. *Have the user add your directory to their workbench.*

## Copying a file or folder to your home directory

Your home directory is displayed at the bottom of the File Manager pane in the Workbench.

To protect the other files and folders in your home directory—those you are not providing permissions to a user to access—we recommended that you:

1. Create a sub-folder.
2. Rename the folder with the name of the user you are granting access to.
3. Copy or move the file you want to grant permissions for to the renamed folder.

The file is copied or moved to the new location and is ready for you to update the file permissions.

### Granting file access

You must select read and execute access for a user to be able to view, but not edit, the files or folders.

1. Right-click the name of the file or folder you are granting access to.
2. In the menu that is displayed, select Permissions.
3. Click the Add button.
4. Type the username of the user to whom you are granting file access and press Enter.

**TIP:** If you grant access to a folder instead of a specific file, you only have to set permissions the first time you share the folder with each user, unless you need to update the permissions.

### Adding file permissions for a user

Once a user is included in your Permissions list, you must *add the correct permissions* for the user, in the same way as you would for a team member.

Once complete, depending on the access granted, the user will be able to view, read, change, and execute the file.

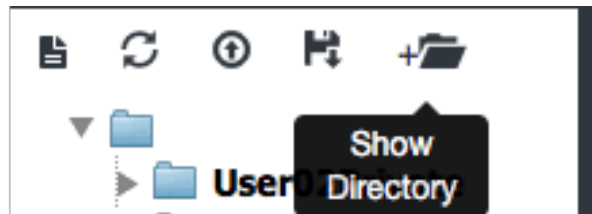
**NOTE:** If you change permissions for a folder instead of a file, the user will be able to see and access any files within that folder.

### Adding a directory to a user's workbench

The user can now add your home directory to their Workbench File Manager.

To add your home directory to another user's workbench, have the other user follow these steps:

1. Click the Show Directory button at the top of the Workbench File Manager:

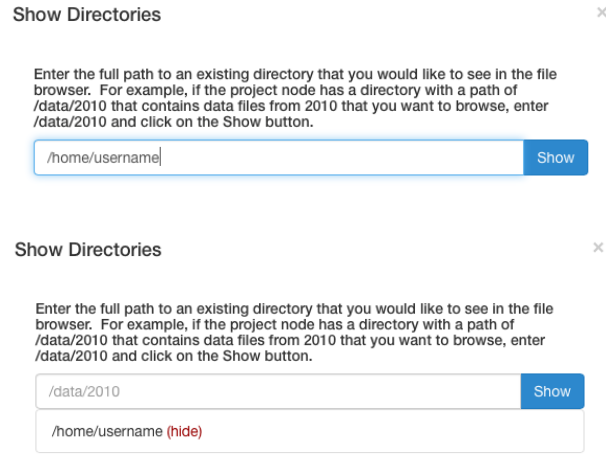


The Show Directories dialog box displays.

2. In the text box, type `/home/[yourusername]`.

**NOTE:** Replace `[yourusername]` with your AEN username.

3. Click the Show button.
4. Verify that the folder is now displayed below the text box:



5. Close the Show Directories dialog box by clicking the X in the upper-right corner or by clicking anywhere outside the box.
6. Click the Refresh button.

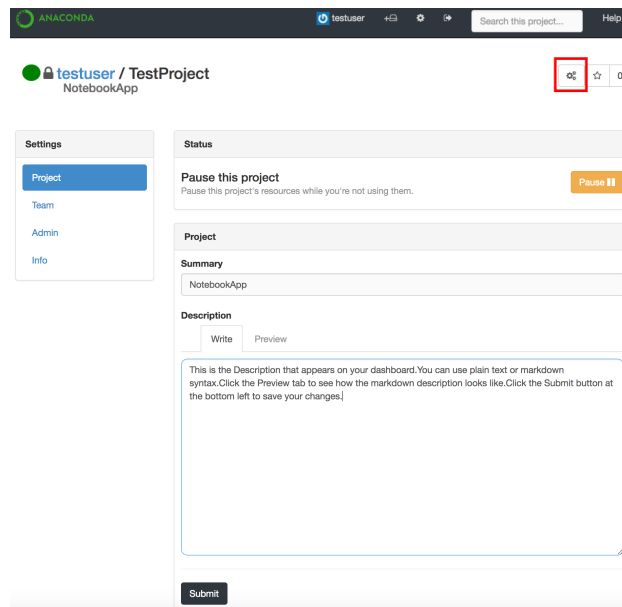
The shared file is displayed in the File Manager:



## Starting and stopping a project

**TIP:** Stopping a project stops all the applications launched for that project that use resources when running, such as memory and compute cycles. It is best to stop projects when they are not in use.

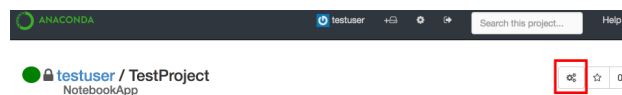
1. On the project home page, click the Project Settings icon to open the Project Settings page.
2. In the **Settings** menu, select Project.



3. In the Status section, click the Start or Stop button to toggle between manually starting and stopping your project.

## Making a project public or private

1. On the project home page, click the Project Settings icon to open the Project Settings page.



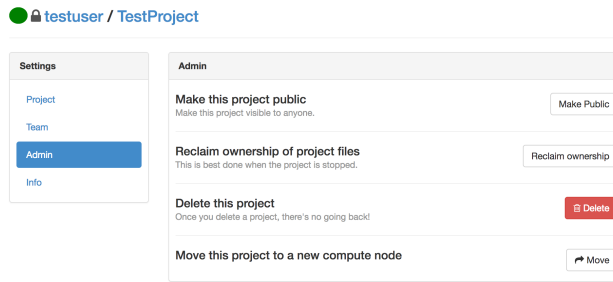
2. In the **Settings** menu, select Admin.
3. Click the Make Public button.
4. If the project is already public and you want to make it private, click the Make Private button.

## Tagging a project

Existing tags assigned to a project are listed in the Tags section on the project's home page.

## Adding a tag

1. In the Tags box, type the name of the tag you want to add:

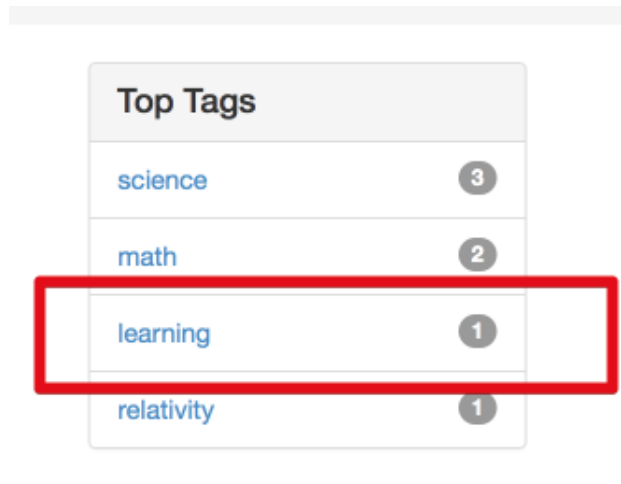
A screenshot of the Anaconda Tags input field. It features a light gray header with the word 'Tags' in bold. Below the header is a white input field containing the text 'learning|'. To the right of the input field is a dark gray button with the word 'Add' in white.

2. Click the Add button.

The new tag is added to the Tags list:

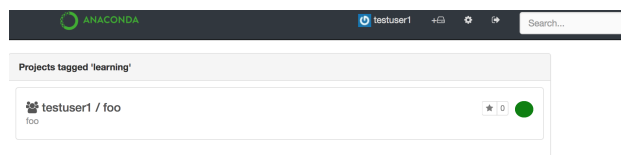
A screenshot of the Anaconda Tags input field, identical to the previous one, showing the 'learning|' text in the input field and the 'Add' button.

If the tag was not already in the Top Tags list on your user home page, it is added. If the tag was already listed because another project used it, the number next to the tag is incremented:



### Removing a tag

1. On your user home page, in the Top Tags list, click the tag name.



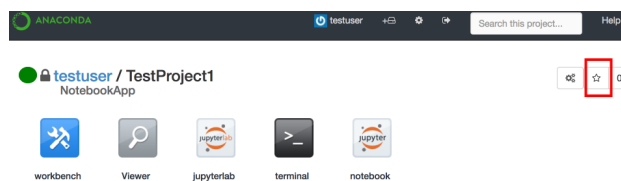
1. In the Tags list, click the X button next to tag name.

### Starring a project (rating)

Starring a project makes it appear on your user home page in the Top Rated list.

Adding or removing stars for a project does not affect the stars added by other users.

1. Open the project that you want to star.
2. On the project home page, click the Star icon at the upper right:

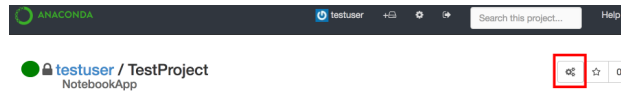


3. To unstar a project, click the Star icon again.

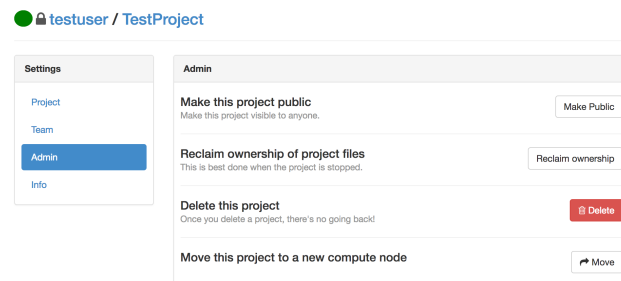
## Claim ownership of a project

When you claim ownership of a project, ownership of all files and folders created by the team members on the project is transferred to you. Project files and folders are copied and renamed.

1. *Stop the project* to prevent team members from making changes while you are changing ownership.
2. On the project home page, click the Project Settings icon to open the Project Settings page.



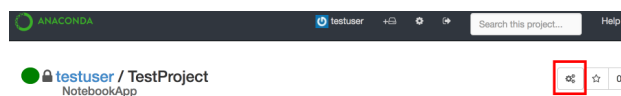
3. In the **Settings** menu, select Admin.



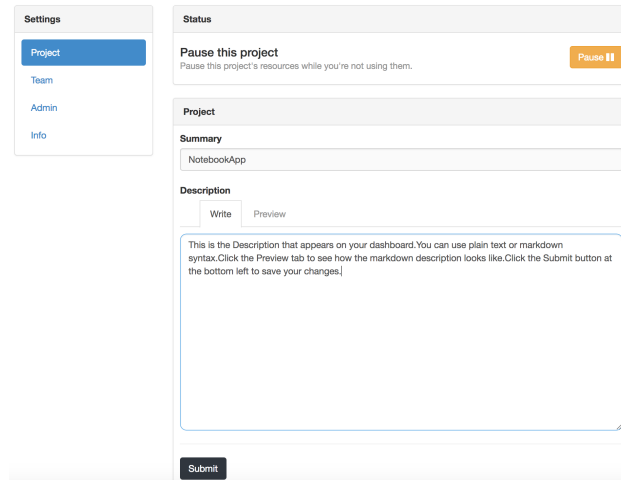
4. Click the Reclaim ownership button.

## Changing a project's summary or description

1. On the project home page, click the Project Settings icon to open the Project Settings page.



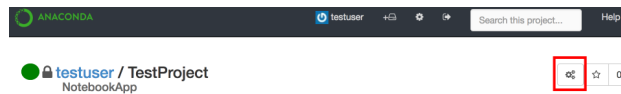
2. In the **Settings** menu, select Project.



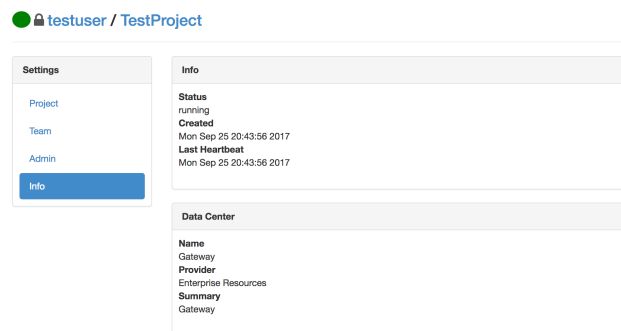
3. Update your project's summary using plain text or its description using Markdown syntax.
4. Click the **Preview** tab to see a preview of the Markdown description.
5. Click the Submit button.

## Viewing a project's status

1. On the project home page, click the Project Settings icon to open the Project Settings page.



2. In the **Settings** menu, select Info.



On the Info page, you can see:



- Whether the project is currently running or stopped.
- When the project was created.
- When the project was last accessed.
- The data center in which the project is running.

### Viewing related projects

Related projects are listed on a project's home page.

**Team**

Add

user02 (owner)

user01 (remove)

**Related Projects**

user01 / TestProject2

No Summary

user02 / User02Private

No Summary

user01 / TestProject

No Summary

These are projects that contain fields that are most similar to the current project.

**TIP:** You will only see projects to which you have been granted access: public projects, and private projects on which you are a team member.

### How related projects are identified

To determine which projects should be listed in Related Projects:

1. The recommendation engine scans the current project's files and weights the terms found to determine which of them to use for the likeness search.
2. The engine performs a search, with extra weight given to the “uses” and “imports” keywords.
3. The engine finds the files and projects that are most similar to the current project and scores the results.
4. The top-scoring matches are displayed in Related Projects. Only public projects and private projects to which you have access are included.

### Viewing top-rated projects

Top-rated projects are listed on your home page:

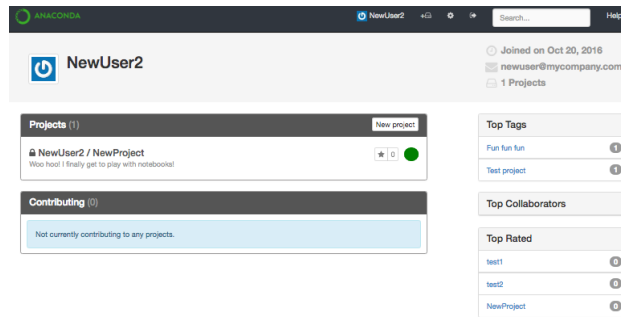
Top Rated	
einstein	2
euler	1
laplace	1
plank	1
Public_project	1

The number next to a project represents the number of stars that have been given to that project.

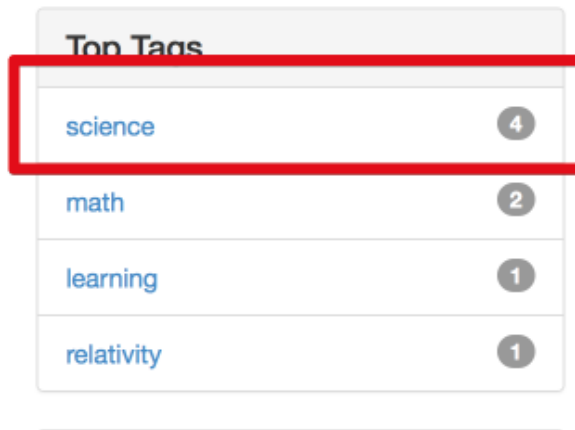
Click a project name to view the project's home page.

### Using tags to find a project

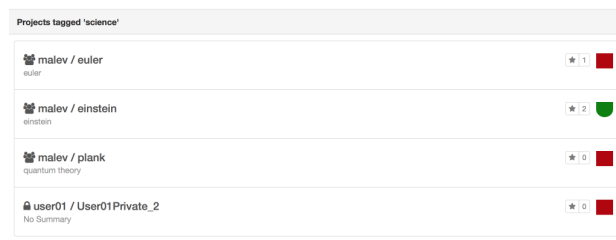
The top tags used on your projects are listed on your home page:



To list all projects that share a specific tag, click the tag name:



A list of projects with the selected tag is displayed:



**TIP:** The list includes only projects that you have access to: public projects, and private projects on which you are a team member.

Click a project name to open the project's home page.

## Viewing your top collaborators

Your top collaborators are listed on your home page:

Top Collaborators	
trento	1
user01	1

These are the team members who have the most projects in common with you.

To view a collaborator's home page—where you can see all public projects and the private projects they have shared with you—click the collaborator's name.

## Sharing projects and notebooks

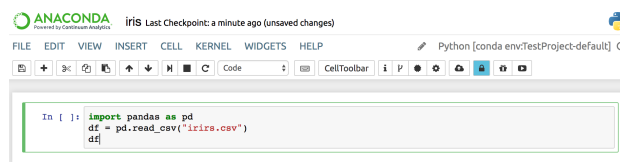
For information on sharing projects via the project settings and access control, see [Sharing projects](#).

To upload a Jupyter Notebook to Anaconda Repository:

1. Log in to Repository by running the `anaconda login` command or by using the login user interface provided by the *nbextension*.

CAUTION: If you are not using a secure connection, we strongly recommended that you use the command line to log in.

2. To share your notebook environment, select the Attach conda environment checkbox. This ensures that your team members will have the right environment for your notebook.
3. Click the Upload button to upload your notebook to your local Repository or to [Anaconda.org](#), depending on how your administrator has set up AEN:



NOTE: If you have not yet logged into Repository or Anaconda Cloud, or have not created an account, you will be asked to do so.

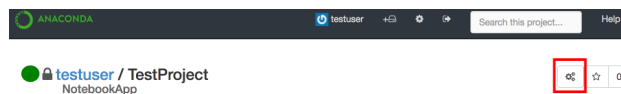
## Other ways to share a notebook

- Print—In the **File** menu, select Print.
- Download and share—In the **File** menu, select one of the following options:
  - Download as Notebook.
  - Download as Python.
  - Download as HTML.
  - Download as Markdown.
  - Download as ReStructured Text.
  - Download as PDF.
- Share and control team members' direct access to read, write and/or execute your notebook file or folder. For more information, see [Controlling access to your project](#).
- Share and control non-team members' file or folder access. For more information, see [Controlling access to your project](#).
- Create a presentation with *NBPresent 4.1*.

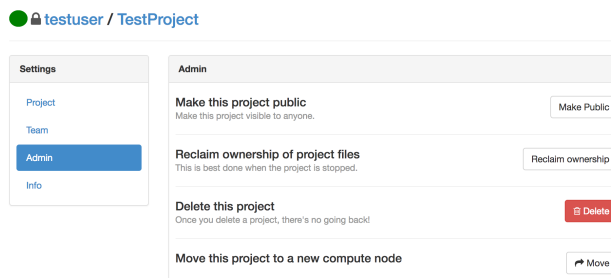
## Deleting a project

CAUTION: Deleting a project deletes all project files and information! There is no undo option.

1. Download a copy of any project files that you need to save.
2. On the project home page, click the Project Settings icon to open the Project Settings page.



3. In the **Settings** menu, select Admin.



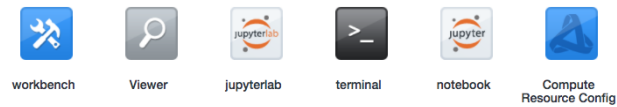
4. Click the Delete button.

## Using AEN applications

The applications in your project make it easy for you to interact with your files and data, manage your project's resources and to customize your AEN experience.

To use applications, log into AEN, then select the project you want to work on or create a new project and open it.

On the project home page, the following application icons are displayed:



**TIP:** Each application opens in a new browser tab. You can run multiple applications at the same time in your project.

For more information on each AEN application, see:

- *Using Workbench*—File viewer and manager, including permissions settings.
- *Using Viewer*—View-only versions of notebooks and other text files.
- *Using JupyterLab*—Alpha preview of the next generation notebook.
- *Using Terminal*—Basic bash shell Terminal.
- *Using Jupyter Notebook*—Jupyter Notebooks with extensions.
- *Using Compute Resource Configuration*—Project information, view and manage applications.

## Using Workbench

- *Opening Workbench*
  - *Using File Manager*
  - *Opening the Workbench terminal*

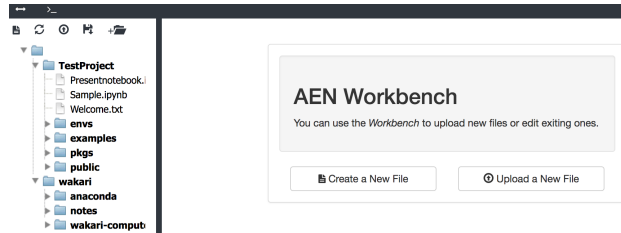
Workbench is a file viewer and manager that includes a file editor and file permissions manager.

You can use Workbench to:

- Upload and download files using the *File Manager*.
- Create new files and folders using the *File Manager*.
- Copy and move files to new locations using the *File Manager*.
- Rename files and/or folders using the *File Manager*.
- Manage the *access permissions* of team members.
- Grant or revoke *access to non-team members*.

Workbench also includes a simple Terminal application, which is convenient because the File Manager is always visible, making navigation simple.

When you first open Workbench, the File Manager is displayed in the left pane, and the Create a New File and Upload a New File buttons are in the right pane:



When you open a file or Workbench Terminal, it is displayed in the right pane. To make the Create or Upload a file options re-appear, refresh your browser window.

Two small icons are displayed in the black navigation bar at the top of the Workbench page. Hovering over them displays tool tips that describe their use:

- The Toggle icon displays or hides the File Manager.
- The Terminal icon opens a simple terminal window.

## Opening Workbench

To open Workbench:

1. Log in to AEN.
2. Select the project you want to work on, or create a new project and open it.
3. On the project home page, click the Workbench icon:



Workbench opens in a new browser window.

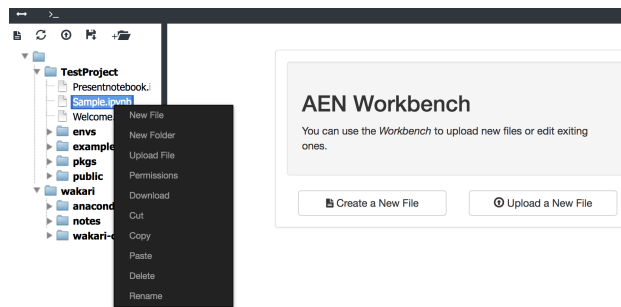
## Using File Manager

The File Manager is an intuitive way to interact with your files and folders.

## Using the options drop-down menu

To perform any of the actions described below:

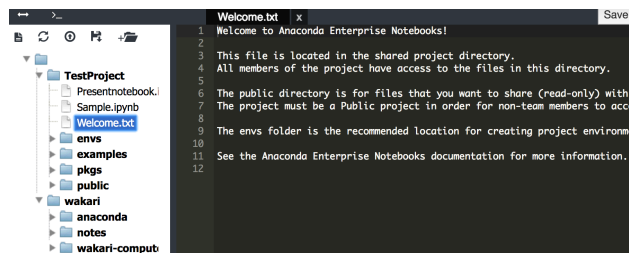
1. Right-click on any folder to display the options drop-down menu.
2. Select one of the following options:
  - New File—Create and edit a new file.
  - New Folder—Create a new folder.
  - Upload File—Upload a file to the selected folder. You can also drag a file to the folder.
  - Permissions—*Control access to files and folders.*
  - Cut—Cut the selected file or folder.
  - Copy—Copy the selected file or folder.
  - Paste—Paste a previously cut or copied file or folder.
  - Delete—Delete the highlighted file or folder.
  - Rename—Rename the highlighted file or folder.



## Editing files using the File Editor

1. Double-click any text file in the File Manager.

The File Editor opens in the right pane:



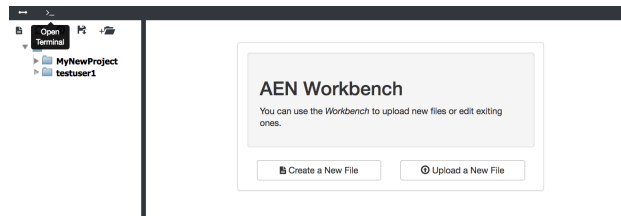


2. When you finish editing the file, click the Save button.

NOTE: To close the file without saving, click the X at the top of the page under the file name.

## Opening the Workbench terminal

In the navigation bar, click the Open terminal icon:



A Terminal—bash shell—is displayed in the right pane.

TIP: You can open additional terminals by clicking the Open terminal icon again, or by clicking the Plus + icon at the top of an open terminal.

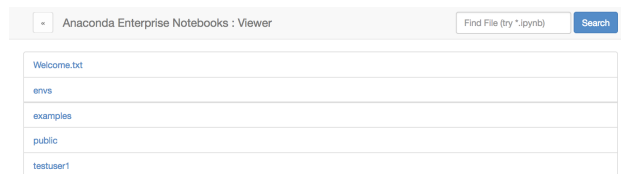
To move between terminal windows, click the **Terminal** tab in the navigation bar, then select the number of the terminal window you want to work in.

## Using Viewer

The Viewer application displays a static, view-only version of your notebooks and other text files by rendering the text files directly and using the NBConvert tool to convert notebooks to static HTML.

1. Log in to AEN.
2. Select the project you want to work on, or create a new project and open it.
3. On the project home page, click the Viewer icon.

Viewer opens in a new browser window:



4. Click any folder to view its contents, or click any filename to view the file.
5. To search for a file or folder name, type text in the Find File box, then press the Enter key. This is not a full-text search, but wildcards are permitted.

## Using JupyterLab

JupyterLab is an early alpha-preview of the next generation of the Jupyter Notebook. It is included so that you can take a tour and play with its capabilities.

**CAUTION:** JupyterLab is experimental. It is not yet intended for production work.

JupyterLab does not include any of the notebook extensions that are available in the *Jupyter Notebook app*.

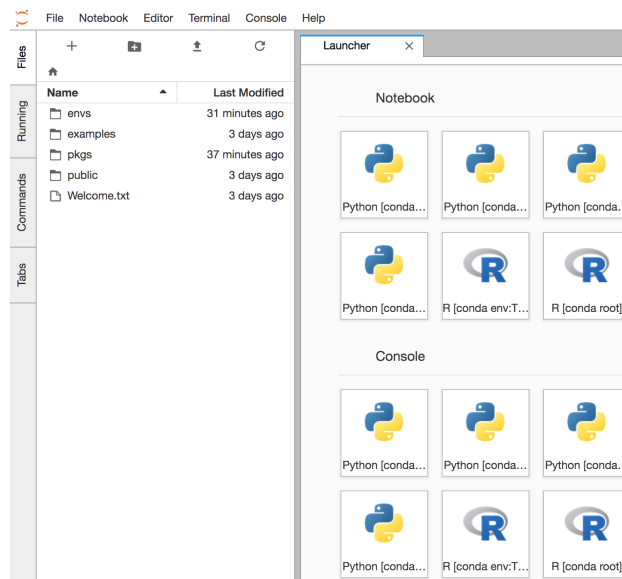
For more information about JupyterLab, see the [documentation](#).

You can also download and print a `Jupyter cheat sheet` on using Jupyter Notebook and the new JupyterLab.

To open JupyterLab:

1. Log in to AEN.
2. Select the project you want to work on, or create a new project and open it.
3. On the project home page, click on the JupyterLab icon.

JupyterLab opens in a new browser window:



Experiment with the application on your own, using the **Notebook**, **Editor**, **Terminal** and **Console** menus.

To review a guided tour of all of the features JupyterLab will contain when it is ready for production, click the [Take a tour](#) link in the right pane.

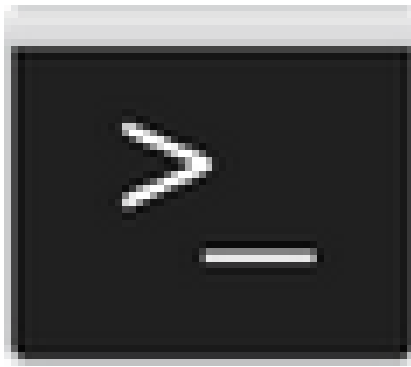
## Using Terminal

The Terminal application is a simple bash shell terminal that runs in your browser:

```
+ 1 bash
(/projects/aen_admin/TestProject/envs/default) ls
envs examples pkgs Presentnotebook.ipynb public Sample.ipynb Welcome
(/projects/aen_admin/TestProject/envs/default)
```

Using Terminal, you can:

- Access your home directory and your project drive.
  - Open multiple shells within one instance of Terminal.
  - Open multiple instances of Terminal in the same browser window.
1. Log in to AEN.
  2. Select a project you want to work on, or create a new project and open it.
  3. On the project home page, click the Terminal icon:



# Terminal

Terminal opens the project directory in a new browser window.

By default, the project directory is `/projects/username/project-name`.

EXAMPLE: `/projects/TestUser/MyFirstNotebook`

4. To see the physical path of your directory, run the Print Working Directory command `pwd -P`.

TIP: The physical path `-P` is important because project attaches data to the beginning of your virtual path to keep your project files together.

5. To navigate out of your project directory to your home directory, run the command `cd`.

6. To return to your project directory, run the command `cd/projects/username/project-name`.

TIP: If you are new to navigating in a terminal, you may want to use [the Workbench terminal](#), which includes a visual navigation tree in the File Manager.

### Using multiple Terminals

You can open as many terminals as you want.

To open another shell in the terminal, in the upper left of the pane, click the plus + icon.



A corresponding number appears after the plus + icon and 1.

To move to another Terminal, click the corresponding number.

The color of the number tab changes to show which terminal is currently selected.

### Using Jupyter Notebook

- *Opening the Jupyter Notebook application*
- *Using example notebooks*
- *Creating a new Jupyter Notebook*

The Jupyter Notebook application allows you to create and edit documents that display the input and output of a Python or R language script. Once saved, you can share these files with others.

NOTE: Python and R language are included by default, but with customization, Notebook can run several other kernel environments.

This page provides a brief introduction to Jupyter Notebooks for AEN users.

For the official Jupyter Notebook user instructions, see [Jupyter documentation](#).

For information on the notebook extensions available in AEN, see [Using Jupyter Notebook extensions](#).

### Opening the Jupyter Notebook application

1. Log in to AEN.
2. Select the project you want to work on, or create a new project and open it.
3. On the project home page, click the Jupyter Notebook icon:



Jupyter Notebook opens in a new browser window:



**TIP:** You can see the same *File Manager* in the Terminal, Workbench, and Viewer applications.

## Using example notebooks

The `Examples` folder in Jupyter Notebook contains several types of Notebook examples created in Python—and one with R language—kernel environments.

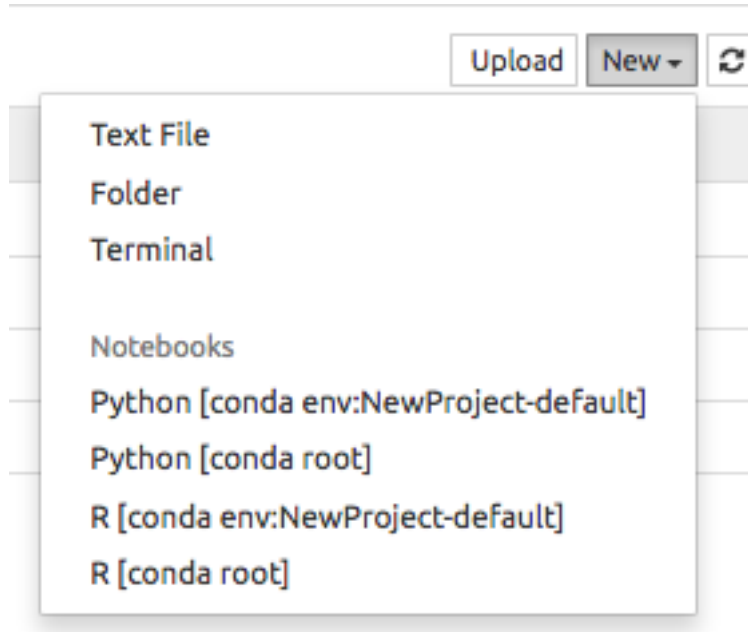
Open any example notebook to experiment and see how it works.

## Creating a new Jupyter Notebook

1. At the top right of the **Files** tab, click the **New** button.

2. Select the kernel environment to create your new notebook in.

**NOTE:** Customizable Python and R Language kernel environments are automatically created for you during project creation.



- Your project's default conda env kernels are a cloned copy of the root environment. You can customize them and install and delete additional packages.
- Root environment is managed by your Administrator. You cannot make or save any changes to it.
- You can switch between Python, R language and any other custom kernels in the notebook as you work in your notebook. For more information, see *Using the Synchronize Environments extension*.

The new notebook is saved in the related project directory and displayed.

## Using Jupyter Notebook extensions

The following extensions are available for use with AEN's Jupyter Notebook application:

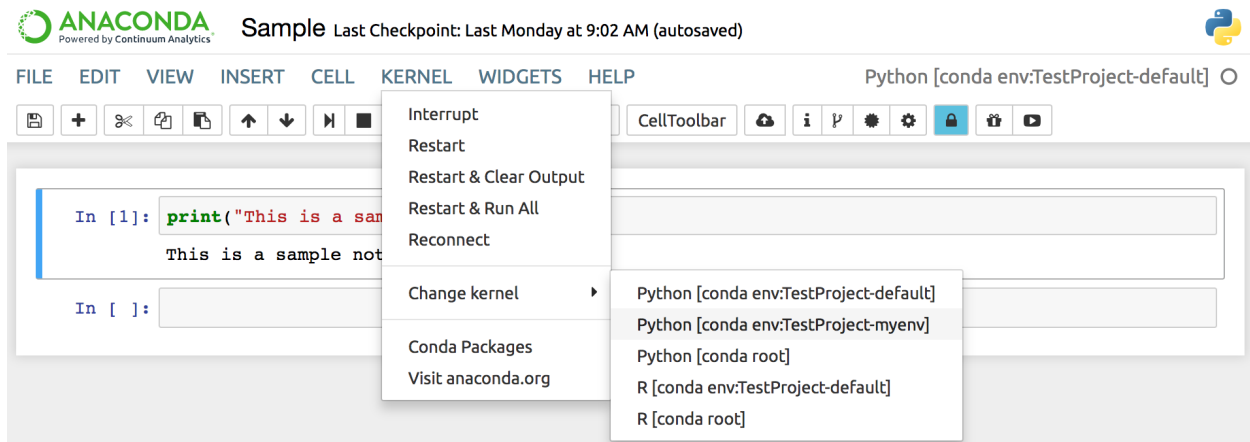
- *Synchronize Environments* with Jupyter from the **Kernel** menu.
- *Locking* adds multi-user capability from the Lock button.
- *Revision Control Mechanism (RCM)* adds Status, Checkout and Commit buttons.
- *Conda environment and package management* tab.
- *Conda notebook* adds conda management inside Notebook from the Kernel > Conda Packages menu option.
- *Anaconda Cloud integration* from the Publish to cloud button.
- *Notebook Present* turns your notebook into a PowerPoint-style presentation.

## Using the Synchronize Environments extension

The Synchronize Environments extension allows you to apply a Python, R language or any other custom environment inside your current notebook session, without needing to start up several Notebook instances using each of the selected environments.

To change environments:

1. Open the **Kernel** menu.



2. Click the Change kernel option.
3. From the list, select the environment to use.

NOTE: In AEN 4.1+ the default kernel for projects is `default`. In versions prior to 4.0, the default kernel for projects is `root Python`.

## Using the Locking extension

Multi-user capabilities are engaged in AEN when multiple users work in the same notebook file.

The Locking extension allows you to lock a notebook to prevent multiple team members from making changes at the same time. Notebooks are automatically locked when you open them.

If team members open a notebook and make changes while it is locked, their save capability is disabled, and they cannot overwrite the notebook.

To override the lock, they must actively take control of the locked file by clicking the Lock icon in the Notebook menu bar:



NOTE: This is a soft locking model. Team members can choose to override your lock to save their work. If you give team members write access to your files, confirm that they understand that they should never unlock your file unless they are making meaningful, non-destructive team contributions.

## Using the Revision Control Mechanism extension

The Revision Control Mechanism (RCM) Jupyter Notebook extension provides simple version control for notebook files. It uses the internal Jupyter functionality to perform tasks.

On the surface, RCM uses a simple linear model, but beneath that is a more complex git-based branching model. To prevent merge conflicts, this model uses a “latest wins” policy as its main merging strategy.

The RCM Jupyter Notebook extension adds four buttons:



- *Status.*
- *Checkout.*
- *Commit.*
- *Configure git.*

TIP: If you do not see the RCM buttons, see *Setting up RCM for the first time.*

### Using the Status button

The Status button allows you to see what revision you are on.

Clicking the Status button displays:

### Using the Checkout button

The Checkout button allows you to view a list of the previous revision points, check out a previous revision or compare differences between revisions.

Clicking the Checkout button displays:

### Checking out a previous revision

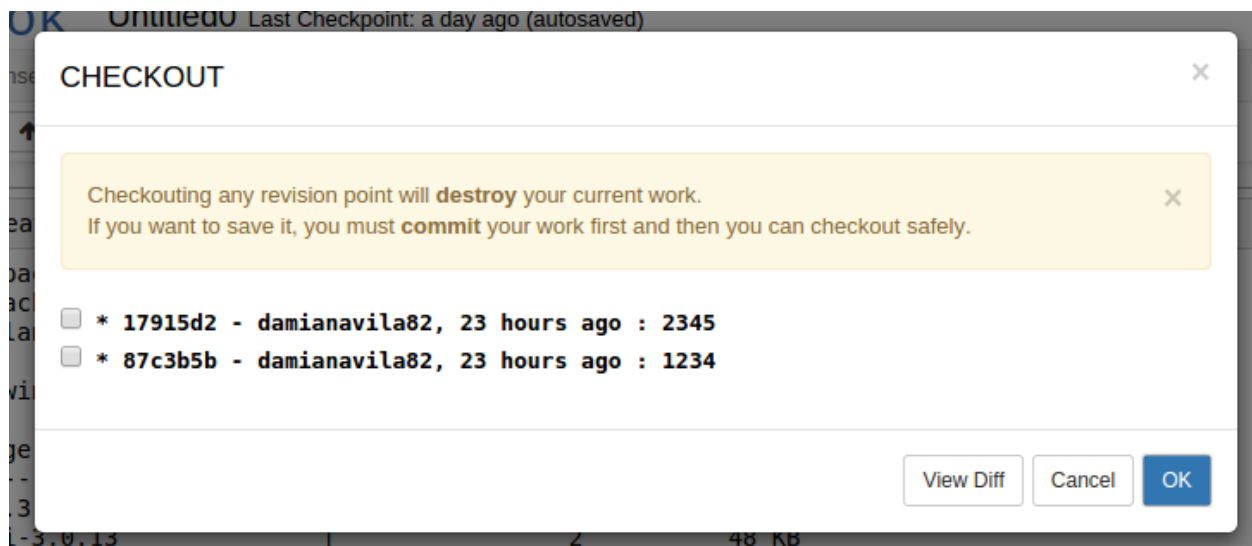
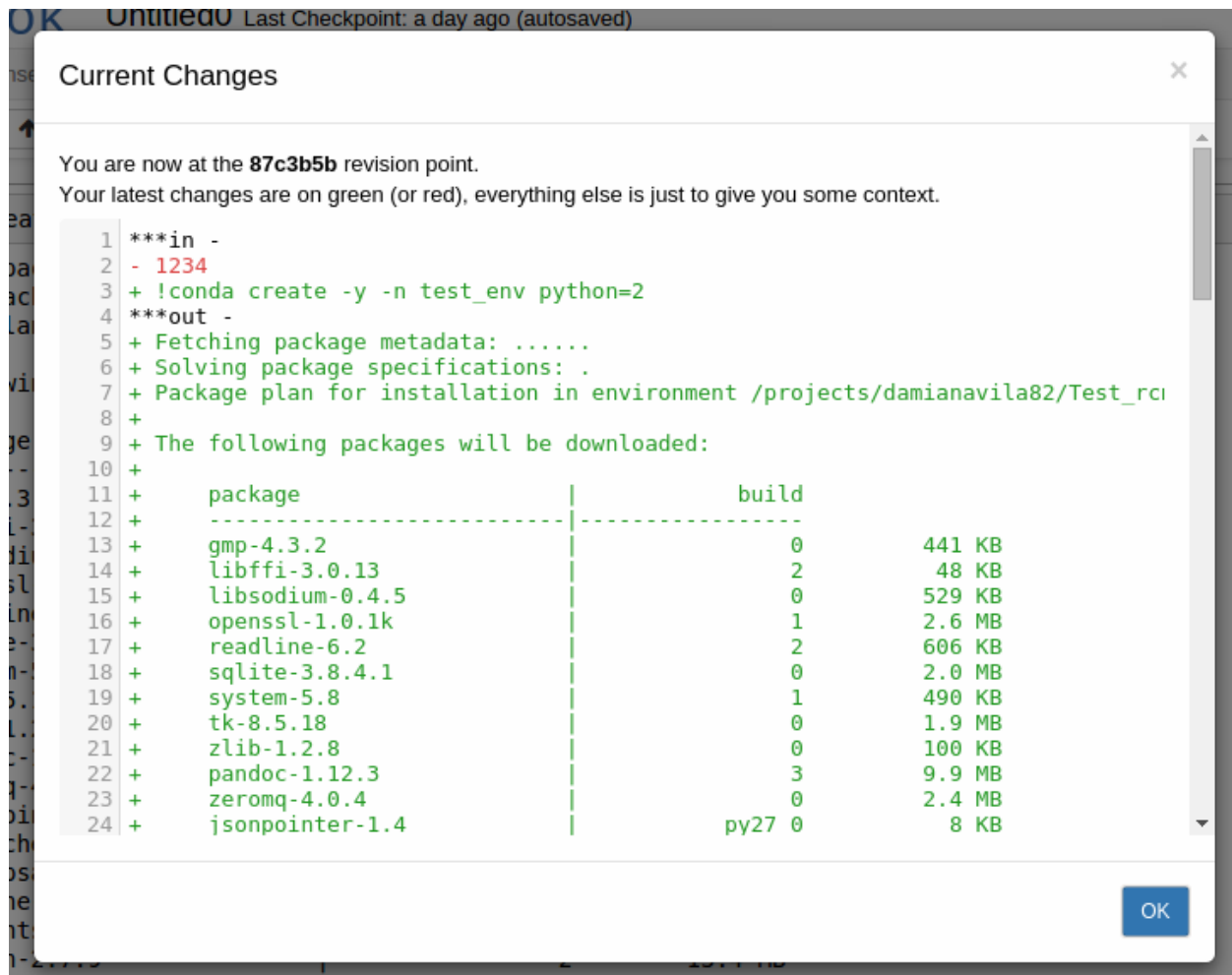
To checkout a notebook at an earlier revision point:

1. Select the checkbox next to the desired revision point.
2. Click the OK button.

A copy of the notebook at the selected revision point is displayed.

NOTE: If you have not saved the work in your current project window, checking out a previous revision destroys it. If in doubt, click the Cancel button and save your work before reverting to a previous revision point.





## Comparing revisions

To compare 2 previous revision points:

1. Select the checkboxes of the revision points to compare.
2. Click the View Diff button.

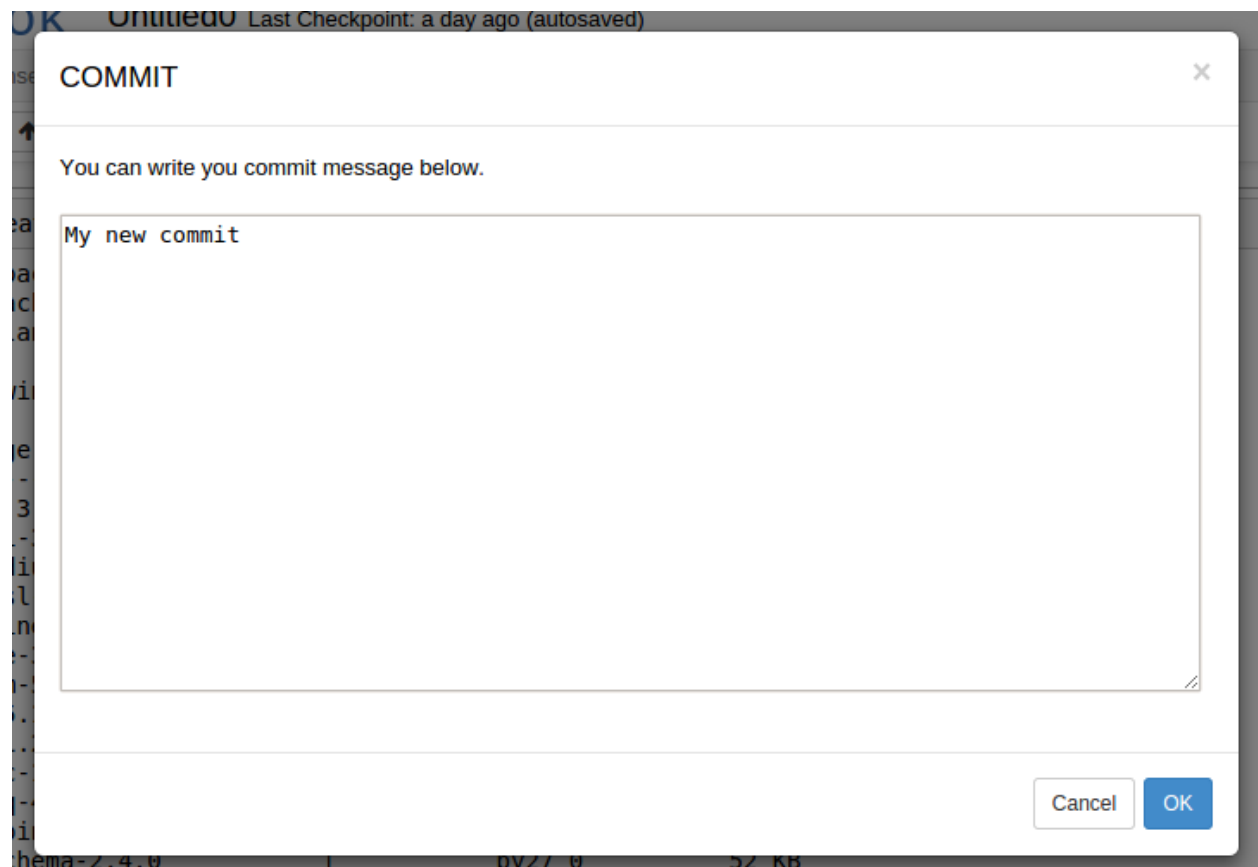
A side-by-side comparison is displayed.

Click the Cancel button to close the differences window.

## Using the Commit button

The Commit button allows you to save or persist the current changes, keeping a permanent record of any changes that are introduced, so that you do not have to worry about losing important data.

Clicking the Commit button displays:



1. Enter a description of the changes in the commit as a reminder in case you need to revert back to it later.
2. Click the OK button.

Your changes are committed and a revision point is created.

If Git user name and user email are not set, the following window appears:



A dialog box titled "COMMIT" with a close button (X) in the top right corner. The main text area contains the message: "Error! You need to configure your Git username and e-mail address first." At the bottom right, there are two buttons: "Cancel" and "Configure Git".

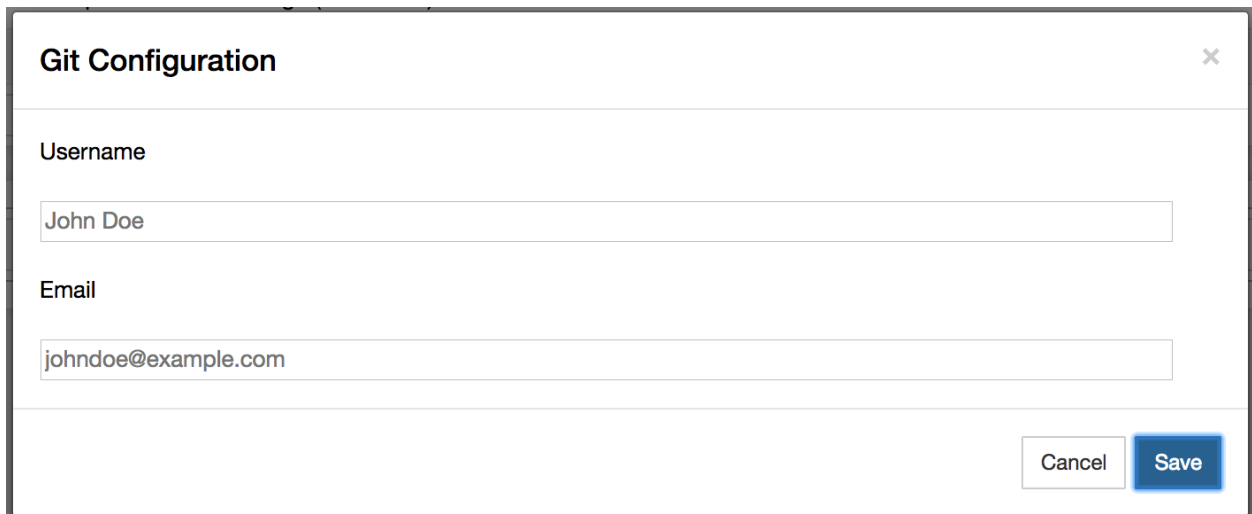
Configure Git and then try to commit again.

TIP: You can roll back committed changes by *checking out a previous version*.

### Using the Configure git button

The Configure git button allows you to configure Git user name and email values.

After clicking the Configure Git button, the following window appears:



A dialog box titled "Git Configuration" with a close button (X) in the top right corner. It contains two text input fields. The first field is labeled "Username" and contains the text "John Doe". The second field is labeled "Email" and contains the text "johndoe@example.com". At the bottom right, there are two buttons: "Cancel" and "Save".

Enter user name and e-mail address. Click the OK button when finished.

### Setting up RCM for the first time

If you do not see the RCM buttons in your notebook:

1. Go to the project home page.
2. Open the Terminal application.
3. In the terminal window, run:

```
git config --global user.email "you@example.com"
git config --global user.name "Your Name"
```

NOTE: Change `you@example.com` to your email address, and `Your Name` to your actual name.

4. Open Jupyter Notebook and refresh the page.

## Using the NBConda extension

The NBConda extension adds a Conda tab to your notebook for easy environment and package management from within the notebook.



Files

Running

IPython Clusters

Conda

2 Conda environments

Action	Name	Default?	Directory
	root		/opt/wakari/anaconda
	default	✓	/projects/aen_admin/TestProject/envs/default

1143 available packages

Search...

→

376 installed packages in environment "default"

Name	Version	Channel
<input type="checkbox"/> _license	1.1	defaults
<input type="checkbox"/> _nb_ext_conf	0.4.0	defaults
<input type="checkbox"/> abstract-rendering	0.5.1	defaults
<input type="checkbox"/> accelerate	2.3.1	defaults
<input type="checkbox"/> accelerate_cudalib	2.0	defaults
<input type="checkbox"/> aen-app-jupyterlab	0.4.0	wakari

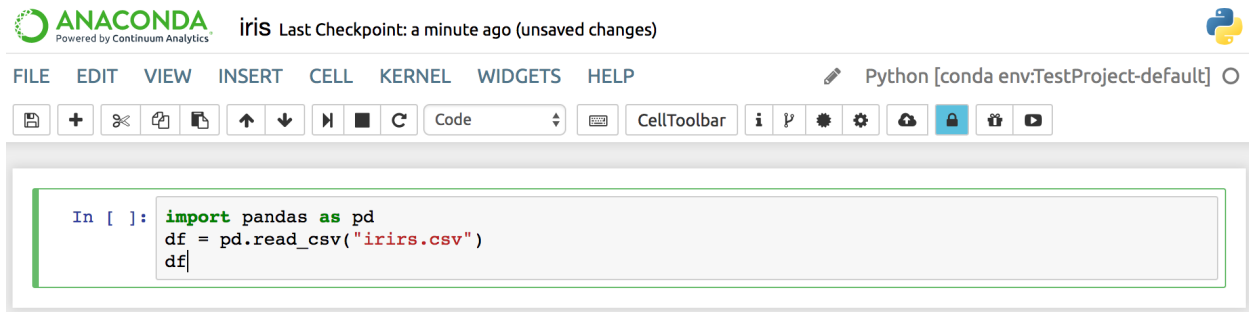
Name	Version	Build	Available
<input type="checkbox"/> _license	1.1	py27_1	
<input type="checkbox"/> alabaster	0.7.10	py27_0	
<input type="checkbox"/> anaconda	custom	py27_0	
<input type="checkbox"/> anaconda-client	1.5.1	py27_0	
<input type="checkbox"/> anaconda-project	0.6.0	py27_0	
<input type="checkbox"/> asn1crypto	0.22.0	py27_0	

Click the Conda tab in a notebook to display:

- Conda environments list—export, clone or delete an environment in the action column, or create a new environment by clicking the plus + icon. Switch to an environment by clicking it; packages for that environment are displayed below in the installed packages list.

- Conda available packages list—for the selected environment in currently configured channels, search for packages and click a package name to install it.
- Installed packages list—in the selected environment, check for updates, update or delete selected packages.

TIP: While you are in any notebook, you can jump to the NBConda extension for that environment by clicking the **Kernel** menu and selecting Conda Packages:



## Using the Conda Notebook extension

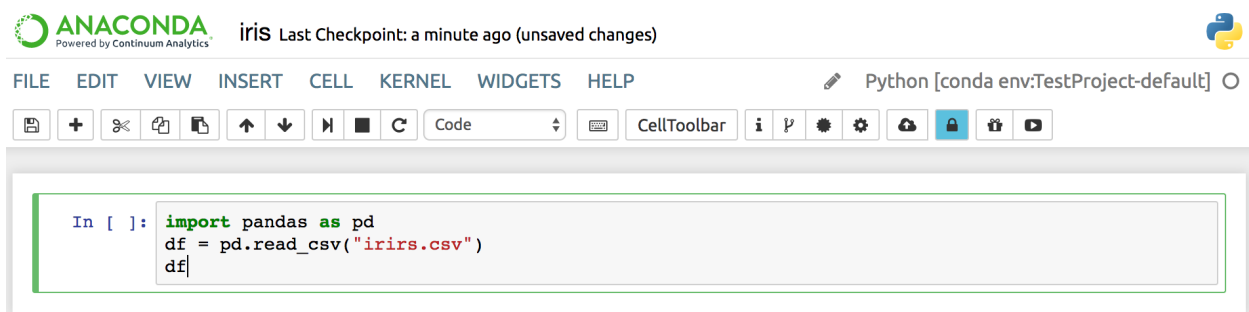
The Conda Notebook extension adds the Conda Packages option to the **Kernel** menu.

Select the Conda Packages option to display a list of all of the Conda packages that are currently used in the environment associated with the running kernel, as well as any available packages.

From the Conda Packages option, you can perform all of the tasks available in the [Conda tab](#), but they will only apply to the current environment.

## Using the Anaconda Cloud extension

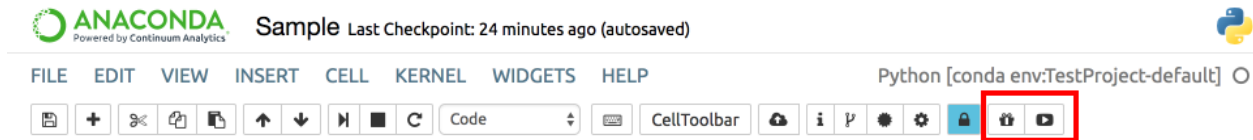
The Anaconda Cloud extension adds the Cloud button to your notebook, allowing you to easily upload your notebook to Cloud:



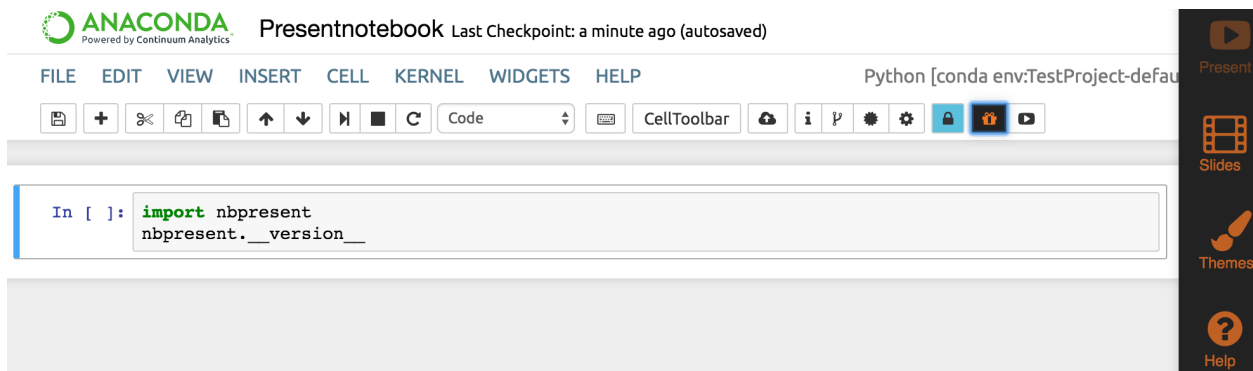
## Using the Notebook Present extension

The AEN Notebook Present extension turns your notebook into a Microsoft PowerPoint-style presentation.

The Present extension adds 2 buttons to Notebook’s menu bar—Edit Presentation and Show Presentation:



To begin using Notebook Present, click the Edit Presentation button.



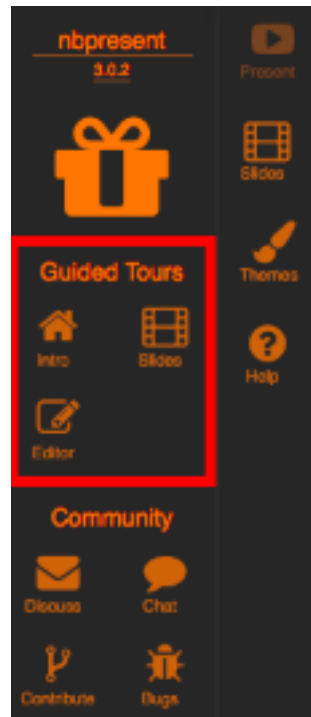
The Notebook Present sidebar is displayed on the right side of your browser:

Clicking each icon changes the menu and layout of your notebook.

Clicking the Help icon displays 3 tours—demonstrations—of the main features of Present:

- *Intro tour.*
- *Slides tour.*
- *Editor tour.*

Select one of the tours to view a short presentation regarding the specifics of that feature.



## Intro tour

The Intro tour is a 2-minute presentation that explains how to use the main features of Present, including a description of each button's purpose.

NOTE: At any time, you can pause, go back to the previous or move forward to the next slide.

The following information is covered in the Intro tour:

- App Bar—When authoring, this allows you control the content and style of your presentation. It also can be used to activate several keyboard shortcuts for editing:
- Stop Authoring—Clicking the Edit Presentation button again stops authoring, and removes all keyboard shortcuts.
- Show Presentation—If you just want to run your presentation without using any authoring tools, just click the Show Presentation button.
- Presenting/Authoring—Once you've made some slides, start presenting, where you can use most Notebook functions with the theme we have defined, as well as customize slides on the fly.
- Slides button—Slides, made of Regions linked to Cell Parts are the bread and butter of any presentation, and can be imported, created, linked, reordered, and edited here.

## Keyboard shortcuts



The Jupyter Notebook has two different keyboard input modes. **Edit mode** allows you to type code/text into a cell and is indicated by a green cell border. **Command mode** binds the keyboard to notebook level actions and is indicated by a grey cell border with a blue left margin.

Mac OS X modifier keys:

: Command

: Control

: Option

: Shift

: Return

: Space

: Tab

### Command Mode (press to enable)

: find and replace

: previous slide

: next slide

: next slide

: enter edit mode

: open the command palette

: run cell, select below

: run selected cells

: run cell, insert below

: to code

: to markdown

: extend selected cells above

: extend selected cells above

: extend selected cells below

: extend selected cells below

: insert cell above

: insert cell below

: cut selected cells

: copy selected cells

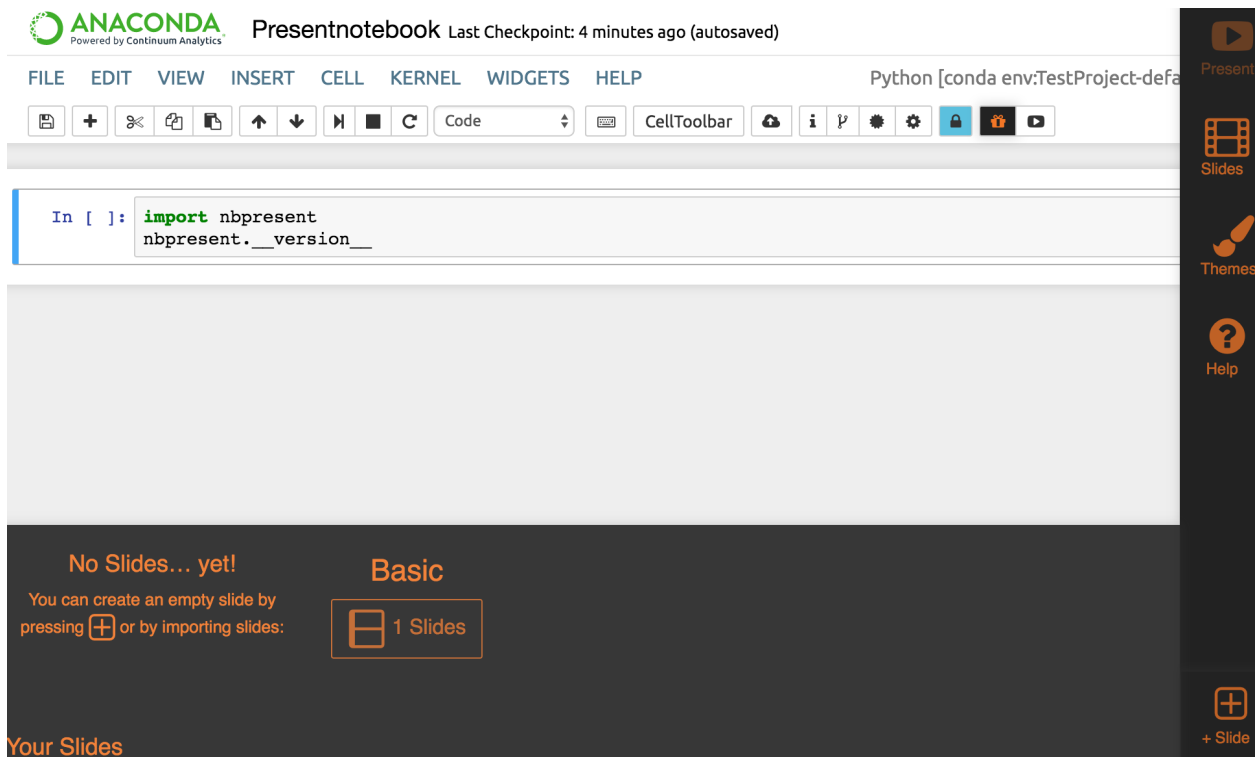
: paste cells above

: paste cells below

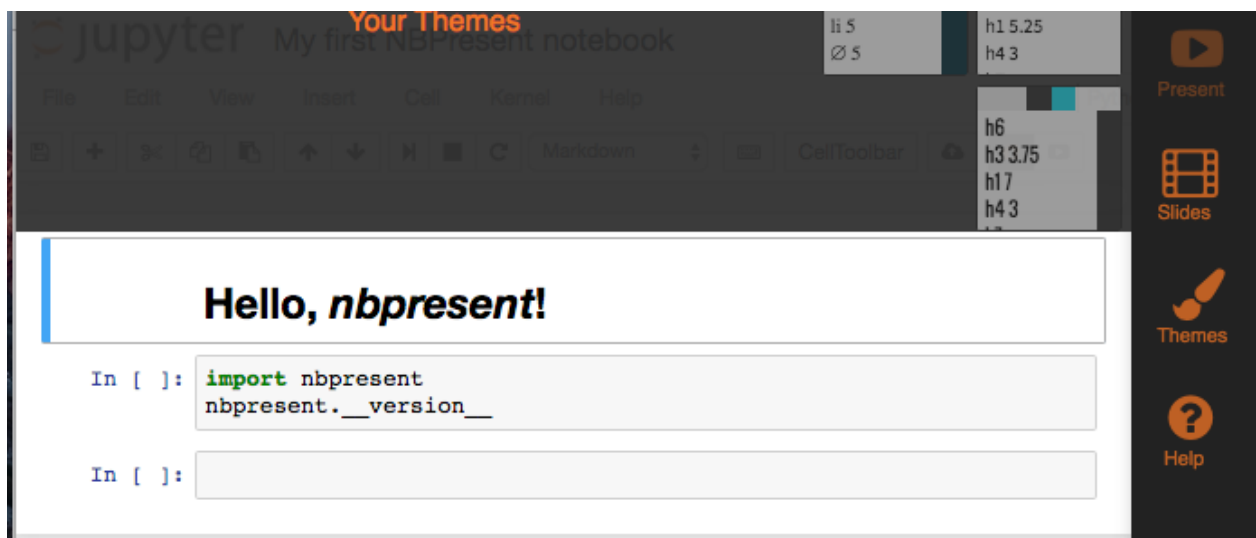
: undo cell deletion

Close





- Theming—Theming lets you select from existing colors, typography, and backgrounds to make distinctive presentations. The first theme you select will become the default, while you can choose custom themes for a particular slide, like a title.

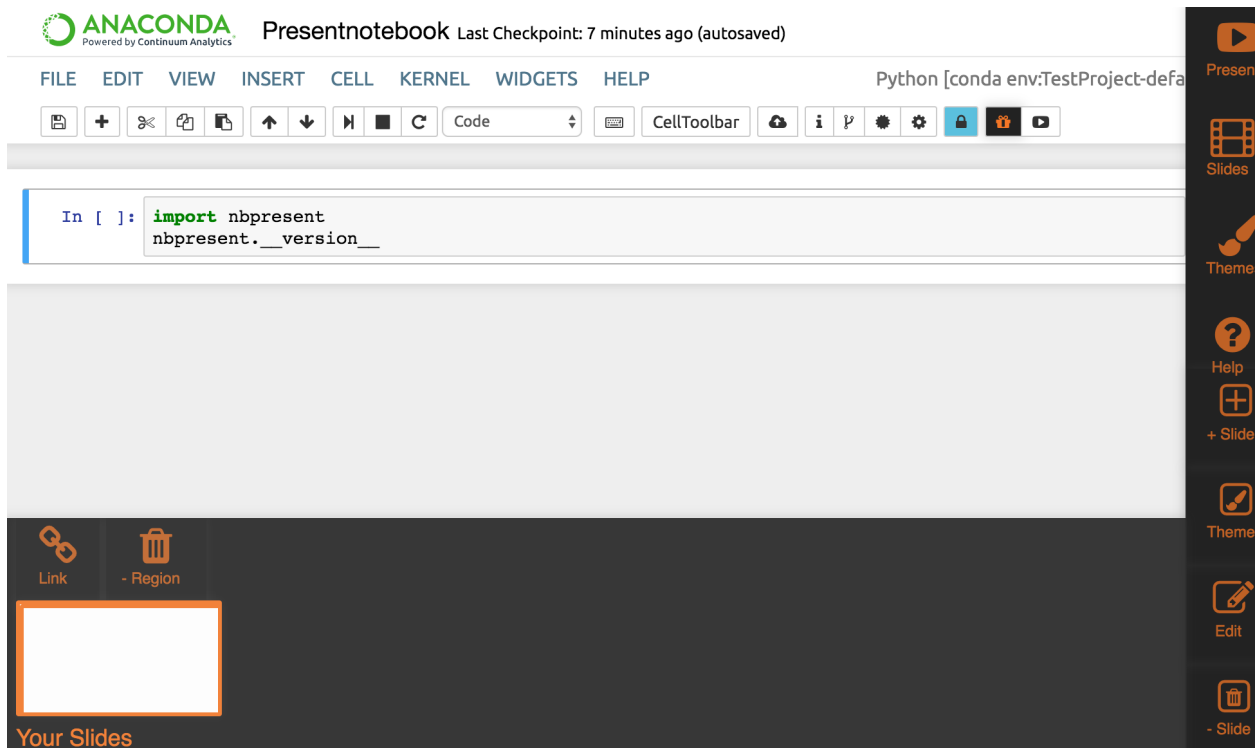


- Saving—Whenever you save your Notebook, all your presentation data will be stored right in the Notebook .ipynb file.

- **Downloading**—After you’ve made a presentation, you can download it as an HTML page by choosing Download → Download As: Presentation (.html) in the menu.
- **Help**—Activate help at any time to try other tours, connect with the present developers and community, and other information.

### Slides tour

Slides make up a presentation. Clicking Slides toggles the sorter view and the Slide Toolbar on and off:



The Slides tour explains how to create and manage slides, including the following information:

- **Slide Toolbar**—Create a new slide. Clicking + Slide will offer some choices for creating your new slide.
- **Import**—The quickest way to create a presentation is to import each cell as a slide. If you’ve already created slides with the official slideshow cell toolbar or RISE, you can import most of that content.
- **Template Library**—You can create a presentation from an existing template.
  - **Reuse Slide as Template**—You can create a presentation based on an existing slide.
  - **Simple Template**—A common template is the Quad Chart, with four pieces of content arranged in a grid.
- **Region**—The Quad Chart has four Regions. To select a region, click it.
  - **Link a Region to a Cell Part**—Each Region can be linked to a single Cell Part using the Link Overlay, which shows all of the parts available.
    - \* **Cell Part: Source (blue)**—Source, such as code and Markdown text.

- \* Cell Part: Outputs (red)—Outputs, such as rich figures and script results.
- \* Cell Part: Widgets (purple)—Jupyter widgets, interactive widgets that provide both visualization and user input.
- \* Cell Part: Whole (orange)—Finally, a Whole Cell, including its Source, Widgets and Outputs can be linked to a single Region.
- Unlink a region from a Cell Part—Unlinking removes the connection between a Region and a Cell Part, without deleting either one.
- Region: Trashing—Trashing a Region permanently deletes it, without affecting any linked Cell Part.
- Part Thumbnail—We’ll try to draw a part thumbnail. It can only be reliably updated when a linked Cell Part is on-screen when you mouse over it, but you should usually be able to get an idea of what you’re seeing. The colors of the regions correspond to the cell types.
- Presenting—Clicking the Present button while editing brings up the Presenter with editing mode still enabled:
  - Linked inputs and widgets are still interactive.
  - Go forward—Click to go to the next slide
  - Go back—Click to go back to the previous slide
  - Go back to the beginning—Click to go back to the first slide
  - My work is done here—Click to go back to the Notebook.

## Editor tour

Once you’ve made a few slides, you’ll likely want to customize them. The Editor tour explains how to edit your notebook, including the following information:

- Editing Slides—Activate the Slide Editor by double-clicking it, or by clicking Edit Slide.
- Region Editor—Click to drag Regions around and resize them.
- Region Tree—Reorder Regions and see the details of how Regions will show their linked Parts.
- Add Region—Add new regions.
- Attribute Editor—Edit the properties of a region.
- Data Layouts—In addition to manually moving regions, you can apply these layouts to automatically fill your slides.
- More Regions—Add more regions—with a weight of 1.
- Tree Weight—Make a Region bigger or smaller, based on its relative weight.
- 12 Grid—A compromise between the Free and Treemap layouts, the 12 Grid option rounds all of the values in a layout to a factor of 12.

## Using Compute Resource Configuration

The Compute Resource Configuration (CRC) application displays information about the current project and allows you to set a custom project environment and view and manage your other AEN applications, including stopping, starting, restarting and viewing the logs of each.

The CRC application screen contains 3 sections:

- *Info.*

- *Conda environment.*
- *Running apps.*

The screenshot shows the Anaconda Cloud interface with three main sections:

- Info:** Displays project details:
  - Hostname: davila-aen-test
  - Project Home: /projects/testuser1/demo
  - Project RC file: /projects/testuser1/demo/.projectrc
- Conda Environment:** Shows the current environment path: /projects/testuser1/demo/envs/default. A yellow warning box states: "Setting the default environment for this project will affect all users by modifying the .projectrc file. All running apps will be shutdown. Make sure **No one working on this project** has any unsaved documents!". A green button labeled "Set Project Environment" is at the bottom.
- Running Apps:** A table showing active applications:
 

User	Application	Status	Last Seen	Terminate	Relaunch	Logs
testuser1	terminal	running	1 hours ago	<a href="#">Terminate</a>	<a href="#">Relaunch</a>	<a href="#">Logs</a>

## Info

The Info section displays:

- Hostname—IP address of the host computer.
- Project Home—File path to the project home.
- Project RC file—File path to the project runtime configuration file `.projectrc`. This file is sourced when a user opens any AEN application. It sets several AEN internal environment variables, sets up the project environment and sets additional user environment variables for the project.

## Conda environment

This section displays the path to the default conda environment.

**CAUTION:** Changing the default environment will affect all users. Be sure that no team members have any unsaved documents before changing the project environment.

To change the default conda environment location:

1. Edit the path to point to your preferred conda environment.
2. Click the Set Project Environment button.

Your `.projectrc` file is modified.

## Running apps

The Running Apps section displays a list of users and the applications that are in use, as well as when the app was last modified.

To terminate any individual application, click the Terminate button.

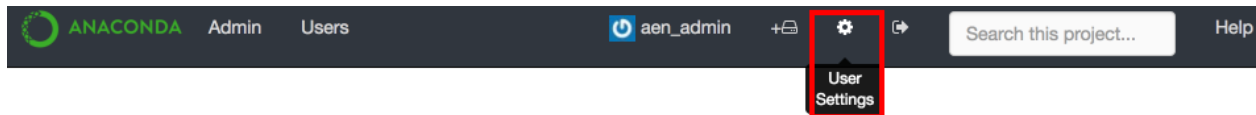
To stop and re-launch any individual application, click the Relaunch button.

To review the run logs of any active application, which may be useful for troubleshooting, click the Logs button.

## Managing your account

- *Updating your public profile*
- *Changing your password*
- *Deleting your AEN account*
- *Viewing account operations*
- *Registering an application*

To access your account information, click the User Settings icon in the AEN navigation bar:



## Updating your public profile

Your public profile is made up of a name, a personal URL, your company and location.

1. In the left navigation pane, click the **Public Profile** tab.
2. To update your profile picture, create a [Gravatar](#) that is associated with the email address you used to create your AEN account. The gravatar will automatically appear.

## Changing your password

1. In the left navigation pane, click the **Account Settings** tab.

## Deleting your AEN account

1. In the left navigation pane, click the **Account Settings** tab.

Viewing account operations

- 1. In the left navigation pane, click the **Security Log** tab to view a list of operations performed on your account.

# Settings

Change your account and profile settings.

Public Profile

Account Settings

Security Log

Applications

Security Log

	aen_admin	oauth.authenticate	2017-09-25 04:52:06.713000+00:00
	aen_admin	oauth.authenticate	2017-09-25 04:51:58.954000+00:00
	aen_admin	oauth.authenticate	2017-09-25 04:51:58.720000+00:00
	aen_admin	oauth.authenticate	2017-09-25 04:51:58.490000+00:00
	aen_admin	oauth.authenticate	2017-09-25 04:51:58.259000+00:00
	aen_admin	oauth.authenticate	2017-09-25 04:51:58.033000+00:00
	aen_admin	oauth.authenticate	2017-09-25 04:51:57.802000+00:00

- 2. For more information about an operation, click the Eye icon to the left of the the operation name.

Registering an application

If you want to create an application for AEN or have already done so, you must register your application.

- 1. In the left navigation pane, click the **Applications** tab.

# Settings

Change your account and profile settings.

Public Profile

Account Settings

Security Log

Applications

Developer Applications

Register New Application

These are applications you have registered to use the Anaconda Enterprise Notebooks API.

Gateway ()

Authorized applications

Gateway ()

revoke

2. Click the Register New Application button to open a form for registering your application.

## Advanced tasks

Advanced tasks are best-suited for users who are comfortable working in a Terminal.

## Working with environments

AEN runs on conda, a package management system and environment management system for installing multiple versions of software packages and their dependencies and switching easily between them.

A conda environment usually includes 1 version of Python or R language and some packages.

The ability to have a custom project environment is one of the most powerful features of AEN. Your project environment is integrated so that all of your project applications recognize it and all of your team members have access to it.

This section contains information about:

- *Creating a default conda environment using the Jupyter Notebook application*
- *Creating a default conda environment using the Jupyter Notebook application*
- *Using your conda environment in a notebook*
- *Customizing your conda environment*
- *Installing a conda package using Terminal*
- *Installing a conda package using Notebook*
- *Uninstalling a conda package*

NOTE: This conda environments guide is specific to AEN. For full conda documentation—including cheat sheets, a conda test drive, and command reference—see the [conda documentation](#).

## Creating a default conda environment using the Jupyter Notebook application

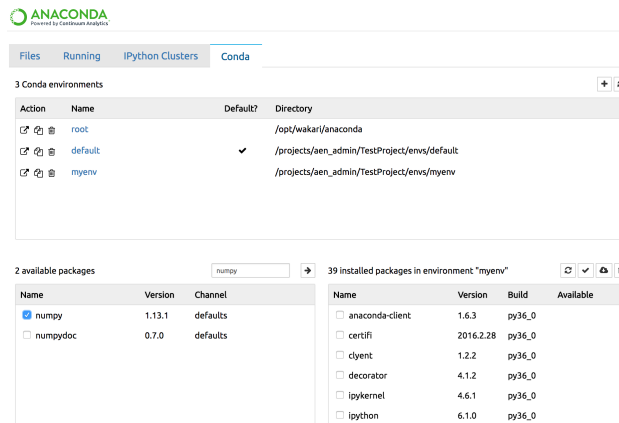
You can create, activate, and install packages and deactivate environments from within the Notebook menu bar.

To install from the Notebook menu bar:

1. Click the **Conda** tab and select the plus sign icon.
2. Search for `numpy` in the package search box.
3. Select `numpy` from the search results.

1. Click the Install button.

The environment is added to the project's `env` directory.



## Creating a default conda environment using Terminal

In AEN, all new environments created with conda automatically include Python, Jupyter Notebooks and pip. You can specify any other packages you want included in your new environment.

**TIP:** By default, conda creates a new environment in your project's `env` directory—so that all team members have access to the environment. For information about limiting your team member's read, write or execute permissions, see [Workbench](#).

To create a new environment within your AEN account, run the command `conda` in a [Terminal](#) application.

**EXAMPLE:** To create a new environment named `WeatherModel` that contains Python, NumPy, pip and Jupyter Notebooks in your project's `env` directory:

1. Log in to AEN.
2. Open a project.
3. On the project home page, click the Terminal application icon to open a Terminal.
4. Create the environment:

```
conda create -n WeatherModel numpy
```

**TIP:** Python, pip and Jupyter Notebooks are automatically installed in each new environment. You only need to specify NumPy in this command.

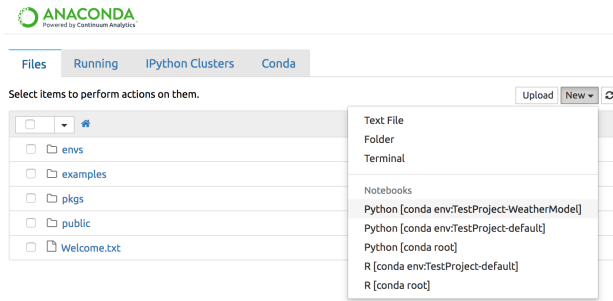
5. Make the new environment your default:

```
source activate WeatherModel
```

6. To use your new environment with Jupyter Notebooks, open the Notebook application.
7. Click the New button to open a new notebook. In the drop-down menu under Notebooks, the environment you just created is displayed.
8. To activate that environment, select it.

The environment is added to the project's `env` directory.





NOTE: You can deactivate the new environment when you are finished with your notebook by opening the Terminal application and running the command `source deactivate`.

## Using your conda environment in a notebook

Whether you have created an environment using conda in a terminal, or from the **Conda** tab in a notebook, you can use the conda environment in the same way.

When working in a notebook, to select the environment you have created and want to use with that notebook, in the **Kernel** menu, select **Change Kernel**.

EXAMPLE: If you have an environment named `my_env` in a project named `test1` that includes NumPy and SciPy and you want to use that environment in your notebook, in the **Kernel** menu, select `Python [conda env:test1-my_env]`.

The notebook code will run in that environment and can import NumPy and SciPy functions.

## Customizing your conda environment

If you need a Python package that AEN doesn't include by default, you can install additional packages into your AEN environment.

TIP: You cannot install packages into the default Anaconda environment. You must create your own environment before installing a new package into that environment.

AEN is built on Anaconda, so you can install additional Python packages using conda or pip—both of which are included with Anaconda.

## Installing a conda package using Terminal

To install a conda package using the Terminal application:

1. Create and activate the environment using the steps in [Creating a default conda environment using the Jupyter Notebook application](#).
2. In your Terminal application, run the command `conda install <packagename>`.

NOTE: Be sure to specify the Python version you want when using conda to create the environment, or it will use the same version as root.

EXAMPLE:

```
conda create -n mypy3 python=3 numpy scipy
```

A conda environment named `mypy3`, running on Python 3 and containing NumPy and SciPy is created. All subsequent packages added to this environment will be the Python 3 compatible versions.

### Installing a conda package using Notebook

You can also install the package within your notebook without using the terminal app:

1. From the Notebook application, click the **Conda** tab.
2. Select the environment you wish to use.
3. Search for the package you want to add.
4. Click the Install button.

### Uninstalling a conda package

To uninstall a package using this method, run the command `conda remove <packagename>`.

NOTE: Replace `<packagename>` with the name of the package you are uninstalling.

### Using visualization packages

AEN supports multiple visualization packages for Python and R language.

For Python, the default environment has *Matplotlib* and *Bokeh* installed.

For R language, the default environment has *r-ggplot2* and *r-bokeh* installed.

### Matplotlib

Matplotlib is a Python 2D and 3D plotting and visualization library that produces publication-quality figures in a variety of hardcopy formats and interactive environments across platforms.

To display Matplotlib figures in the output cells of a notebook running the default environment, run:

```
import matplotlib.pyplot as plt
%matplotlib inline
```

Any Matplotlib figures in the notebook are displayed in it's output cells.

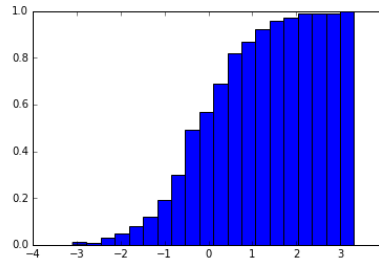
EXAMPLE: The following screenshot is of a cumulative density function (CDF) plot using values taken from a normal distribution:

For more information, including a [gallery](#), [examples](#), [documentation](#) and a [list of plotting commands](#), see the [Matplotlib website](#).

```
In [1]: import matplotlib.pyplot as plt
        %matplotlib inline

In [2]: import numpy as np
        x = np.random.normal(size=100)

In [3]: plt.hist(x, normed=True, cumulative=True, bins=20);
```



## Bokeh

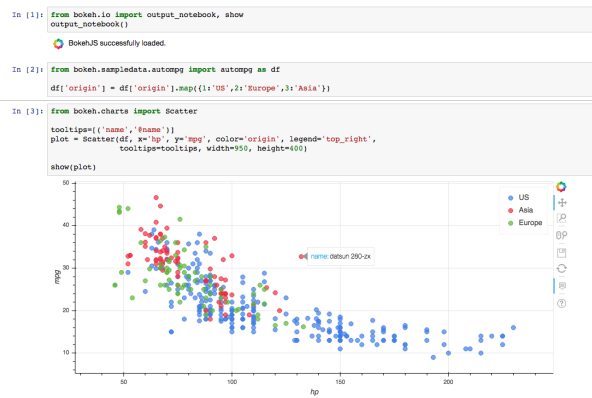
**Bokeh** is an interactive visualization library that targets modern web browsers to provide elegant, concise construction of novel graphics.

To display Bokeh figures in the output cells of a notebook running the default environment, run:

```
from bokeh.io import output_notebook, show
output_notebook()
```

Any Bokeh figures in the notebook are displayed in its output cells.

The following screenshot is of a scatter plot of miles-per-gallon vs. horsepower for 392 automobiles using the `autompg` sample dataset:



## ggplot2

**Ggplot2** is a plotting system for R language which is based on the grammar of graphics. Ggplot2 tries to take only the good parts of base and lattice graphics and none of the bad parts.

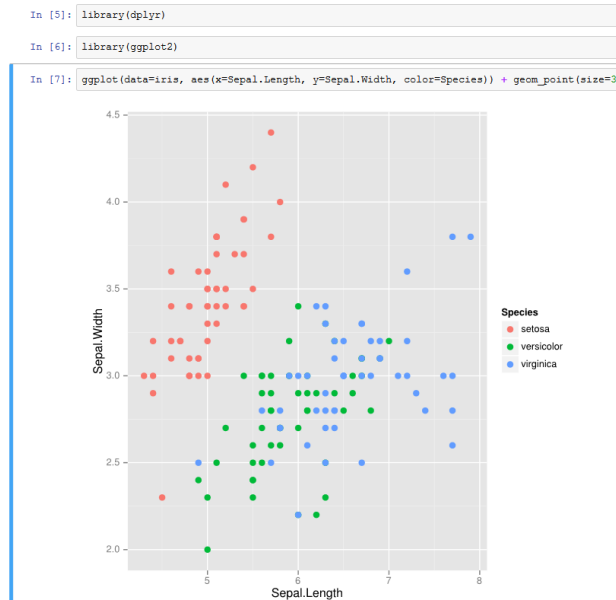
To use ggplot2 with AEN:

1. Open a new Notebook using the R kernel.
2. Load the ggplot2 library with the following code:

```
library(ggplot2)
```

The ggplot2 library is loaded and ready for use in AEN.

The following screenshot is of a scatter plot of sepal width vs sepal length using the `iris` dataset provided by the `dplyr` library:



## Using environment variables

Some Python packages depend on environment variables for correct operation.

EXAMPLE: Theano requires that the directory containing the CUDA compiler is included in the `$PATH` environment variable in order for GPU acceleration to be enabled.

To change environment variables for all AEN applications, modify the project runtime configuration file `.projectrc`. For more information, see [Using Compute Resource Configuration](#).

`.projectrc` sets several AEN internal environment variables, sets up the project environment and can set additional user environment variables for that project. This file is sourced when a user opens any AEN application—including Jupyter Notebook—and Jupyter kernels will be able to read the included environment variables.

## Cheat sheet

See the [Anaconda Enterprise Notebooks cheat sheet PDF \(232 KB\)](#) for a single-page summary of the most important information about using AEN.

## Troubleshooting

This troubleshooting guide provides you with ways to deal with issues that may occur with your AEN installation.

### AEN application not working properly

An AEN application is not working as expected.

#### Cause

There are several reasons an application may not work as expected.

#### Solution

Most AEN application issues can be resolved by following these steps:

1. Refresh the page.
2. If the issue is not resolved, close and open the application.
3. If the issue is not resolved, *stop and restart your project*.
4. If the issue is not resolved, check that you are using the latest version of your web browser—Chrome, Safari, Edge, or Firefox.
5. Log out of AEN.
6. Restart your browser, and log back in.

If you continue to have issues, then please contact your administrator or enterprise support representative.

### Admin guide

This administrator guide provides information about the administration of an AEN installation.

Most AEN system management is done from the administrative user interface (admin UI). Some advanced tasks are done *using the command line*.

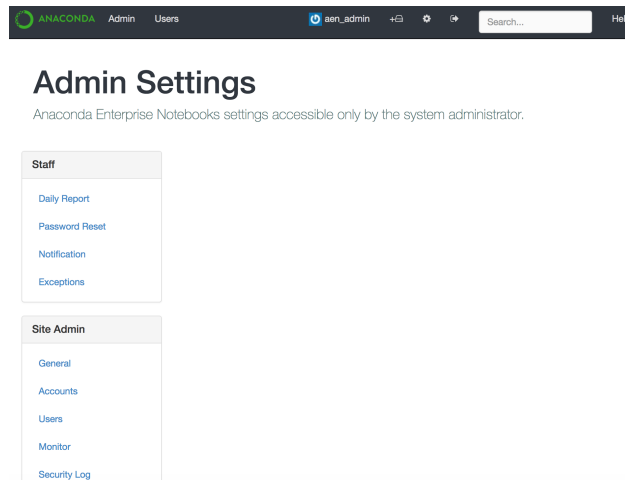
Any AEN user account can be *upgraded to an administrator account* to have both user and administrator privileges.

Administrators see two additional links in the AEN Navigation bar—Admin and Users:

All of the other navigation bar items are the same as for a user account.

## Concepts

- *System overview*



- *Server node*
- *Gateway node*
- *Compute node(s)*
- *Supervisor and supervisord*
- *Service Account*
- *Anaconda environments*
- *Projects and permissions*

## System overview

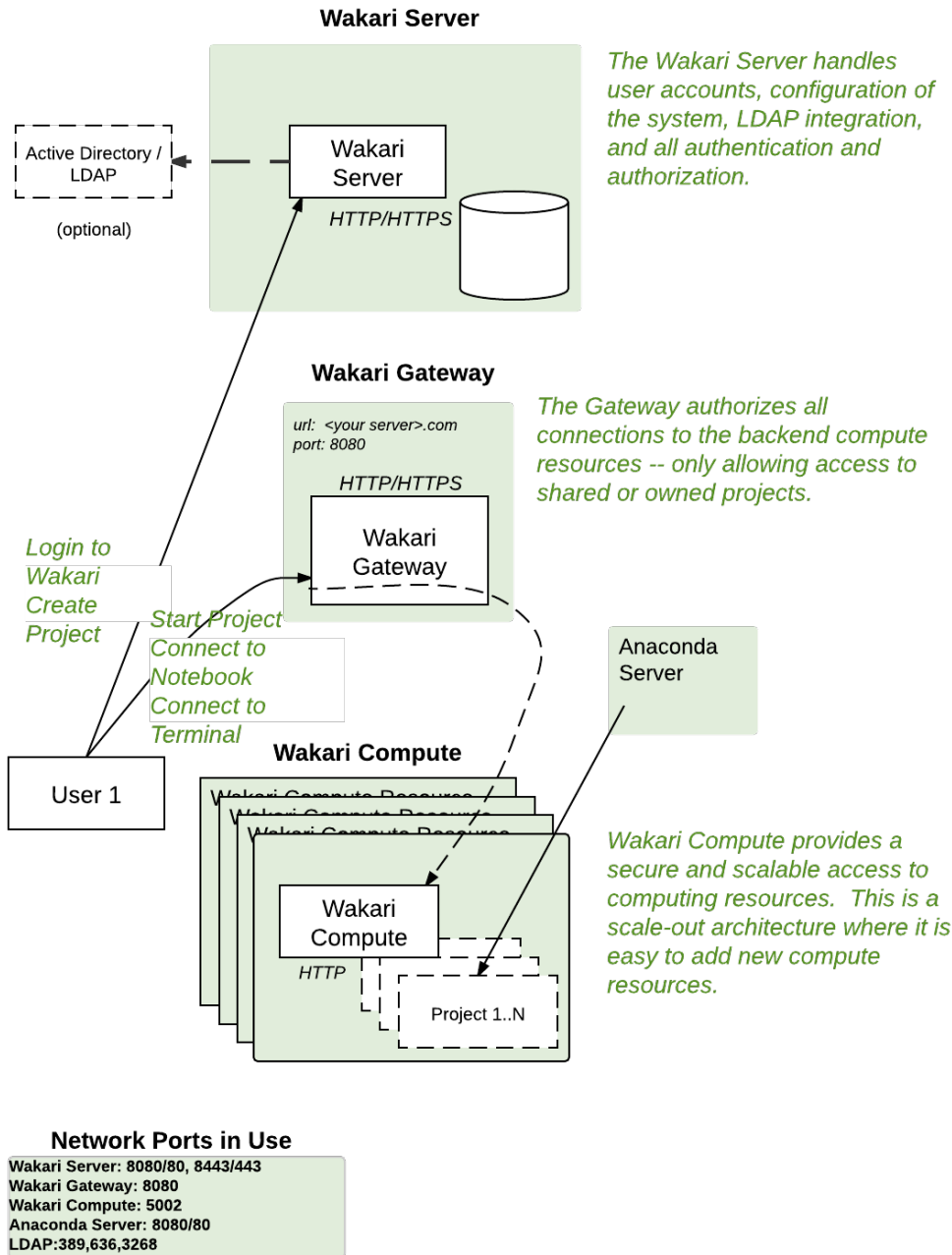
The Anaconda Enterprise Notebooks platform consists of 3 main service groups: AEN server, AEN gateway and AEN compute, which are called “nodes”:

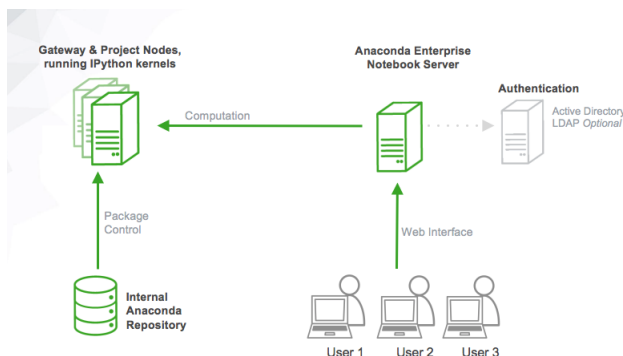
- *Server node*—The administrative front-end to the system where users login, user accounts are stored, and administrators manage the system.
- *Gateway node(s)*—A reverse proxy that authenticates users and directs them to the proper compute node for their project. Users will not notice this node after installation as it automatically routes them.
- *Compute nodes*—Where projects are stored and run.

These services can be run on a single machine or distributed across multiple servers.

Organizationally, each AEN installation has exactly 1 server instance and 1 or more gateway instances. Each compute node can only be connected to a single gateway. The collection of compute nodes served by a single gateway is called a **data center**. You can add data centers to the AEN installation at any time.

## Anaconda Enterprise Notebooks





EXAMPLE: An AEN deployment with 2 data centers, where 1 gateway has a cluster of 20 physical computers, and the second gateway has 30 virtual machines, must have the following services installed and running:

- 1 AEN server instance
- 2 AEN gateway instances
- 50 AEN compute instances (20 + 30)

Nodes must be configured and maintained separately.

## Server node

The server node controls login, accounts, admin, project creation and management as well as interfacing with the database. It is the main entry point to AEN for all users. The server node handles project setup and ensures that users are sent to the correct project data center.

Since AEN is web-based, it uses the standard HTTP port 80 or HTTPS port 443 on the server.

AEN uses MongoDB for its internal data persistency. It is typically run on the same host as the server but can also be *installed* on a separate host.

Server nodes use NGINX to handle the user-facing AEN web interface. NGINX acts as a request proxy for the actual server web-process which runs on a high numbered port that only listens on localhost. NGINX is also responsible for static content.

Server is installed in the `/opt/wakari/wakari-server` directory.

## Server processes

When you *view the status of server processes*, you may see the processes explained below.

supervisord	details
description	Manage wakari-worker, multiple processes of wk-server.
user	wakari
configuration	/opt/wakari/wakari-server/etc/supervisord.conf
log	/opt/wakari/wakari-server/var/log/supervisord.log
control	service wakari-server
ports	none



wk-server	details
description	Handles user interaction and passing jobs on to the wakari gateway. Access to it is managed by NGINX.
user	wakari
command	/opt/wakari/wakari-server/bin/wk-server
configuration	/opt/wakari/wakari-server/etc/wakari/
control	service wakari-server
logs	/opt/wakari/wakari-server/var/log/wakari/server.log
ports	Not used in versions after 4.1.2 *

\* AEN 4.1.2 and earlier use port 5000. This port is used only on localhost. Later versions of AEN use Unix sockets instead. The Unix socket path is: `unix:/opt/wakari/wakari-server/var/run/wakari-server.sock`

wakari-worker	details
description	Asynchronously executes tasks from wk-server.
user	wakari
logs	/opt/wakari/wakari-server/var/log/wakari/worker.log
control	service wakari-server

nginx	details
description	Serves static files and acts as proxy for all other requests passed to wk-server process. *
user	nginx
configuration	/etc/nginx/nginx.conf      /opt/wakari/wakari-server/etc/conf.d/www.enterprise.conf
logs	/var/log/nginx/woc.log /var/log/nginx/woc-error.log
control	service nginx status
port	80

\* In AEN 4.1.2 and earlier the wk-server process runs on port 5000 on localhost only. In later versions of AEN the wk-server process uses the Unix socket path `unix:/opt/wakari/wakari-server/var/run/wakari-server.sock`.

NGINX runs at least two processes:

- Master process running as root user.
- Worker processes running as nginx user.

## Gateway node

The gateway node serves as an access point for a given group of compute nodes. It acts as a proxy service and manages the authorization and mapping of URLs and ports to services that are running on those nodes. The gateway nodes provide a consistent uniform interface for the user.

NOTE: The gateway may also be referred to as a data center because it serves as the proxy for a collection of compute nodes.

You can put a gateway in each data center in a tiered scale-out fashion.

AEN gateway is installed in the `/opt/wakari/wakari-gateway` directory.

## Gateway processes

When you *view the status of server processes*, you may see the processes explained below.

supervisord	details
description	Manages the wk-gateway process.
user	wakari
configuration	/opt/wakari/wakari-gateway/etc/supervisord.conf
log	/opt/wakari/wakari-gateway/var/log/supervisord.log
control	service wakari-gateway
ports	none

wakari-gateway	details
description	Passes requests from the AEN Server to the Compute nodes.
user	wakari
configuration	/opt/wakari/wakari-gateway/etc/wakari/wk-gateway-config.json
logs	/opt/wakari/wakari-gateway/var/log/wakari/gateway.application.log /opt/wakari/wakari-gateway/var/log/wakari/gateway.log
working dir	/ (root)
port	8089 (webcache)

## Compute node(s)

Compute nodes are where applications such as Jupyter Notebook and Workbench actually run. They are also the hosts that a user sees when using the Terminal app or when using SSH to access a node. Compute nodes contain all user-visible programs.

Compute nodes only need to communicate with a gateway, so they can be completely isolated by a firewall.

Each project is associated with one or more compute nodes that are part of a single data center.

AEN compute nodes are installed in the /opt/wakari/wakari-compute directory.

Each compute node in the AEN system requires a compute launcher service to mediate access to the server and gateway.

## Compute processes

When you *view the status of server processes*, you may see the processes explained below.

supervisord	details
description	Manages the wk-compute process.
user	wakari
configuration	/opt/wakari/wakari-compute/etc/supervisord.conf
log	/opt/wakari/wakari-compute/var/log/supervisord.log
control	service wakari-compute
working dir	/opt/wakari/wakari-compute/etc
ports	none

wk-compute	details
de-scription	Launches compute processes.
user	wakari
con-figuration	/opt/wakari/wakari-compute/etc/wakari/wk-compute-launcher-config.json /opt/wakari/wakari-compute/etc/wakari/scripts/config.json
logs	/opt/wakari/wakari-compute/var/log/wakari/compute-launcher. application.log /opt/wakari/wakari-compute/var/log/wakari/ compute-launcher.log
work-ing dir	/ (root)
con-trol	service wakari-compute
port	5002 (rfe)

Wk-compute loads each of the following configuration files, in this order:

- /etc/wakari/config.json.
- /etc/wakari/compute-launcher-config.json.
- ./compute-launcher-config.json.
- Any configuration file specified by the `-c` option.

If an option is specified in multiple files, the last one encountered takes precedence.

## Supervisor and supervisord

AEN uses a process control system called “Supervisor” to run its services. Supervisor is run by the AEN Service Account user, usually wakari or aen\_admin.

The Supervisor daemon process is called “supervisord”. It runs in the background and should rarely need to be restarted.

## Service Account

AEN must be installed and executed by a Linux account called the AEN Service Account. The username of the AEN Service Account is called the AEN Functional ID (NFI). The AEN Service Account is created during AEN installation—if it does not exist—and is used to run all AEN services.

The default NFI username is wakari. Another popular choice is aen\_admin.

**WARNING:** The Service Account should only be used for administrative tasks, and should not be used for operating AEN the way an ordinary user would. If the Service Account creates or starts projects, the permissions on the AEN package cache will be reset to match the Service Account, which will interfere with the normal operation of AEN for all other users.

### Anaconda environments

Each project has an associated conda environment containing the packages needed for that project. When a project is first started, AEN clones a default environment with the name “default” into the project directory.

Each release of AEN 4 includes specific tested versions of conda and the conda packages included with AEN. These tested conda packages include Python, R, and other packages, and these tested conda packages include all of the packages in Anaconda.

If you upgrade or install different versions of conda or different versions of any of these conda packages, the new packages will not have been tested as part of the AEN 4 release.

These different packages will usually work, especially if they are newer versions, but they are not tested or guaranteed to work, and in some cases they may break product functionality.

You can use a new conda environment to test a new version of a package before installing it in your existing environments.

If using conda to change the version of a package breaks product functionality, you can use conda to change the version of the package back to the version known to work.

For more information about environments, see [Working with environments](#).

### Projects and permissions

AEN users interact with the system predominantly through *projects*.

Projects are associated with a single data center within the AEN environment. The team of users includes one owner, which is the user that created the project.

Projects live in the `projectRoot` folder on the compute node—by default, `/projects`.

The project directory is created the first time a project is started. The `start-project` script clones it from `/opt/wakari/wakari-compute/lib/node_modules/wakari-compute-launcher/skeleton`.

Project directory permissions are:

```
owner: rwx, user who created the project
group: rwx, group of the owner
other: --x, to allow access to the Public folder
ACL: rwx for any other team members
```

Files and subdirectories within the project directory have the same permissions as the project directory, except:

- The public folder and everything in it are open to anyone.
- Any files hardlinked into the root anaconda environment—`/opt/wakari/anaconda`—are owned by the root or wakari users.

Project file and directory permissions are maintained by the `start-project` script. All files and directories in the project will have their permissions set when the project is started, except for files owned by root or the AEN\_SRVC\_ACCT user—by default, wakari or aen\_admin.

The permissions set for files owned by root or the AEN\_SRVC\_ACCT user are not changed to avoid changing the permissions settings of any linked files in the `/opt/wakari/anaconda` directory.

**CAUTION:** Do not start a project as the AEN\_SRVC\_ACCT user. The permissions system does not correctly manage project files owned by this user.

## Installation

### Installation requirements

- *Hardware requirements*
- *Software requirements*
- *Security requirements*
- *Network requirements*
- *Other requirements*
- *What's next*

### Hardware requirements

AEN server—At least:

- 2+GB RAM.
- 2+CPU cores.
- 20GB storage.

AEN gateway—At least:

- 2 GB RAM.
- 2 CPU cores.

AEN compute (N-machines)—Configured to meet the needs of the projects. At least:

- 2GB RAM.
- 2 CPU cores.
- 20 GB.

NOTE: We recommend putting `/opt/wakari` and `/projects` on the same filesystem. If the project and conda env directories are on separate filesystems then more disk space will be required on compute nodes and performance will be worse.

### Software requirements

- RHEL/CentOS on all nodes. Versions from 6.5 through 7.4 are supported. Other operating systems are supported. However, this document assumes RHEL or CentOS.
- Linux home directories—Jupyter looks in `$HOME` for profiles and extensions.
- Ability to install in AEN directory `/opt/wakari` with at least 10 GB of storage.
- Ability to install in Projects directory `/projects` with at least 20 GB of storage. Size depends on number and size of projects.

NOTE: To install AEN in a different location see *Installing AEN in a custom location*.

## Linux system accounts

Some Linux system accounts (UIDs) are added to the system during installation.

If your organization requires special actions, the following list is available:

- mongod (RHEL) or mongod (Ubuntu/Debian)—created by the RPM or deb package.
- elasticsearch—created by RPM or deb package.
- nginx—created by RPM or deb package.
- AEN\_SRVC\_ACCT—created during installation of AEN, and defaults to wakari.
- ANON\_USER—An account such as “public” or “anonymous” on the compute node.

NOTE: If ANON\_USER is not found, AEN\_SRVC\_ACCT will attempt to create it. If it fails, the project(s) will fail to start.

- ACL directories need the filesystem mounted with Posix ACL support (Posix.1e).

NOTE: You can verify ACL from the command line by running `mount` and `tune2fs -l /path/to/filesystem | grep options`.

## Software prerequisites

- AEN server:
  - Mongo—Equal to or higher than version 2.6.8 and lower than version 3.0.
  - NGINX—Equal to or higher than version 1.6.2.
  - Elasticsearch—Equal to or higher than version 1.7.2.
  - Oracle JRE version 7 or 8.
  - bzip2.
- AEN Gateway:
  - bzip2.
- AEN compute:
  - git
  - bzip2
  - bash or zsh
  - X Window System

NOTE: If you don’t want to install the whole X Window System, you must install the following packages to have R plotting support:

```
sudo yum install -y libXrender libXext libXdmc6 libSM libICE libXt \
dejavu-sans-fonts dejavu-serif-fonts dejavu-fonts-common \
fontpackages-filesystem
```

## Security requirements

- Root or sudo access.
- File permissions: `umask 0022` is required during the installation.
- SELinux in permissive or disabled mode.

Edit the following file using either root or sudo access:

```
/etc/sysconfig/selinux
```

Edit the following:

```
# This file controls the state of SELinux on the system.
# SELINUX= can take one of these three values:
#   enforcing - SELinux security policy is enforced.
#   permissive - SELinux prints warnings instead of enforcing.
#   disabled - No SELinux policy is loaded.

SELINUX=enforcing

# SELINUXTYPE= can take one of these two values:
#   targeted - Targeted processes are protected,
#   mls - Multi Level Security protection.

SELINUXTYPE=targeted
```

NOTE: You must reboot for the changes to take effect.

Verify changes with `getenforce`.

## Network requirements

TCP Ports:

Direction	Type	Default Port	Protocol	Optional	Configurable	Comments
Inbound	TCP	80	HTTP or HTTPS	No	Yes	Server
Inbound	TCP	8089	HTTP or HTTPS	No	Yes	Gateway
Inbound	TCP	5002	HTTP	No	Yes	Compute

## Other requirements

As long as the above requirements are met, there are no additional dependencies for AEN.

See also system requirements for Anaconda Repository and Anaconda Scale.

## What's next

*Prepare for installation.*

## Preparing for installation

- *Downloading AEN installers*
- *Gathering IP addresses or FQDNs*
- *Set up variables*
- *What's next*

## Downloading AEN installers

Download the installers and copy them to the corresponding servers.

```
RPM_CDN="https://820451f3d8380952ce65-4cc6343b423784e82fd202bb87cf87cf.ssl.cf1.
↪rackcdn.com"
curl -O $RPM_CDN/aen-server-4.3.0-Linux-x86_64.sh
curl -O $RPM_CDN/aen-gateway-4.3.0-Linux-x86_64.sh
curl -O $RPM_CDN/aen-compute-4.3.0-Linux-x86_64.sh
```

NOTE: The current \$RPM\_CDN server will be confirmed in an email provided by your sales rep.

NOTE: These instructions use `curl` or `wget` to download packages, but you may use other means to move the necessary files into the installation directory.

## Gathering IP addresses or FQDNs

AEN is very sensitive to the IP address or domain name used to connect to the server and gateway nodes. If users will be using the domain name, you should install the nodes using the domain name instead of the IP addresses. The authentication system requires the proper hostnames when authenticating users between the services.

Print this page and fill in the domain names or IP addresses of the nodes below and record the user name and auto-generated password for the administrative user account in the box below after installing the AEN server node:

Node   Name or IP address	Port Number	Username   Password	
AEN server			
AEN gateway			
AEN compute			

NOTE: The values of these IP entries or DNS entries are referred to as `<AEN_SERVER_IP>` or `<AEN_SERVER_FQDN>`, particularly in examples of shell commands. Consider actually assigning those values to environment variables with similar names.

## Set up variables

Certain variables need to have values assigned to them before you start the installation.



## AEN server address

To define an environment variable for the AEN server address—FQDN or IP:

```
export AEN_SERVER=<AEN_SERVER_IP> # <from table above>
```

NOTE: The address—FQDN or IP—specified for the AEN server must be resolvable by your intended AEN users' web clients.

To verify your hostname, run `echo $AEN_SERVER`.

## AEN functional ID

AEN must be installed and executed by a Linux account called the AEN Service Account. The username of the AEN Service Account is called the AEN Functional ID (NFI). The AEN Service Account is created during AEN installation—if it does not exist—and is used to run all AEN services.

The default NFI username is `wakari`. Another popular choice is `aen_admin`.

To set the environment variable `AEN_SRVC_ACCT` to `wakari` or your chosen name before installation, run `export AEN_SRVC_ACCT="aen_admin"`.

This name is now the username of the AEN Service Account and of the AEN administrator account.

When upgrading AEN, set the NFI to the NFI of the current installation.

WARNING: The Service Account should only be used for administrative tasks, and should not be used for operating AEN the way an ordinary user would. If the Service Account creates or starts projects, the permissions on the AEN package cache will be reset to match the Service Account, which will interfere with the normal operation of AEN for all other users.

## AEN functional group

The AEN Functional Group (NFG) may be given any name. Most often, it is set to `aen_admin` or `wakari`. This Linux group includes the AEN service account, so all files and directories that have the owner NFI also have the group NFG.

When upgrading AEN, set the NFG to the NFG of the current installation.

To set the NFG before installation, run:

```
export AEN_SRVC_GRP="<NFG>"
```

NOTE: Replace `<NFG>` with your NFG name.

## AEN install sudo command

During AEN installation the installers perform various operations that require root level privileges. By default, the installers use the `sudo` command to perform these operations.

Before installation, set the `AEN_SUDO_CMD_INSTALL` environment variable to perform root level operations. You can also set it to no command at all if the user running the installer(s) has root privileges and the `sudo` command is not needed or is not available.

EXAMPLES:

```
export AEN_SUDO_CMD_INSTALL=""  
export AEN_SUDO_CMD_INSTALL="sudo2"
```

### AEN sudo command

By default the AEN services uses `sudo -u` to perform operations on behalf of other users—including `mkdir`, `chmod`, `cp` and `mv`.

To override the default `sudo` command when `sudo` is not available on the system, before installing, set the `AEN_SUDO_CMD` environment variable.

AEN must have the ability to perform operations on behalf of other users. Therefore, this environment variable cannot be set to an empty string or to `null`.

**CAUTION:** Any command that replaces `AEN_SUDO_CMD` must support the `-u` command line parameter—similarly to the `sudo` command.

**EXAMPLE:**

```
export AEN_SUDO_CMD="sudo2"
```

The optional environmental variable `AEN_SUDO_SH` is another way to customize AEN sudo operations. When AEN executes any `sudo` command, it will include the value of `AEN_SUDO_SH`, if it is set.

**EXAMPLE:** If your username is “jsmith” and the values are set as:

```
AEN_SUDO_CMD=sudo  
OWNER=jsmith  
AEN_SUDO_SH=sudologger  
PROJECT_HOME=/projects/jsmith/myproj
```

Then AEN will resolve:

```
$AEN_SUDO_CMD -u ${OWNER} $AEN_SUDO_SH rm -rf $PROJECT_HOME
```

As:

```
sudo -u jsmith sudologger rm -rf /projects/jsmith/myproj
```

In this case the `sudologger` utility could be a pass-through utility that logs all `sudo` usage and then executes the remaining parameters.

### Post-installation Sudo configuration

While `root/sudo` privileges are required during installation, `root/sudo` privileges are not required during normal operations after install, if user accounts are managed outside the software. However `root/sudo` privileges are required to start the services, thus in the service config files there may still need to be an `AEN_SUDO_CMD` entry.

For more information, see [Configuring sudo customizations](#).

### AEN remote database settings

By default AEN server uses a local database. To override the default database location, see [Install AEN connected to a remote Mongo DB instance](#).

## What's next

*Install the AEN server.*

## Installing the AEN server

- *Installing the bzip2 package*
- *Downloading prerequisite RPMs*
- *Installing prerequisite RPMs*
- *Setting variables and changing permissions*
- *Running the AEN server installer*
- *Starting NGINX and Elasticsearch*
- *Testing AEN server installation*
- *Updating your license*
- *What's next*

The AEN server is the administrative front end to the system. This is where users log in to the system, where user accounts are stored, and where admins can manage the system.

Server is installed in the `/opt/wakari/wakari-server` directory.

## Installing the bzip2 package

Be sure you have the `bzip2` package installed. If this package is not installed on your system, install it:

```
sudo yum install bzip2
```

## Downloading prerequisite RPMs

To install AEN on a CentOS 6 server:

```
RPM_CDN="https://820451f3d8380952ce65-4cc6343b423784e82fd202bb87cf87cf.ssl.cf1.
↪rackcdn.com"
curl -O $RPM_CDN/nginx-1.6.2-1.el6ngx.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-tools-2.6.8-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-shell-2.6.8-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-server-2.6.8-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-mongos-2.6.8-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-2.6.8-1.x86_64.rpm
curl -O $RPM_CDN/elasticsearch-1.7.2.noarch.rpm
curl -O $RPM_CDN/jre-8u65-linux-x64.rpm
```

To install AEN on a CentOS 7 server:

```
RPM_CDN="https://820451f3d8380952ce65-4cc6343b423784e82fd202bb87cf87cf.ssl.cf1.
↳rackcdn.com"
curl -O $RPM_CDN/nginx-1.10.2-1.el7ngx.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-tools-2.6.12-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-shell-2.6.12-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-server-2.6.12-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-mongos-2.6.12-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-2.6.12-1.x86_64.rpm
curl -O $RPM_CDN/jre-8u112-linux-x64.rpm
curl -O $RPM_CDN/elasticsearch-1.7.6.noarch.rpm
```

### Installing prerequisite RPMs

Run:

```
sudo yum install -y *.rpm
sudo service mongod start
sudo chkconfig --add elasticsearch
```

### Setting variables and changing permissions

Run:

```
export AEN_SERVER=<FQDN HOSTNAME OR IP ADDRESS> # Use the real FQDN
chmod a+x aen-*.sh # Set installer to be executable
```

NOTE: Change <FQDN HOSTNAME OR IP ADDRESS> to the actual fully qualified domain hostname or IP address.

### Running the AEN server installer

Run:

```
sudo -E ./aen-server-4.3.0-Linux-x86_64.sh -w $AEN_SERVER
<license text>
...
...

PREFIX=/opt/wakari/wakari-server
Logging to /tmp/wakari_server.log
Checking server name
Ready for pre-install steps
Installing miniconda
...
...
Checking server name
Loading config from /opt/wakari/wakari-server/etc/wakari/config.json
Loading config from /opt/wakari/wakari-server/etc/wakari/wk-server-config.json

=====
```

(continues on next page)

(continued from previous page)

```
Created password '<RANDOM_PASSWORD>' for user 'aen_admin'
```

```
=====
```

```
Starting Wakari daemons...
installation finished.
```

After successfully completing the installation script, the installer creates the administrator account—AEN\_SRVC\_ACCT user—and assigns it a password.

EXAMPLE:

```
Created password '<RANDOM_PASSWORD>' for user 'aen_admin'
```

**TIP:** Record this password. It will be needed in the following steps. It is also available in the installation log file `/tmp/wakari_server.log`.

## Starting NGINX and Elasticsearch

When SELinux is enabled, it blocks NGINX from connecting to the socket created by Gunicorn. If you have SELinux enabled, run these commands to correct these permissions and allow connections between NGINX and Gunicorn:

```
sudo semanage fcontext -a -t httpd_var_run_t "/opt/wakari/wakari-server/var/run/
↳ wakari-server.sock"
sudo restorecon -r /opt/wakari/wakari-server/var/run
```

To start NGINX and Elasticsearch to read the new config file:

```
sudo service nginx start
sudo service elasticsearch start
```

**TIP:** If the AEN web page shows an NGINX 404 error, restart NGINX:

```
sudo nginx -s stop
sudo nginx
```

## Testing AEN server installation

Visit `http://protect\T1\textdollarAEN_SERVER`.

The License expired page is displayed.

## Updating your license

From the License expired page, follow the onscreen instructions to upload your license file.

After your license is submitted, you will see this page:

No license found!

[Acquire a license](#)

Thank you for using Anaconda Enterprise Notebooks.

After 45 days, or the end of your paid license agreement, you must renew your license.

### Software updates and technical support

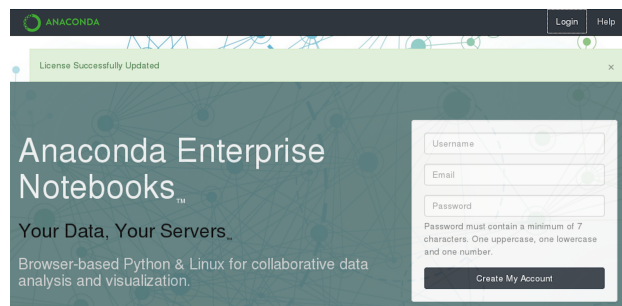
Software updates are free of charge during the initial 1-year period after the license purchase. Each subsequent update automatically terminates your rights to use the previous versions of the software. A commercial license qualifies you for unlimited access to technical support.

[Contact support for more information.](#)

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License File

No file selected.



## What's next

*Install the AEN gateway.*

## Installing the AEN gateway

- *Setting variables and changing permissions*
- *Running the AEN gateway installer*
- *Registering your gateway*
- *What's next*

The gateway is a reverse proxy that authenticates users and automatically directs them to the proper AEN compute node for their project. Users will not notice this node as it automatically routes them.

Gateway is installed in the `/opt/wakari/wakari-gateway` directory.

## Setting variables and changing permissions

Run:

```
export AEN_SERVER=<FQDN HOSTNAME OR IP ADDRESS> # Use the real FQDN
export AEN_GATEWAY_PORT=8089
export AEN_GATEWAY=<FQDN HOSTNAME OR IP ADDRESS> # will be needed shortly
chmod a+x aen-*.sh # Set installer to be executable
```

NOTE: Change <FQDN HOSTNAME OR IP ADDRESS> to the actual fully qualified domain hostname or IP address.

NOTE: You must perform the entire procedure before closing the terminal to ensure the variable export persists. If the terminal is closed before successful installation, export the variables to continue with the installation.

## Running the AEN gateway installer

Run:

```
sudo -E ./aen-gateway-4.3.0-Linux-x86_64.sh -w $AEN_SERVER
<license text>
...
...
PREFIX=/opt/wakari/wakari-gateway
Logging to /tmp/wakari_gateway.log
...
...
Checking server name
Please restart the Gateway after running the following command
to connect this Gateway to the AEN Server
...
```

## Registering your gateway

The gateway needs to register with the AEN server.

This needs to be authenticated, so the NFI user's credentials created during the AEN server install must be used.

To write the configuration file `/opt/wakari/wakari-gateway/etc/wakari/wk-gateway-config.json`, run the following as `sudo` or `root`:

```
sudo /opt/wakari/wakari-gateway/bin/wk-gateway-configure \
--server http://$AEN_SERVER --host $AEN_GATEWAY \
--port $AEN_GATEWAY_PORT --name Gateway --protocol http \
--summary Gateway --username $AEN_SRVC_ACCT \
--password '<NFI USER PASSWORD>'
```

NOTE: replace <NFI USER PASSWORD> with the password of the NFI user that was generated during *server installation*.

## Setting permissions

Run:

```
sudo chown $AEN_SRVC_ACCT /opt/wakari/wakari-gateway/etc/wakari/wk-gateway-config.json
```

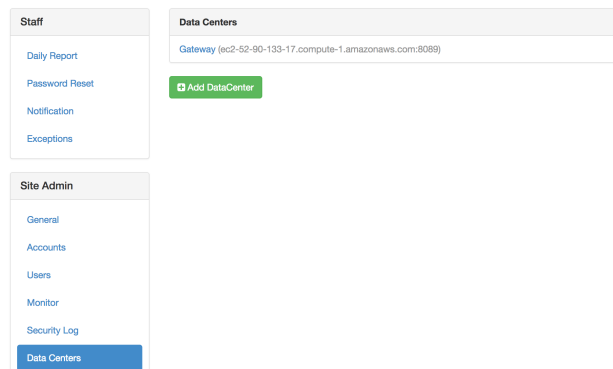
### Starting the gateway

Run:

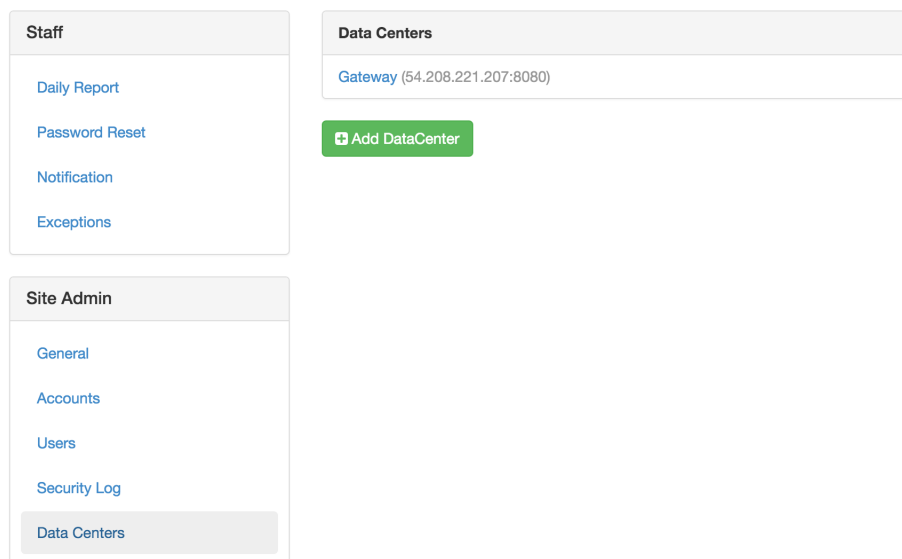
```
sudo service wakari-gateway start
```

### Verifying your gateway registration

1. Log into the AEN server using the Chrome or Firefox browser and the AEN\_SRVC\_ACCT user.
2. In the AEN navigation bar, click Admin to open the Admin Settings page.
3. In the **Site Admin** menu, select Data Centers:



4. Click your data center:



5. Verify that your data center is registered and the status is {"status": "ok", "messages": []}:



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Datacenter Gateway

Provider

wk\_server.plugins.providers.enterprise

Client ID

59c119cd3f94c30fe45ff5db

Client Secret

50cc629d-4e8e-44a5-9a2e-a46fee7c1921

Redirect URIs

http://ec2-52-90-133-17.compute-1.amazonaws.com:8089/login/authorized

wk-gateway-config.json

```
{
  "CDN": "http://ec2-204-236-198-47.compute-1.amazonaws.com/static/",
  "SUBDOMAIN_ROUTING": false,
  "client_id": "59c119cd3f94c30fe45ff5db",
  "client_secret": "50cc629d-4e8e-44a5-9a2e-a46fee7c1921",
  "WAKARI_SERVER": "http://ec2-204-236-198-47.compute-1.amazonaws.com",
  "port": 8089
}
```

status

```
{"status": "ok", "messages": []}
```

Back

Remove

## What's next

*Install the AEN compute node(s).*

## Installing the AEN compute node(s)

- *Setting variables and changing permissions*
- *Running the AEN compute installer*
- *Restart the AEN Server*
- *Configuring your compute node(s)*
- *What's next*

Compute nodes are where projects are stored and run.

Adding multiple AEN compute machines allows you to scale-out horizontally to increase capacity. Projects can be created on individual compute nodes to spread the load.

Repeat this procedure on each compute machine.

## Setting variables and changing permissions

Run:

```
export AEN_SERVER=<FQDN HOSTNAME OR IP ADDRESS> # Use the real FQDN
chmod a+x aen-*.sh                               # Set installer to be executable
```

NOTE: Change <FQDN HOSTNAME OR IP ADDRESS> to the actual fully qualified domain hostname or IP address.

NOTE: You must perform the entire procedure before closing the terminal, to ensure the variable export persists.

### Running the AEN compute installer

Run:

```
sudo -E ./aen-compute-4.3.0-Linux-x86_64.sh -w $AEN_SERVER
...
...
PREFIX=/opt/wakari/wakari-compute
Logging to /tmp/wakari_compute.log
Checking server name
...
...
Initial clone of root environment...
Starting Wakari daemons...
installation finished.
Do you wish the installer to prepend the wakari-compute install location
to PATH in your /root/.bashrc ? [yes|no]
[no] >>> yes
```

### Restart the AEN Server

Once configured, restart the AEN server:

```
sudo service wakari-server restart
```

### Configuring your compute node(s)

Once installed, you must configure the compute launcher on your server:

1. In your browser, go to your AEN server.
2. Log in as the AEN\_SRVC\_ACCT user.
3. In the AEN navigation bar, click Admin to open the Admin Settings page.
4. In the **Providers** menu, select Enterprise Resources:
5. Click the Add Resource button to open the new resource form.
6. Select the data center to associate this compute node with.

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Providers

[Enterprise Resources](#)

Resources

Add Resource

Gateway

ec2-54-210-232-251.compute-1.amazonaws.com

remove

Resources / new

Data Center

Gateway 59c119cd3f94c30fe45ff5db

Name

Compute Node1

URL

http://ec2-54-210-232-251.compute-1.amazonaws.com:5002

Description

Configuring Compute Node

☒ Public

Uncheck this if you want to control exactly who has access to this compute node

Add Resource

7. In the URL box, type: `http://$AEN_COMPUTE:5002`.

NOTE: If the compute launcher is located on the same box as the gateway, we recommended that you type `http://localhost:5002` instead.

8. Type a Name and Description for the compute node.
9. Click the Add Resource button to save the changes.

Your AEN compute node is configured.

### What's next

*Configure conda to use your local on-site AEN repository.*

### Configuring conda to use your local on-site AEN repository

You can configure AEN to use a local on-site Anaconda Repository server instead of Anaconda.org.

To configure AEN to use a local on-site Repository, you must:

1. *Edit conda on the compute node.*
2. *Configure the Anaconda client.*

### Editing conda on the compute node

NOTE: If there are channels that you haven't mirrored, you must remove them from the configuration.

Edit the file `.condarc` to match the following:

```
#/opt/wakari/anaconda/.condarc
channels:
  - defaults

create_default_packages:
  - anaconda-client
  - ipykernel

# Default channels is needed for when users override the system .condarc
# with ~/.condarc. This ensures that "defaults" maps to your Anaconda Repository and
↪not
# repo.anaconda.com
default_channels:
  - http://<your Anaconda Repository name>:8080/conda/anaconda
  - http://<your Anaconda Repository name>:8080/conda/wakari
  - http://<your Anaconda Repository name>:8080/conda/r-channel

# Note: You must add the "conda" subdirectory to the end
channel_alias: http://<your Anaconda Repository name>:8080/conda
```

NOTE: Replace `<your Anaconda Repository name>` with the actual name or IP address of your local Anaconda Repository installation.

## Configuring the Anaconda client

Anaconda client lets users work with Repository from the command-line—including searching for packages, logging in, uploading packages, and more.

To set the default configuration of anaconda-client for all users on your compute node:

```
sudo /opt/wakari/anaconda/bin/anaconda config --set url http://<your Anaconda_
↳Repository>:8080/api -s
```

NOTE: Sudo access is required because the configuration file is written to the root file system: `/etc/xdg/binstar/config.yaml`.

NOTE: Replace `<your Anaconda Repository>` with the actual name or IP address of your local Anaconda Repository installation.

## What's next

Review the *optional configuration* tasks to see if any apply to your system.

## Optional configuration

### Using configuration files

- *AEN configuration keys*
- *Checking configuration file syntax*

The default locations for each component's configuration files are:

- Server—`/opt/wakari/wakari-server/etc/wakari/config.json`.
- Gateway—`/opt/wakari/wakari-gateway/etc/wakari/config.json`.
- Compute—`/opt/wakari/wakari-compute/etc/wakari/config.json`.

Additionally, service-specific configuration files may also be present in the following locations:

- Server—`/opt/wakari/wakari-server/etc/wakari/wk-server-config.json`.
- Gateway—`/opt/wakari/wakari-gateway/etc/wakari/wk-gateway-config.json`.
- Compute—`/opt/wakari/wakari-compute/etc/wakari/wk-compute-config.json`.

Each service loads each of the configuration files in the following order and updates the AEN configuration at each step:

1. `/etc/wakari/config.json`.
2. `/etc/wakari/wk-gateway-config.json`.
3. `/opt/wakari/wakari-SERVICE/etc/wakari/config.json`.
4. `/opt/wakari/wakari-SERVICE/etc/wakari/wk-SERVICE-config.json`.
5. `./config.json`.
6. `./wk-gateway-config.json`.

## **AEN configuration keys**

The following is a list of AEN supported configuration keys:

Table 19: Server Configuration Keys

Key	Default	Description
CDN	\$WAKARI_SERVER/ static/	The location of static assets.
MONGO_DB	wakari	The name of the AEN database in mongodb.
MONGO_URL	mongodb:// localhost/	The URL of your AEN server's mongodb instance. Format: mongodb://<username>:<password>@<host>:<port>/
WAKARI_SERVER		The URL of this AEN server.
DEFAULT_PRIVACY	public	The default project privacy setting—can be either public or private.
SESSION_COOKIE_NAME	wk. enterprise. session	The cookie name used to maintain Anaconda Enterprise Notebooks Enterprise login sessions.
PERMANENT_SESSION	True	Sets cookie session to permanent. This will keep the session open after the browser is closed. The session will still expire after the number of minutes set in the SESSION_LIFETIME key.
SESSION_LIFETIME	120	Time in minutes until the session expires. The counter resets with each request.
USE_SES	false	Sets whether AEN will use Amazon SES to send emails.
SMTP		Sets the SMTP email settings.
- host		A SMTP subkey—the SMTP mail server hostname.
- user		SMTP subkey—the username for SMTP server authentication.
- password		SMTP subkey—the password for SMTP server authentication.
- from_addr		SMTP subkey—the From address for emails sent through SMTP.
verify_gateway_certificate	true	A boolean setting that indicates whether your AEN server should verify the gateway SSL certificate.
accounts	wk_server. plugins .accounts.cloud	The account provider class. For LDAP, this should be set to wk_server.plugins.accounts.ldap_accounts.
uniqueEmail	true	A boolean setting that indicates whether unique user email addresses are required. See <a href="#">note below</a> about updating the database when setting uniqueEmail.
has_internet	true	Boolean for retrieving the avatar from the gravatar URL. If false a local default is used instead.
LDAP	389	LDAP configurations.
- SERVER		LDAP subkey—A list of LDAP servers. At least one server name must be listed. The primary server should be listed first. All secondary or fail-over servers should be listed after the primary.
- PORT	389	LDAP subkey—The LDAP port on the LDAP server.
- AUTH_TYPE		LDAP subkey—LDAP Authentication types. simple—no encryption not secure. “TLS”—encrypted secure requires the TLS_CERT to be set.
- TLS_CERT		LDAP subkey—the full path to the TLS certificate file. The certificate file must also be provided by the Enterprise.
- BASEDN		LDAP subkey—the LDAP Base DN value.
- OU		LDAP subkey—a list of Organizational Units. Some enterprises group users by OUs in their LDAP server records. AEN will loop over the list of OUs when authenticating a user. The OU value is a list of lists to support multiple OUs where each OU is a single name or a hierarchy of names.
ANON_USER	anonymous	Username—such as public or anonymous—assigned users who are not logged in to access projects. To disable public access use the special value disabled. For more information, see <a href="#">Configuring sudo customizations</a> .
<b>4.1. Anaconda Enterprise 4</b>		<b>823</b>
SEARCH_ENABLED	true	Boolean indicating whether ElasticSearch is enabled
SEARCH_SERVER	'localhost:9200'	IP address or domain name and port of ElasticSearch server

NOTE: If you set `uniqueEmail` to `false`, you must drop the existing index in the database. EXAMPLE: If the index name is `email_1`, run `db.users.dropIndex("email_1")`.

Table 20: Gateway Configuration Keys

Key	Default	Description
WAKARI_SERVER		The URL of the AEN WAKARI_SERVER.
port	8089	The Port number used by the gateway application. Must be a non-privileged port ( $\geq 1024$ ).
client_id		The client ID assigned to this gateway by the server during <code>wk-gateway-configure</code> .
client_secret		The Client secret assigned to this gateway by the server during <code>wk-gateway-configure</code> .
httpTimeout	600	Timeout in seconds. The default is 10 minutes to allow project creation.
logLevel	info	Log verbosity. One of: 'error' 'warn' 'info' 'debug'.
https		Enable SSL encryption. For more information, see <a href="#">Configuring SSL</a> .
- key		A https subkey-Path to gateway key.
- cert		A https subkey-Path to gateway cert.
- ca		A https subkey-Required if cert was signed by a private root CA or signed by an intermediate authority. It must contain separate values for the paths to the CA root, any intermediates and the certificate for the Server.
- passphrase		A https subkey-Passphrase required to decrypt SSL certs.



Table 21: Compute Node Configuration Keys

Key	Default	Description
WAKARI_SERVER		The URL of the AEN WAKARI_SERVER.
MANAGE_ACCOUNTS	true	A boolean setting that indicates whether AEN should manage system user accounts. Set to false for LDAP installations.
identicalGID	false	<b>To make the AEN compute service create groups with the same uid. Set to true</b> /projects folder resides on an NFSv3 volume. For more information, see <a href="#">Group and user permissions for NFS</a> .
port	2227	The port number used by the compute-launcher application. Note that individual applications use dynamic ports.
projectRoot	/projects	The location of project file storage.
logLevel	info	Log verbosity. One of: 'error' 'warn' 'info' 'debug'
logMaxSize	10000000	Max size in bytes of the logfile. Default is 10 MB. If the size is exceeded then a new file is created and a counter will become a suffix of the log file.
logMaxFiles	30	Limit the number of files created when the size of the logfile is exceeded
appIdleTime	172800000 (48 hours)	The amount of idle time before applications will be auto-terminated (in msec).
idleCheckInterval	13600000 (1 hour)	The frequency of idle checks.
numericUsernames	false	A boolean setting that indicates whether numeric usernames are permitted.
httpTimeout	600	The time before a timeout—in seconds. The default is 10 minutes—600 seconds—to allow time for project creation.
ANON_USER	anonymous	Username such as public or anonymous for users who are not logged in to access projects. To disable public access use the special value disabled. For more information, see <a href="#">Configuring sudo customizations</a> .
projDirsAsHome	false	A boolean setting. When false AEN apps use /home/<username> as HOME. When true AEN apps use /projects/<username> as HOME.

Table 22: Server Internal Configuration Keys - Do not change

Key	Default	Description
PROVIDERS	["wk_server. plugins providers. enterprise"]	A list of compute provider classes.
MONGO_ACTION_LOG_SIZE	262144000	The size of the Mongo action log in bytes.
SITE_ADMINS		A list of site administrator email addresses—used for crash notifications and LDAP password reset requests.
FROM_EMAIL_ADDR		The From address for notification emails sent by AEN.
uniqueUserName	true	A boolean setting that indicates whether unique usernames are required.

Table 23: Gateway Internal Configuration Keys - Do not change

Key	Default	Description
CDN	\$WAKARI_SERVER/ static/	The location of static assets.
SUBDOMAIN_ROUTING	false	A boolean that indicates whether subdomains are being used.
refreshTokenExpiration	60000	Idle time in milliseconds before the Gateway session expires.

Table 24: Compute Node Internal Configuration Keys - Do not change

Key	Default	Description
CDN	\$WAKARI_SERVER/ static/	The location of static assets.
USE_SES	false	Sets whether AEN will use Amazon SES to send emails.
multiUser	true	A boolean that indicates whether multi-user support is enabled.
multiProject	true	A boolean that indicates whether multi-project support is enabled.
ANACONDA_ROOT	/opt/wakari/ anaconda	The location of your Anaconda installation.
appLogs	/opt/wakari/ wakari- compute/var/ log/wakari/ compute-launcher-apps	The directory where application logs are stored.
appPIDs	/opt/wakari/ wakari-compute/ var/run/ compute-launcher-apps	The directory where application PID files are stored.
applicationLog	/opt/wakari/ wakari-compute/ var/log/ wakari/ compute-launcher. application. log	The path to the compute launcher log.
accessLog	opt/wakari/ wakari-compute/ var/log/ wakari/ compute-launcher. access.log	Path to compute launcher access log

## Checking configuration file syntax

To verify that the configuration file contains valid JSON, run:

```
root@server # python -m json.tool /opt/wakari/wakari-server/etc/wakari/*.json
root@gateway # python -m json.tool /opt/wakari/wakari-gateway/etc/wakari/*.json
root@compute # python -m json.tool /opt/wakari/wakari-compute/etc/wakari/*.json
```

If the file is correct, the contents are displayed.

If there is a syntax error in the file, a “No JSON object could be decoded” message is displayed instead.

To fix any errors, edit the configuration file and verify that it contains the correct JSON syntax.

## Increasing HTTP timeout between gateway and compute nodes

The default HTTP timeout is 600 seconds (10 minutes).

This setting works for HTTP timeout only, not HTTPS.

To modify the HTTP timeout setting:

1. Open the `/opt/wakari/wakari-compute/etc/wakari/wk-compute-launcher-config.json` file and modify the `httpTimeout` key:

```
"httpTimeout": 600
```

2. Update the gateway node by modifying the `httpTimeout` key in the `/opt/wakari/wakari-gateway/etc/wakari/wk-gateway-config.json` file to match the above settings.
3. Restart the AEN compute service:

```
sudo service wakari-compute restart
```

## Installing AEN in a custom location

To install AEN in a custom location:

1. Make the custom install folder owned by `$AEN_SRVC_ACCT`. EXAMPLE: `/data/aen/`.
2. Make a symlink from `/opt/wakari` to `/data/aen`.
3. Run the installers.
4. Move the folder from `/projects` to your chosen custom location. EXAMPLE: `/data/aen/projects`.
5. Make a symlink from `/projects` to `/data/aen/projects`.

NOTE: We recommend putting `/opt/wakari` and `/projects` on the same filesystem. If the conda environment and project directories are on separate filesystems, more disk space will be required on compute nodes and performance will be impacted.

## Changing where projects are stored

NOTE: We recommend putting `/opt/wakari` and `/projects` on the same filesystem. If the project and conda env directories are on separate filesystems then more disk space will be required on compute nodes and performance will be worse.

To make `aen-compute` service use a different directory than `/projects` to store your AEN projects:

1. Modify the `/opt/wakari/wakari-compute/etc/wakari/wk-compute-launcher-config.json` file:

```
"projectRoot" : "/nfs/storage/services/wakari/projects",
```

NOTE: The directory `/nfs/storage/services/wakari/projects` specified as `projectRoot` must already exist for this command to resolve properly.

2. Restart the AEN compute service:

```
sudo service wakari-compute restart
```

## Group and user permissions for NFS

To install AEN with multiple compute nodes and a `/projects` folder on an NFSv3 volume, manually pre-create both the anonymous user and the `$AEN_SRVC_ACCOUNT` user on all nodes. Each of these users must have the same user identity number (UID) and group identity number (GID) on all nodes.

By default AEN creates local users with a different GID on each node. To make the AEN compute service create groups with the same GID:

1. In the `/opt/wakari/wakari-compute/etc/wakari/wk-compute-launcher-config.json` file, change the `identicalGID` key value to `true`:

```
, "identicalGID": true
```

If you don't see the `identicalGID` key, add it.

NOTE: You must add the comma at the beginning of the line. If you add this line as the last key, you must remove any comma at the end of the line.

2. Restart the AEN compute service:

```
sudo service wakari-compute restart
```

## Using numeric usernames

1. In the `/opt/wakari/wakari-compute/etc/wakari/wk-compute-launcher-config.json` file, change the `numericUsernames` key value to `true`.

```
, "numericUsernames": true
```

If you don't see the `numericUsernames` key, add it.

NOTE: You must add the comma at the beginning of the line. If you add this line as the last key, you must remove any comma at the end of the line.

2. Restart the AEN compute service:

```
sudo service wakari-compute restart
```

## Using project directories as home directories

The `projDirsAsHome` option changes the AEN home directories from the standard `/home/<username>` location to the project directories and the location `/projects/<username>/<project_name>/<username>/`. This ensures that AEN and AEN apps will not be affected by configuration files in a user's home directory, such as `.bashrc` or configuration files in subdirectories such as `.ipython` and `.jupyter`.

## Package cache locations

AEN version 4.1.3 stores the cache of packages in `/home/<username>`, while AEN versions 4.2.0 and higher store the cache of packages in `/projects/<username>/<project_name>/<username>/`. By moving the

package cache to the same filesystem as the project, AEN versions 4.2.0 and higher can use hardlinks and save disk space and time when creating or cloning environments.

These package cache locations are not affected by the `projDirsAsHome` option.

After upgrading from AEN 4.1.3 to AEN 4.2.0 or higher, existing projects will still use the package cache in `/home/<username>`. Do not remove this cache, or the existing projects will break.

When users create new projects or install packages, the newly installed packages will use the new cache location.

If you wish to remove the older package cache in `/home/<username>`:

- Upgrade AEN to 4.2.0 or higher.
- Use `conda remove` to remove every non-default package in every project.
- Use `conda install` to replace them. The replaced packages will link to the new package cache in `/projects/<username>/<project_name>/<username>/`.
- You can now safely remove the older package cache.

## Enabling `projDirsAsHome`

NOTE: The `projDirsAsHome` option should be enabled immediately after performing the installation process and before any users have logged in to AEN. This ensures that users will not have home directories in different places due to some creating their home directories when the option was disabled and others creating their home directories when the option was enabled.

1. In the `/opt/wakari/wakari-compute/etc/wakari/wk-compute-launcher-config.json` file, add the `projDirsAsHome` key value and set it to `true`.

```
, "projDirsAsHome": true
```

NOTE: You must add the comma at the beginning of the line. If you add this line as the last key, you must remove any comma at the end of the line.

2. Restart the AEN compute service:

```
sudo service wakari-compute restart
```

## Setting up a default project environment

AEN includes a full installation of the Anaconda Python distribution—along with several additional packages—located within the root conda environment in `/opt/wakari/anaconda`.

The first time any new AEN project is started, this default project environment is cloned into the new project's workspace.

To configure a different set of packages than the default:

1. Create a new conda environment in the `/opt/wakari/anaconda/envs/default` directory.

EXAMPLE: Using a Python 3.4 base environment, run:

```
sudo -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda \
  create -p /opt/wakari/anaconda/envs/default python=3.4
```

2. Use `conda` to install any additional packages into the environment.
3. After the environment is created, clone it to ensure that it works correctly:

```
sudo -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda \  
    create -p /opt/wakari/testenv --clone /opt/wakari/anaconda/envs/default  
sudo -u $AEN_SRVC_ACCT rm -rf /opt/wakari/testenv
```

For more information and examples about creating a default project environment with Microsoft R Open (MRO), see *Using MRO in AEN*.

## Converting an existing project

1. Run the following command to clone the environment:

```
sudo -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda \  
    create -n /projects/owner/project/envs/<ENV_NAME> \  
    --clone /opt/wakari/anaconda/envs/default
```

NOTE: Replace `/projects/owner/project/envs/<ENV_NAME>` with the path to the new environment you would like to create within the project.

2. Open the *Compute Resource Configuration application* for your project and set the project environment path there as well.

## Using MRO in AEN

In AEN 4.2.2 and higher, you can choose to create environments with the Microsoft R Open (MRO) interpreter by installing the `mro-base` package, or create environments with the R interpreter by installing the `r-base` package. Unless you request a change, conda will continue to use the existing interpreter in each environment. In AEN `r-base` is the default.

EXAMPLE: To create a custom environment called `mro_env` with MRO and R Essentials:

```
.. code-block:: bash  
  
sudo -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda \  
    create -c https://repo.anaconda.com/pkgs/main \  
    -n mro_env r-essentials
```

NOTE: Conda 4.4 and higher include the `main` channel by default. Earlier versions of conda do not.

## Making a default project environment with MRO

You can also create an environment with MRO and make this the default AEN project environment.

The first time a new project is started, the default project environment is cloned into the new project's workspace.

1. Create a new conda environment in the `/opt/wakari/anaconda/envs/default` directory.

The command is similar to the one used in the previous example to create a custom environment.

```
sudo -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda \  
    create -c https://repo.anaconda.com/pkgs/main \  
    -p /opt/wakari/anaconda/envs/default r-essentials
```

2. Use `conda` to install any additional packages into the environment.
3. After the environment is created, clone it to check that it works correctly, and then clean up the clone.

```
sudo -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda \
    create -p /opt/wakari/testenv --clone /opt/wakari/anaconda/envs/default
sudo -u $AEN_SRVC_ACCT rm -rf /opt/wakari/testenv
```

NOTE: To convert existing projects, see *Converting an existing project*.

## Install AEN connected to a remote Mongo DB instance

To install AEN with a remote database:

1. Connect to the Mongodb instance and create the user for AEN:

```
> user = { user: "<username>",
  pwd: "<super-secure-password>",
  roles: [
    { role: "dbOwner", db: "<db_name>" },
    { role: "dbOwner", db: "<db_name>_mq" }
  ]
}
> db.createUser(user)
Successfully added user: { ... }
```

2. Before installing AEN-server export the database URL and name:

```
$ export MONGO_URL="mongodb://<username>:<password>@<host>:<port>/"
$ export MONGO_DB="<database_name>"
```

3. Continue the installation process: *Install the AEN server*.

## Migrate from local to remote MongoDB

To configure your remote database to work with an already installed AEN server:

1. Stop the server, gateway and compute nodes:

```
sudo service wakari-server stop
sudo service wakari-gateway stop
sudo service wakari-compute stop
```

2. Open the `/opt/wakari/wakari-server/etc/wakari/config.json` file and create the `MONGO_URL` key. For the value parameter, add the database information.

The final file should read:

```
{
  "MONGO_URL": "mongodb://MONGO-USER:MONGO-PASSWORD@MONGO-URL:MONGO-PORT",
  "MONGO_DB": "MONGO-DB-NAME",
  "WAKARI_SERVER": "http://YOUR-IP",
  "USE_SES": false,
  "CDN": "http://YOUR-IP/static/",
  "ANON_USER": "anonymous"
}
```

For more information about configuration keys, see *Using configuration files*.

3. Migrate the data from the former database into the new one. For more information, see the [MongoDB documentation website](#).
4. After migration, restart the nodes:

```
sudo service wakari-server start
sudo service wakari-gateway start
sudo service wakari-compute start
```

### Running SELinux in enforcing mode

To run SELinux in Enforcing mode, a few ports must be set up using the `semanage port` command.

The `semanage` command relies on `polycoreutils-python`. To install `polycoreutils-python`, if needed, run:

```
sudo yum -y install polycoreutils-python
```

Enable ports 9200 and 9300 for Elasticsearch:

```
sudo semanage port -a -t http_port_t -p tcp 9200
sudo semanage port -a -t http_port_t -p tcp 9300
```

### Changing server hostnames

It is possible to change the domain names (hostnames) of the various AEN nodes by updating the configuration files.

NOTE: After the configuration files are updated, the associated nodes need to be restarted.

To edit the information for all of the data centers that you are changing the base domain name for:

1. Go to the Site Admin section of the Admin Settings page.
2. In the Data Centers section, click the Edit button.
3. Make any necessary updates.

NOTE: This must include the service port if it is different from the default—80 for HTTP and 443 for HTTPS.

4. In the Enterprise Resources sub-section of the Providers section, edit each compute node that has a changed domain name.

NOTE: These URLs should include the protocol, hostname and port.

### Authenticating with LDAP

Anaconda Enterprise Notebooks performs local authentication against accounts in the AEN database by default.

To configure AEN to authenticate against accounts in an LDAP (Lightweight Directory Access Protocol) server, follow the instructions below.

### Installing OpenLDAP libraries

The system needs OpenLDAP libraries to be installed and accessible by AEN. AEN uses the OpenLDAP libraries to establish an LDAP connection to your LDAP servers.



To install OpenLDAP on CentOS or Redhat:

```
sudo yum install openldap
```

To install OpenLDAP on Ubuntu or Debian, follow the official [OpenLDAP installation instructions](#).

## Configuring OpenLDAP

1. Open the `/opt/wakari/wakari-server/etc/wakari/wk-server-config.json` file.
2. Add the following LDAP settings:

```
{
  "accounts": "wk_server.plugins.accounts.ldap2",
  "LDAP" : {
    "URI": "ldap://openldap.EXAMPLE.COM",
    "BIND_DN": "cn=Bob Jones,ou=Users,DC=EXAMPLE,DC=COM",
    "BIND_AUTH": "secretpass",
    "USER_SEARCH": { "base": "DC=EXAMPLE,DC=COM",
                     "filter": "(| (& (ou=Payroll)
                                   (uid=%(username)s))
                               (& (ou=Facilities)
                                   (uid=%(username)s)))"
                   },
    "KEY_MAP": { "email": "mail",
                 "name": "cn"
               }
  }
}
```

- **URI**—The IP address or hostname of your OpenLDAP server. For SSL/TLS, use the `ldaps://` prefix and specify a `TLS_CACERT` as described in the SSL/TLS configuration section below.
- **BIND\_DN**—The full directory path of the user you want AEN server to bind as.
- **BIND\_AUTH**—The password of the **BIND\_DN** user.
- **USER\_SEARCH**:
  - **base**—The level at which you want to start the search.
  - **filter**—The default is to search for the `sAMAccountName` attribute, and use its value for the AEN server username field.
- **KEY\_MAP**—Maps user attributes in AEN server to LDAP user attributes.

EXAMPLE: The `mail` attribute in LDAP maps to the `email` attribute in AEN server.

3. Restart AEN server to load new settings.
4. Log in with the admin account. This creates the admin user in the local database.
5. As soon as LDAP is installed, LDAP authentication takes over, so you need to add your admin account again:

```
/opt/wakari/wakari-server/bin/wk-server-admin superuser --add "jsmith"
```

## Configuring Active Directory

Microsoft Active Directory is a server program that provides directory services and uses the open industry standard Lightweight Directory Access Protocol (LDAP).

To enable Active Directory support:

1. Open the `/opt/wakari/wakari-server/etc/wakari/wk-server-config.json` file.
2. Add the following LDAP settings:

```
{
  "accounts": "wk_server.plugins.accounts.ldap2",
  "LDAP" : {
    "URI": "ldap://<ad.EXAMPLE.COM>",
    "BIND_DN": "CN=Bind User,CN=Users,DC=EXAMPLE,DC=COM",
    "BIND_AUTH": "secretpass",
    "USER_SEARCH": { "base": "CN=Users,DC=EXAMPLE,DC=COM",
                     "filter": "sAMAccountName=%(username)s"
                   },
    "KEY_MAP": { "email": "mail",
                 "name": "cn"
               }
  }
}
```

- URI—The IP address or hostname of your Active Directory server. Replace `<ad.EXAMPLE.COM>` with the actual URI. For SSL/TLS, use the `ldaps://` prefix and specify a `TLS_CACERT` as described in the SSL/TLS configuration section below.
- BIND\_DN—The full directory path of the user you want AEN server to bind as.
- BIND\_AUTH—The password of the BIND\_DN user.
- USER\_SEARCH:
  - base—the level at which you want to start the search.
  - filter—default is to search for the `sAMAccountName` attribute, and use its value for the AEN server `username` field.
- KEY\_MAP—Maps user attributes in AEN server to LDAP user attributes.

EXAMPLE: The `mail` attribute in LDAP maps to the `email` attribute in AEN server.

3. Restart AEN server to load new settings.
4. Log in with the admin account. This creates the admin user in the local database.
5. As soon as LDAP is installed, LDAP authentication takes over, so you need to add your admin account again:

```
/opt/wakari/wakari-server/bin/wk-server-admin superuser --add "jsmith"
```

## Configuring SSL/TLS

AEN uses system-wide LDAP settings, including SSL/TLS support.

- On Redhat/CentOS systems, these settings are located in the `/etc/openldap/ldap.conf` file.
- On Ubuntu/Debian systems, these settings are located in the `/etc/ldap/ldap.conf` file.

Typically, the only configuration necessary is updating the file to read:

```
TLS_CACERT /path/to/CA.cert
```

NOTE: `CA.cert` is the Certificate Authority used to sign the LDAP server's SSL certificate. In the case of a self-signed SSL certificate, this is the path to the SSL certificate itself.

## Testing LDAP configuration

Test your LDAP configuration using `flask-ldap-login-check`:

```
/opt/wakari/wakari-server/bin/flask-ldap-login-check \
  wk_server.wsgi:app \
  -u [username] \
  -p [password]
```

NOTE: `username` is the username of a valid user and `password` is that user's `BIND_AUTH` password.

## Configuring sudo customizations

If your organization's IT security policy does not allow root access or has restrictions on the use of `sudo`, after AEN installation, you may customize AEN to meet their requirements.

Your organization may choose to implement any or all of the following:

- *Remove root access* for AEN service account (Note: this restricts AEN from managing user accounts).
- *Configurable sudo command*.
- *Restrict sudo access to all processes*.

These customizations must be done in a terminal window after copying the files to the server node.

## Removing all root access from the service account

Because root access is required for `useradd`, the following process restricts AEN from managing user accounts.

1. Modify the `/etc/sudoers.d/wakari_sudo` file to read:

```
Defaults:wakari !requiretty, visiblepw
Runas_Alias    OP = ALL,!root
wakari ALL=(OP) NOPASSWD: ALL
```

NOTE: If you used a service account name other than `wakari`, enter that name instead of `wakari`.

2. Modify the `/opt/wakari/wakari-compute/etc/wakari/config.json` file to read:

```
"MANAGE_ACCOUNTS": false,
```

Using this option means that your IT department must create and manage all user accounts at the OS level.

After an OS-level account exists, you may create on the main AEN web page an AEN account using the same name. The password you choose is not linked in any way to the OS-level password for the account.

Alternatively, you can configure the system to *use LDAP for authenticating users*.

## Allowing public users to have access to your AEN projects

A public account is visible to anyone who can access the AEN server. The name of this account can be configured to any name you wish. For example, `public` or `anonymous`. To disable this feature use the special value `disabled`.

1. In the `/opt/wakari/wakari-compute/etc/wakari/wk-compute-launcher-config.json` file, modify the `ANON_USER` line to read:

```
"ANON_USER": "public"
```

2. Restart AEN compute node:

```
sudo service wakari-compute restart
```

3. In the `/opt/wakari/wakari-server/etc/wakari/wk-server-config.json` file, modify the `ANON_USER` line to read:

```
"ANON_USER": "public"
```

4. Restart AEN server:

```
sudo service wakari-server restart
```

For more information about configuration keys, see [Using configuration files](#).

## Using a sudo alternative

You can use a sudo alternative as long as it supports the same execution semantics as the original sudo. The alternative must be configured to give the service account permission to run commands on behalf of AEN users.

1. In your terminal window, open the `/opt/wakari/wakari-compute/etc/wakari/config.json` file.
2. Modify the `AEN_SUDO_CMD` line to read:

```
"AEN_SUDO_CMD": "/path/to/alternative/sudo",
```

NOTE: If the alternate sudo command is available on `PATH`, then the full path is not required.

## Restricting sudo access to a single gatekeeper

By default, sudoers is configured to allow AEN to run any command as a particular user which allows the platform to initiate processes as the logged-in end user. If more restrictive control is required, it should be implemented using a suitable sudoers policy. If that is not possible or practical, it is also possible to route all AEN ID-changing operations through a single gatekeeper.

This gatekeeper wraps the desired executable and provides an alternate way to log, monitor, or control which processes can be initiated by AEN on behalf of a user.

CAUTION: Gatekeeper is a special case configuration and should only be used if required.

To configure an AEN gatekeeper:

1. Modify the `/etc/sudoers.d/wakari_sudo` file to contain:

```
Defaults:wakari !requiretty, visiblepw
Runas_Alias    OP = ALL,!root
wakari ALL=(OP) NOPASSWD: /path/to/gatekeeper
```

2. In the `/opt/wakari/wakari-compute/etc/wakari/config.json` file, modify the `AEN_SUDO_SH` line to read:

```
"AEN_SUDO_SH": "/path/to/gatekeeper"
```

EXAMPLE: The gatekeeper can be as simple as a script with contents such as:

```
#!/bin/bash
first_cmd=$1
if [ 'bash' == $1 ]; then
    shift
    export HOME=~
    export SHELL=/bin/bash
    export PATH=$PATH:/opt/wakari/anaconda/bin
    bash "$@"
else
    exec $@
fi
```

## Configuring SSL

The server node uses NGINX to proxy all incoming http(s) requests to the server running on a local port, and uses NGINX for SSL termination. The default setup uses http—non-SSL—since cert files are required to configure SSL and each enterprise will have their own cert files.

The `www.enterprise.conf` file is the default `nginx.conf` file used for AEN. It is copied to the `/etc/nginx/conf.d` directory during server installation.

NOTE: This section describes setting up SSL after your gateway node has been installed and registered with the server node.

## Copying the required files

To configure SSL on AEN, you will need the following files:

- Server certificate and key
- Server CA bundle
- Gateway certificate and key
- Gateway CA bundle

Configure SSL on AEN:

1. Copy the Gateway certificate and key to `/opt/wakari/wakari-gateway/etc/` on the Gateway as `gateway.crt` and `gateway.key`.
2. Copy the Gateway CA bundle to `/opt/wakari/wakari-server/etc/` on the Server.
3. Copy the Server certificate and key to `/etc/nginx` on the Server as `server.crt` and `server.key`.
4. Copy the Server CA bundle to `/opt/wakari/wakari-gateway/etc/` on the Gateway.

If you have a certificate that was signed by a private root CA and/or an intermediate authority:

- The Gateway CA bundle must contain the full chain: root CA, any intermediate authority and the certificate.

```
cat gateway.crt intermediate.crt root.crt >> gateway-crt-int-root.crt
```

- The Server CA bundle must be separated into individual files for the root CA, any intermediate and the certificate.

## Configuring SSL on the server node

The `www.enterprise.https.conf` is an NGINX configuration file for SSL. It is set up to use the `server.crt` and `server.key` cert files.

**CAUTION:** You must change these values to point to the signed cert files for your domain.

**NOTE:** Self-signed certs or those signed by a private root CA require additional configuration.

Perform the following steps as root:

1. Stop NGINX:

```
service nginx stop
```

2. Move the `/etc/nginx/conf.d/www.enterprise.conf` file to a backup directory.
3. Copy the `/opt/wakari/wakari-server/etc/nginx/conf.d/www.enterprise.https.conf` file to `/etc/nginx/conf.d`.  
**NOTE:** `/etc/nginx/conf.d` may have `www.enterprise.conf` or `www.enterprise.https.conf` but it may not have both.
4. Edit the `/etc/nginx/conf.d/www.enterprise.https.conf` file and change the `server.crt` and `server.key` values to the names of the real cert and key files if they are different.
5. Restart NGINX by running:

```
service nginx start
```

6. Update the `WAKARI_SERVER` and `CDN` settings to use `https` instead of `http` in the following configuration files:

```
/opt/wakari/wakari-server/etc/wakari/config.json  
/opt/wakari/wakari-gateway/etc/wakari/wk-gateway-config.json  
/opt/wakari/wakari-compute/etc/wakari/config.json
```

7. Copy the gateway certificate, `gateway.crt` to `/opt/wakari/wakari-server/etc/`.
8. In an editor, open `/opt/wakari/wakari-server/etc/wakari/wk-server-config.json` and add:

```
"verify_gateway_certificate": "/opt/wakari/wakari-server/etc/gateway.crt"
```

9. Restart AEN services on the server by running:

```
service wakari-server restart
```

**NOTE:** This step may return an error since the gateway has not yet been configured for SSL.

10. In AEN, verify that the browser uses `https`. On the Admin Settings page, under Data Centers, click Gateway, then select `https`:

# Admin Settings

Anaconda Enterprise Notebooks settings accessible only by the administrator

The screenshot shows two side-by-side panels. The left panel, titled 'Staff', contains three links: 'Daily Report', 'Password Reset', and 'Notification'. The right panel, titled 'Data Centers / Register a datacenter', contains a 'Name' field with the value 'Gateway 1', a checkbox for 'Subdomain Routing' which is unchecked, and a checkbox for 'Https' which is checked.

## Configuring SSL on the gateway

1. For all types of SSL certificates, in `/opt/wakari/wakari-gateway/etc/wakari/wk-gateway-config.json`, add:

```
{
  EXISTING_CONFIGURATION,
  "https": {
    "key": "/opt/wakari/wakari-gateway/etc/gateway.key",
    "cert": "/opt/wakari/wakari-gateway/etc/gateway.crt"
  }
}
```

2. For a server certificate signed by a private root CA or signed by an intermediate authority, add:

```
{
  EXISTING_CONFIGURATION,
  "https": {
    "key": "/opt/wakari/wakari-gateway/etc/gateway.key",
    "cert": "/opt/wakari/wakari-gateway/etc/gateway.crt",
    "ca": ["/opt/wakari/wakari-gateway/etc/server.crt"]
  }
}
```

NOTE: When the certificate chain has more than one intermediate cert signed by a higher root CA authority, you must manually break up the certs in the chain into individual files, and enumerate them in the `ca` key:

```
{
  EXISTING_CONFIGURATION,
  "https": {
```

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```

    "key": "/opt/wakari/wakari-gateway/etc/gateway.key",
    "cert": "/opt/wakari/wakari-gateway/etc/gateway.crt",
    "ca": ["/opt/wakari/wakari-gateway/etc/server1.crt",
           "/opt/wakari/wakari-gateway/etc/server2.crt",
           "/opt/wakari/wakari-gateway/etc/server3.crt"]
  }
}

```

3. For a gateway certificate that is encrypted using a passphrase, add:

```

{
  EXISTING_CONFIGURATION,
  "https": {
    "key": "/opt/wakari/wakari-gateway/etc/gateway.key",
    "cert": "/opt/wakari/wakari-gateway/etc/gateway.crt",
    "passphrase": "mysecretpassphrase"
  }
}

```

NOTE: Alternatively, the passphrase can be passed using an environment variable or entered when the wakari-gateway service is manually started.

#### EXAMPLES:

```

# using an environment variable
AEN_GATEWAY_SSL_PASSPHRASE='mysecretpassphrase' wk-gateway

```

```

# starting wakari-gateway manually
sudo service wakari-gateway start --ask-for-passphrase
Passphrase?

```

4. Restart the gateway:

```

sudo service wakari-gateway restart

```

## Configuring SSL on compute nodes

Anaconda Enterprise does not support direct SSL on Compute Nodes. If you need SSL on Compute Nodes, you must install each Compute Node on the same server as a Gateway using `http://localhost:5002` for the URL value while adding it as a resource, and you must use a Gateway for each and every Compute Node.

## Security reminder

The permissions on the cert files must be set correctly to prevent them from being read by others. Since NGINX is run by the root user, only the root user needs read access to the cert files.

EXAMPLE: If the cert files are called `server.crt` and `server.key`, then use the root account to set permissions:

```

chmod 600 server.key
chmod 600 server.crt

```



## Enabling or disabling the Strict-Transport-Security header

By default, Strict-Transport-Security (STS) is enabled in the `www.enterprise.https.conf` file:

```
add_header Strict-Transport-Security max-age=31536000;
```

It can remain enabled if either of the following is true:

- The gateway is running on a different host than the server.
- or
- SSL has been enabled for the gateway.

You must comment out this line if both of the following are true:

- The gateway is running on the same host as the server.
- and
- SSL has not been enabled for the gateway.

Leaving STS enabled when these conditions are true will cause a mismatch in protocols between the server and gateway, causing your apps to fail to launch correctly.

## Configuring single sign-on

AEN's single sign-on (SSO) capability creates a new authentication provider that defers to your Anaconda Repository for login and authentication cookies.

To enable SSO:

1. Deploy AEN and Repository on the same machine.
2. In the `/opt/wakari/wakari-server/etc/wakari/config.json` file, add:

```
{
  EXISTING_CONFIGURATION,
  "SECRET_KEY": "<repo signing secret>",
  "REPO_LOGIN_URL":
    "http://example_repo.com:8080/account/login?next=http://example_repo.com/"
}
```

3. Copy the `SECRET_KEY` from the Repository configuration file.
4. In the `/opt/wakari/wakari-server/etc/wakari/wk-server-config.json` file, modify:

```
{
  EXISTING_CONFIGURATION,
  "accounts": "wk_server.plugins.accounts.repo",
}
```

5. If you are using Repository version 2.33.3 through 2.33.10, set `USE_SERVER_BASED_SESSIONS: false` in the Repository configuration.

This setting affects the network security properties of AEN and Repository. Specifically, if `USE_SERVER_BASED_SESSIONS` is set to false, and if a new cross-site scripting (XSS) vulnerability is discovered, it could expose an additional server fixation vulnerability. Please discuss this with your Anaconda representative and be sure the feature is compatible with your network requirements before setting `USE_SERVER_BASED_SESSIONS: false`.

6. To activate the changes restart `wakari-server`:

```
sudo service wakari-server restart
```

SSO is enabled.

### Adding a third-party extension

Anaconda officially supports and tests functionality of the default environment(s) only for those extensions that ship with AEN.

It is possible to add third-party and custom extensions from `conda-forge` or `pip`, but doing so may cause instability in your default project environments or kernels.

**CAUTION:** Anaconda does not officially support third-party extensions. This section is informational only.

### Installing unofficial Jupyter Notebook extensions for AEN

**TIP:** Always back up and verify your complete system before installing extensions.

The `jupyter-contrib-nbextensions` extensions are installed on a compute node.

The default `conda` executable directory for AEN is `/opt/wakari/anaconda/bin/conda`. If you are installing a Jupyter extension, it must be installed in the `wakari-compute` directory.

**EXAMPLE:** Run:

```
/opt/wakari/anaconda/bin/conda install -p /opt/wakari/wakari-compute/ -c conda-forge_
↪ jupyter_contrib_nbextension
```

For more information, see [Unofficial Jupyter Notebook Extensions](#).

### Configure search indexing

For search indexing to work correctly, verify that the AEN Compute node can communicate with the AEN Server.

```
curl -m 5 $AEN_SERVER > /dev/null
```

There must be at least one `inotify` watch available for the number of subdirectories within the project root filesystem. Some Linux distributions default to a low number of watches, which can prevent the search indexer from monitoring project directories for changes.

```
cat /proc/sys/fs/inotify/max_user_watches
```

If necessary, increase the number of max user watches with the following command:

```
echo fs.inotify.max_user_watches=100000 | sudo tee -a /etc/sysctl.conf && sudo sysctl_
↪ -p
```

There must be at least one `inotify` user instance available per project.

```
cat /proc/sys/fs/inotify/max_user_instances
```

If necessary, this can be increased with the following command:

```
echo fs.inotify.max_user_instances=1000 | sudo tee -a /etc/sysctl.conf && sudo sysctl_
↪-p
```

## Create custom Jupyter kernel for Pyspark

These instructions add a custom Jupyter Notebook option to allow users to select PySpark as the kernel.

### Install Spark

The easiest way to install Spark is with [Cloudera CDH](#).

You will use YARN as a resource manager. After installing Cloudera CDH, [install Spark](#). Spark comes with a PySpark shell.

### Create a notebook kernel for PySpark

You may create the kernel as an administrator or as a regular user. Read the instructions below to help you choose which method to use.

#### 1. As an administrator

Create a new kernel and point it to the root env in each project. To do so create a directory 'pyspark' in /opt/wakari/wakari-compute/share/jupyter/kernels/.

Create the following kernel.json file:

```
{ "argv": [ "/opt/wakari/anaconda/bin/python",
  "-m", "ipykernel", "-f", "connection_file", "--profile", "pyspark"],
  "display_name": "PySpark", "language": "python" }
```

You may choose any name for the 'display\_name'.

This configuration is pointing to the python executable in the root environment. Since that environment is under admin control, users cannot add new packages to the environment. They will need an admin to help update the environment.

#### 2. As an administrator without IPython profile

To have an admin level PySpark kernel, without the user .ipython space:

```
{ "argv":
  [ "/opt/wakari/wakari-compute/etc/ipython/pyspark.sh", "-f", "{connection_file}" ],
  "display_name": "PySpark", "language": "python" }
```

NOTE: The pyspark.sh script is defined in *Without IPython profile* section below.

#### 3. As a regular user

Create a new directory in the user's home directory: .local/share/jupyter/kernels/pyspark/. This way the user will be using the default environment and able to upgrade or install new packages.

Create the following `kernel.json` file:

```
{
  "argv": ["/projects/<username>/<project_name>/envs/default/bin/python",
    "-m", "ipykernel", "-f", "connection_file", "--profile", "pyspark"],
  "display_name": "PySpark",
  "language": "python"
}
```

NOTE: Replace `<username>` with the correct user name and `<project_name>` with the correct project name.

You may choose any name for the `display_name`.

## Create an IPython profile

The above profile call from the kernel requires that we define a particular PySpark profile. This profile should be created for each user that logs in to AEN to use the PySpark kernel.

In the user's home, create the directory and file `~/.ipython/profile_pyspark/startup/00-pyspark-setup.py` with the file contents:

```
import os
import sys

# The place where CDH installed spark, if the user installed Spark locally it can be
↪ changed here.
# Optionally we can check if the variable can be retrieved from environment.

os.environ["SPARK_HOME"] = "/usr/lib/spark"

os.environ["PYSPARK_PYTHON"] = "/opt/wakari/anaconda/bin/python"

# And Python path
os.environ["PYLIB"] = os.environ["SPARK_HOME"] + "/python/lib"
sys.path.insert(0, os.environ["PYLIB"] + "/py4j-0.9-src.zip") #10.4-src.zip")
sys.path.insert(0, os.environ["PYLIB"] + "/pyspark.zip")

os.environ["PYSPARK_SUBMIT_ARGS"] = "--name yarn pyspark-shell"
```

Now log in using the user account that has the PySpark profile.

## Without IPython profile

If it is necessary to avoid creating a local profile for the users, a script can be made to be called from the kernel. Create a bash script that will load the environment variables:

```
sudo -u $AEN_SRVC_ACCT mkdir /opt/wakari/wakari-compute/etc/ipython
sudo -u $AEN_SRVC_ACCT touch /opt/wakari/wakari-compute/etc/ipython/pyspark.sh
sudo -u $AEN_SRVC_ACCT chmod a+x /opt/wakari/wakari-compute/etc/ipython/pyspark.sh
```

The contents of the file should look like:

```
#!/usr/bin/env bash
# setup environment variable, etc.

export PYSPARK_PYTHON="/opt/wakari/anaconda/bin/python"
export SPARK_HOME="/usr/lib/spark"
```

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```
# And Python path
export PYLIB=$SPARK_HOME:/python/lib
export PYTHONPATH=$PYTHONPATH:$PYLIB:/py4j-0.9-src.zip
export PYTHONPATH=$PYTHONPATH:$PYLIB:/pyspark.zip

export PYSARK_SUBMIT_ARGS="--name yarn pyspark-shell"

# run the ipykernel
exec /opt/wakari/anaconda/bin/python -m ipykernel $@
```

## Using PySpark

When creating a new notebook in a project, now there will be the option to select PySpark as the kernel. When creating such a notebook you'll be able to import pyspark and start using it:

```
from pyspark import SparkConf
from pyspark import SparkContext
```

NOTE: You can always add those lines and any other command you may use frequently in the PySpark setup file 00-pyspark-setup.py as shown above.

## Upgrading AEN

- *Before you upgrade*
- *Upgrading the AEN server node*
- *Upgrading the AEN gateway node*
- *Upgrading AEN compute nodes*
- *After upgrading*

CAUTION: These instructions are for upgrading AEN to the current version 4.3.0 from 4.2.2 ONLY. Each version must be upgraded iteratively from the previous version. Do not skip versions.

Upgrade instructions for previous versions:

- *AEN 4.2.2 upgrade instructions*
- *AEN 4.2.1 upgrade instructions*
- *AEN 4.2.0 upgrade instructions*
- *AEN 4.1.3 upgrade instructions*
- *AEN 4.1.2 upgrade instructions*
- *AEN 4.1.1 upgrade instructions.*
- *AEN 4.1.0 upgrade instructions.*
- *AEN 4.0.0 upgrade instructions.*

For upgrades from versions before those listed above, please contact your enterprise support representative.

NOTE: Named Service Account functionality is available with AEN 4.0.0+ for new installations only. It is not available for upgraded installations. Contact your enterprise support representative for more information.

An AEN platform update requires that each instance of the 3 node types be upgraded individually:

- AEN Server
- AEN Gateway
- AEN Compute

The upgrade process requires that all AEN service instances be stopped, upgraded, and then restarted.

NOTE: Any commands that call for the root user can also be done using `sudo`.

If you encounter any difficulty during the upgrade process, see [Troubleshooting](#) which provides guidance on:

- processes
- configuration files
- log files
- ports

If you are unable to resolve an installation or upgrade problem, please contact your enterprise support representative.

### Before you upgrade

CAUTION: Make a tested backup of your installation before starting the upgrade. Upgrading to a higher version of AEN is not reversible. Any errors during the upgrade procedure may result in partial or complete data loss and require restoring data from backups.

CAUTION: Terminate all AEN applications and stop all projects before starting the upgrade process.

Before upgrading each service on each host:

1. Suspend the services on each of the nodes:

```
sudo service wakari-server stop
sudo service wakari-gateway stop
sudo service wakari-compute stop
```

2. Set the AEN Functional ID (“NFI”) and AEN Functional Group (“NFG”) to the NFI and NFG of the current installation:

```
export AEN_SRVC_ACCT="wakari"
export AEN_SRVC_GRP="wakari"
```

NOTE: The default NFI is `wakari`, but `aen_admin` or any other name may be used instead.

For more information on NFI and NFG, see the [installation instructions](#).

3. Install `wget`:

```
yum install wget
```

## Upgrading the AEN server node

NOTE: If you are using LDAP-based authentication, back up the `/opt/wakari/wakari-server/etc/wakari/wk-server-config.json` configuration file. After the server has been upgraded, copy that file back into the same location as before the upgrade.

Complete the following steps on the server host:

1. Stop the Elasticsearch service:

```
sudo service elasticsearch stop
```

2. Remove any previous index:

```
sudo rm -rf /var/lib/elasticsearch/*
```

NOTE: You can choose to keep the old index, but if you detect any issues with the search capabilities after the upgrade, you will need to run the following to start with a clean index:

```
sudo service wakari-server stop
sudo service elasticsearch stop
sudo rm -rf /var/lib/elasticsearch/*
sudo service elasticsearch start
sudo service wakari-server start
```

3. Upgrade the server:

```
pushd /tmp
wget http://j.mp/aen-server-update-4_3_0

sudo -E -u $AEN_SRVC_ACCT /opt/wakari/miniconda/bin/conda install \
    -p /opt/wakari/wakari-server \
    --file aen-server-update-4_3_0

sudo -E -u $AEN_SRVC_ACCT /opt/wakari/miniconda/bin/conda install \
    -p /opt/wakari/wakari-server \
    --no-deps \
    wakari-enterprise-server-conf-update=2.0.10

popd
```

4. Start Elasticsearch:

```
sudo service elasticsearch start
```

Or, if you do not want to use the search features, edit your server's `/opt/wakari/wakari-server/etc/wakari/config.json` file by adding the line `"SEARCH_ENABLED": false`.

5. Restart the *NGINX* server:

AEN server version `>= 4.1.3` uses Unix sockets for communication with NGINX. Restart NGINX to load this new configuration:

```
sudo service nginx restart
```

Alternatively, you can restart NGINX with:

```
sudo nginx -s stop
sudo nginx
```

6. Start the server:

```
sudo service wakari-server start
```

7. Check that the server is running properly:

```
sudo service wakari-server status
```

8. If you see NGINX errors, please check the configuration at `/opt/wakari/wakari-server/etc/nginx/conf.d/www.enterprise.conf:18`.
9. Connect to AEN server using your web browser with the correct protocol (http or https), hostname and port number.

## Upgrading the AEN gateway node

Complete the following steps on each gateway host:

1. Upgrade the gateway:

```
pushd /tmp
wget http://j.mp/aen-gateway-update-4_3_0

sudo -E -u $AEN_SRVC_ACCT /opt/wakari/miniconda/bin/conda install \
    -p /opt/wakari/wakari-gateway \
    --file aen-gateway-update-4_3_0

sudo -E -u $AEN_SRVC_ACCT /opt/wakari/miniconda/bin/conda install \
    -p /opt/wakari/wakari-gateway \
    --no-deps \
    wakari-enterprise-gateway-conf-update=2.0.10

popd
```

2. Start the gateway:

```
sudo service wakari-gateway start
```

3. Check that the gateway is running properly:

```
sudo service wakari-gateway status
```

4. Connect to the gateway using your web browser with the correct http/https, hostname and port number.

## Upgrading AEN compute nodes

Complete the following steps on each host where an AEN compute service is running:

1. Check for any `wakari-indexer` processes running:

```
ps aux | grep wakari-indexer
```

NOTE: If you stopped all the projects, you will not see any `wakari-indexer` processes running.

Terminate any remaining `wakari-indexer` processes:

```
sudo killall wakari-indexer
```



NOTE: The processes killed with `killall` are run by the `$AEN_SRVC_ACCT` user, so they can be killed as root with `sudo killall` or killed as the `$AEN_SRVC_ACCT` user with `sudo -u $AEN_SRVC_ACCT killall`. Example commands show the `sudo killall` option.

2. Check for any AEN applications processes running—Workbench, Viewer, Terminal or Notebook:

```
ps aux | grep wk-app-gateone
ps aux | grep wk-app-workbench
ps aux | grep wk-app-viewer
ps aux | grep wk-app-terminal
ps aux | grep jupyter-notebook
```

NOTE: If you stopped all the projects, you will not see any AEN app processes running.

Terminate any remaining AEN application processes by running one or more of the following:

```
sudo killall wk-app-gateone
sudo killall wk-app-workbench
sudo killall wk-app-viewer
sudo killall wk-app-terminal
sudo killall jupyter-notebook
```

3. Verify the contents of `/opt/wakari/anaconda/.condarc`. Modify it to contain the following entries, and possibly others if you customized the `.condarc` file.

NOTE: Modify the file as the `AEN_SRVC_ACCT` user (or be sure to keep the same ownership).

```
channels:
- https://conda.anaconda.org/t/<TOKEN>/anaconda-nb-extensions
- r
- https://conda.anaconda.org/wakari
- defaults

create_default_packages:
- anaconda-client
- ipykernel
```

NOTE: Contact your enterprise support representative to get your token for the Anaconda channel referenced above. Replace `<TOKEN>` with the actual token from your enterprise support representative.

4. Upgrade *Anaconda* in the root environment:

```
pushd /tmp
wget http://j.mp/aen-anaconda-update-4_3_0

sudo -E -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda install \
    -p /opt/wakari/anaconda \
    --file aen-anaconda-update-4_3_0

popd
```

5. Upgrade each compute service:

```
pushd /tmp
wget http://j.mp/aen-compute-update-4_3_0

sudo -E -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda install \
    -p /opt/wakari/wakari-compute \
    --file aen-compute-update-4_3_0
```

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```
sudo -E -u $AEN_SRV_CCT /opt/wakari/anaconda/bin/conda install \
    --no-deps \
    -p /opt/wakari/wakari-compute \
    wakari-enterprise-compute-conf-update=2.0.14
popd
```

NOTE: When upgrading the wakari-compute environment, you may see ImportError warnings with some nbextensions. As long as the Validating message is OK, the ImportError warnings are harmless—a consequence of the post-link presence on those packages.

6. Initialize the root environment to prime the package cache:

```
sudo -E -u $AEN_SRV_CCT /opt/wakari/anaconda/bin/conda create \
    -p /opt/wakari/testenv \
    --clone root
```

7. Test the offline cloning step:

```
sudo -E -u $AEN_SRV_CCT /opt/wakari/anaconda/bin/conda create \
    -p /opt/wakari/testenvoffline \
    --clone root --offline
```

8. Remove the test environments:

```
sudo rm -rf /opt/wakari/testenv
sudo rm -rf /opt/wakari/testenvoffline
```

9. Install necessary dependencies:

NOTE: Skip this step if you already have these dependencies installed from previous installations.

```
sudo yum groupinstall "X Window System" -y
sudo yum install git -y
```

NOTE: If you don't want to install the whole X Window System, you must install the following packages to have R plotting support:

```
sudo yum install -y libXrender libXext libXdmp libSM libICE libXt \
    dejavu-sans-fonts dejavu-serif-fonts dejavu-fonts-common \
    fontpackages-filesystem
```

10. Start the compute service:

```
sudo service wakari-compute start
```

11. Verify the compute service is running properly:

```
sudo service wakari-compute status
```

12. Restart the AEN Server with:

```
sudo service wakari-server restart
```

13. Repeat this upgrade procedure for all compute nodes in your Data Center.

## After upgrading

1. Restart the projects and start using AEN applications.
2. If you have a *customized default environment*, you may choose to upgrade it depending on the needs of your users.

Upgrade the customized default environment at `/opt/wakari/anaconda/envs/default` with the `$AEN_SRVC_ACCT` user:

```
pushd /tmp
wget http://j.mp/aen-anaconda-update-4_3_0

sudo -E -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda install \
    -p /opt/wakari/anaconda/envs/default \
    --file aen-anaconda-update-4_3_0

popd
```

To upgrade the customized default environments for every user and every project at `/projects/<USER>/<PROJECT>/envs/default`, run these commands for **every** user as that user:

```
pushd /tmp
wget http://j.mp/aen-anaconda-update-4_3_0

sudo -E -u <USER> /opt/wakari/anaconda/bin/conda install \
    -p /projects/<USER>/<PROJECT>/envs/default \
    --file aen-anaconda-update-4_3_0

popd
```

NOTE: Replace `<USER>` with the user's name. Replace `<PROJECT>` with the project name.

NOTE: Upgrading the default environment at `/opt/wakari/anaconda/envs/default` does NOT automatically upgrade the default environment in the users pre-existing projects. For pre-existing projects, the upgrade, if requested, should be done on a per-user basis.

NOTE: These commands update packages listed in `aen-anaconda-update-4_3_0` and do not update any other package.

3. If you did not stop all your projects before upgrading, then the first time you start an application you will see an error page requesting that you restart the application.
4. Restart the application to complete the upgrade.
5. If you still see old applications or icons after restart, reload the page to reset the browser cache.

## Uninstalling AEN

Each AEN node must be uninstalled separately.

- *Uninstalling a server node*
- *Uninstalling a gateway node*
- *Uninstalling a compute node*
- *OPTIONAL: Removing projects from compute nodes*

Begin by setting the AEN Functional ID (NFI). The NFI is the username of the AEN Service Account which is used to run all AEN services and is also the username of the AEN Admin account. The NFI may be any name. The default NFI is `wakari`. The NFI is also often set to `aen_admin`. The NFI (and AEN Functional Group or NFG) are described in [the installation instructions](#).

Set the NFI with this command:

```
export AEN_SRVC_ACCT="aen_admin"
```

Replace the name `aen_admin` with the NFI that was set in your installation of Anaconda Enterprise Notebooks.

### Uninstalling a server node

To remove a server node, run the following commands as root or sudo on the server node's host system:

1. Stop the server processes:

```
service wakari-server stop
```

2. Stop MongoDB:

```
service mongod stop
```

3. Remove AEN server software, AEN database files and NGINX configuration:

```
rm -Rf /opt/wakari/wakari-server
rm -Rf /opt/wakari/miniconda
rm -Rf /var/lib/mongo/wakari*
rm -Rf /etc/nginx/conf.d/www.enterprise.conf
```

NOTE: Remove `/etc/nginx/conf.d/www.enterprise.https.conf` if SSL is enabled on the Server node.

4. Restart MongoDB and NGINX:

```
service mongod restart
service nginx restart
```

5. Check for any outstanding server processes and stop them:

```
ps -ef | grep -e wakari-server -e wk-server
```

6. Remove the AEN Service Account:

```
userdel $AEN_SRVC_ACCT
```

7. Check for and remove any references to “aen” or “wakari” from the root user's `.condarc` file:

```
grep -i aen ~/.condarc
grep -i wakari ~/.condarc
```

### Uninstalling a gateway node

To uninstall a gateway node, run the following commands as root or sudo on the gateway host system:

1. Stop the gateway processes:

```
service wakari-gateway stop
```

2. Remove gateway software:

```
rm -Rf /opt/wakari/wakari-gateway
```

3. Check for any outstanding gateway processes and stop them:

```
ps -ef | grep -e wakari-gateway -e wk-gateway
```

4. Remove the AEN Service Account:

```
userdel $AEN_SRVC_ACCT
```

5. Check for and remove any references to “aen” or “wakari” from the root user’s `.condarc` file:

```
grep -i aen ~/.condarc  
grep -i wakari ~/.condarc
```

## Uninstalling a compute node

To remove a compute node, run the following commands as root or sudo on each compute node host system:

1. Stop the compute processes:

```
service wakari-compute stop
```

2. Remove the compute software:

```
rm -Rf /opt/wakari/wakari-compute  
rm -Rf /opt/wakari/miniconda  
rm -Rf /opt/wakari/anaconda
```

3. Check for any outstanding compute processes and stop them:

```
ps -ef | grep -e wakari-compute -e wk-compute
```

4. Remove the AEN Service Account:

```
userdel $AEN_SRVC_ACCT
```

5. Check for and remove any references to “aen” or “wakari” from the root user’s `.condarc` file:

```
grep -i aen ~/.condarc  
grep -i wakari ~/.condarc
```

## OPTIONAL: Removing projects from compute nodes

**CAUTION:** This is an extreme measure and is not necessary in most instances. We recommend you create and verify a backup before doing this or any other file removal.

To remove all AEN projects from all of your compute nodes:

```
rm -Rf /projects
```

This is a step-by-step guide to installing an Anaconda Enterprise Notebooks system comprised of a front-end server, a gateway and compute machines.

If you have any questions about these instructions or you encounter any issues while installing AEN, please contact your sales representative or Priority Support team.

When you have completed the installation process, review the *optional configuration tasks* to see if any are appropriate for your system.

### Distributed install

In a distributed install the server and gateway run on separate hosts.

### Single-box install

In a single-box install, both the server and the gateway need separate external ports since they are independent services that are running on the same host in the single-box installation.

Both port 80 and port 8089 must be open on the firewall for a single-box install.

The compute node only receives connections from the gateway and server nodes and typically runs on port 80 or port 443.

## User management

### Adding or removing an administrative user

An administrator can make any other user an administrator—or remove their administrator permissions—by using administrator commands in the Terminal application.

A user can also be designated as a superuser or as staff, giving them greater administrative privileges within the system.

### Designating a user as an administrator/superuser

To designate a user as an administrator and superuser:

```
/opt/wakari/wakari-server/bin/wk-server-admin superuser --add <username>
```

NOTE: Replace <username> with the actual username.

EXAMPLE: To give administrative privileges to the user named “jsmith” and set them as a superuser, run:

```
/opt/wakari/wakari-server/bin/wk-server-admin superuser --add jsmith
```

### Removing an administrator/superuser

To remove a user’s administrative privileges:

```
/opt/wakari/wakari-server/bin/wk-server-admin superuser --remove <username>
```

NOTE: Replace <username> with the actual username.

## Allowing and restricting new user registration

When Open Registration is enabled, anyone who has access to the URL of your AEN server can create their own account.

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select Accounts.

The screenshot shows the Admin Settings page. On the left, there are two sidebars. The top sidebar is titled 'Staff' and contains links for 'Daily Report', 'Password Reset', 'Notification', and 'Exceptions'. The bottom sidebar is titled 'Site Admin' and contains links for 'General' and 'Accounts'. The main content area is titled 'Cloud Registration' and contains a checkbox labeled 'Open Registration' with the text 'Allow new user signups' below it. The checkbox is checked. Below the checkbox is a green 'Update' button.

3. To open user registration, select the Open Registration checkbox. To close registration, clear the checkbox.
4. Click the Update button.

## Resetting a user password

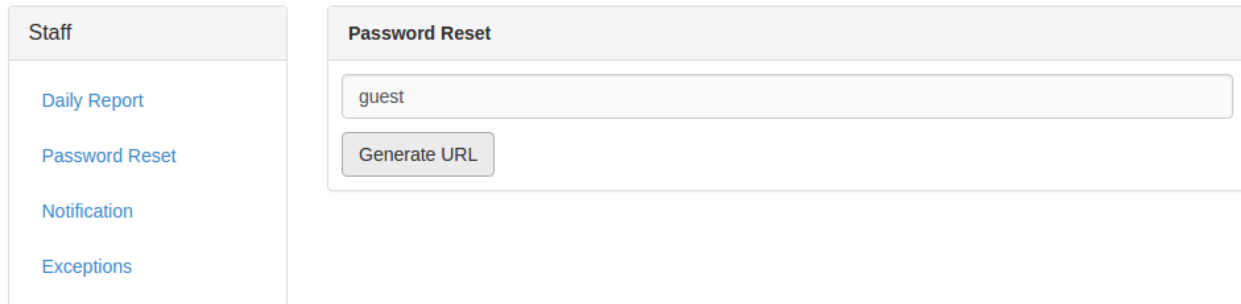
1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Staff** menu, select Password Reset:

3. Enter the username of the user whose password needs to be reset.
4. Click the Generate URL button.

A password reset link is generated that you can email to the user.

Alternatively you may use the command line interface:

Anaconda Enterprise Notebooks settings accessible only by the system administrator.



The screenshot shows a web interface for managing staff. On the left is a sidebar titled 'Staff' with links to 'Daily Report', 'Password Reset', 'Notification', and 'Exceptions'. The 'Password Reset' link is selected. The main content area is titled 'Password Reset' and contains a text input field with the value 'guest' and a button labeled 'Generate URL'.

1. Use ssh to log into the server as root.
2. Run:

```
/opt/wakari/wakari-server/bin/wk-server-admin reset-password -u SOME_USER -p SOME_
↪PASSWORD
```

NOTE: Replace SOME\_USER with the username and SOME\_PASSWORD with the password.

3. Log into AEN as the user.

## Managing permissions

This page explains the admin commands used to manage user permissions.

### Checking file ownership

To verify that all files in the `/opt/wakari/anaconda` directory are owned by the `wakari` user or group:

```
root@server # find /opt/wakari/anaconda \! -user wakari -print
root@server # find /opt/wakari/anaconda \! -group wakari -print
```

### Fixing file ownership settings

To fix the ownership settings of any files that are listed in the output:

```
chown -R wakari:wakari /opt/wakari/anaconda
```

### Setting a file owner and permissions

To set a file owner and set its permissions:

```
chown wakari:wakari /opt/wakari/wakari-server/bin/wk-*
chmod 700 /opt/wakari/wakari-server/bin/wk-*
```



## Verifying that POSIX ACLs are enabled

The `acl` option must be enabled on the file system that contains the project root directory.

NOTE: By default, the project root directory is `/projects`.

To determine the project root directory where a custom `projectRoot` is configured:

```
root@compute # grep projectRoot /opt/wakari/wakari-compute/etc/wakari/config.json
```

The mount options or default options listed by `tune2fs` should indicate that the `acl` option is enabled.

EXAMPLE:

```
root@compute # fs=`df /projects | tail -1 | cut -d " " -f 1`
root@compute # mount | grep $fs
/dev/vda on / type ext4 (rw)
root@compute # tune2fs -l $fs | grep options
Default mount options:    user_xattr acl
```

## Viewing a list of users

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select Users:

Staff

[Daily Report](#)
[Password Reset](#)
[Notification](#)
[Exceptions](#)

Site Admin

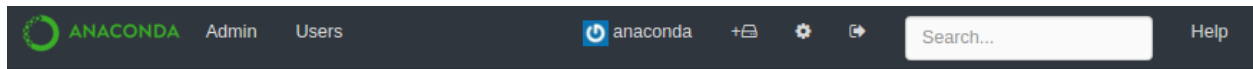
[General](#)
[Accounts](#)
[Users](#)

Users		
Username	Projects	Last Seen
<a href="#">aen_admin</a>	6	Sep 25, 2017 10:05:58 CDT

The Users section lists the all users who are signed up, the number of projects they have created and the last time they logged on to AEN.

### Viewing a list of currently active users

In the AEN navigation bar, click Users.



## Users

List of currently active users in the system.


 anaconda
 andrew
 bokeh
 christine
 guest
 hubert
 ivan
 paula
 simon
 tanya
 wakari

Click a username to open the user's profile page.


### Viewing a user profile




A user's profile page includes a summary of the projects created by that user and a list of projects on which the user is a team member.

1. In the AEN navigation bar, click Users to see a list of users who are currently logged into the system.
2. On the Users page, click the username of the user whose profile page you want to view.

 ANACONDA

[Admin](#) [Users](#)

 anaconda

[Help](#)

# Users

List of currently active users in the system.

 anaconda
 andrew
 bokeh
 christine
 guest
 hubert
 ivan
 paula
 simon
 tanya
 wakari

## Sending a system message

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Staff** menu, select Notification:

The screenshot shows the 'Notification Settings' page. On the left is a navigation sidebar with three main sections: 'Staff' (containing links for Daily Report, Password Reset, Notification, and Exceptions), 'Site Admin' (containing links for General, Accounts, Users, Security Log, Data Centers, Task Queue, and License), and 'Providers' (containing Enterprise Resources). The main content area is titled 'Notification Settings' and contains three radio button options: 'Off' (selected), 'SES - Amazon Simple Email Service', and 'SMTP Email Server'. The 'Off' option has a subtext 'No email notification will be sent'. The 'SES' option has a subtext 'This requires a .boto file in the wakari home dir'. The 'SMTP Email Server' option is currently selected, and its settings are displayed in a light gray box titled 'SMTP Settings'. These settings include fields for 'SMTP Hostname', 'SMTP Username (optional)', 'SMTP Password (optional)', and 'SMTP From Address (optional)'. A green 'Update' button is located at the bottom left of the settings box.

**Staff**  
Daily Report  
Password Reset  
Notification  
Exceptions

**Site Admin**  
General  
Accounts  
Users  
Security Log  
Data Centers  
Task Queue  
License

**Providers**  
Enterprise Resources

**Notification Settings**  
☒ **Off**  
No email notification will be sent  
  
☐ **SES - Amazon Simple Email Service**  
This requires a .boto file in the wakari home dir  
  
☐ **SMTP Email Server**  
  
**SMTP Settings**  
SMTP Hostname  
  
SMTP Username (optional)  
  
SMTP Password (optional)  
  
SMTP From Address (optional)

The Notification Settings section allows you to create a system message that can be relayed to users.

By default, notifications are off.

3. To turn on email notifications, select the radio button for the type of email service to use:
  - SES to use Amazon Simple Email Service (SES).
  - SMTP Email Server.

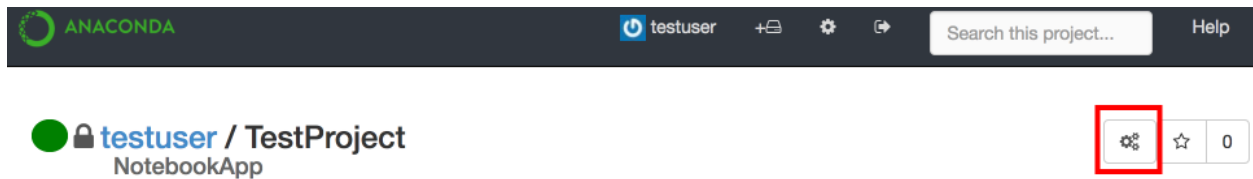
4. If you select SMTP Email Server, complete the SMTP Settings.

NOTE: If you get an error message after changing the SMTP settings, you may need to restart the server.

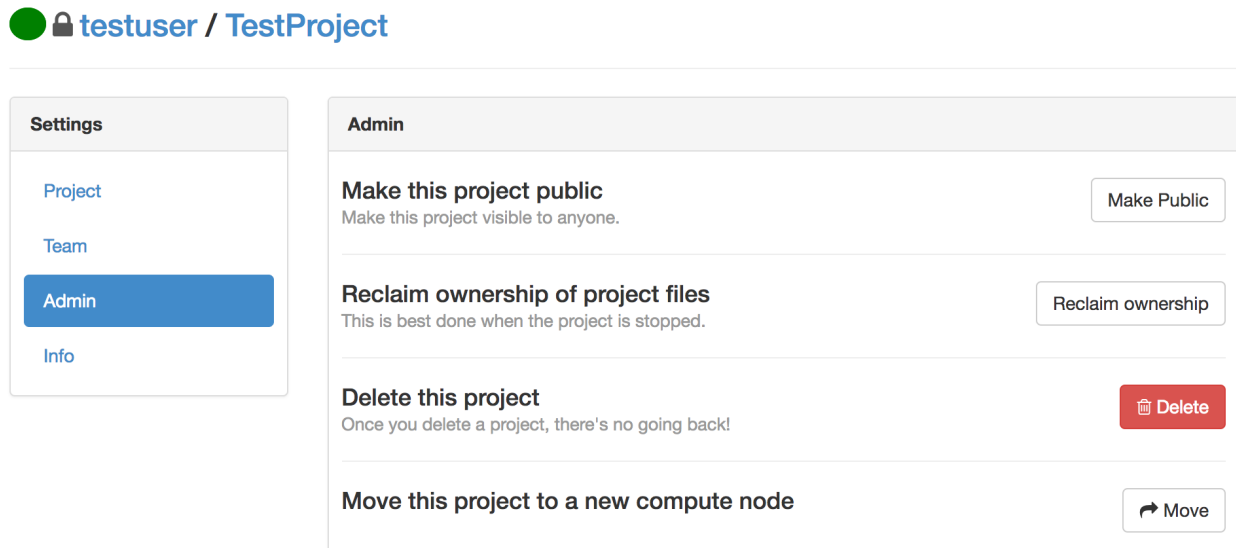
## Moving a project to another compute node

If you have multiple compute nodes available and want to move a project from one to another, the project must exist on both nodes.

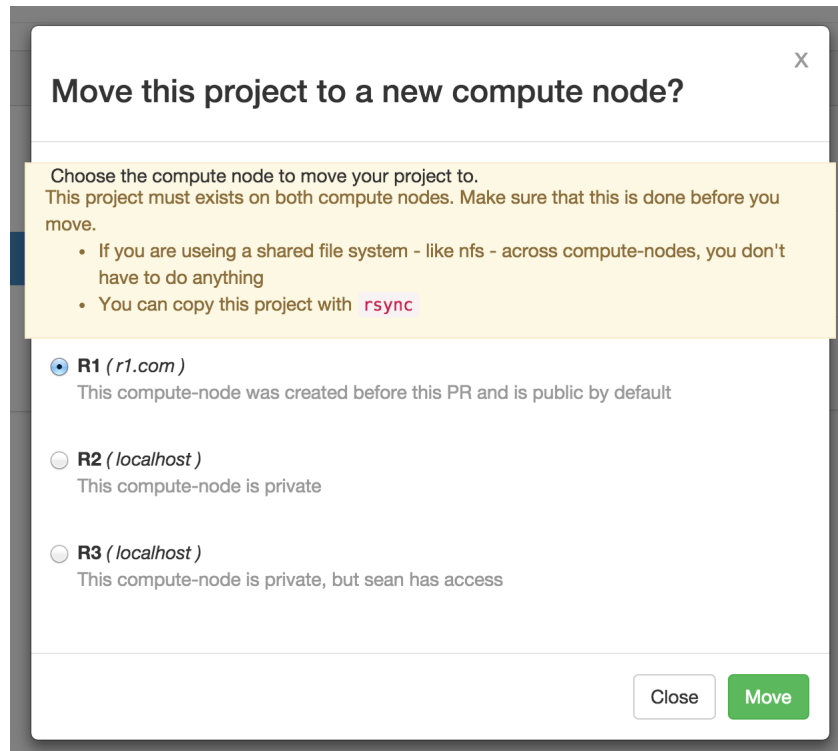
1. Verify that the project has been created on both compute nodes. You can use `rsync` for this job unless you have a shared file system like `nfs`.
2. On the project home page, click the Project Settings icon to open the Project Settings page.



3. In the **Settings** menu, select Admin.



4. Click the Move button.
5. In the move dialog box, click to choose the compute node destination, and click the Move button.



## Deleting a user

To remove a user from the AEN database:

```
/opt/wakari/wakari-server/bin/wk-server-admin remove-user <username>
```

NOTE: Replace `<username>` with the actual username.

NOTE: Changing the owner of a project requires that both the previous owner and the new owner are still AEN users. Before deleting a user, *change the owner* of that user's projects.

## Deleting a project

To remove a project from the AEN database:

```
/opt/wakari/wakari-server/bin/wk-server-admin remove-project <username> <projectname>
```

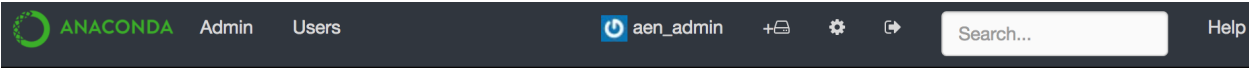
NOTE: Replace `<username>` with the actual username and `<projectname>` with the actual project name you are removing.

## System management

### Opening the Admin dashboard

If you have administrator privileges, you see two additional links in the AEN navigation bar—Admin and Users:

To open the Admin dashboard, click the Admin link.



# Admin Settings

Anaconda Enterprise Notebooks settings accessible only by the system administrator.

Staff
<a href="#">Daily Report</a>
<a href="#">Password Reset</a>
<a href="#">Notification</a>
<a href="#">Exceptions</a>

Site Admin
<a href="#">General</a>
<a href="#">Accounts</a>
<a href="#">Users</a>
<a href="#">Monitor</a>
<a href="#">Security Log</a>

## Backing up and restoring AEN

- *Document purpose*
- *Important notes*
- *Server component steps*
  - *Backup*
    - \* *Mongo database*
    - \* *AEN Server config files (including License file)*
    - \* *Nginx config (if needed)*
    - \* *SSL certificates (if needed)*
  - *Restore*
    - \* *Reinstall AEN-Server*
    - \* *Restore Mongo database*
    - \* *AEN Server config files (including License file)*
    - \* *Nginx config (if needed)*
    - \* *SSL certificates (if needed)*
    - \* *Restart server*
- *Gateway component steps*
  - *Backup*
    - \* *Config files*
    - \* *Custom .condarc file (if needed)*
    - \* *SSL certificates (if needed)*
  - *Restore*
    - \* *Reinstall AEN-Gateway*
    - \* *Config files*
    - \* *Custom .condarc file (if needed)*
    - \* *SSL certificates (if needed)*
    - \* *Restart gateway*
- *Compute component steps*
  - *Backup*
    - \* *Config files*
    - \* *Custom Changes (rare)*
    - \* *Create user list*



- \* *Project files*
- \* *Full Anaconda (option 1)*
- \* *Partial Anaconda (option 2)*
- *Restore*
  - \* *Reinstall AEN-Compute*
  - \* *Config files*
  - \* *Custom changes (rare)*
  - \* *Create users*
  - \* *Project files*
  - \* *Full Anaconda (option 1)*
  - \* *Partial Anaconda (option 2)*
  - \* *Custom environments (if needed)*
  - \* *Restart compute node*

## Document purpose

This document lays out the steps to backup and restore Anaconda Enterprise Notebooks (AEN) for Disaster Recovery. It is not intended to provide High Availability. Each of the components (Server, Gateway and Compute) has its own instructions and each may be done individually as needed. The steps primarily involve creating tar files of important configuration files and data.

This document is written for a system administrator who is comfortable with basic Linux command line navigation and usage.

To migrate to a new cluster, use these backup and restore instructions to back up the system from the old cluster and restore it to the new cluster.

## Important notes

Review the [Concepts](#) page to become familiar with the different components and how they work together.

Root or sudo access is required for some commands.

**CAUTION:** All commands **MUST** be run by \$AEN\_SRVC\_ACCT (the account used to run AEN) except for those commands explicitly indicated to run as root or sudo. If the commands are not run by the correct user, the installation will not work, and a full uninstallation and reinstallation will be required!

These instructions assume that the fully qualified domain name (FQDN) has not changed for any of the component nodes. If any of the FQDNs are not the same, additional steps will be needed.

## Server component steps

### Backup

### Mongo database

This will create a single tar file called `aen_mongo_backup.tar` that includes only the database named “wakari” that is used by AEN. It also generates a log of the database backup.

NOTE: These commands must be run by `$AEN_SRVC_ACCT`.

```
mongodump -db wakari -o aen_main >> mongo_backup.log
tar -cvf aen_mongo_backup.tar aen_main
```

### AEN Server config files (including License file)

Create a tar file of all of the configuration files, including any license files.

NOTE: This command must be run by `$AEN_SRVC_ACCT`.

```
tar -cvf aen_server_config.tar -C /opt/wakari/ wakari-server/etc/wakari/
```

### Nginx config (if needed)

Make a copy of the nginx configuration file if it has been customized. The default configuration for the AEN server is a symlink.

NOTE: This command must be run by `$AEN_SRVC_ACCT`.

```
/etc/nginx/conf.d/www.enterprise.conf -> /opt/wakari/wakari-server/etc/nginx/conf.d/
↪ www.enterprise.conf
```

### SSL certificates (if needed)

Make a copy of the SSL certificates files (certfiles) for the server, including the key file, and a copy of the certfile for the gateway, which is needed for verification if using self-signed or private CA signed certs.

## Restore

### Reinstall AEN-Server

See *the instructions for installing the current version of AEN-Server*.

It is not necessary to upload the license, because it will be restored with the config files.

NOTE: The new installation will generate a new password for the local `$AEN_SRVC_ACCT` account.

### Restore Mongo database

This assumes that mongo was reinstalled as part of the reinstallation of the server component. Untar the mongo database and restore it.

NOTE: These commands must be run by `$AEN_SRVC_ACCT`.

```
tar -xvf aen_mongo_backup.tar
mongorestore --drop aen_main
```

NOTE: The `--drop` option resets the `$AEN_SRVC_ACCT` user password and restores the database to the exact state it was in at the time of backup. Please see the [MongoDB documentation](#) for more information about mongorestore options for Mongo 2.6.

NOTE: AEN uses Mongo 2.6 by default. If you are using a different version, consult the documentation for your version.

### AEN Server config files (including License file)

Untar the tar file of all of the configuration files, including any license files.

NOTE: This command must be run by `$AEN_SRVC_ACCT`.

```
tar -xvf aen_server_config.tar -C /opt/wakari/
```

Make sure the files are in `/opt/wakari/wakari-server/etc/wakari/` and are owned by the `$AEN_SRVC_ACCT`.

### Nginx config (if needed)

Make sure any modifications to the nginx configuration are either in `/etc/nginx/conf.d` or in `/opt/wakari/wakari-server/etc/nginx/conf.d/` with a proper symlink.

NOTE: This command must be run by `$AEN_SRVC_ACCT`.

```
/etc/nginx/conf.d/www.enterprise.conf -> /opt/wakari/wakari-server/etc/nginx/conf.d/
↪www.enterprise.conf
```

### SSL certificates (if needed)

Move any SSL certificate files to the locations indicated in the config files.

### Restart server

Restart the server application.

NOTE: This command must be run as root or with `sudo`.

```
service wakari-server restart
```

## Gateway component steps

### Backup

### Config files

Create a tar file of all of the configuration files.

NOTE: This command must be run by \$AEN\_SRVC\_ACCT.

```
tar -cvf aen_gateway_config.tar -C /opt/wakari/ wakari-gateway/etc/wakari/
```

### Custom .condarc file (if needed)

Make a copy of any /opt/wakari/miniconda/.condarc if it has been modified.

### SSL certificates (if needed)

Make a copy of SSL certificate files for the gateway (including the key file) and the certfile for the server (needed for verification if using self-signed or private CA signed certs).

### Restore

### Reinstall AEN-Gateway

### Setting variables and changing permissions

NOTE: These commands must be run by \$AEN\_SRVC\_ACCT.

Run:

```
export AEN_SERVER=<FQDN HOSTNAME OR IP ADDRESS> # Use the real FQDN
export AEN_GATEWAY_PORT=8089
export AEN_GATEWAY=<FQDN HOSTNAME OR IP ADDRESS> # will be needed shortly
chmod a+x aen-*.sh # Set installer to be executable
```

NOTE: Change <FQDN HOSTNAME OR IP ADDRESS> to the actual fully qualified domain hostname or IP address.

NOTE: You must perform the entire procedure before closing the terminal to ensure the variable export persists. If the terminal is closed before successful installation, export the variables to continue with the installation.

### Running the AEN gateway installer

Run:

```
sudo -E ./aen-gateway-4.3.0-Linux-x86_64.sh -w $AEN_SERVER
<license text>
...
...

PREFIX=/opt/wakari/wakari-gateway
Logging to /tmp/wakari_gateway.log
...
...
Checking server name
Please restart the Gateway after running the following command
to connect this Gateway to the AEN Server
...
```

## Config files

Untar the configuration files.

NOTE: This command must be run by \$AEN\_SRVC\_ACCT.

```
tar -xvf aen_gateway_config.tar -C /opt/wakari
```

Verify that the files are in `/opt/wakari/wakari-gateway/etc/wakari/` and are owned by the \$AEN\_SRVC\_ACCT.

## Custom .condarc file (if needed)

Move the custom .condarc file to `/opt/wakari/miniconda/.condarc`.

## SSL certificates (if needed)

Move any SSL certificate files to the locations indicated in the config files.

## Restart gateway

Restart the gateway application.

NOTE: This command must be run as root or with sudo.

```
service wakari-gateway restart
```

## Compute component steps

### Backup

### Config files

Create a tar file of all of the configuration files.

NOTE: This command must be run by \$AEN\_SRVC\_ACCT.

```
tar -cvf aen_compute_config.tar -C /opt/wakari/ wakari-compute/etc/wakari
```

## Custom Changes (rare)

Manually backup any custom changes that were applied to the code. One change might be additional files in the skeleton folder:

```
/opt/wakari/wakari-compute/lib/node_modules/wakari-compute-launcher/skeleton
```

### Create user list

AEN uses POSIX access control lists (ACLs) for project sharing, so the backup must preserve the ACL information. This is done with a script that creates a file named `users.lst` containing a list of all users that have access to projects on a given compute node. Download and run the script.

NOTE: These commands must be run by `$AEN_SRVC_ACCT`.

```
wget https://s3.amazonaws.com/continuum-airgap/misc/wk-compute-get-acl-users.py
chmod 755 wk-compute-get-acl-users.py
./wk-compute-get-acl-users.py
```

### Project files

Create a tar of the projects directory with ACLs enabled. The default projects base location is `/projects`.

NOTE: This command must be run as root or with `sudo`.

```
tar --acls -cpvf projects.tar -C <projects base location>/*
```

### Full Anaconda (option 1)

If any changes have been made to the default Anaconda installation (additional packages installed or packages removed), it is necessary to backup the entire Anaconda installation.

NOTE: This command must be run by `$AEN_SRVC_ACCT`.

```
tar -cvf aen_anaconda.tar -C /opt/wakari/anaconda/*
```

If no changes have been made to the default installation of Anaconda, you may just backup the `.condarc` file and any custom environments.

### Partial Anaconda (option 2)

#### Custom `.condarc` file

Make a copy of `/opt/wakari/anaconda/.condarc`.

#### Custom environments (if needed)

Create a tar file of any custom shared environments.

NOTE: This command must be run by `$AEN_SRVC_ACCT`.

```
tar -cvf aen_compute_envs.tar -C /opt/wakari/ anaconda/envs
```

NOTE: If no custom shared environments have been created, the `envs` folder will not be present.

## Restore

### Reinstall AEN-Compute

#### Setting variables and changing permissions

NOTE: These commands must be run by \$AEN\_SRVC\_ACCT.

Run:

```
export AEN_SERVER=<FQDN HOSTNAME OR IP ADDRESS> # Use the real FQDN
chmod a+x aen-*.sh # Set installer to be executable
```

NOTE: Change <FQDN HOSTNAME OR IP ADDRESS> to the actual fully qualified domain hostname or IP address.

NOTE: You must perform the entire procedure before closing the terminal, to ensure the variable export persists.

#### Running the AEN compute installer

Run:

```
sudo -E ./aen-compute-4.3.0-Linux-x86_64.sh -w $AEN_SERVER
...
...
PREFIX=/opt/wakari/wakari-compute
Logging to /tmp/wakari_compute.log
Checking server name
...
...
Initial clone of root environment...
Starting Wakari daemons...
installation finished.
Do you wish the installer to prepend the wakari-compute install location
to PATH in your /root/.bashrc ? [yes|no]
[no] >>> yes
```

#### Config files

Untar the config files.

NOTE: This command must be run by \$AEN\_SRVC\_ACCT.

```
tar -xvf aen_compute_config.tar -C /opt/wakari
```

NOTE: Verify that they are located in /opt/wakari/wakari-compute/etc/wakari and are owned by the \$AEN\_SRVC\_ACCT.

#### Custom changes (rare)

Manually restore any custom changes you saved in the backup section. If there are changes in the skeleton directory, these files must be world readable or projects will refuse to start.

### Create users

NOTE: Only create users with these instructions if your Linux machine is not bound to LDAP.

In order for the ACLs to be set properly on restore, all users that have permissions to the files must be available on the machine. Ask your system administrator for the proper way to do this for your system, such as using the “useradd” tool. A list of users that are needed was created in the backup process as a file named `users.lst`.

A process similar to the following `useradd` example will be suitable for most Linux systems.

NOTE: This command must be run by `$AEN_SRVC_ACCT`.

```
xargs -0 -n 1 useradd --user-group < users.lst
```

### Project files

Create the `projects` directory in the location specified in `projectRoot` in `wk-compute-launcher-config.json`.

NOTE: By default this directory is `/projects`.

Then untar the `projects` directory with ACLs.

NOTE: This command must be run as root or with `sudo`:

```
tar --acls -xpvf projects.tar -C <projects base location>
```

### Full Anaconda (option 1)

If you did a full backup of the full Anaconda installation, untar this file to `/opt/wakari/anaconda`.

NOTE: This command must be run by `$AEN_SRVC_ACCT`.

```
tar -xvf aen_anaconda.tar -C /opt/wakari
```

### Partial Anaconda (option 2)

Restore the custom `.condarc` file.

If you did a partial backup of the Anaconda installation, move the copy of the `.condarc` file to `/opt/wakari/anaconda/.condarc`.

### Custom environments (if needed)

Untar any custom environments that were created to `/opt/wakari/anaconda/envs`.

NOTE: This command must be run by `$AEN_SRVC_ACCT`.

```
tar -xvf aen_compute_envs.tar -C /opt/wakari
```



## Restart compute node

Restart the compute-launcher application.

NOTE: This command must be run as root or with sudo.

```
service wakari-compute restart
```

## Viewing a list of admin commands

A user who is promoted to administrator can access administrator commands to perform advanced administrator tasks.

NOTE: Utility files are owned by, and should only be executed by, the AEN user who owns the files.

To display a list of all administrator commands:

```
ls -al /opt/wakari/wakari-server/bin/wk-*
```

## Viewing help for admin commands

To view help information for command, run the command followed by `-h` or `--help`.

EXAMPLE: To view help for the `remove-user` command:

```
/opt/wakari/wakari-server/bin/wk-server-admin remove-user -h  
/opt/wakari/wakari-server/bin/wk-server-admin remove-project -h
```

## Running daily reports

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Staff** menu, select Daily Report:

The Report section displays the following:

- Users—The number of users and projects.
- New User Emails—If *open registration is enabled*, the user names and emails for new users.
- Actions—The actions—projects created, projects updated, user authentications and added users—that have occurred in during the selected time frame—today, yesterday, this week, or this month.

## Viewing system errors

When an error occurs, a red dot is displayed in the AEN navigation bar next to the Admin link. The red dot is removed when all exceptions are marked as “read.”

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Staff** menu, select Exceptions:

Staff

Daily Report

Password Reset

Notification

Exceptions

Site Admin

General

Accounts

Users

Monitor

Security Log

Data Centers

Task Queue

License

Providers

Enterprise Resources

Report

Today

Yesterday

This Week

This Month

From:

Sun Sep 24 15:09:03 2017

Until:

Mon Sep 25 15:09:03 2017

Date Range

1 day, 0:00:00

Users

	New	Total
Users	0	1
Projects	0	6

New User Emails

Username	Email
----------	-------

Actions

Count	Action
82	<a href="#">oauth.authenticate</a>

Staff

Daily Report

Password Reset

Notification

Exceptions

Site Admin

General

Accounts

Users

Security Log

Data Centers

Task Queue

License

Providers

Enterprise Resources

Exceptions

Mark all as read

☒ jinja2.exceptions.UndefinedError: 'wk\_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'

☐ jinja2.exceptions.UndefinedError: 'wk\_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'

☐ jinja2.exceptions.UndefinedError: 'wk\_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'

☐ jinja2.exceptions.UndefinedError: 'wk\_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'

☐ jinja2.exceptions.UndefinedError: 'wk\_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'

☐ jinja2.exceptions.UndefinedError: 'wk\_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'

☐ jinja2.exceptions.UndefinedError: 'wk\_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'

☐ jinja2.exceptions.UndefinedError: 'wk\_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'

☐ jinja2.exceptions.UndefinedError: 'wk\_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'

☐ elasticsearch.exceptions.ConnectionError:

☐ elasticsearch.exceptions.ConnectionError:

☐ elasticsearch.exceptions.ConnectionError:

☐ elasticsearch.exceptions.ConnectionError:

The Exceptions section lists all errors that have occurred while AEN is running.

3. To see the details of an error, click the radio button next to the error. This also marks the error as “read.”
4. To mark all errors as read without reviewing each one, click the Mark all as read button.

## Viewing security errors

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select Security Log:

Staff

Daily Report

Password Reset

Notification

Exceptions

Site Admin

General

Accounts

Users

Monitor

Security Log

View	Actor	Action	Date
	aen_admin	oauth.authenticate	Sep 25, 2017 09:46:09 CDT
	aen_admin	oauth.authenticate	Sep 25, 2017 09:39:17 CDT
	aen_admin	oauth.authenticate	Sep 25, 2017 09:22:04 CDT
	aen_admin	oauth.authenticate	Sep 25, 2017 09:10:31 CDT
	aen_admin	oauth.authenticate	Sep 25, 2017 08:45:50 CDT
	aen_admin	oauth.authenticate	Sep 25, 2017 08:43:12 CDT
	aen_admin	oauth.authenticate	Sep 25, 2017 08:10:30 CDT
	aen_admin	oauth.authenticate	Sep 25, 2017 08:09:38 CDT
	aen_admin	oauth.authenticate	Sep 24, 2017 23:52:06 CDT
	aen_admin	oauth.authenticate	Sep 24, 2017 23:51:58 CDT
	aen_admin	oauth.authenticate	Sep 24, 2017 23:51:58 CDT
	aen_admin	oauth.authenticate	Sep 24, 2017 23:51:58 CDT

The Security Log section lists all errors that have occurred that could potentially affect AEN security.

3. To view a user’s profile page, click their username in the Actor column.
4. To see the details of an error, click the Eye icon next to the error.

The error details are displayed:

5. To close the error details, click the Back link.

Public Profile

Account Settings

Security Log

Applications

oauth.authenticate

_id	59c907f03f94c30fe45ffb9e
action	oauth.authenticate
actor_id	59c069b1ae55d1b3fe9fa45e
actor_username	aen_admin
client_id	59c119cd3f94c30fe45ff5db
remote_addr	None
time	2017-09-25 13:43:12.479000+00:00
token_id	59c907f03f94c30fe45ffb9d

[← Back](#)

Managing data centers

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select Data Centers:

Staff

[Daily Report](#)

[Password Reset](#)

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Site Admin

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[Data Centers](#)

Data Centers

[Gateway](#) (ec2-52-90-133-17.compute-1.amazonaws.com:8089)

[+ Add DataCenter](#)

The Data Centers section displays current data center information.

## Adding a data center

1. Click the Add DataCenter button to display the the Register a datacenter form.
2. In the Name box, type a Name for the new data center:

**Data Centers / Register a datacenter**

**Name**

☐ Subdomain Routing  
☐ Https

**Base Domain Name**

**summary**

**Provider**

3. Select the Subdomain Routing and/or Https checkboxes.
4. In the Base Domain Name box, type the base domain name.
5. In the Summary box, type a description of the data center.
6. In the Provider list, select a provider.
7. Click the Submit button.

## Managing enterprise resources

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Providers** menu, select Enterprise Resources:

Staff

Daily Report

Password Reset

Notification

Exceptions

Site Admin

General

Accounts

Users

Monitor

Security Log

Data Centers

Task Queue

License

Providers

Enterprise Resources

Resources

Add Resource

Gateway

ec2-54-210-232-251.compute-1.amazonaws.com

remove

The Resources section lists your existing cloud and local resources.

### Adding a resource

1. Click the Add Resource button to open the new resource form.
2. Complete the form:

**Resources / new**

**Data Center**  
Gateway 59c119cd3f94c30fe45ff5db

**Name**  
Compute Node1

**URL**  
http://ec2-54-210-232-251.compute-1.amazonaws.com:5002

**Description**  
Configuring Compute Node

☒ **Public**  
Uncheck this if you want to control exactly who has access to this compute node

Add Resource

3. Click the Add Resource button.

### Viewing or changing the resource details

1. Click a resource name to open the Local Resource form.
2. If necessary, change the resource details:



**Data Center**

Gateway 59c119cd3f94c30fe45ff5db

**Name**

ec2-54-210-232-251.compute-1.amazonaws.com

**URL**

http://ec2-54-210-232-251.compute-1.amazonaws.com:5002

**Description****Public**

Uncheck this if you want to control exactly who has access to this compute node

**Update****status**

```
{"status": "ok", "messages": []}
```

3. Click the Update button.

### Making a node public or private

1. Click the resource name to open the Local Resource form.
2. Select or clear the Public checkbox:

**Data Center**  

Gateway 59c119cd3f94c30fe45ff5db

**Name**  

ec2-54-210-232-251.compute-1.amazonaws.com

**URL**  

http://ec2-54-210-232-251.compute-1.amazonaws.com:5002

**Description**

☒ **Public**  
Uncheck this if you want to control exactly who has access to this compute node

Update

**status**  

{"status": "ok", "messages": []}

3. Click the Update button.

## Removing a resource

Click the Remove button next to the resource you want to remove.

NOTE: When you remove a resource assigned to a project, the project becomes orphaned. To fix an orphaned project, *move the project to a valid Compute Resource*.

## Managing services

The tasks on this page assume that the 3 AEN nodes are installed in the following locations:

- Server—`/opt/wakari/wakari-server/`.
- Gateway—`/opt/wakari/wakari-gateway/`.
- Compute-Launcher—`/opt/wakari/wakari-compute/`.

- *Checking the status of server node processes*
- *Checking the status of gateway node processes*
- *Checking the status of compute node processes*
- *Starting AEN services*
- *Verifying that AEN services are set to start with the system*
- *Stopping AEN services*
- *Restarting AEN services*
- *Identifying extraneous processes*
- *Removing extraneous processes*

## Checking the status of server node processes

1. Run:

```
# service wakari-server status
wk-server          RUNNING      pid 20758, uptime 5 days, 0:30:23
worker             RUNNING      pid 20757, uptime 5 days, 0:30:23
```

OR

```
root@server # ps -Hu wakari
PID TTY          TIME CMD
20756 ?              00:02:26 .supervisord
20757 ?              00:05:58 mtq-worker
20758 ?              00:00:08 wk-server
```

(continues on next page)

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```
20765 ?      00:02:00    wk-server
20766 ?      00:01:55    wk-server
20767 ?      00:02:20    wk-server
20770 ?      00:02:02    wk-server
```

## 2. Run:

```
root@server # service nginx status
nginx (pid 26303) is running...
```

For more information on server processes, see *Server processes*.

## Checking the status of gateway node processes

### Run:

```
# service wakari-gateway status
wk-gateway          RUNNING      pid 1137, uptime 5 days, 1:59:28
```

### OR

```
root@gateway # ps -Hu wakari
  PID TTY          TIME CMD
 1136 ?            00:01:59 .supervisord
 1137 ?            00:00:02  wk-gateway
```

For more information on gateway processes, see *Gateway processes*.

## Checking the status of compute node processes

### Run:

```
# service wakari-compute status
wk-compute          RUNNING      pid 22050, uptime 3 days, 1:03:19
```

### OR

```
root@compute # ps -Hu wakari
  PID TTY          TIME CMD
 1150 ?            00:02:01 .supervisord
 1152 ?            00:00:01  wk-compute
```

For more information on compute node processes, see *Compute processes*.

## Starting AEN services

Services should start automatically both when they are first installed and at any point when the system is restarted.

If you need to manually start an AEN service, you must start each node independently, because they may be running on separate machines.

NOTE: The process is basically the same for each node, but the path to the correct commands vary.

To manually start a service:

- On the server node, run:

```
service wakari-server start
```

- On the gateway node, run:

```
service wakari-gateway start
```

- On a compute node, run:

```
service wakari-compute start
```

## Verifying that AEN services are set to start with the system

To verify that AEN services are set up to start automatically:

1. Run the following command on each node:

```
chkconfig --list | grep wakari
```

2. If services are missing, add them:

```
chkconfig --add [wakari-server|wakari-gateway|wakari-compute]
```

3. *Restart the services.*

## Stopping AEN services

CAUTION: Do not stop or kill supervisord without first stopping wk-compute and any other processes that use it.

You must stop services on each node independently, because they may be running on separate machines.

To stop an AEN service:

- On the server node, run:

```
service wakari-server stop
```

- On the gateway node, run:

```
service wakari-gateway stop
```

- On a compute node, run:

```
service wakari-compute stop
```

Compute nodes may have running processes that are not automatically stopped. To stop them, run:

```
sudo /opt/wakari/wakari-compute/bin/wk-compute-apps kill-all
```

## Restarting AEN services

- On the server node, run:

```
service wakari-server restart
```

- On the gateway node, run:

```
service wakari-gateway restart
```

- On a compute node, run:

```
service wakari-compute restart
```

## Identifying extraneous processes

To get a complete list of the processes running under the wakari user account, run `ps -Hu wakari`.

EXAMPLE:

```
root@server # ps -Hu wakari
  PID TTY          TIME CMD
 20756 ?            00:02:26 .supervisord
 20757 ?            00:05:58 mtq-worker
 20758 ?            00:00:08 wk-server
 20765 ?            00:02:00 wk-server
 20766 ?            00:01:55 wk-server
 20767 ?            00:02:20 wk-server
 20770 ?            00:02:02 wk-server

root@server # ps -f -C nginx
UID      PID  PPID  C  STIME TTY          TIME CMD
root    26303    1   0  12:18 ?        00:00:00 nginx: master process /usr/sbin/nginx -c /
→etc/nginx/nginx.conf
nginx   26305 26303   0  12:18 ?        00:00:00 nginx: worker process

root@gateway # ps -Hu wakari
  PID TTY          TIME CMD
 1136 ?            00:01:59 .supervisord
 1137 ?            00:00:02 wk-gateway

root@compute # ps -Hu wakari
  PID TTY          TIME CMD
 1150 ?            00:02:01 .supervisord
 1152 ?            00:00:01 wk-compute
```

- wk-server, wk-gateway and wk-compute should have PIDs reported by supervisorctl.
- The nginx master process should have a PID reported by service nginx status.
- If you have installed more than one AEN node on a single machine, the processes from all of the installed nodes should be displayed for that machine.
- On compute node(s), any AEN applications currently being run by users will be present.

EXAMPLE:

```
root@compute # ps -Hu wakari
  PID TTY          TIME CMD
 1150 ?            00:00:00 .supervisord
 1152 ?            00:00:00 wk-compute
```

(continues on next page)

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```
1340 ?      00:00:00 bash
1341 ?      00:00:00 notebookwrapper
```

## Removing extraneous processes

If extra `wk-server`, `wk-gateway`, `wk-compute`, or `supervisord` processes are present, use the `kill` command to remove them to prevent issues with AEN.

You can safely *restart* any process that you remove in error.

## Making sure NGINX and MongoDB are running

In order for AEN to run, the dependencies `mongodb` and `nginx` must be up and running. If either of these fail to start, AEN will not be served on port 80.

Check if `nginx` and `mongod` are both running (RHEL 6x):

```
$ sudo service nginx status
nginx (pid 25956) is running...

$ sudo service mongod status
mongod (pid 25928) is running...
```

If either of these failed to start, tail the log files. The default location of log files is:

```
$ tail -n 50 /var/log/mongodb/mongod.log

# nginx errors reported in error.log
$ tail -n 50 /var/log/nginx/error.log
```

## Viewing, terminating, and relaunching applications

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select Monitor:

The Monitor menu lists started applications by user and project.

The list includes columns for the application name, current running status, running node and last seen date.

3. Use the buttons to terminate or relaunch an application.
4. To view an application's logs, click the Logs button with the document icon.

## Viewing the task queue

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select Task Queue:

Staff

[Daily Report](#)  
[Password Reset](#)  
[Notification](#)  
[Exceptions](#)

Site Admin

[General](#)  
[Accounts](#)  
[Users](#)  
[Monitor](#)

Running Apps								
User	Project	Application	Status	Node	Last Seen	Terminate	Relaunch	Logs
aen_admin	asd	notebook	running	localhost	Jul 24, 2017 15:15:24 CDT	<a href="#">Terminate</a>	<a href="#">Relaunch</a>	<a href="#">Logs</a>
aen_admin	Test	notebook	running	localhost	Jul 25, 2017 11:54:05 CDT	<a href="#">Terminate</a>	<a href="#">Relaunch</a>	<a href="#">Logs</a>

Staff

[Daily Report](#)  
[Password Reset](#)  
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Site Admin

[General](#)  
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## Task Queue

Workers

ip-172-31-10-196.4053 | [high](#) [default](#) [low](#)

Queues

[high](#)  
Backlog: 0  
Failed: 1

[default](#)  
Backlog: 0  
Failed: 3



The Workers section lists the workers in the task queue and whether each worker is set at high, default or low priority.

The Queues section provides information on the default and high priority queues.

3. To view all the tasks in a particular queue, in the Queues section, click the queue name.

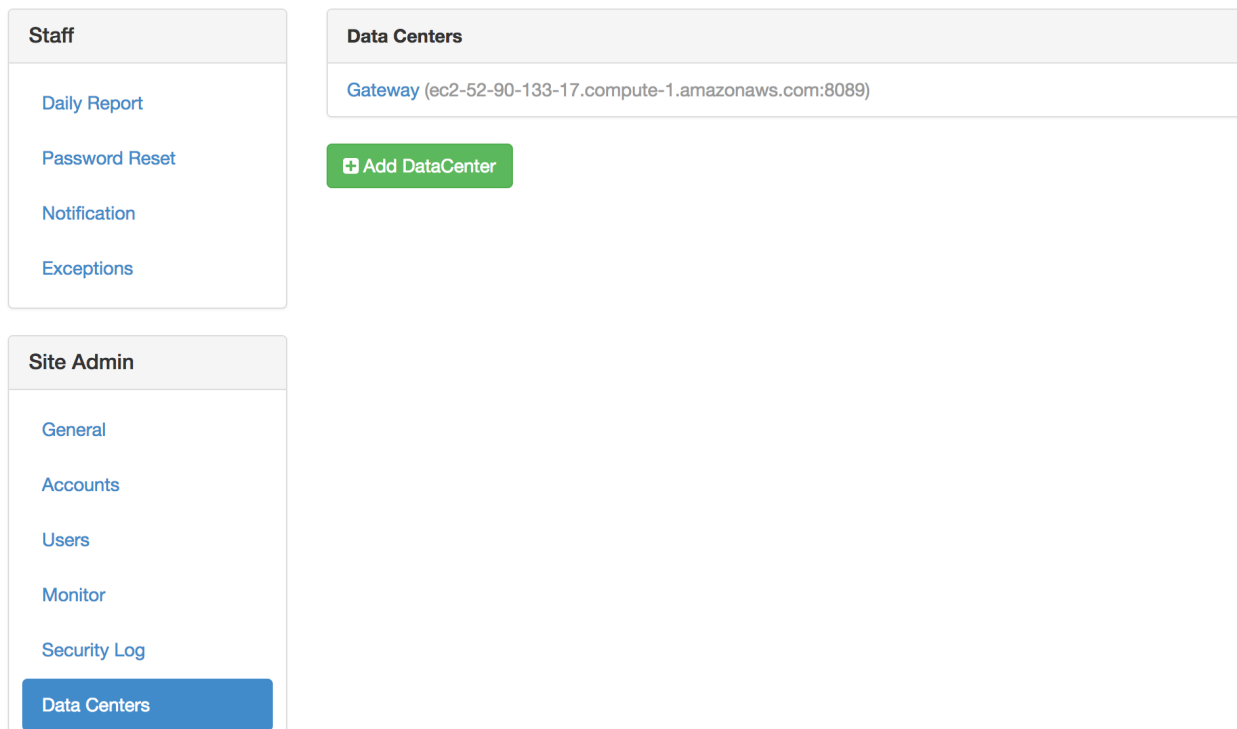
## Checking node connections

When the AEN nodes cannot communicate with each other as intended, it can cause issues with you AEN platform installation.

- *Verifying server to gateway connectivity*
- *Verifying gateway to compute node connectivity*
- *Verifying gateway to server connectivity*

## Verifying server to gateway connectivity

1. On the server, in the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select Data Centers:



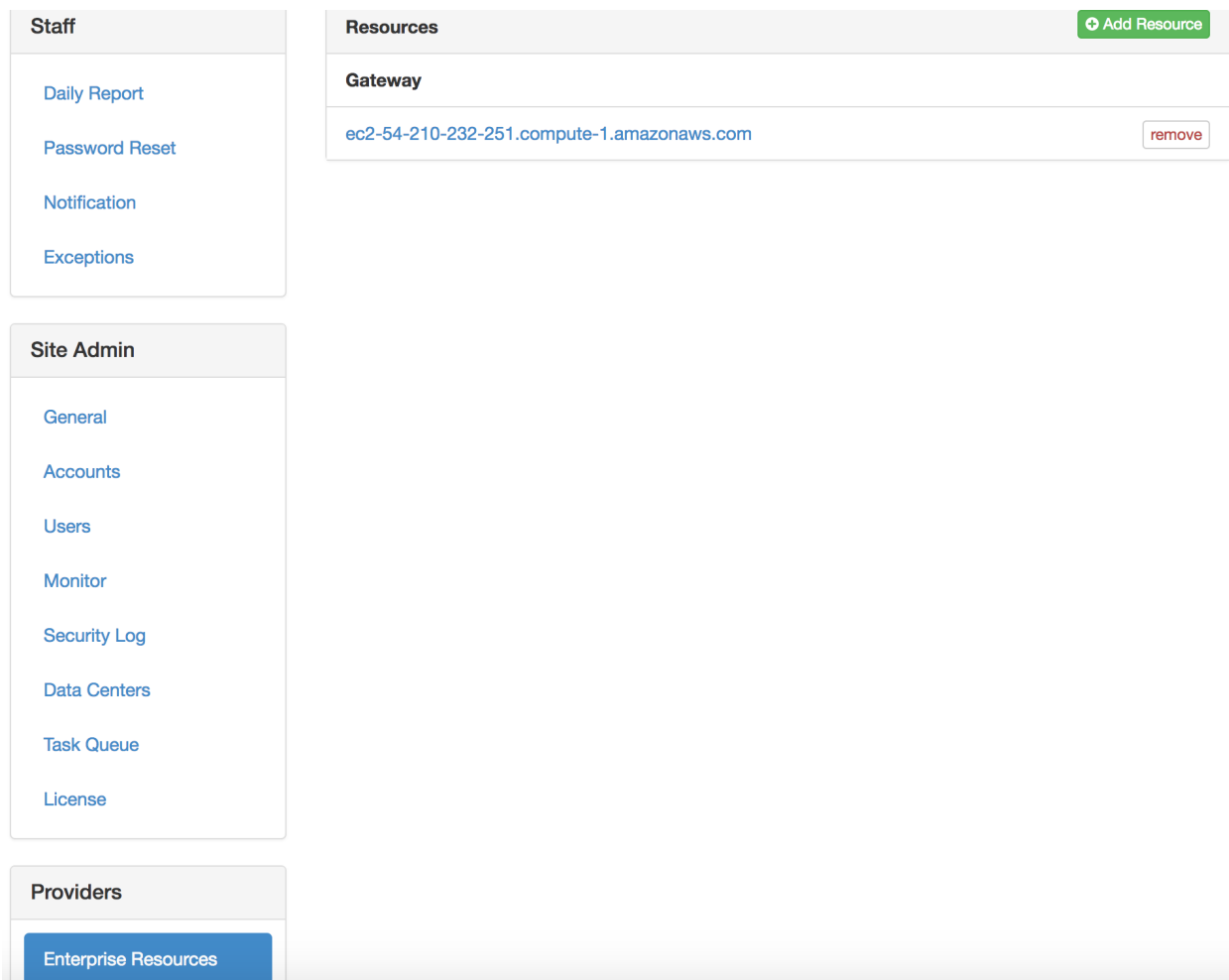
3. For each data center in the list, check connectivity from the server to that gateway.

EXAMPLE: The gateway in this example is `http://gateway.example.com:8089`:

```
root@server # curl --connect-timeout 5 http://gateway.example.com:8089 > /dev/null
```

## Verifying gateway to compute node connectivity

1. On the server, in the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Providers** menu, select Enterprise Resources:



3. Open each compute node in the Resources section.
4. Verify that the contents of the URL field begin with either `http` or `https`.

**Data Center**

Gateway 59c119cd3f94c30fe45ff5db

**Name**

ec2-54-210-232-251.compute-1.amazonaws.com

**URL**

http://ec2-54-210-232-251.compute-1.amazonaws.com:5002

**Description****Public**

Uncheck this if you want to control exactly who has access to this compute node

**Update****status**

```
{"status": "ok", "messages": []}
```

5. Check connectivity to that URL from the corresponding gateway.

EXAMPLE: The gateway in this example is `http://gateway.example.com:8089`:

```
root@gateway # curl --connect-timeout 5 http://compute.example.com:5002 > /dev/
↪null
```

## Verifying gateway to server connectivity

The gateway-to-server path is used by the gateway configuration command `wk-gateway-configure`.

1. Verify that the gateway is linked to the correct server in the configuration file.
2. Verify that the full server URL is specified.
3. Check connectivity to the server:

```
root@gateway # grep WAKARI_SERVER /opt/wakari/wakari-gateway/etc/wakari/wk-
↪gateway-config.json
"WAKARI_SERVER": "http://wakari.example.com",

root@gateway # curl --connect-timeout 5 http://wakari.example.com > /dev/null
root@gateway # curl --connect-timeout 5 http://error.example.com > /dev/null
curl: (7) Failed to connect to error.example.com port 80: Connection refused
```

4. If a connection fails:
  1. Ensure that gateways (data centers) and compute nodes (Enterprise Resources) are correctly configured on the server.
  2. Verify that processes are listening on the configured ports:

```
$ sudo netstat -nplt
Active Internet connections (only servers)
Proto Recv-Q Send-Q Local Address   Foreign Address State  PID/Program
tcp        0      0 *:80            :::*           LISTEN 26409/nginx
tcp        0      0 *:22            :::*           LISTEN 986/sshd
tcp        0      0 127.0.0.1:25    :::*           LISTEN 1063/master
tcp        0      0 *:5000          :::*           LISTEN 26192/python
tcp        0      0 127.0.0.1:27017 :::*           LISTEN 29261/mongod
tcp        0      0 *:22            :::*           LISTEN 986/sshd
tcp        0      0 127.0.0.1:25    :::*           LISTEN 1063/master
```

3. Check the firewall setting and logs on both hosts to ensure that packets are not being blocked or discarded.

## Verifying and tuning search indexing

For search indexing to work correctly, a compute node must be able to communicate with the server. To verify this:

1. Run:

```
curl -m 5 $AEN_SERVER > /dev/null
```

2. Verify that there are sufficient inotify watches available for the number of subdirectories within the project root file system:

```
cat /proc/sys/fs/inotify/max_user_watches
```

NOTE: Some Linux distributions default to a low number of watches, which may prevent the search indexer from monitoring project directories for changes.

3. If necessary, increase the number of watches:

```
echo fs.inotify.max_user_watches=100000 | sudo tee -a /etc/sysctl.conf && sudo  
→ sysctl -p
```

4. Verify that there are sufficient inotify user instances available—at least one per project:

```
cat /proc/sys/fs/inotify/max_user_instances
```

5. If necessary, increase the number of inotify user instances:

```
echo fs.inotify.max_user_instances=1000 | sudo tee -a /etc/sysctl.conf && sudo  
→ sysctl -p
```

## Changing the AEN server URL

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select General:
3. In the Wakari Server box, type the main URL where the site can be viewed.
4. Click the Update button.

## Changing the static URL for JavaScript files

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select General:
3. In the Static URL box, type the static URL where JavaScript files can be accessed.
4. Click the Update button.

## Changing the AEN account type

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select General:

Staff

[Daily Report](#)  
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Site Admin

General

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Providers

General Admin Settings

**Wakari Server**  
Set the main URL where this site will be accessed

http://anaconda-enterprise.trl

**Static URL**  
Set static URL where the js can be accessed

http://anaconda-enterprise.trl/static/

**Default Project Access**  
This will be the default when a user creates a project

☐ Public  
Anyone can see this project. Collaborators have write access

☒ Private  
No one can see this project except collaborators.

**Account Type**

wk\_server.plugins.accounts.cloud

Update

Config Files

<b>Staff</b>	<b>General Admin Settings</b>
<a href="#">Daily Report</a>	<b>Wakari Server</b> Set the main URL where this site will be accessed
<a href="#">Password Reset</a>	<input type="text" value="http://anaconda-enterprise.trl"/>
<a href="#">Notification</a>	
<a href="#">Exceptions</a>	<b>Static URL</b> Set static URL where the js can be accessed
	<input type="text" value="http://anaconda-enterprise.trl/static/"/>
<b>Site Admin</b>	<b>Default Project Access</b> This will be the default when a user creates a project
<b>General</b>	<input type="radio"/> <b>Public</b> Anyone can see this project. Collaborators have write access
<a href="#">Accounts</a>	<input checked="" type="radio"/> <b>Private</b> No one can see this project except collaborators.
<a href="#">Users</a>	
<a href="#">Monitor</a>	<b>Account Type</b>
<a href="#">Security Log</a>	<input type="text" value="wk_server.plugins.accounts.cloud"/>
<a href="#">Data Centers</a>	
<a href="#">Task Queue</a>	<input type="button" value="Update"/>
<a href="#">License</a>	
<b>Providers</b>	<b>Config Files</b>

<b>Staff</b>	<b>General Admin Settings</b>
<a href="#">Daily Report</a>	<b>Wakari Server</b> Set the main URL where this site will be accessed
<a href="#">Password Reset</a>	<input type="text" value="http://anaconda-enterprise.trl"/>
<a href="#">Notification</a>	
<a href="#">Exceptions</a>	<b>Static URL</b> Set static URL where the js can be accessed
	<input type="text" value="http://anaconda-enterprise.trl/static/"/>
<b>Site Admin</b>	<b>Default Project Access</b> This will be the default when a user creates a project
<b>General</b>	<input type="radio"/> <b>Public</b> Anyone can see this project. Collaborators have write access
<a href="#">Accounts</a>	<input checked="" type="radio"/> <b>Private</b> No one can see this project except collaborators.
<a href="#">Users</a>	
<a href="#">Monitor</a>	<b>Account Type</b>
<a href="#">Security Log</a>	<input type="text" value="wk_server.plugins.accounts.cloud"/>
<a href="#">Data Centers</a>	
<a href="#">Task Queue</a>	<input type="button" value="Update"/>
<a href="#">License</a>	
<b>Providers</b>	<b>Config Files</b>



3. In the Account Type box, select the account type—cloud or LDAP.
4. Click the Update button.

### Changing the default for project access

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select General:

<div>Staff</div> <div>Daily Report</div> <div>Password Reset</div> <div>Notification</div> <div>Exceptions</div>	<div>General Admin Settings</div> <div> <b>Wakari Server</b>  Set the main URL where this site will be accessed  <input type="text" value="http://anaconda-enterprise.trl"/> </div> <div> <b>Static URL</b>  Set static URL where the js can be accessed  <input type="text" value="http://anaconda-enterprise.trl/static/"/> </div> <div> <b>Default Project Access</b>  This will be the default when a user creates a project  <div> <input type="radio"/> <b>Public</b>  Anyone can see this project. Collaborators have write access </div> <div> <input checked="" type="radio"/> <b>Private</b>  No one can see this project except collaborators. </div> </div> <div> <b>Account Type</b>  <input type="text" value="wk_server.plugins.accounts.cloud"/> </div> <div> <input type="button" value="Update"/> </div>
<div>Site Admin</div> <div>General</div> <div>Accounts</div> <div>Users</div> <div>Monitor</div> <div>Security Log</div> <div>Data Centers</div> <div>Task Queue</div> <div>License</div>	<div>Config Files</div>
<div>Providers</div>	

3. Under Default Project Access, select the default access type for new projects: Public or Private.
4. Click the Update button.

## Changing the owner of a project

To change the owner of a project:

1. Collect the project name, the user name of the previous owner, and the user name of the new owner.
2. Run the `wakari-server` executable command `wk-server-admin`:

```
/opt/wakari/wakari-server/bin/wk-server-admin project-owner --project PROJECT --  
↪old OLD_OWNER --new NEW_OWNER --delete --keep-owner
```

- **PROJECT**: The project name.
- **OLD\_OWNER**: The user name of the previous owner.
- **NEW\_OWNER**: The user name of the new owner.
- **--delete**: An optional flag that deletes the old project directory in the `projects` directory of **OLD\_OWNER**. If this flag is not used, the old project directory is preserved but no longer used.
- **--keep-owner**: An optional flag that makes **OLD\_OWNER** a collaborator of the project after it is transferred to **NEW\_OWNER**. If this flag is not used, **OLD\_OWNER** will no longer have collaborator access to the project.

**NOTE:** The **OLD\_OWNER** user must still exist when the project's owner is changed. Before deleting any user, be sure to change the owner of the user's projects.

## Editing configuration files

1. In the AEN navigation bar, click **Admin** to open the Admin Settings page.
2. In the **Site Admin** menu, select **General**.
3. In the **Config Files** section, change the configuration settings for your AEN installation. For more information on configuration files, see [Using configuration files](#).
4. Click the **Update** button.

## Managing your AEN license

1. In the AEN navigation bar, click **Admin** to open the Admin Settings page.
2. In the **Site Admin** menu, select **License**:

The **Current License** section displays information regarding your AEN license, including the name of the product, vendor, license holder's name, end and issued dates, company name, license type, and contact email.

Staff	General Admin Settings
<a href="#">Daily Report</a>	<b>Wakari Server</b> Set the main URL where this site will be accessed <input type="text" value="http://anaconda-enterprise.trl"/>
<a href="#">Password Reset</a>	<b>Static URL</b> Set static URL where the js can be accessed <input type="text" value="http://anaconda-enterprise.trl/static/"/>
<a href="#">Notification</a>	<b>Default Project Access</b> This will be the default when a user creates a project  <input type="radio"/> <b>Public</b> Anyone can see this project. Collaborators have write access <input checked="" type="radio"/> <b>Private</b> No one can see this project except collaborators.
<a href="#">Exceptions</a>	<b>Account Type</b> <input type="text" value="wk_server.plugins.accounts.cloud"/>
	<input type="button" value="Update"/>
Site Admin	Config Files
<a href="#">General</a>	
<a href="#">Accounts</a>	
<a href="#">Users</a>	
<a href="#">Monitor</a>	
<a href="#">Security Log</a>	
<a href="#">Data Centers</a>	
<a href="#">Task Queue</a>	
<a href="#">License</a>	
Providers	

Staff

[Daily Report](#)
[Password Reset](#)
[Notification](#)
[Exceptions](#)

Site Admin

[General](#)
[Accounts](#)
[Users](#)
[Monitor](#)
[Security Log](#)
[Data Centers](#)
[Task Queue](#)
[License](#)

Current License

You have **166 days** remaining on your current license.

Renew your license

<b>product</b>	Anaconda Enterprise Notebooks
<b>vendor</b>	Continuum Analytics, Inc.
<b>name</b>	Continuum Development
<b>end_date</b>	2018-03-10
<b>issued</b>	2017-03-10
<b>company</b>	Continuum Analytics
<b>type</b>	undefined
<b>email</b>	dev@continuum.io

Upload New License

License File

No file chosen

Update

## Renewing your AEN license

1. Click the Renew your license button.
2. In the Upload New License section, click the Choose File button.
3. Select the new license file.
4. Click the Open button.
5. Click the Update button.

Your renewed license information is displayed.

## Cheat sheet

The Admin dashboard includes three menus in the left column: **Staff**, **Site Admin** and **Providers**.

### Staff menu

- Daily Report—See the number of users and projects.
- Password Reset—Reset a user password.
- Notification—Send system messages to users via SES or SMTP.

- Exceptions—If errors are raised while AEN is running, a red dot appears in the AEN navigation bar. Review errors and mark them as read.

## Site Admin menu

- General—Change the configuration settings for your AE Notebook server installation.
- Accounts—Turns on or off Open Registration.
- Users—View usernames, number of projects and last logins.
- Monitor—View status of applications with related data, terminate or restart
- Security Log—View errors that could affect security.
- Data Centers—View current data centers and add a new data center.
- Task Queue—View workers in the task queue and priority.
- License—View current AEN license or upload a new license.

## Providers menu

Enterprise Resources—View, add or remove local or cloud services and designate public or private to control access to a compute node.

## Troubleshooting

This troubleshooting guide provides you with ways to deal with issues that may occur with your AEN installation.

- *General troubleshooting steps*
- *Browser error: too many redirects*
- *Browser error: too many redirects when starting project apps*
- *Exception: exceptions.TypeError: 'NoneType' object has no attribute '\_\_getitem\_\_'*
- *Error: unix:///opt/wakari/wakari-server/etc/supervisor.sock no such file*
- *Error: “Data Center Not Found” when deleting a project*
- *Forgotten administrator password*
- *Log files being deleted*
- *Error: This socket is closed*
- *Service error 502: Cannot connect to the application manager*
- *502 communication error on Amazon web services (AWS)*
- *Invalid username*
- *Notebook Error: Cannot download notebook as PDF via LaTeX*
- *Unresponsive wk-server thread without error messages*
- *Unresponsive wk-gateway thread without error messages*

- *Error starting projects*
- *Changes in .condarc file are ignored*

### General troubleshooting steps

1. Clear browser cookies. When you change the AEN configuration or upgrade AEN, cookies remaining in the browser can cause issues. Clearing cookies and logging in again can help to resolve problems.
2. *Make sure NGINX and MongoDB are running.*
3. Make sure that AEN services are *set to start at boot*, on all nodes.
4. *Make sure that services are running* as expected. If any services are not running or are missing, *restart them*.
5. *Check for and remove extraneous processes.*
6. *Check the connectivity between nodes.*
7. *Check the configuration file syntax.*
8. *Check file ownership.*
9. *Verify that POSIX ACLs are enabled.*

### Browser error: too many redirects

#### Cause

Browser cookies are out of date.

#### Solution

1. Log out.
2. Clear the browser's cookies.
3. Clear the browser cache.
4. Log in.

### Browser error: too many redirects when starting project apps

Browser shows “Too many redirects” when the user tries to start an application.

#### Cause

The project's Compute Resource is invalid or was deleted.

#### Solution

*Move the project to a valid Compute Resource.*

**Exception: exceptions.TypeError: 'NoneType' object has no attribute '\_\_getitem\_\_'**

This exception appears on the Admin > Exceptions page when a project does not have a Compute Resource assigned.

**Cause**

The project's Compute Resource is invalid or was deleted.

**Solution**

*Move the project to a valid Compute Resource.*

**Error: unix:///opt/wakari/wakari-server/etc/supervisor.sock no such file**

This is a supervisorctl error.

**Cause**

supervisord is not running on the Server.

**Solution**

Ensure that supervisord is included in the crontab. Then restart supervisord manually.

**Error: "Data Center Not Found" when deleting a project****Cause**

The data center has been removed.

**Solution**

As root, run:

```
/opt/wakari/wakari-server/bin/wk-server-admin remove-project --db-only <user>  
↪<project>
```

**Forgotten administrator password**

1. Use ssh to log into the server as root.
2. Run:

```
/opt/wakari/wakari-server/bin/wk-server-admin reset-password -u SOME_USER -p SOME_  
↪PASSWORD
```

NOTE: Replace SOME\_USER with the administrator username and SOME\_PASSWORD with the password.

3. Log into AEN as the administrator user with the new password.

Alternatively you may add an administrator user:

1. Use ssh to log into the server as root.
2. Run:

```
/opt/wakari/wakari-server/bin/wk-server-admin add-user SOME_USER --admin -p SOME_
↵PASSWORD -e YOUR_EMAIL
```

NOTE: Replace SOME\_USER with the username, replace SOME\_PASSWORD with the password, and replace YOUR\_EMAIL with your email address.

3. Log into AEN as the administrator user with the new password.

### Log files being deleted

Log files are being deleted.

NOTE: Locations of AEN log files for each process and application are shown in the node sections in [Concepts](#).

### Cause

AEN installers log into `/tmp/wakari\_server, gateway, compute}.log`. If the log files grow too large, they might be deleted.

### Solution

To set the logs to be more or less verbose, Jupyter Notebooks uses `Application.log_level`.

To make the logs less verbose than the default, but still informative, set `Application.log_level` to `ERROR`.

### Error: This socket is closed

You receive the “This socket is closed” error message when you try to start an application.

### Cause

When the `supervisord` process is killed, information sent to the standard output `stdout` and the standard error `stderr` is held in a pipe that will eventually fill up.

Once full, attempting to start any application will cause the “This socket is closed” error.

### Solution

To prevent this issue:

- Follow the instructions in [Managing services](#) to stop and restart processes.
- Do not stop or kill `supervisord` without first stopping `wk-compute` and any other processes that use it.



To resolve the “This socket is closed” error:

1. Stop wk-compute by running `sudo kill -9`.
2. Restart the supervisord and wk-compute processes:

```
sudo /etc/init.d/wakari-compute stop
sudo /etc/init.d/wakari-compute start
```

## Service error 502: Cannot connect to the application manager

Gateway node displays “Service Error 502: Can not connect to the application manager.”

### Cause

A compute node is not responding because the wk-compute process has stopped.

### Solution

Stop and then restart the supervisord and wk-compute processes:

```
sudo /etc/init.d/wakari-compute stop
sudo /etc/init.d/wakari-compute start
```

## 502 communication error on Amazon web services (AWS)

You receive the “502 Communication Error: This gateway could not communicate with the Wakari server” error message.

### Cause

An AEN gateway cannot communicate with the Wakari server on AWS. There may be an issue with the IP address of the Wakari server.

### Solution

Configure your AEN gateway to use the DNS hostname of the server. On AWS this is the DNS hostname of the Amazon Elastic Compute Cloud (EC2) instance.

## Invalid username

### Cause

The username does not follow 1 or more of these rules:

- Must be at least 3 characters and no more than 25 characters.
- The first character must be a letter (A-Z) or a digit (0-9).

- Other characters can be a letter, digit, period (.), underscore (\_) or hyphen (-).
- The [POSIX standard](#) specifies that these characters are the portable filename character set, and that portable usernames have the same character set.

### Solution

Follow the above rules for usernames.

## Notebook Error: Cannot download notebook as PDF via LaTeX

### Cause

LaTeX is not properly installed.

### CentOS/6 Solution

1. Install TeXLive from the [TUG site](#). Follow the described steps. The installation may take some time.
2. Add the installation to the PATH in the file `/etc/profile.d/latex.sh`. Add the following, replacing the year and architecture as needed:

```
PATH=/usr/local/texlive/2017/bin/x86_64-linux:$PATH
```

3. Restart the compute node.

### CentOS/7 Solution

1. Install the missing packages running the command:

```
yum install texlive texlive-xetex texlive-xetexconfig texlive-xetex-def texlive-  
↪adjustbox texlive-upquote texlive-ulem
```

## Unresponsive `wk-server` thread without error messages

### Cause

Two things can cause the `wk-server` thread to freeze without error messages:

- LDAP freezing
- MongoDB freezing

If LDAP or MongoDB are configured with a long timeout, Gunicorn can time out first and kill the LDAP or MongoDB process. Then the LDAP or MongoDB process dies without logging a timeout error.

### Solution

1. Check for frozen LDAP or MongoDB server processes.
2. You may also wish to configure the Gunicorn timeout to more than 30 seconds.

## Unresponsive `wk-gateway` thread without error messages

### Cause

If TLS is configured with a passphrase protected private key, `wk-gateway` will freeze without any error messages.

### Solution

Update the TLS configuration so that it does not use a passphrase protected private key.

## Error starting projects

Project's status page shows "There was an error starting this project".

### Cause

Lack of disk space in compute nodes prevents projects from starting.

### Solution

1. Verify that the project node meets the *system requirements*.
2. Check if there is enough free space on the compute node's partition where `/projects` lives:

```
df -h /projects
```

3. Free up some disk space to meet the system requirements.
4. Restart the project.

## Changes in `.condarc` file are ignored

Changes applied to `.condarc` are ignored by conda.

### Cause

Conda loads its configuration by merging multiple files together.

### Solution

Check if you are applying the changes to the correct file.

To show the merged state that conda is currently using:

```
conda config --show
```

To show all config files that conda is currently reading:

```
conda config --show-sources
```

### Frequently asked questions

- *What is AEN?*
- *Can notebooks be shared with anyone?*
- *Can I disable the option, “publish your notebook to anaconda.org”?*
- *How can I check the version number of my AEN server?*
- *Can I use AEN to access CSV or Amazon S3 data?*
- *Can I install other Python packages?*
- *Can I create a Python environment from the command line?*
- *Can I connect to GitHub with AEN?*
- *Can I print or print preview my Jupyter Notebooks?*
- *Is there a set amount of storage on AEN?*
- *How do I get help, give feedback, suggest features or report a bug?*

### What is AEN?

For information on AEN, see *Anaconda Enterprise 4 Notebooks*.

### Can notebooks be shared with anyone?

Yes. When you share a Jupyter Notebook through AEN, it can be viewed and run without the need to install anything special, regardless of what libraries were used to create the notebook. Each notebook also includes the Python environment that it needs to run in.

AEN allows users to clone a shared Jupyter Notebook into their AEN account to make whatever changes or modifications they want. The notebook’s Python environment is also cloned, so it runs in the same environment as the shared Jupyter Notebook unless it is changed.

### Can I disable the option, “publish your notebook to anaconda.org”?

Yes. The upload button in the notebook app executes the option “publish your notebook to anaconda.org”. To disable it, log in as the AEN\_SRVC\_ACCT and run these commands:

```
source activate /opt/wakari/wakari-compute
jupyter-nbextension disable nb_anacondacloud --py --sys-prefix
jupyter-serverextension disable nb_anacondacloud --py --sys-prefix
```

## How can I check the version number of my AEN server?

Go to this URL in a browser: `http://$AEN_SERVER/admin/list`

NOTE: Replace `$AEN_SERVER` with the domain name or the domain name and port number of your AEN server.

## Can I use AEN to access CSV or Amazon S3 data?

Yes. If your data is in CSV files, upload the CSV files to your AEN account using the upload controls in the File Browser of the Workbench Application or the File Transfer Application.

To access data stored on Amazon S3, use the Boto interface from AEN. See the public data files in AEN for examples of how to use Boto to pull your data from Amazon S3 into AEN. For more information, see [Boto documentation](#).

You can also use IOPro to simplify and optimize the conversion of your data into Python arrays.

## Can I install other Python packages?

Yes, by creating a custom environment for your packages within your project.

For more information, see [Using the NBConda extension](#).

## Can I create a Python environment from the command line?

Yes, you can use the `conda create` command to create custom Python environments with whatever packages you choose. All AEN environments are shared with all the team members of a project.

EXAMPLE: In this example, `myenv` is a new environment containing the NumPy package.

```
conda create -n myenv numpy
```

NOTE: Python, Jupyter Notebooks and PIP are installed by default in all new AEN environments.

To use your new environment, activate it by running `source activate myenv`.

## Can I connect to GitHub with AEN?

Yes, you have full access to GitHub through an AEN Terminal application.

To generate an SSH key from your AEN account and add it to your GitHub account:

1. [Generate a GitHub SSH key](#).
2. Copy your key by running `cat ~/.ssh/id_rsa.pub`.
3. Select and copy the contents of the `id_rsa.pub` file to the clipboard.
4. Follow [GitHub's instructions](#) to go to your GitHub account and paste it from your clipboard into the appropriate box in your GitHub settings.

## Can I print or print preview my Jupyter Notebooks?

Yes, you can print your notebooks using your browser's regular printing capabilities.

You can also preview the printed page by clicking the **File** menu and selecting Print Preview.

### Is there a set amount of storage on AEN?

No, there is no set limit for storage in AEN. You are limited only by the size of the disk where AEN is installed.

If you need more storage, contact your system administrator.

### How do I get help, give feedback, suggest features or report a bug?

See *Help and support*.

### Help and support

Priority support is included with the purchase of an Anaconda subscription.

Contact your administrator first if you are having problems. Your administrator has a service level agreement where your issue will be responded to within a specific response time, depending on type and severity.

### Training and consulting

Training and consulting is available for AEN and any other Anaconda product.

For more information, please contact your account representative or [email the sales team](#).

### Providing feedback

Your feedback is very important to us!

Please, send us any [product feedback](#) while you are thinking about it.

TIP: Be sure to select AEN as the Platform Component Name.

### Submitting feature requests

We'd love to hear your ideas for consideration in future releases!

Your ideas help us build a better product. Your administrator can submit a support ticket for you.

NOTE: You can also request new features by using the [product feedback](#) form.

### Reporting a bug

If you think you have found a bug, please contact your administrator immediately. They will open a support ticket for your issue.

### Additional resources

The following resources are useful for getting started with Jupyter Notebooks:

- [Jupyter Notebook quick start guide](#)
- [Jupyter Notebook user documentation](#)

- [GitHub](#) shows the most popular Jupyter notebooks of the [month](#), [week](#), and [day](#).

## Release notes

### v4.3.0 October 24, 2018

#### Administrator-facing changes:

- Fix bug where compute logging wasn't respecting the `logMaxFiles` key
- Log and display a descriptive error message when there is a problem creating the users index
- Log and display a descriptive error message when there is a problem creating a new user with a duplicated e-mail address when the `uniqueEmail` setting is enabled
- Add footer server pages with server host data (IP, AEN version and server version)
- Fix admin script to change the status of private projects
- Fix validation error when updating/editing an existing resource
- Docs: Add KB article about using MongoDB to update old projects with new Data Center information
- Docs: Add restarting service step to SSO documentation
- Docs: Add support for newer versions of MongoDB
- Docs: Add documentation on `uniqueEmail`
- Docs: Add `projDirsAsHome` key to config docs
- Docs: Rewrite the “Using project directories as home directories” section
- Docs: Add full path to admin commands
- Docs: Warn about upgrading away from tested pkgs
- Docs: Add missing steps to “Authenticating with LDAP” section
- Docs: Add troubleshooting documentation about orphaned projects
- Docs: Warn about not using IP address when you connect to AEN
- Docs: Add an entry about ‘Error starting projects’ in the troubleshooting page
- Docs: Rewrite “Group and user permissions for NFS” section and description of the `identicalGID` key in the config pages
- Docs: Add a new section about using MRO packages in AEN
- Docs: Preserve username capitalization when using LDAP/AD
- Docs: Add `umask 0022` to security requirements
- Docs: Add new section about changing install location
- Docs: Add note about how to manually break out Root CA for the gateway
- Docs: Add note about upgrading custom environments
- Docs: Add notes about how to find conda config files inside AEN
- Docs: Add note about using `USE_SERVER_BASED_SESSIONS: false` when configuring SSO between AEN and versions 2.33.3 through 2.33.10 of the Repository

#### User-facing changes:

- Increase Workbench file upload limit
- Fix Bokeh examples
- Extend `nb_locker` to detect a server disconnection and generate an alert if it occurs
- Docs: Update the notebook app to correctly point to AEN docs
- Docs: Emphasize that permissions are not applied recursively in the workbench

Internal fixes:

- Update Nginx version to v1.12.2
- Remove unused server config file during the compute upgrade process
- Remove already defined compute default settings from the post-script step
- Pin `widgetsnbextension` version to prevent version mismatch issue (ipywidgets)
- Remove `--offline` flag from the conda clone operations
- Support MongoDB 3.4.14 and update pymongo to version 3.2.2
- Fix LDAP username case sensitivity
- Security fixes and enhancements

### v4.2.2 March 1, 2018

Administrator-facing changes:

- Add admin command to change project owner
- Server: Add ability to disable public projects
- Gateway: Add support for SSL private key passphrase
- Docs: Add backup and restore runbook to the docs
- Docs: Emphasize backups before upgrading process
- Docs: Recommend putting AEN and projects folder on the same filesystem
- Docs: Add RHEL version 7.4 to supported versions
- Docs: Add troubleshooting instructions to fix problems when downloading notebook as PDF via LaTeX

User-facing changes:

- Upgrade bokeh to version 0.12.7
- Upgrade holoviews to version 1.8.3
- Upgrade numba to version 0.35.0
- Upgrade scikit-learn to version 0.19.0

Internal fixes:

- Fix bug in init scripts when `requiretty` is enabled
- Fix bugs related to `AEN_SUDO_SSH` option
- Fix bug in `fix_ownership` function when directories contain spaces
- Docs: Fix error in Active Directory configuration example
- Server: Fix bug when updating user/group in supervisor configuration files in post-install for server and gateway



- Server: Fix bug Admin reports on user totals are inconsistent
- Server: Fix error in login screen when open registration and LDAP are enabled
- Server: Fix bug in Last seen date
- Server: Fix bug Monitor Report blank
- Server: Load JS files from local CDN
- Server: Fix error when terminating or relaunching an application from Monitor
- Server: Fix error creating projects when using Internet Explorer 11
- Compute: Fix 404 errors when using pivottablesjs
- Remove Wakari Cloud leftovers

#### **v4.2.1 December 18, 2017**

Administrator-facing changes:

- None

User-facing changes:

- None

Internal fixes:

- Fix undetected “ca” key when using self-signed certificates signed by a private CA
- Fix login redirects when using SSL
- Add verify gateway SSL certificate for get and post requests

#### **v4.2.0 November 22, 2017**

Administrator-facing changes:

- Feature/allow remote MongoDB
- Allow for configuration for login timeout and set default
- Add verbose option to conda create clone
- Avoid duplicate name for resources / compute-nodes
- Allow renaming main and message queue databases
- PAM-based authentication module
- Change wakari logos to Anaconda logos
- Replace ‘wakari’ wording
- New config option to move the user’s home directory into the user’s project directory
- Make logging less verbose in AEN
- Documentation for PySpark kernel installation
- Improve SSL documentation

User-facing changes:

- New config option to move the user's home directory into the user's project directory
- Package cache was moved from user's home directory into the user's project directory
- Change wakari logos to Anaconda logos
- Fix error for deleting tags to work
- Define shell prompt in `.projectrc` template
- Replace 'wakari' wording

Internal fixes:

- Move server unix socket from `/tmp` to `/opt/wakari/wakari-server/var/run`
- Make project deletion synchronous for consistency
- Avoid storing `csrf` token in the user profile
- Expire gateway session when server logs out
- Allow log rotation in the three components
- Fix permissions on static files
- Change log level to debug in gateway
- Do not log private keys in gateway
- Save request remote address when logging action
- Unify logs formatting and timezone in compute nodes with Winston
- Several fixes and documentation improvements

### v4.1.3 August 16, 2017

- Upgrade conda to version 4.3.24
- Upgrade anaconda to version 4.4.0
- Admin application monitor
- Block access to package list view
- Add placeholders in password reset form
- Change static content location
- Fix error when checking for package updates in notebook application
- Replace slashes in project tags
- Fix submit errors in password reset form
- Replace/remove "wakari" word from multiple places
- Fix missing commands missing sudo in start-project
- Improve gateway and compute node validators
- Check if bzip2 is installed during server setup process
- Include port number in host header
- Forbid creation of empty tags
- Repair "Create Account" link in login page

- Use UTC for server logs
- Mark datacenters as trusted by default
- Disable heart beating
- Compute resource: Show full path to log file
- Improve init scripts
- Allow deleting all projects
- mtq: Implement exponential backoff on connection error to mongodb
- In the general admin display, do not show the bind password for LDAP
- The accelerate package has been removed from the installation
- Other minor bugfixes

#### **v4.1.2 March 29, 2017**

This is mainly a maintenance release improving internal machinery and upgrading the root packages.

- Upgrade conda to version 4.3.14
- Upgrade Anaconda to 4.3.1
- Upgrade r-base to 3.2.2
- Fixed AEN nb\_conda to be compatible with conda 4.3.x series
- Several documentation fixes
- Other minor bugfixes

#### **v4.1.1 December 15, 2016**

- Added CentOS 7 support
- Support dots in usernames
- More usernames validation
- Fixed creation (through nb\_conda) of single letter environment names
- Environment names (through nb\_conda) validation
- Fixed uploading of notebook using nb\_anacondacloud
- Fixed attaching of environments in published notebooks through nb\_anacondacloud
- Several documentation fixes
- Other bugfixes

#### **v4.1.0 October 21, 2016**

- Added JupyterLab application
- Removed GateOne terminal application
- Included additional notebook extensions (nbpresent and nb\_anaconda\_theme)

- Updated to conda 4.2.9 in default project environments
- Added HTTP timeout setting for gateway and compute launcher
- Changed default gateway port to 8089
- Added support for all-numeric usernames
- Add R channel to default conda configuration file
- Other bugfixes

### **v4.0.0 June 30, 2016**

- Customized installation with:
  - AEN Functional ID and Group
  - AEN (installation and run) `sudo` commands
  - Removal of root access from the AEN service account
  - Configurable `sudo` command
  - Restriction of `sudo` access to all the processes
- Upgrade Jupyter to 4.2
- Upgrade the anaconda-nb-extensions to the latest versions
- Upgrade Anaconda to 4.0
- Deprecate wakari-publisher
- Security enhancements
- SSL configuration documented between all AEN Server components
- Several bugfixes
- Overall documentation revision and general improvement

### **v0.10.0 February 2, 2016**

- New projects dashboard
- Capability to star and tag a project
- Sticky searches
- New Jupyter Notebook extensions
- Updates to all packages. Highlights: bokeh 0.11, ipython/jupyter 4.1.

### **v0.9.1 October 19, 2015**

- New Search capability to find projects and files within a project.
- Added “Related Projects” list to the project view, based on code similarity.
- New UI for fine-grained access control of project files in the Workbench app
- Viewer app now renders plain text files correctly

- Updated LDAP configuration docs
- Updates to all packages. Highlights: bokeh 0.10, ipython/jupyter 4.0.

**Note** ElasticSearch, and an Oracle JRE, must be installed on the server in order to use the new search features. Indexing of project files will begin when the project is started (or paused and re-started). If search features are not desired, set `"SEARCH_ENABLED": false` in the server configuration file to avoid errors.

## v0.8.0 August 21, 2015

### New Features

- Updated packages based on Anaconda 2.3, and removed older packages no longer in Anaconda.
- Updated IPython to version 3.2.1
- Documentation is now installed with the server (use the Help link in the top navigation bar)
- Added the ability for the administrator to define a customized default project environment.
- The server has been updated to use python 2.7.10.
- Init scripts are now provided for each Anaconda Enterprise Notebooks service.
- Added relevant links to some error pages

### Problems Resolved in this Release

- Project status indicators (e.g. starting, pausing) now automatically update.
- If an access is unauthorized, the server now returns a 403 (Unauthorized) status code and prompts the user to log in.
- Modified nginx configuration to support running the server on non-standard ports.
- The server installation no longer uses a default password for the wakari user. A random password is generated and displayed during installation.
- Prevent double-click from attempting to create a project twice
- Removed an obsolete script reference that was causes a 404 error to be logged in the browser console when opening the Terminal app.
- The installer scripts no longer fail if the database already contains the 'wakari' user.
- Updated example notebooks to work with latest Bokeh release.
- Fixed terminal app key bindings to allow Mac command key to work normally
- Installers now indicate where the installation logs are stored
- LDAP user attributes containing binary data are now ignored.

### Documentation Updates

- Updated and consolidated Troubleshooting guide.
- Simplified some steps in the installation procedure.
- Updated notebooks in the Examples directory for use with the latest IPython Notebook and Bokeh.

- Added a section on project permissions to the Troubleshooting guide.
- Added notes on how to remove a project if the datacenter has already been removed.

### v0.7.0 June 12, 2015

#### New Features

- Updated Bokeh to v0.9
- Ability to list packages installed on the server
- Administrators now have full access to all projects.
- Added automated checking and display of connection status between server, data centers, and compute resources.
- When creating a new project, an environment for the project is automatically created as a clone of the root Anaconda environment.

#### Problems Resolved in this Release

- Problem with checking in files with revision control extension
- Revision control extension can't handle notebook names with spaces
- Problem moving files from one compute node to another if configured for LDAP
- Should default to UTF-8 encoding and warn user if no locale is detected
- Adding a compute resource via the command line admin tool does not work
- The installer now sets `umask 0022` to ensure correct file permissions

#### Documentation Updates

- Added a *Troubleshooting* section to the documentation.
- Added notes on how to configure crontab to start the Anaconda Enterprise Notebooks services at startup
- Example SSL config file now has correct log paths
- Added instructions on how to ensure that POSIX ACL support is enabled on the projects directory.
- Fixed syntax problem in sample LDAP config.json
- Added section on how to use self-signed or private CA certificates

### v0.6.3 March 27, 2015

- Updated LDAP module
- LDAP user filtering
- Added Notebook locking
- Added Notebook integrated revision control system
- Move projects between compute nodes

- User-specific binding to compute nodes (private compute nodes)
- Improved installation process and dependency checking
- Incorporated support for SSL for Server and Gateway nodes
- Improved Gateway error handling
- Fixed package dependencies for update process
- Documentation updates

## Anaconda Enterprise Notebooks 4

*Empower the Data Science Team with cross-collaboration*

AEN is a browser-based Python data analysis environment and visualization tool from Anaconda®. AEN is a ready-to-use, powerful, fully-configured data analytics environment all in a secure, governed environment.

AEN allows data science team members to create and share private notebooks, manage access, control notebook revisions, compare and identify differences across notebook versions, search notebooks for keywords and packages, use enhanced collaborative notebook features—including revision control and locking—and to access an on-premises and/or cloud collaborative notebook server.

The current version of AEN is 4.2.2, released March 1st, 2018.

### User guide

AEN's browser-based management of private packages, notebooks, and environments allows data science team members to:

- Create, share and manage private notebooks.
- Control notebook revisions.
- Compare and identify differences across notebook versions.
- Search notebooks for keywords and packages.
- Use enhanced collaborative notebook features including revision control and locking.
- Access on-premises and/or cloud-based collaborative notebook servers.
- Utilize multiple language kernels like Python and R language in the same notebook.
- Create new notebook environments on the fly without leaving the notebook or entering commands in a prompt.
- Publish results to business stakeholders as interactive visualizations and presentations.

To quickly get up and running with AEN, see [Getting started](#).

Download the [Cheat sheet](#) for easy reference.

### Concepts

- [Projects](#)
- [Team collaboration](#)

- [Access control](#)
- [Sharing projects](#)
- [Project tags](#)

## Projects

AEN users interact with the system predominantly through projects.

A project is a set of conda environments, Jupyter Notebooks, and other files.

Each project has a project drive that all team members can access. The size of the drive is not limited by AEN. Contact your system administrator if you find you do not have sufficient space.

Each project has a separate project directory on the project drive.

The project directory is a directory for project files and data that is separate from the project owner's and team members' home directories, so that team members can share and have equal access.

The path to your project directory is `/projects/<project_owner>/<project_name>`.

For administrative information about projects, directories, and permissions, see [Projects and permissions](#).

## Team collaboration

Teams collaborate in AEN using projects. Projects allow a team to easily come together by sharing the resources, applications, and environments that are necessary to collaborate effectively.

The AEN project owner and any team members connected to their project will have access to the same:

- Shared files and home directories.
- Shared Python and R environments.
- Shared nodes and hardware.
- Common applications.
- Web user interface.

For more information, see [Working with projects](#).

## Access control

AEN access controls allow you to:

- Add and remove project access for new team members.
- Limit the access to specific folders and files to members of your project team.
- Use permissions to extend execute access to team members. By default, all of the team members on a project have read and write access to all project assets.

Access control is performed from each project's Workbench application.

For more information, see [Controlling access to your project](#).



## Sharing projects

AEN supports both public and private sharing.

A project can be “public,” which means that anyone with access to the system can view the project assets.

Any content placed in the `public` folder in a project is publicly accessible using its URL.

A project can be “private,” which means that only the project owner and team members can view the project assets.

You can also *limit who can access specific files*.

## Sharing Jupyter Notebooks

In addition to general project sharing capabilities, you can also publish Jupyter Notebooks to Anaconda Repository. This automatically versions the notebook and allows you to define who can view the notebook.

## Project tags

Tags are used to:

- Group similar or related projects.
- Identify your project so that it is easier to find.
- Let others know about your project.

You can *add and remove tags* for any project that you have access to.

## Getting started

This section contains information and tasks for first-time AEN users.

In this getting started guide, you will:

- 1. *Download the AEN cheat sheet*
- 2. *Access your user home page*
- 3. *Create a new project*
- 4. *Add collaborators*
- 5a. *Open an example notebook, OR*
- 5b. *Create a new environment and notebook*
- 6. *Create checkpoints for version control*
- 7. *Share your notebook and environment with others*
- 8. *See what to do next*

### 1. Download the AEN cheat sheet

Before you start, download and print the *AEN cheat sheet* for easy reference.

## 2. Access your user home page

After your administrator has set up your server and new Anaconda account, you will receive a welcome email.

1. Click the link in the email to open the AEN login page.

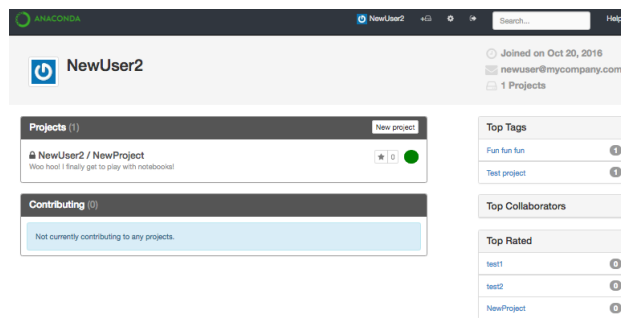
NOTE: Use the domain name and not the IP address when you connect to AEN. Using the IP address can cause TLS and security certificate errors.

2. Enter your AEN account username and password.

NOTE: Some administrators allow you to create your own account. If your administrator has allowed this, in the create a new account section, create your own username and password.

3. Click the Login button.

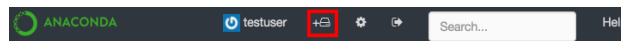
Your user home page, where all good things happen, is displayed:



## 3. Create a new project

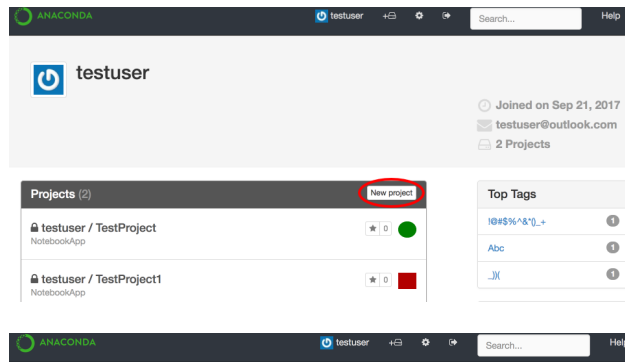
1. There are 2 ways to create a new project in AEN:

- On the right side of the AEN task bar, click on the New Project icon:



- On your home page, click the New project button:

2. On the Project page that is displayed, type a name for your project, such as “Testing.”



## New Project

Create your project here!

Project Name

Project names must start with a letter and contain only alphanumeric characters.

Summary

☐ Public

Anyone can see this project. Collaborators have write access.

☒ Private

No one can see this project except collaborators.

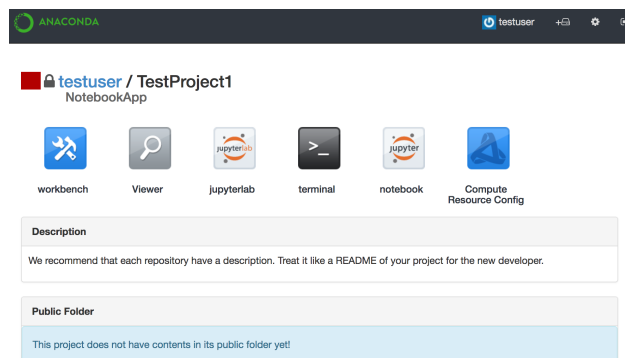
Next

3. Type a summary of the project so you can recognize it later.
4. Select whether your project will be public or private.
5. Verify that the default data center is selected.

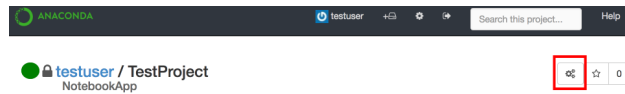
TIP: You can update the project summary and description at any time from the **Project** menu in the Project Settings. To return to your project at any time, click the project name.

6. Click the Next button.

Your new project's home page is displayed:



7. To change the project settings, click the Project Settings icon on at the top right.



8. Modify the summary or add a description of the project.

TIP: A project description is recommended, and may be written in Markdown syntax (plain text valid Markdown).

To see how Markdown will be displayed, in the description area, click the **Preview** tab.

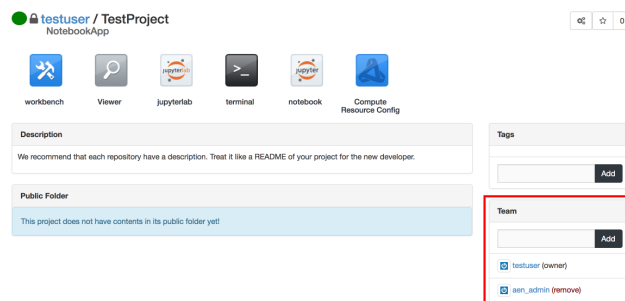
#### 4. Add collaborators

You can add team members to your project as collaborators. Adding team members to your projects makes collaboration easy because they have full access to the project's applications, files and services.

When you add team members, their home directory is mounted in the project. There is no need to download and email data or scripts—team members can work on the same files in the same environment in which you are working.

To add collaborators to your project:

1. From your project home page, in the Team box, begin typing a teammate's username.
2. In the list that is displayed, select the teammate's username.
3. Click the Add button.

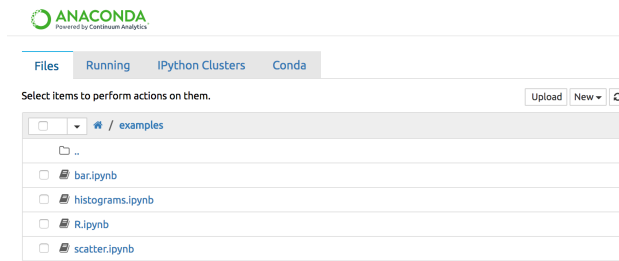


1. Repeat these steps for each team member you want to add as a collaborator.

TIP: You can add or remove team members any time from the **Team** menu in Project Settings. You can also modify a team member's read, write or execute permissions at any time from the [Using Workbench](#).

#### 5a. Open an example notebook, OR

1. From your project home page, click the Jupyter Notebooks icon.
2. On the File View page, click the Examples folder.
1. Select any of the example notebooks.
2. To see the default results of the formulas used in the displayed notebook, in the **Cell** menu, select Run All.
3. To experiment with changing the notebook, edit any of the formulas in the notebook.
4. In the **Cell** menu, select Run All.



Any differences resulting from your edits are displayed.

## 5b. Create a new environment and notebook

If you are already familiar with creating notebooks, you can easily set up a new environment with the programs you need—like SciPy and NumPy—then open a new notebook and make your edits.

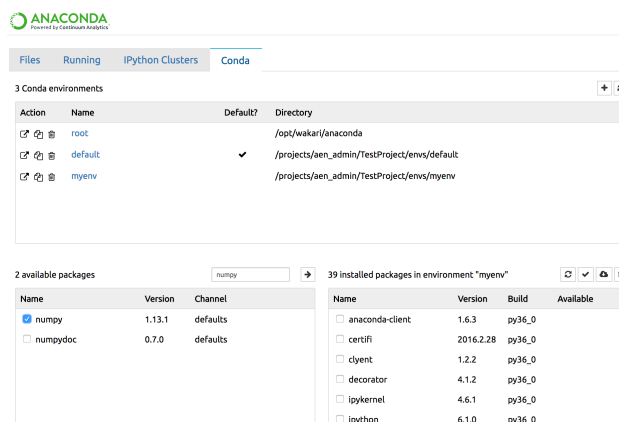
To create a new environment:

1. From your project home page, click the Jupyter Notebooks icon.
2. On the File View page, click the **Conda** tab.
3. To add a new conda environment, on the top right of the **Conda** tab, click the + icon.
4. Type a name for your environment.
5. Select Python 2, Python 3 or R language kernel.
6. Click the Create button.
7. To activate your new environment, click its name.

The packages that are available and installed in your new environment are displayed.

## Adding SciPy and Numpy packages

1. In the available packages section, search for the package name `numpy`—all lower case.
2. In the results section, next to `numpy`, select the checkbox.



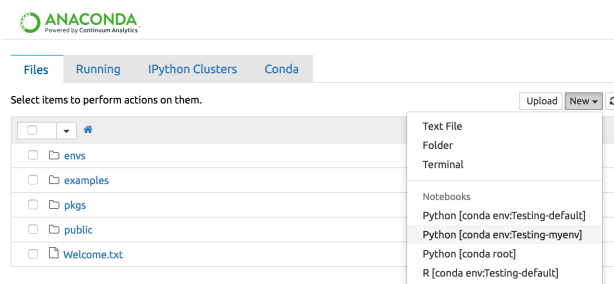
1. Click the Install icon.
2. To confirm your installation, click the Install button.

Numpy is displayed in the installed packages section—if not, click the Refresh button. Repeat these steps to install the Scipy package—searching for `scipy` in step 1.

TIP: You can return to this screen at any time to add additional packages to this environment.

## Creating a new notebook in your environment

1. From the AEN homepage, click the **Files** tab.
2. On the top right of the **Files** tab, click the New button.
3. Under Notebooks, select the Python environment with the name you entered while *creating a new environment*.



NOTE: If you do not see your new environment listed under Notebooks, next to the New button, click the Refresh button.

A new locked notebook is displayed. Paste or write some code to execute when you are ready.

## 6. Create checkpoints for version control

Whether you are exploring an existing notebook, or creating a new one, you can easily create checkpoints, return to an earlier version, compare two different versions and save them for reference.

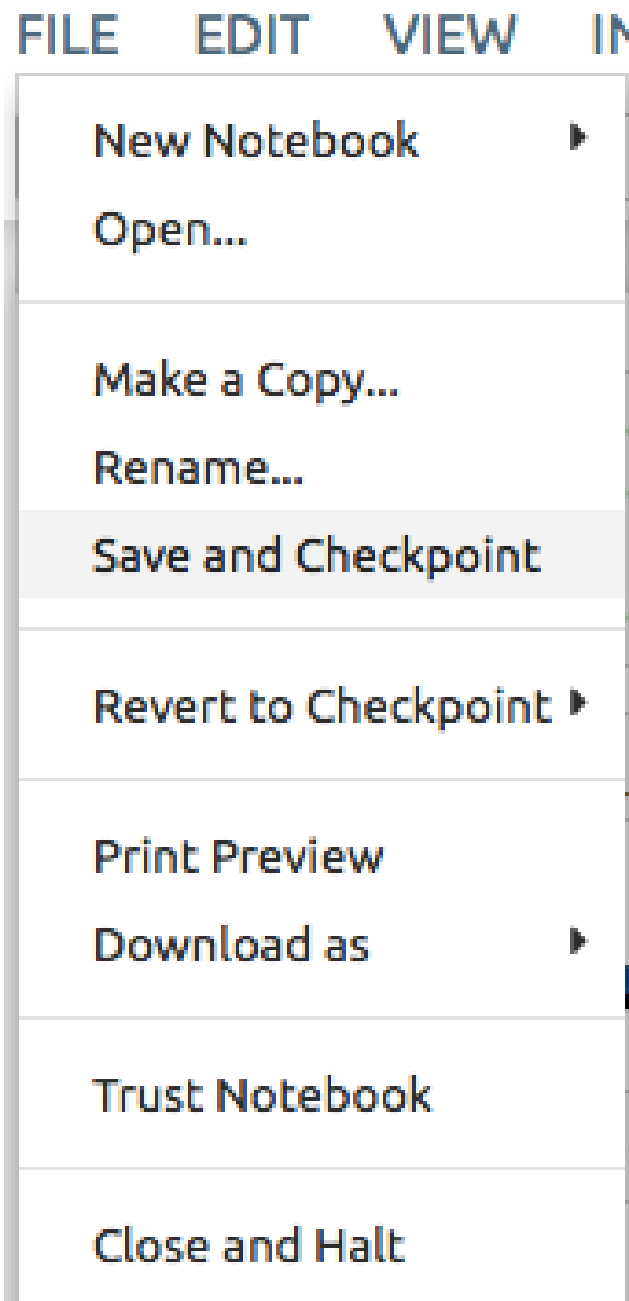
To create a checkpoint, in the **File** menu, select Save and Checkpoint:

To revert your notebook to a previous checkpoint, in the **File** menu, select Revert to Checkpoint.

NOTE: For more information about revision control features, including creating commits and comparing differences, see *Using the Revision Control Mechanism extension*.

## 7. Share your notebook and environment with others

See *Sharing projects and notebooks*.



### 8. See what to do next

Now that you have completed the Getting Started guide, you are ready to move on to [basic tasks](#) and [advanced tasks](#).

#### Basic tasks

This section contains information and tasks that use the web browser to manage projects and is best-suited for any beginning AEN user:

#### Working with projects

Almost everything in AEN starts by opening an existing project or creating a new one.

After that, you can set up a special environment with the packages you want, set their access permissions and modify your project settings.

#### Searching for a project or file

- *Types of files searched*
- *Search indexing*
- *Using search constructs*
- *Searching metadata fields*
- *Searching a project*
- *Saving a search*
- *Removing a saved search*

To search for projects and files, use the Search box in the AEN navigation bar. The search provides different results depending on which page you search from:

- On a project home page, search results include any files that match your search criteria within the current project.
- On any other AEN page, search results include any files that match your search criteria within all projects.

TIP: Your search results include only files and projects that you can view: public projects, and private projects to which you have a minimum of view access.

#### Types of files searched

The following types of files are included in search results:

- `.py`—Python source files.
- `.ipynb`—IPython/Jupyter notebooks.
- `.txt`—plain text files.
- `.md`—Markdown files.



## Search indexing

Files that are modified while a project is running are automatically re-indexed shortly after the files are modified. If you create or update a large number of files—such as cloning a git repository or copying a directory—search results may take several minutes to update.

Files that are modified while the project is not running are re-indexed only after the project is started.

## Using search constructs

You can use the following search constructs:

- Ordinary words will match the full-text contents of any file.
- Wildcards are permitted.

EXAMPLE: `John*` will match John and Johnny. These are glob patterns and are similar to their usage in the command line.

- Combine queries using AND or OR, and group them using parentheses `()`.

Regular expression patterns can be embedded in the query string by wrapping them in forward-slashes `/`:

```
name:/joh?n(ath[oa]n)/
```

The supported regular expression syntax is explained in [the Elasticsearch reference](#).

NOTE: Wildcards apply inside a regular expression. A query string such as `/. *n/` would force the search to visit every term in the index.

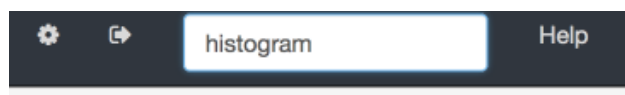
## Searching metadata fields

You can search in specific metadata fields:

- `imports:name`—matches files that import the module name.
- `uses:name`—matches files that reference the identifier name. Referenced names include any functions and globals imported from other modules, as well as the names of any methods invoked on any object.
- `defines:name`—matches files that define the identifier name. Defined names include functions defined at global scope, class names, and method names within classes.
- `acl:user`—matches files in which the named user has read access or higher.

## Searching a project

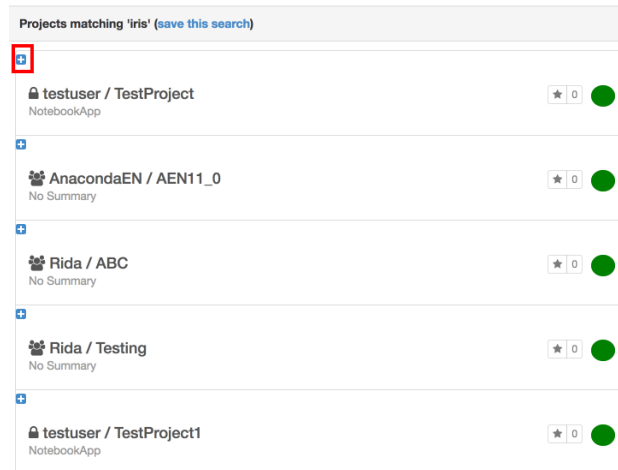
1. In the Search box, type a string of text:



TIP: Search by glob patterns, which are similar to file matching in the command line.

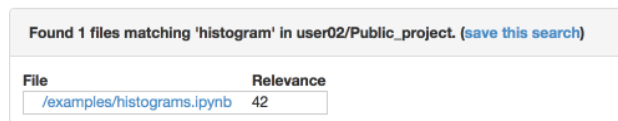
EXAMPLE: To find projects in the test family that are numbered from 00 to 99, search for `Test-??`. To find all projects whose name ends with “Stats,” search for `*Stats`.

2. Press Enter.
3. In the search results, click the plus + icon above a project name to show a list of matching files in the selected project:



TIP: Click the project name to open the project’s home page.

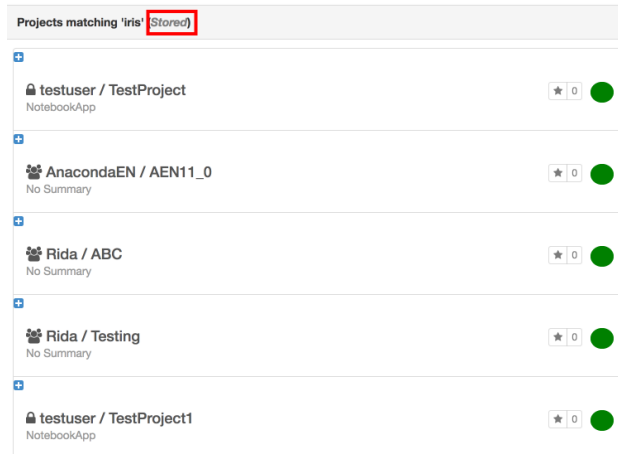
4. To view a file, click its file name in the matching files list:



## Saving a search

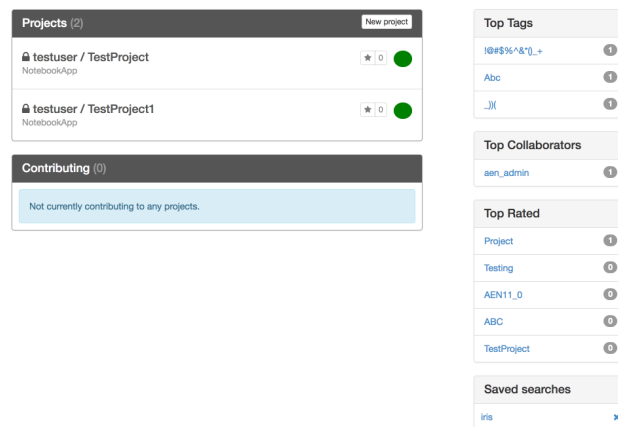
1. At the top of the search results, click Save this search:

The “save this search” text changes to “stored” and your search is saved. Your saved searches are listed on your home page.



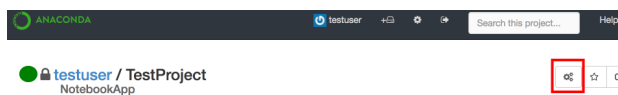
## Removing a saved search

On your home page, in the Saved searches section, click X next the saved search that you want to remove:

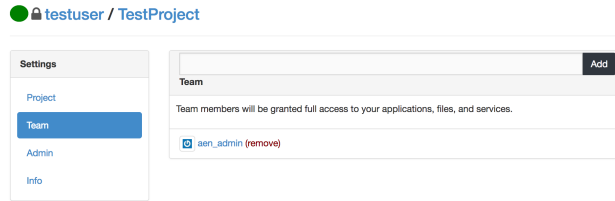


## Adding and removing team members on a project

1. On the project home page, click the Project Settings icon to open the Project Settings page.



2. In the **Settings** menu, select Team.



## Adding a team member

1. In the username box, type in the first few letters of the username for the team member you want to add to the project.
2. In the list of usernames that displays, click the user to add.
3. Click the Add button.

## Removing a team member

Click the red Remove link next to the name of the user you want to remove from the project.

## Controlling access to your project

- *Controlling team member access*
- *Controlling non-team member access*

## Controlling team member access

By default, all of the team members on a project have read and write access permissions for all project assets.

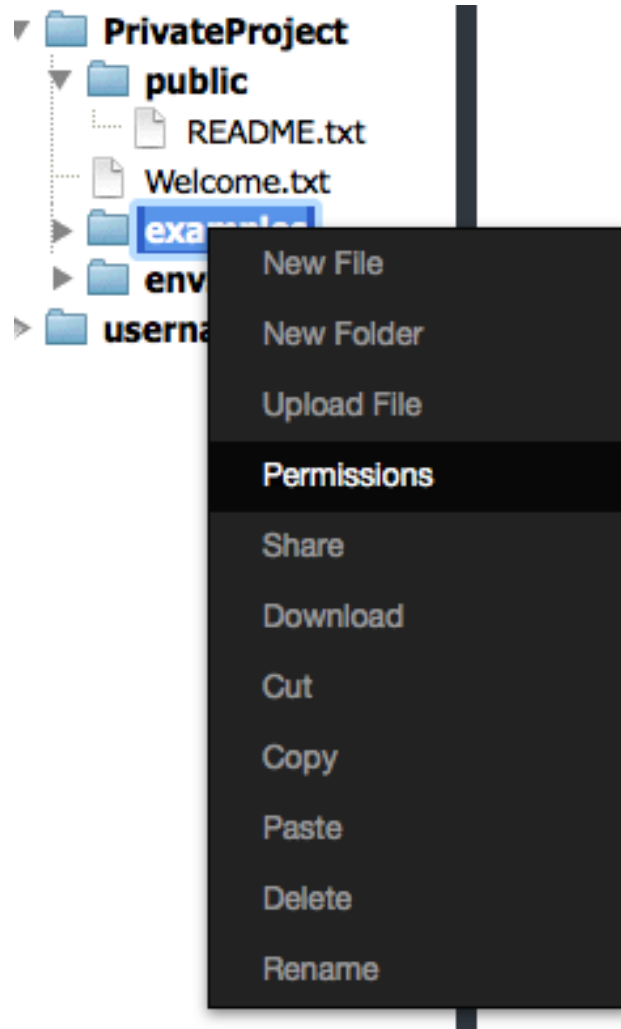
The available permissions are read, write and execute. If you remove all individual or group permissions for a project asset, team members will not be able to access that asset.

To change a project's permissions:

1. Open the project's home page.
2. Click the Workbench icon.
3. In the Workbench app, right-click the file or folder you want to limit access to.

NOTE: When you change a folder's permissions, the permissions of files and folders inside it do not change. You may change the permissions of those files and folders manually.

4. In the menu that displays, select Permissions:



A list of owners and team members who have access to your project is displayed.

- Find the team member you want to change access for:

Permissions for examples

Owner:  Group:

Who	Type	Read	Write	Execute
owner		<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
group		<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
others		<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>
Mask		true	true	true
<input type="text" value="username"/>	User	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input type="text" value="username"/>	Group	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
<input type="text" value="username2"/>	User	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>
<input type="text" value="username2"/>	Group	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
<input type="text" value="username3"/>	User	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
<input type="text" value="username3"/>	Group	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

- Next to the team member's name, select or deselect the permissions for that user.

NOTE: You can add a team member and set their access at the same time by typing their name in a username box, setting their permissions, and then clicking the Add button.

- Click the Submit button.

The selected permissions are added, and the deselected permissions are removed.

NOTE: If a team member is in the Workbench application when you give them access, they must refresh their browser window to see their current permissions.

## Controlling non-team member access

You can choose to grant file or folder access to someone who is not part of the project team, as long as that person has an AEN account.

Sharing with individuals outside the team is a four step process:

- Copy or move the file or folder to your home directory.*
- Give the user read and execute access to your home directory.*
- Add the user to the file's permissions.*
- Have the user add your directory to their workbench.*

## Copying a file or folder to your home directory

Your home directory is displayed at the bottom of the File Manager pane in the Workbench.

To protect the other files and folders in your home directory—those you are not providing permissions to a user to access—we recommended that you:

1. Create a sub-folder.
2. Rename the folder with the name of the user you are granting access to.
3. Copy or move the file you want to grant permissions for to the renamed folder.

The file is copied or moved to the new location and is ready for you to update the file permissions.

## Granting file access

You must select read and execute access for a user to be able to view, but not edit, the files or folders.

1. Right-click the name of the file or folder you are granting access to.
2. In the menu that is displayed, select Permissions.
3. Click the Add button.
4. Type the username of the user to whom you are granting file access and press Enter.

**TIP:** If you grant access to a folder instead of a specific file, you only have to set permissions the first time you share the folder with each user, unless you need to update the permissions.

## Adding file permissions for a user

Once a user is included in your Permissions list, you must *add the correct permissions* for the user, in the same way as you would for a team member.

Once complete, depending on the access granted, the user will be able to view, read, change, and execute the file.

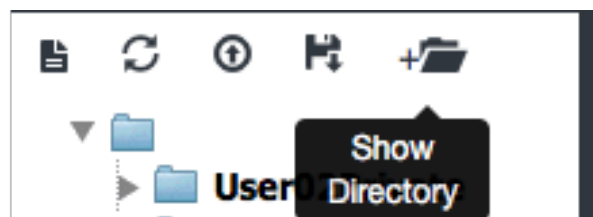
**NOTE:** If you change permissions for a folder instead of a file, the user will be able to see and access any files within that folder.

## Adding a directory to a user's workbench

The user can now add your home directory to their Workbench File Manager.

To add your home directory to another user's workbench, have the other user follow these steps:

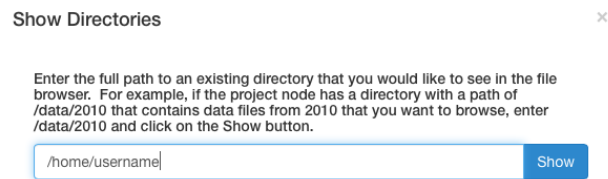
1. Click the Show Directory button at the top of the Workbench File Manager:



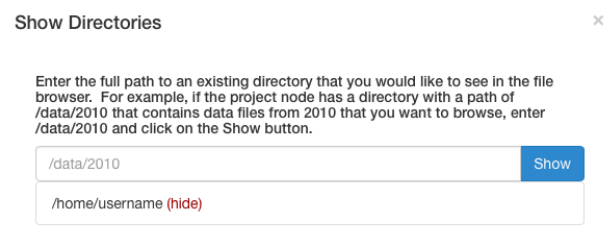
The Show Directories dialog box displays.

- In the text box, type `/home/[yourusername]`.

NOTE: Replace `[yourusername]` with your AEN username.



- Click the Show button.
- Verify that the folder is now displayed below the text box:



- Close the Show Directories dialog box by clicking the X in the upper-right corner or by clicking anywhere outside the box.
- Click the Refresh button.

The shared file is displayed in the File Manager:

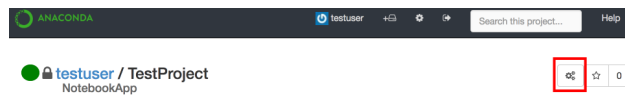


## Starting and stopping a project

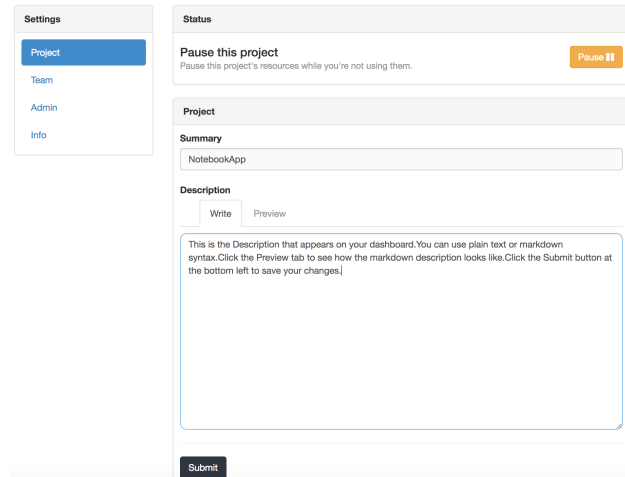
TIP: Stopping a project stops all the applications launched for that project that use resources when running, such as memory and compute cycles. It is best to stop projects when they are not in use.



1. On the project home page, click the Project Settings icon to open the Project Settings page.



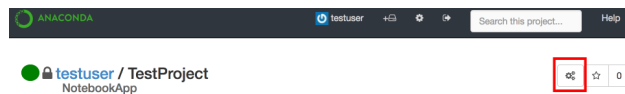
2. In the **Settings** menu, select Project.



3. In the Status section, click the Start or Stop button to toggle between manually starting and stopping your project.

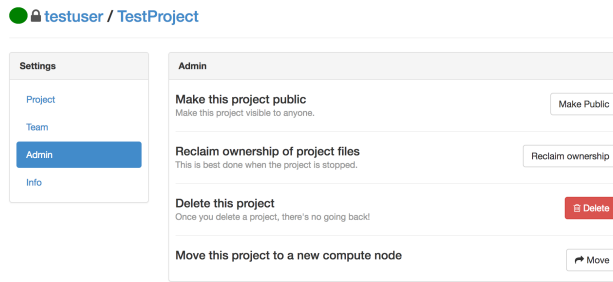
## Making a project public or private

1. On the project home page, click the Project Settings icon to open the Project Settings page.



2. In the **Settings** menu, select Admin.

3. Click the Make Public button.



4. If the project is already public and you want to make it private, click the Make Private button.

## Tagging a project

Existing tags assigned to a project are listed in the Tags section on the project's home page.

## Adding a tag

1. In the Tags box, type the name of the tag you want to add:

Tags

learning Add

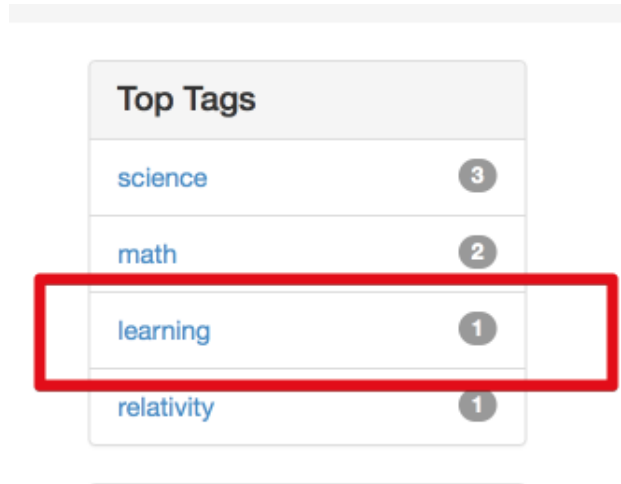
2. Click the Add button.

The new tag is added to the Tags list:

Tags

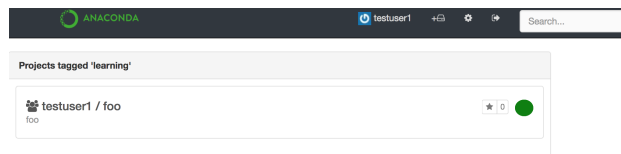
learning Add

If the tag was not already in the Top Tags list on your user home page, it is added. If the tag was already listed because another project used it, the number next to the tag is incremented:



## Removing a tag

1. On your user home page, in the Top Tags list, click the tag name.



1. In the Tags list, click the X button next to tag name.

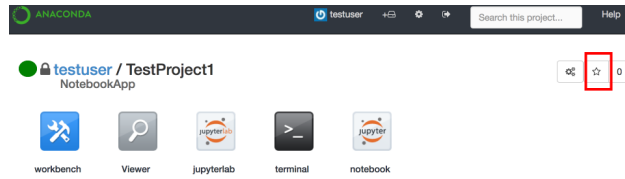
## Starring a project (rating)

Starring a project makes it appear on your user home page in the Top Rated list.

Adding or removing stars for a project does not affect the stars added by other users.

1. Open the project that you want to star.
2. On the project home page, click the Star icon at the upper right:

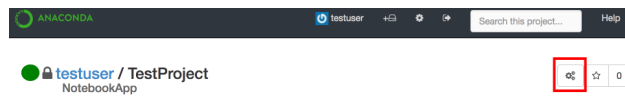
3. To unstar a project, click the Star icon again.



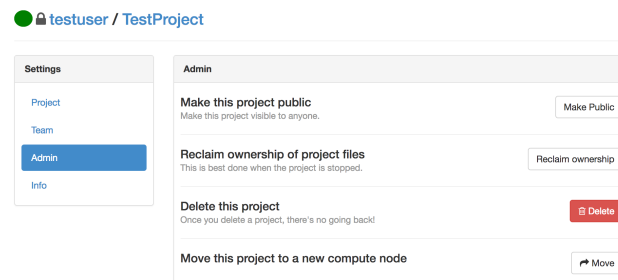
## Claim ownership of a project

When you claim ownership of a project, ownership of all files and folders created by the team members on the project is transferred to you. Project files and folders are copied and renamed.

1. *Stop the project* to prevent team members from making changes while you are changing ownership.
2. On the project home page, click the Project Settings icon to open the Project Settings page.



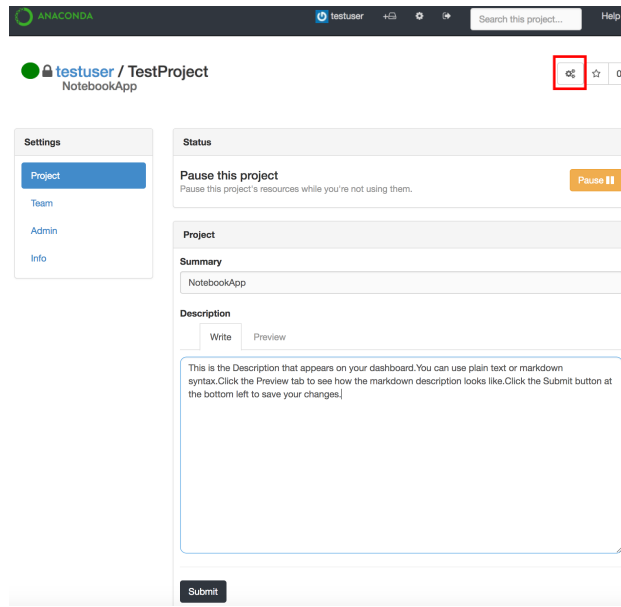
3. In the **Settings** menu, select Admin.



4. Click the Reclaim ownership button.

## Changing a project's summary or description

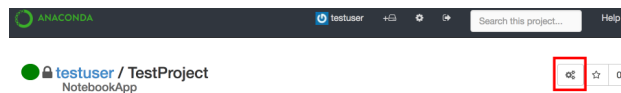
1. On the project home page, click the Project Settings icon to open the Project Settings page.
2. In the **Settings** menu, select Project.



3. Update your project's summary using plain text or its description using Markdown syntax.
4. Click the **Preview** tab to see a preview of the Markdown description.
5. Click the Submit button.

## Viewing a project's status

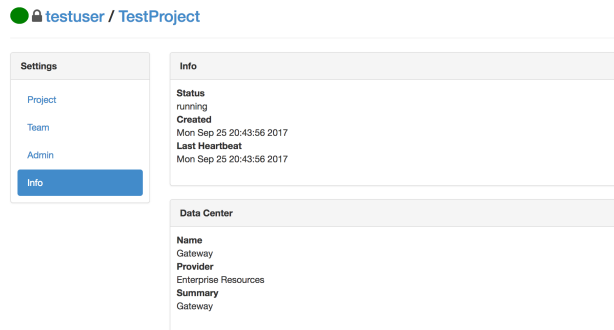
1. On the project home page, click the Project Settings icon to open the Project Settings page.



2. In the **Settings** menu, select Info.

On the Info page, you can see:

- Whether the project is currently running or stopped.
- When the project was created.
- When the project was last accessed.



- The data center in which the project is running.

## Viewing related projects

Related projects are listed on a project's home page.

These are projects that contain fields that are most similar to the current project.

**TIP:** You will only see projects to which you have been granted access: public projects, and private projects on which you are a team member.

## How related projects are identified

To determine which projects should be listed in Related Projects:

1. The recommendation engine scans the current project's files and weights the terms found to determine which of them to use for the likeness search.
2. The engine performs a search, with extra weight given to the “uses” and “imports” keywords.
3. The engine finds the files and projects that are most similar to the current project and scores the results.
4. The top-scoring matches are displayed in Related Projects. Only public projects and private projects to which you have access are included.

## Viewing top-rated projects

Top-rated projects are listed on your home page:

The number next to a project represents the number of stars that have been given to that project.

Click a project name to view the project's home page.

Team

Add

user02 (owner)

user01 (remove)

Related Projects

user01 / TestProject2

No Summary

user02 / User02Private

No Summary

user01 / TestProject

No Summary

Top Rated	
einstein	2
euler	1
laplace	1
plank	1
Public_project	1

### Using tags to find a project

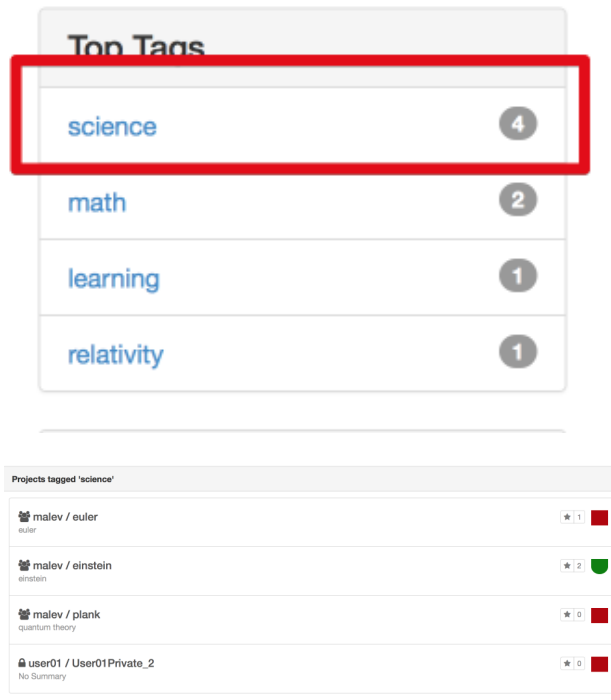
The top tags used on your projects are listed on your home page:

The screenshot shows the Anaconda Cloud user interface for a user named NewUser2. The interface includes a sidebar with 'Projects (1)' and 'Contributing (0)'. The main content area displays a project named 'NewUser2 / NewProject' with a description 'Woo hoo! I finally get to play with notebooks!'. On the right, there are sections for 'Top Tags' (Fun fun fun, Test project), 'Top Collaborators', and 'Top Rated' (test1, test2, NewProject).

To list all projects that share a specific tag, click the tag name:

A list of projects with the selected tag is displayed:



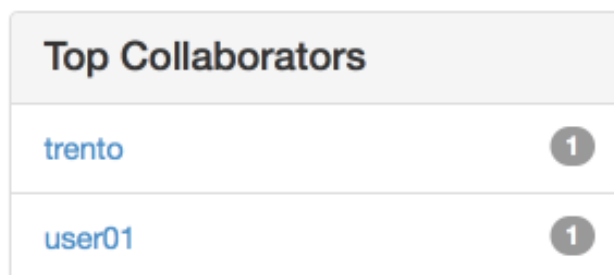


TIP: The list includes only projects that you have access to: public projects, and private projects on which you are a team member.

Click a project name to open the project's home page.

### Viewing your top collaborators

Your top collaborators are listed on your home page:



These are the team members who have the most projects in common with you.

To view a collaborator's home page—where you can see all public projects and the private projects they have shared with you—click the collaborator's name.

## Sharing projects and notebooks

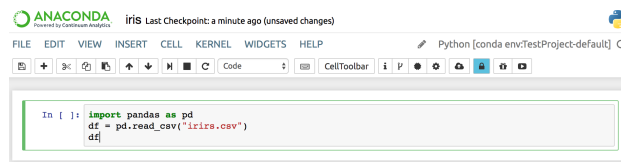
For information on sharing projects via the project settings and access control, see [Sharing projects](#).

To upload a Jupyter Notebook to Anaconda Repository:

1. Log in to Repository by running the `anaconda login` command or by using the login user interface provided by the [nbextension](#).

CAUTION: If you are not using a secure connection, we strongly recommended that you use the command line to log in.

2. To share your notebook environment, select the Attach conda environment checkbox. This ensures that your team members will have the right environment for your notebook.
3. Click the Upload button to upload your notebook to your local Repository or to [Anaconda.org](#), depending on how your administrator has set up AEN:



NOTE: If you have not yet logged into Repository or Anaconda Cloud, or have not created an account, you will be asked to do so.

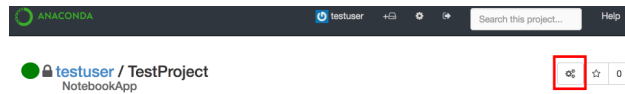
## Other ways to share a notebook

- Print—In the **File** menu, select Print.
- Download and share—In the **File** menu, select one of the following options:
  - Download as Notebook.
  - Download as Python.
  - Download as HTML.
  - Download as Markdown.
  - Download as ReStructured Text.
  - Download as PDF.
- Share and control team members' direct access to read, write and/or execute your notebook file or folder. For more information, see [Controlling access to your project](#).
- Share and control non-team members' file or folder access. For more information, see [Controlling access to your project](#).
- Create a presentation with [NBPresent 4.1](#).

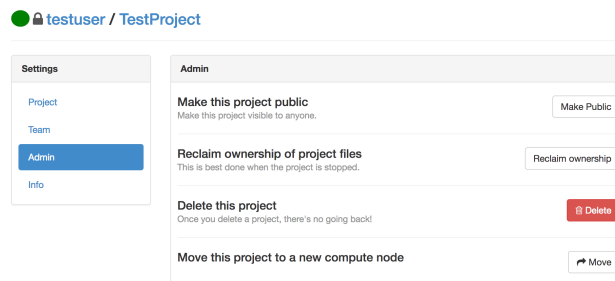
## Deleting a project

CAUTION: Deleting a project deletes all project files and information! There is no undo option.

1. Download a copy of any project files that you need to save.
2. On the project home page, click the Project Settings icon to open the Project Settings page.



3. In the **Settings** menu, select Admin.



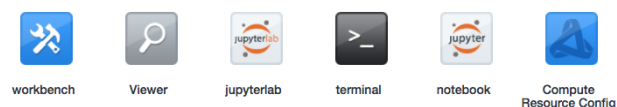
4. Click the Delete button.

## Using AEN applications

The applications in your project make it easy for you to interact with your files and data, manage your project's resources and to customize your AEN experience.

To use applications, log into AEN, then select the project you want to work on or create a new project and open it.

On the project home page, the following application icons are displayed:



TIP: Each application opens in a new browser tab. You can run multiple applications at the same time in your project. For more information on each AEN application, see:

- *Using Workbench*—File viewer and manager, including permissions settings.
- *Using Viewer*—View-only versions of notebooks and other text files.
- *Using JupyterLab*—Alpha preview of the next generation notebook.
- *Using Terminal*—Basic bash shell Terminal.
- *Using Jupyter Notebook*—Jupyter Notebooks with extensions.
- *Using Compute Resource Configuration*—Project information, view and manage applications.

## Using Workbench

- *Opening Workbench*
- *Using File Manager*
- *Opening the Workbench terminal*

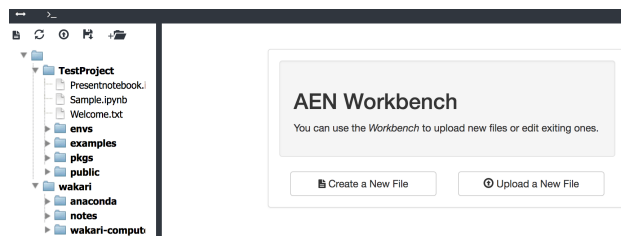
Workbench is a file viewer and manager that includes a file editor and file permissions manager.

You can use Workbench to:

- Upload and download files using the *File Manager*.
- Create new files and folders using the *File Manager*.
- Copy and move files to new locations using the *File Manager*.
- Rename files and/or folders using the *File Manager*.
- Manage the *access permissions* of team members.
- Grant or revoke *access to non-team members*.

Workbench also includes a simple Terminal application, which is convenient because the File Manager is always visible, making navigation simple.

When you first open Workbench, the File Manager is displayed in the left pane, and the Create a New File and Upload a New File buttons are in the right pane:



When you open a file or Workbench Terminal, it is displayed in the right pane. To make the Create or Upload a file options re-appear, refresh your browser window.

Two small icons are displayed in the black navigation bar at the top of the Workbench page. Hovering over them displays tool tips that describe their use:

- The Toggle icon displays or hides the File Manager.
- The Terminal icon opens a simple terminal window.

## Opening Workbench

To open Workbench:

1. Log in to AEN.
2. Select the project you want to work on, or create a new project and open it.
3. On the project home page, click the Workbench icon:



Workbench opens in a new browser window.

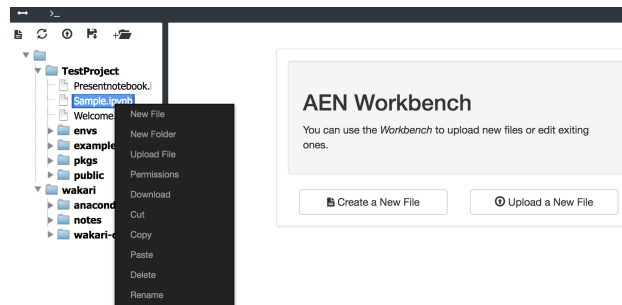
## Using File Manager

The File Manager is an intuitive way to interact with your files and folders.

## Using the options drop-down menu

To perform any of the actions described below:

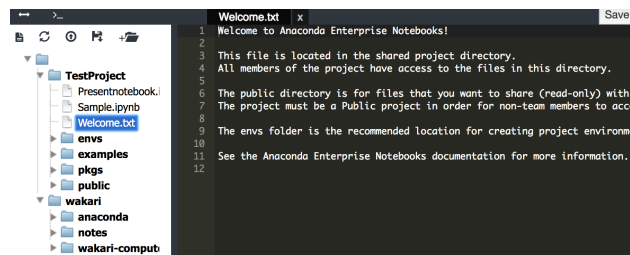
1. Right-click on any folder to display the options drop-down menu.
2. Select one of the following options:
  - New File—Create and edit a new file.
  - New Folder—Create a new folder.
  - Upload File—Upload a file to the selected folder. You can also drag a file to the folder.
  - Permissions—*Control access to files and folders.*
  - Cut—Cut the selected file or folder.
  - Copy—Copy the selected file or folder.
  - Paste—Paste a previously cut or copied file or folder.
  - Delete—Delete the highlighted file or folder.
  - Rename—Rename the highlighted file or folder.



## Editing files using the File Editor

1. Double-click any text file in the File Manager.

The File Editor opens in the right pane:

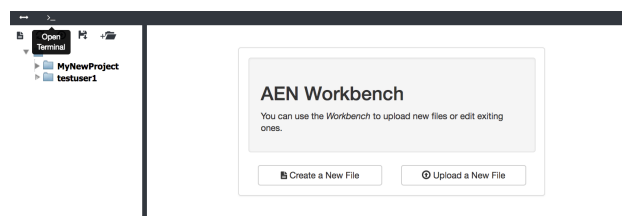


2. When you finish editing the file, click the Save button.

NOTE: To close the file without saving, click the X at the top of the page under the file name.

## Opening the Workbench terminal

In the navigation bar, click the Open terminal icon:



A Terminal—bash shell—is displayed in the right pane.

**TIP:** You can open additional terminals by clicking the Open terminal icon again, or by clicking the Plus + icon at the top of an open terminal.

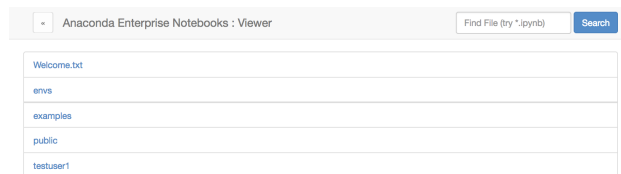
To move between terminal windows, click the **Terminal** tab in the navigation bar, then select the number of the terminal window you want to work in.

## Using Viewer

The Viewer application displays a static, view-only version of your notebooks and other text files by rendering the text files directly and using the NBConvert tool to convert notebooks to static HTML.

1. Log in to AEN.
2. Select the project you want to work on, or create a new project and open it.
3. On the project home page, click the Viewer icon.

Viewer opens in a new browser window:



4. Click any folder to view its contents, or click any filename to view the file.
5. To search for a file or folder name, type text in the Find File box, then press the Enter key. This is not a full-text search, but wildcards are permitted.

## Using JupyterLab

JupyterLab is an early alpha-preview of the next generation of the Jupyter Notebook. It is included so that you can take a tour and play with its capabilities.

**CAUTION:** JupyterLab is experimental. It is not yet intended for production work.

JupyterLab does not include any of the notebook extensions that are available in the *Jupyter Notebook app*.

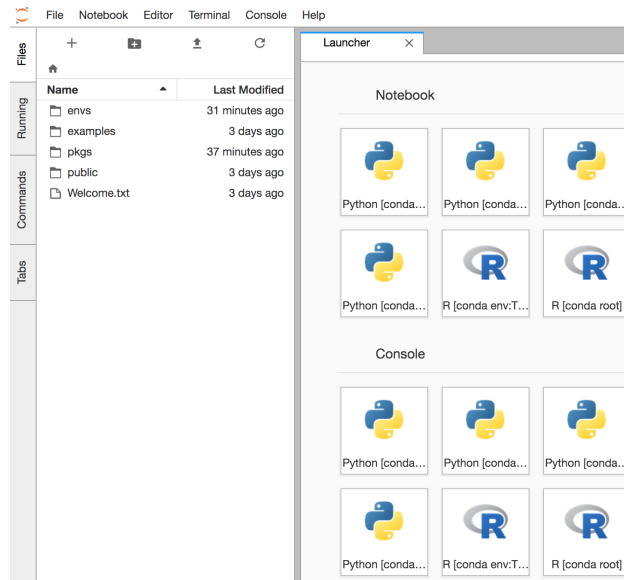
For more information about JupyterLab, see the [documentation](#).

You can also download and print a `Jupyter cheat sheet` on using Jupyter Notebook and the new JupyterLab.

To open JupyterLab:

1. Log in to AEN.
2. Select the project you want to work on, or create a new project and open it.
3. On the project home page, click on the JupyterLab icon.

JupyterLab opens in a new browser window:



Experiment with the application on your own, using the **Notebook**, **Editor**, **Terminal** and **Console** menus.

To review a guided tour of all of the features JupyterLab will contain when it is ready for production, click the Take a tour link in the right pane.

## Using Terminal

The Terminal application is a simple bash shell terminal that runs in your browser:

```
+ 1 bash
(/projects/aen_admin/TestProject/envs/default) ls
envs  examples  pkgs  Presentnotebook.ipynb  public  Sample.ipynb  Welcome
(/projects/aen_admin/TestProject/envs/default) █
```

Using Terminal, you can:

- Access your home directory and your project drive.
- Open multiple shells within one instance of Terminal.
- Open multiple instances of Terminal in the same browser window.

1. Log in to AEN.
2. Select a project you want to work on, or create a new project and open it.
3. On the project home page, click the Terminal icon:





## Terminal

Terminal opens the project directory in a new browser window.

By default, the project directory is `/projects/username/project-name`.

EXAMPLE: `/projects/TestUser/MyFirstNotebook`

4. To see the physical path of your directory, run the Print Working Directory command `pwd -P`.

TIP: The physical path `-P` is important because project attaches data to the beginning of your virtual path to keep your project files together.

5. To navigate out of your project directory to your home directory, run the command `cd`.
6. To return to your project directory, run the command `cd/projects/username/project-name`.

TIP: If you are new to navigating in a terminal, you may want to use *the Workbench terminal*, which includes a visual navigation tree in the File Manager.

### Using multiple Terminals

You can open as many terminals as you want.

To open another shell in the terminal, in the upper left of the pane, click the plus + icon.



A corresponding number appears after the plus + icon and 1.

To move to another Terminal, click the corresponding number.

The color of the number tab changes to show which terminal is currently selected.

### Using Jupyter Notebook

- *Opening the Jupyter Notebook application*
- *Using example notebooks*
- *Creating a new Jupyter Notebook*

The Jupyter Notebook application allows you to create and edit documents that display the input and output of a Python or R language script. Once saved, you can share these files with others.

NOTE: Python and R language are included by default, but with customization, Notebook can run several other kernel environments.

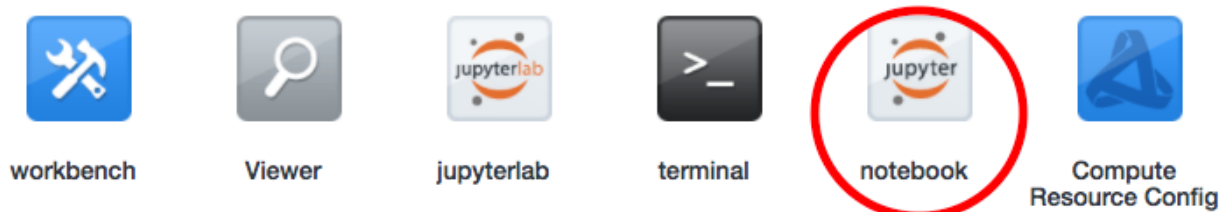
This page provides a brief introduction to Jupyter Notebooks for AEN users.

For the official Jupyter Notebook user instructions, see [Jupyter documentation](#).

For information on the notebook extensions available in AEN, see [Using Jupyter Notebook extensions](#).

### Opening the Jupyter Notebook application

1. Log in to AEN.
2. Select the project you want to work on, or create a new project and open it.
3. On the project home page, click the Jupyter Notebook icon:



Jupyter Notebook opens in a new browser window:

TIP: You can see the same *File Manager* in the Terminal, Workbench, and Viewer applications.



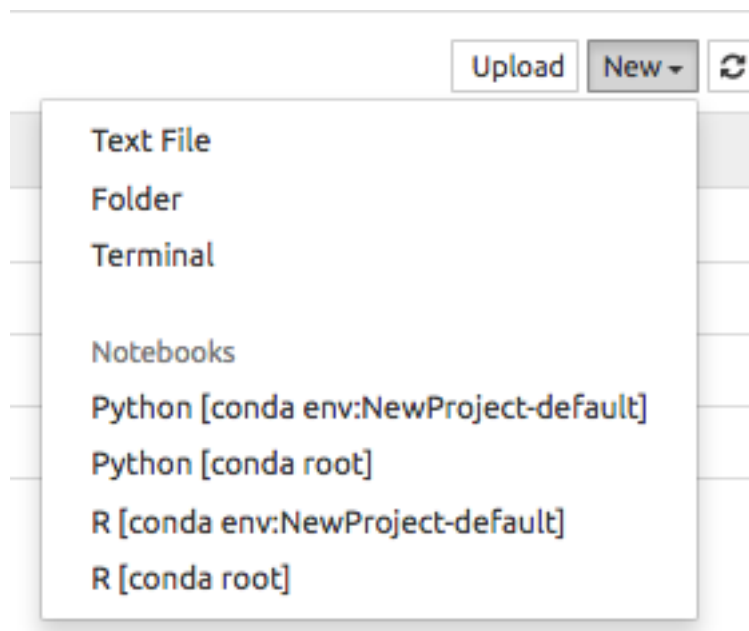
## Using example notebooks

The `Examples` folder in Jupyter Notebook contains several types of Notebook examples created in Python—and one with R language—kernel environments.

Open any example notebook to experiment and see how it works.

## Creating a new Jupyter Notebook

1. At the top right of the **Files** tab, click the New button.



2. Select the kernel environment to create your new notebook in.

NOTE: Customizable Python and R Language kernel environments are automatically created for you during project creation.

- Your project's default conda env kernels are a cloned copy of the root environment. You can customize them and install and delete additional packages.
- Root environment is managed by your Administrator. You cannot make or save any changes to it.
- You can switch between Python, R language and any other custom kernels in the notebook as you work in your notebook. For more information, see [Using the Synchronize Environments extension](#).

The new notebook is saved in the related project directory and displayed.

## Using Jupyter Notebook extensions

The following extensions are available for use with AEN's Jupyter Notebook application:

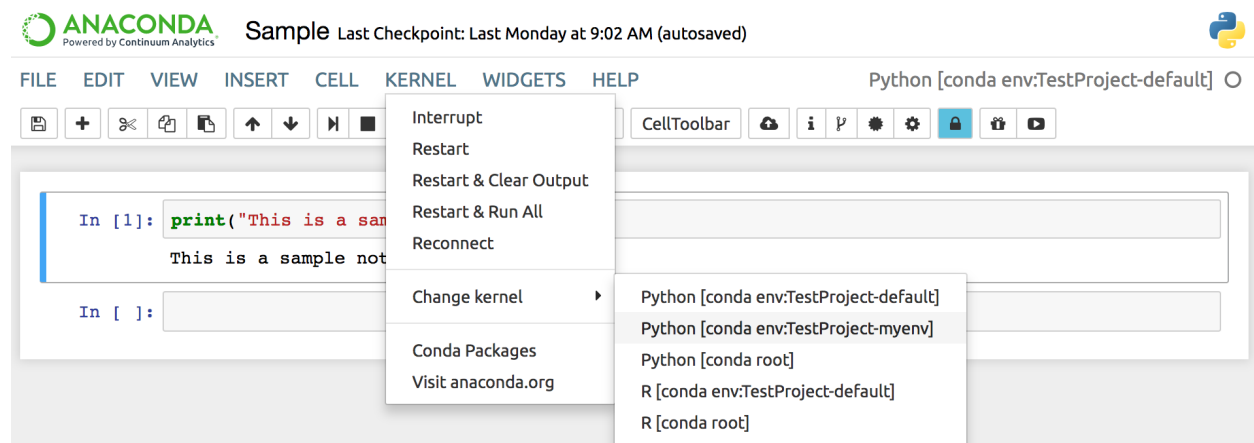
- [Synchronize Environments](#) with Jupyter from the **Kernel** menu.
- [Locking](#) adds multi-user capability from the Lock button.
- [Revision Control Mechanism \(RCM\)](#) adds Status, Checkout and Commit buttons.
- [Conda environment and package management](#) tab.
- [Conda notebook](#) adds conda management inside Notebook from the Kernel > Conda Packages menu option.
- [Anaconda Cloud integration](#) from the Publish to cloud button.
- [Notebook Present](#) turns your notebook into a PowerPoint-style presentation.

## Using the Synchronize Environments extension

The Synchronize Environments extension allows you to apply a Python, R language or any other custom environment inside your current notebook session, without needing to start up several Notebook instances using each of the selected environments.

To change environments:

1. Open the **Kernel** menu.



2. Click the Change kernel option.
3. From the list, select the environment to use.

NOTE: In AEN 4.1+ the default kernel for projects is `default`. In versions prior to 4.0, the default kernel for projects is `root Python`.

## Using the Locking extension

Multi-user capabilities are engaged in AEN when multiple users work in the same notebook file.

The Locking extension allows you to lock a notebook to prevent multiple team members from making changes at the same time. Notebooks are automatically locked when you open them.

If team members open a notebook and make changes while it is locked, their save capability is disabled, and they cannot overwrite the notebook.

To override the lock, they must actively take control of the locked file by clicking the Lock icon in the Notebook menu bar:



NOTE: This is a soft locking model. Team members can choose to override your lock to save their work. If you give team members write access to your files, confirm that they understand that they should never unlock your file unless they are making meaningful, non-destructive team contributions.

## Using the Revision Control Mechanism extension

The Revision Control Mechanism (RCM) Jupyter Notebook extension provides simple version control for notebook files. It uses the internal Jupyter functionality to perform tasks.

On the surface, RCM uses a simple linear model, but beneath that is a more complex git-based branching model. This model uses the latest wins as its main merging strategy to prevent merge conflicts.

The RCM Jupyter Notebook extension adds four buttons:



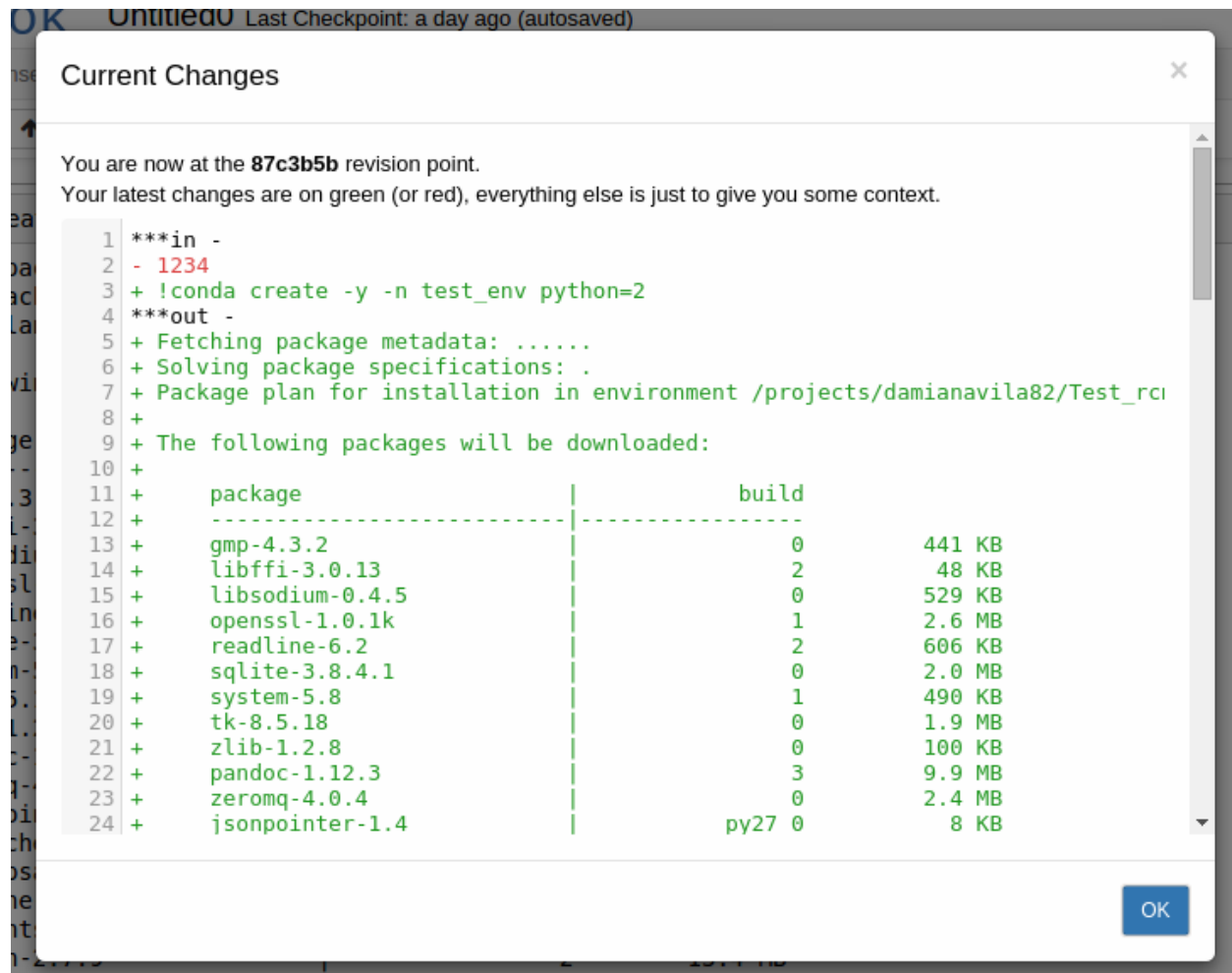
- *Status.*
- *Checkout.*
- *Commit.*
- *Configure git.*

TIP: If you do not see the RCM buttons, see *Setting up RCM for the first time.*

## Using the Status button

The Status button allows you to see what revision you are on.

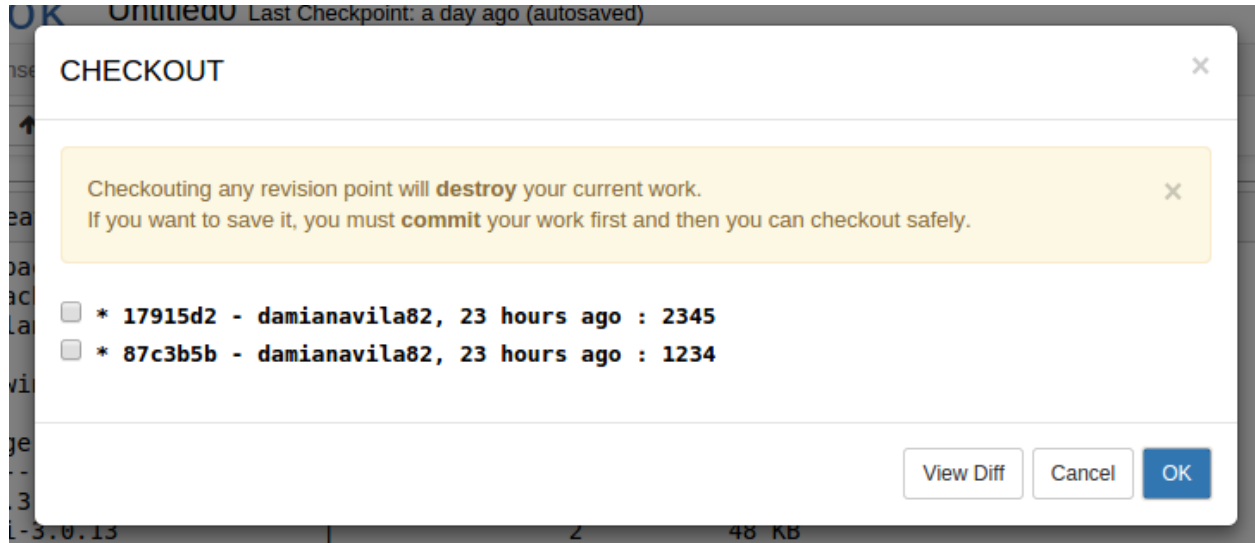
Clicking the Status button displays:



## Using the Checkout button

The Checkout button allows you to view a list of the previous revision points, check out a previous revision or compare differences between revisions.

Clicking the Checkout button displays:



## Checking out a previous revision

To checkout a notebook at an earlier revision point:

1. Select the checkbox next to the desired revision point.
2. Click the OK button.

A copy of the notebook at the selected revision point is displayed.

**NOTE:** If you have not saved the work in your current project window, checking out a previous revision destroys it. If in doubt, click the Cancel button and save your work before reverting to a previous revision point.

## Comparing revisions

To compare 2 previous revision points:

1. Select the checkboxes of the revision points to compare.
2. Click the View Diff button.

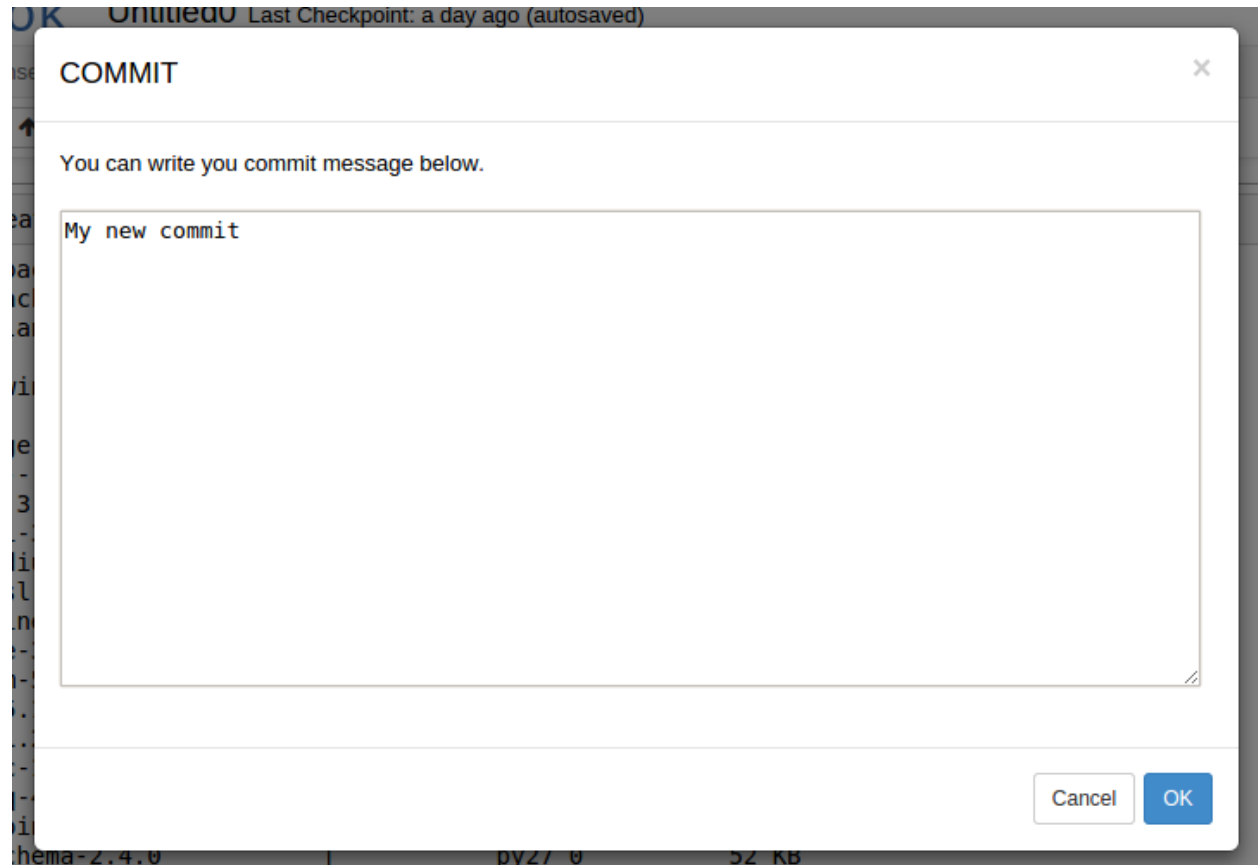
A side-by-side comparison is displayed.

Click the Cancel button to close the differences window.

## Using the Commit button

The Commit button allows you to save or persist the current changes, keeping a permanent record of any changes that are introduced, so that you do not have to worry about losing important data.

Clicking the Commit button displays:



1. Enter a description of the changes in the commit as a reminder in case you need to revert back to it later.
2. Click the OK button.

Your changes are committed and a revision point is created.

If Git user name and user email are not set, the following window appears:

Configure Git and then try to commit again.

TIP: You can roll back committed changes by *checking out a previous version*.

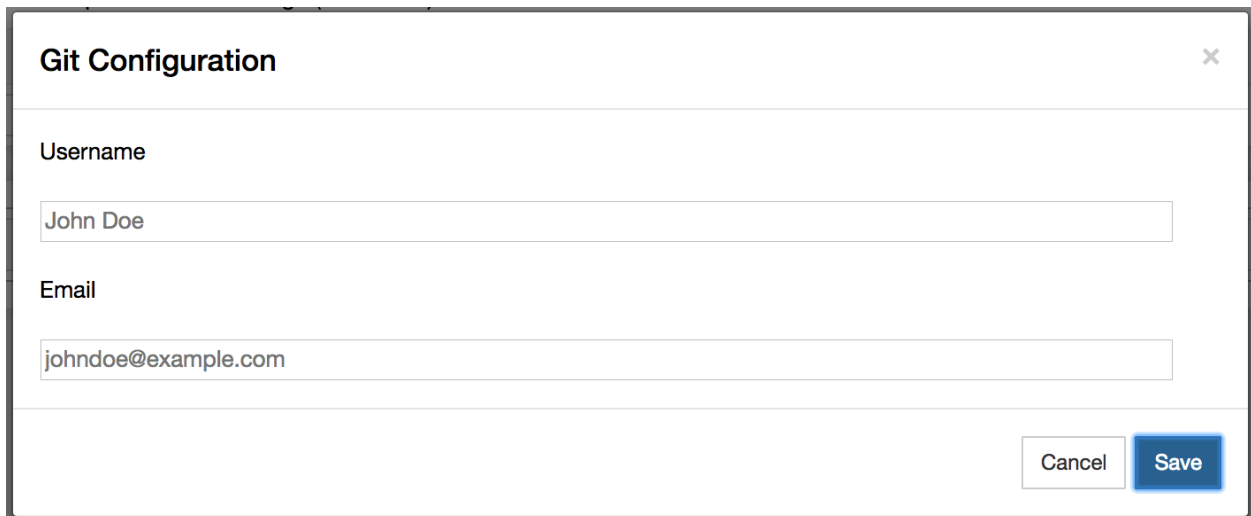




### Using the Configure git button

The Configure git button allows you to configure Git user name and email values.

After clicking the Configure Git button, the following window appears:



Enter user name and e-mail address. Click the OK button when finished.

### Setting up RCM for the first time

If you do not see the RCM buttons in your notebook:

1. Go to the project home page.
2. Open the Terminal application.
3. In the terminal window, run:

```
git config --global user.email "you@example.com"  
git config --global user.name "Your Name"
```

NOTE: Change `you@example.com` to your email address, and `Your Name` to your actual name.

4. Open Jupyter Notebook and refresh the page.

## Using the NBConda extension

The NBConda extension adds a Conda tab to your notebook for easy environment and package management from within the notebook.



Files

Running

IPython Clusters

Conda

2 Conda environments

Action	Name	Default?	Directory
	root		/opt/wakari/anaconda
	default	✓	/projects/aen_admin/TestProject/envs/default

1143 available packages

Search...

→

376 installed packages in environment "default"

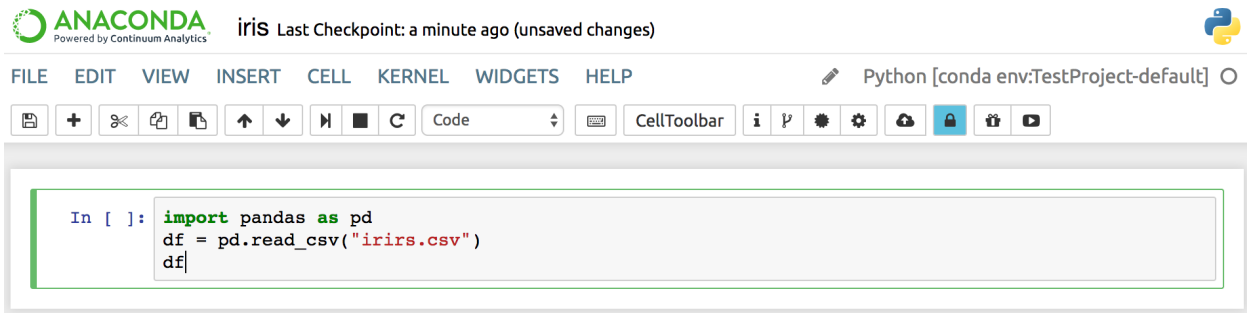
Name	Version	Channel
<input type="checkbox"/> _license	1.1	defaults
<input type="checkbox"/> _nb_ext_conf	0.4.0	defaults
<input type="checkbox"/> abstract-rendering	0.5.1	defaults
<input type="checkbox"/> accelerate	2.3.1	defaults
<input type="checkbox"/> accelerate_cudalib	2.0	defaults
<input type="checkbox"/> aen-app-jupyterlab	0.4.0	wakari

Name	Version	Build	Available
<input type="checkbox"/> _license	1.1	py27_1	
<input type="checkbox"/> alabaster	0.7.10	py27_0	
<input type="checkbox"/> anaconda	custom	py27_0	
<input type="checkbox"/> anaconda-client	1.5.1	py27_0	
<input type="checkbox"/> anaconda-project	0.6.0	py27_0	
<input type="checkbox"/> asn1crypto	0.22.0	py27_0	

Click the Conda tab in a notebook to display:

- Conda environments list—export, clone or delete an environment in the action column, or create a new environment by clicking the plus + icon. Switch to an environment by clicking it; packages for that environment are displayed below in the installed packages list.
- Conda available packages list—for the selected environment in currently configured channels, search for packages and click a package name to install it.
- Installed packages list—in the selected environment, check for updates, update or delete selected packages.

**TIP:** While you are in any notebook, you can jump to the NBConda extension for that environment by clicking the **Kernel** menu and selecting Conda Packages:



## Using the Conda Notebook extension

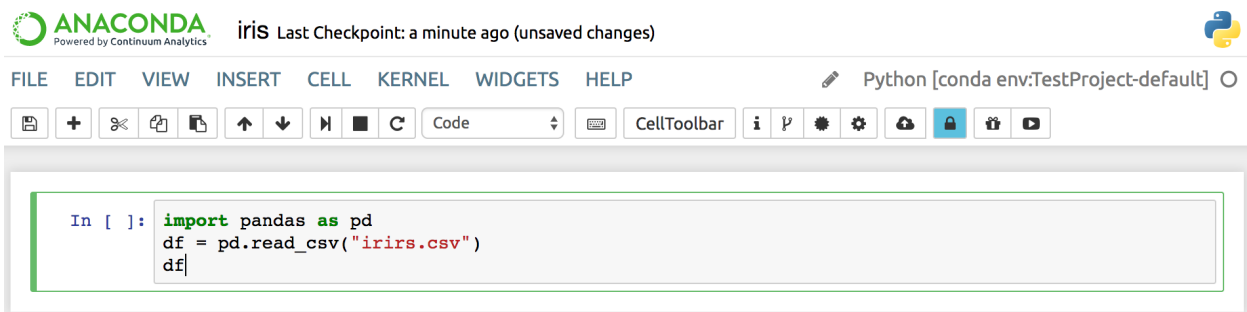
The Conda Notebook extension adds the Conda Packages option to the **Kernel** menu.

Select the Conda Packages option to display a list of all of the Conda packages that are currently used in the environment associated with the running kernel, as well as any available packages.

From the Conda Packages option, you can perform all of the tasks available in the [Conda tab](#), but they will only apply to the current environment.

## Using the Anaconda Cloud extension

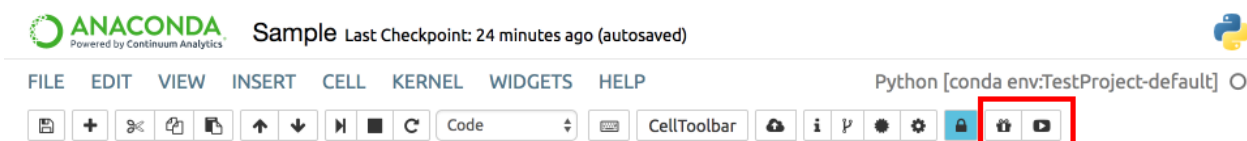
The Anaconda Cloud extension adds the Cloud button to your notebook, allowing you to easily upload your notebook to Cloud:



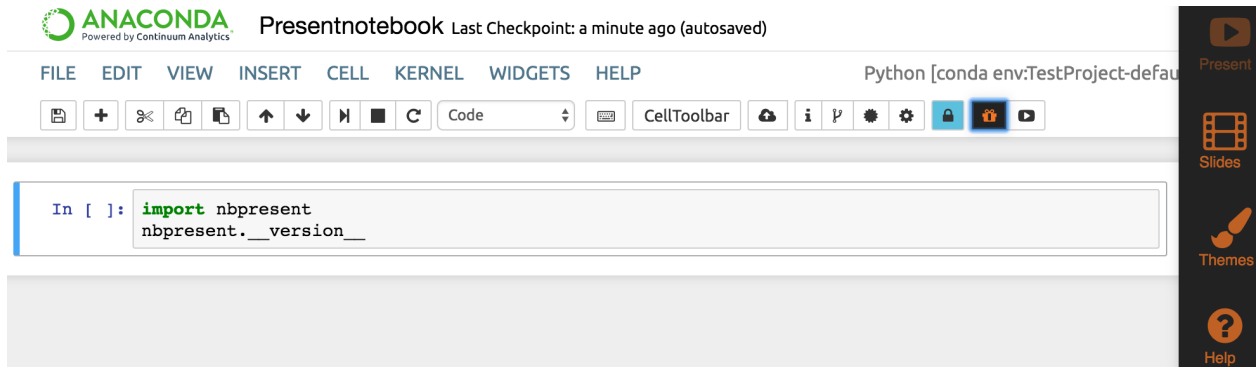
## Using the Notebook Present extension

The AEN Notebook Present extension turns your notebook into a Microsoft PowerPoint-style presentation.

The Present extension adds 2 buttons to Notebook's menu bar—Edit Presentation and Show Presentation:



To begin using Notebook Present, click the Edit Presentation button.

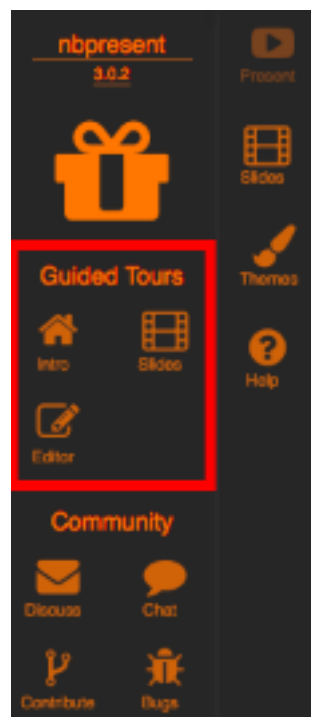


The Notebook Present sidebar is displayed on the right side of your browser:

Clicking each icon changes the menu and layout of your notebook.

Clicking the Help icon displays 3 tours—demonstrations—of the main features of Present:

- *Intro tour.*
- *Slides tour.*
- *Editor tour.*



Select one of the tours to view a short presentation regarding the specifics of that feature.

## Intro tour

The Intro tour is a 2-minute presentation that explains how to use the main features of Present, including a description of each button's purpose.

NOTE: At any time, you can pause, go back to the previous or move forward to the next slide.

The following information is covered in the Intro tour:

- App Bar—When Authoring, this allows you control the content and style of your presentation. It also can be used to activate several keyboard shortcuts for editing:
- Stop Authoring—Clicking the Edit Presentation button again stops Authoring, and removes all keyboard shortcuts.
- Show Presentation—If you just want to run your presentation without using any Authoring tools, just click the Show Presentation button.
- Presenting/Authoring—Once you've made some slides, start Presenting, where you can use most Notebook functions with the Theme we have defined, as well as customize slides on the fly.
- Slides button—Slides, made of Regions linked to Cell Parts are the bread and butter of any presentation, and can be imported, created, linked, reordered, and edited here.
- Theming—Theming lets you select from existing colors, typography, and backgrounds to make distinctive presentations. The first theme you select will become the default, while you can choose custom themes for a particular slide, like a title.
- Saving—Whenever you save your Notebook, all your presentation data will be stored right in the Notebook .ipynb file.
- Downloading—After you've made a presentation, you can download it as an HTML page by choosing Download → Download As: Presentation (.html) in the menu.
- Help—Activate Help at any time to try other tours, connect with the Present developers and community, and other information.

## Keyboard shortcuts



The Jupyter Notebook has two different keyboard input modes. **Edit mode** allows you to type code/text into a cell and is indicated by a green cell border. **Command mode** binds the keyboard to notebook level actions and is indicated by a grey cell border with a blue left margin.

Mac OS X modifier keys:

: Command

: Control

: Option

: Shift

: Return

: Space

: Tab

### Command Mode (press to enable)

: find and replace

: previous slide

: next slide

: next slide

: enter edit mode

: open the command palette

: run cell, select below

: run selected cells

: run cell, insert below

: to code

: to markdown

: extend selected cells above

: extend selected cells above

: extend selected cells below

: extend selected cells below

: insert cell above

: insert cell below

: cut selected cells

: copy selected cells

: paste cells above

: paste cells below

: undo cell deletion

Close

The screenshot shows the Anaconda Presentnotebook interface. At the top, the Anaconda logo is on the left, and the text "Presentnotebook Last Checkpoint: 4 minutes ago (autosaved)" is on the right. Below this is a menu bar with "FILE", "EDIT", "VIEW", "INSERT", "CELL", "KERNEL", "WIDGETS", and "HELP". To the right of the menu bar, it says "Python [conda env:TestProject-defa". Below the menu bar is a toolbar with various icons for file operations, navigation, and execution. The main area contains a code cell with the following code:

```
In [ ]: import nbpresent
        nbpresent.__version__
```

Below the code cell, there is a large gray area with the text "No Slides... yet!" and "You can create an empty slide by pressing or by importing slides:". To the right of this text is a button labeled "Basic" with a slide icon and "1 Slides". At the bottom left, it says "Your Slides". On the right side, there is a vertical sidebar with icons for "Present", "Slides", "Themes", "Help", and a "+ Slide" button at the bottom.

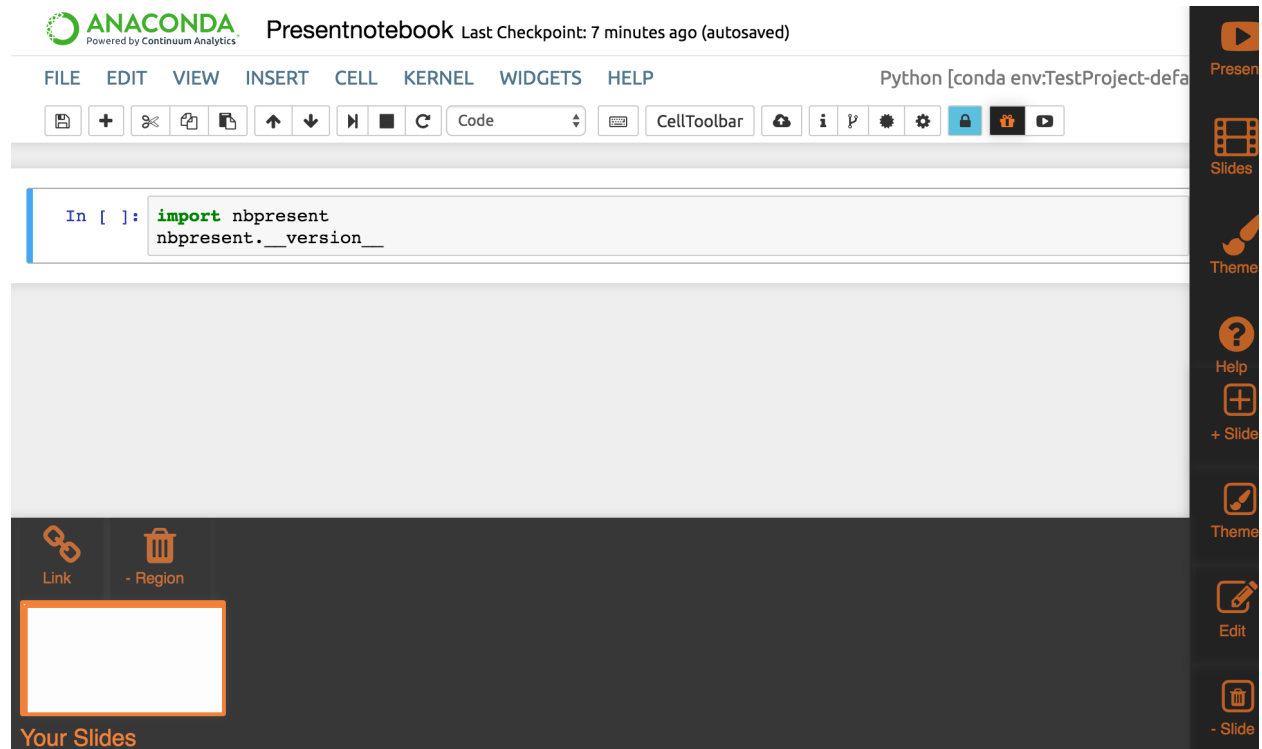
The screenshot shows the Anaconda Presentnotebook interface with a slide titled "Hello, *nbpresent!*". The slide content includes a code cell with the following code:

```
In [ ]: import nbpresent
        nbpresent.__version__
```

Below the code cell, there is another code cell with the prompt "In [ ]:". On the right side, there is a vertical sidebar with icons for "Present", "Slides", "Themes", "Help", and a "+ Slide" button at the bottom. The top of the interface shows the Jupyter logo and the text "My first NBPresent notebook".

## Slides tour

Slides make up a presentation. Clicking Slides toggles the sorter view and the Slide Toolbar on and off:



The Slides tour explains how to create and manage slides, including the following information:

- Slide Toolbar—Create a new slide. Clicking + Slide will offer some choices for creating your new slide.
- Import—The quickest way to create a presentation is to import each cell as a slide. If you’ve already created slides with the official slideshow cell toolbar or RISE, you can import most of that content.
- Template Library—You can create a presentation from an existing template.
  - Reuse Slide as Template—You can create a presentation based on an existing slide.
  - Simple Template—A common template is the Quad Chart, with four pieces of content arranged in a grid.
- Region—The Quad Chart has four Regions. To select a region, click it.
  - Link a Region to a Cell Part—Each Region can be linked to a single Cell Part using the Link Overlay, which shows all of the parts available.
    - \* Cell Part: Source (blue)—Source, such as code and Markdown text.
    - \* Cell Part: Outputs (red)—Outputs, such as rich figures and script results.
    - \* Cell Part: Widgets (purple)—Jupyter widgets, interactive widgets that provide both visualization and user input.



- **Cell Part: Whole (orange)**—Finally, a Whole Cell, including its Source, Widgets and Outputs can be linked to a single region.
- **Unlink a region from a Cell Part**—Unlinking removes the connection between a region and a cell part, without deleting either one.
- **Region: Trashing**—Trashing a Region permanently deletes it, without affecting any linked Cell Part.
- **Part Thumbnail**—We'll try to draw a part thumbnail. It can only be reliably updated when a linked Cell Part is on-screen when you mouse over it, but you should usually be able to get an idea of what you're seeing. The colors of the regions correspond to the cell types.
- **Presenting**—Clicking the Present button while editing brings up the Presenter with editing mode still enabled:
  - Linked inputs and widgets are still interactive.
  - **Go forward**—Click to go to the next slide
  - **Go back**—Click to go back to the previous slide
  - **Go back to the beginning**—Click to go back to the first slide
  - **My work is done here**—Click to go back to the Notebook.

## Editor tour

Once you've made a few slides, you'll likely want to customize them. The Editor tour explains how to edit your notebook, including the following information:

- **Editing Slides**—Activate the Slide Editor by double-clicking it, or by clicking Edit Slide.
- **Region Editor**—Click to drag Regions around and resize them.
- **Region Tree**—Reorder Regions and see the details of how Regions will show their linked Parts.
- **Add Region**—Add new regions.
- **Attribute Editor**—Edit the properties of a region.
- **Data Layouts**—In addition to manually moving regions, you can apply these layouts to automatically fill your slides.
- **More Regions**—Add more regions—with a weight of 1.
- **Tree Weight**—Make a Region bigger or smaller, based on its relative weight.
- **12 Grid**—A compromise between the Free and Treemap layouts, the 12 Grid option rounds all of the values in a layout to a factor of 12.

## Using Compute Resource Configuration

The Compute Resource Configuration (CRC) application displays information about the current project and allows you to set a custom project environment and view and manage your other AEN applications, including stopping, starting, restarting and viewing the logs of each.

The CRC application screen contains 3 sections:

- *Info.*
- *Conda environment.*
- *Running apps.*

The screenshot shows the Anaconda Cloud interface with three main sections:

- Info:** Displays system information including Hostname (davila-aen-test), Project Home (/projects/testuser1/demo), and Project RC file (/projects/testuser1/demo/.projectrc).
- Conda Environment:** Shows the default environment path (/projects/testuser1/demo/envs/default) and a warning that setting the default environment will affect all users and shut down running apps. A green button labeled "Set Project Environment" is present.
- Running Apps:** A table listing active applications.

User	Application	Status	Last Seen	Terminate	Relaunch	Logs
testuser1	terminal	running	1 hours ago	<a href="#">Terminate</a>	<a href="#">Relaunch</a>	<a href="#">Logs</a>

## Info

The Info section displays:

- Hostname—IP address of the host computer.
- Project Home—File path to the project home.
- Project RC file—File path to the project runtime configuration file `.projectrc`. This file is sourced when a user opens any AEN application. It sets several AEN internal environment variables, sets up the project environment and sets additional user environment variables for the project.

## Conda environment

This section displays the path to the default conda environment.

**CAUTION:** Changing the default environment will affect all users. Be sure that no team members have any unsaved documents before changing the project environment.

To change the default conda environment location:

1. Edit the path to point to your preferred conda environment.
2. Click the Set Project Environment button.

Your `.projectrc` file is modified.

## Running apps

The Running Apps section displays a list of users and the applications that are in use, as well as when the app was last modified.

To terminate any individual application, click the Terminate button.

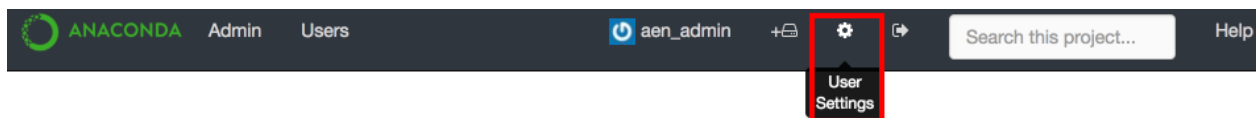
To stop and re-launch any individual application, click the Relaunch button.

To review the run logs of any active application, which may be useful for troubleshooting, click the Logs button.

## Managing your account

- *Updating your public profile*
- *Changing your password*
- *Deleting your AEN account*
- *Viewing account operations*
- *Registering an application*

To access your account information, click the User Settings icon in the AEN navigation bar:



## Updating your public profile

Your public profile is made up of a name, a personal URL, your company and location.

1. In the left navigation pane, click the **Public Profile** tab.
2. To update your profile picture, create a [Gravatar](#) that is associated with the email address you used to create your AEN account. The gravatar will automatically appear.

## Changing your password

1. In the left navigation pane, click the **Account Settings** tab.

## Deleting your AEN account

1. In the left navigation pane, click the **Account Settings** tab.

## Viewing account operations

1. In the left navigation pane, click the **Security Log** tab to view a list of operations performed on your account.

# Settings

Change your account and profile settings.

Public Profile

Account Settings

Security Log

Applications

Security Log

	aen_admin	oauth.authenticate	2017-09-25 04:52:06.713000+00:00
	aen_admin	oauth.authenticate	2017-09-25 04:51:58.954000+00:00
	aen_admin	oauth.authenticate	2017-09-25 04:51:58.720000+00:00
	aen_admin	oauth.authenticate	2017-09-25 04:51:58.490000+00:00
	aen_admin	oauth.authenticate	2017-09-25 04:51:58.259000+00:00
	aen_admin	oauth.authenticate	2017-09-25 04:51:58.033000+00:00
	aen_admin	oauth.authenticate	2017-09-25 04:51:57.802000+00:00

- 2. For more information about an operation, click the Eye icon to the left of the the operation name.

## Registering an application

If you want to create an application for AEN or have already done so, you must register your application.

- 1. In the left navigation pane, click the **Applications** tab.

# Settings

Change your account and profile settings.

Public Profile

Account Settings

Security Log

Applications

Developer Applications

Register New Application

These are applications you have registered to use the Anaconda Enterprise Notebooks API.

Gateway ()

Authorized applications

Gateway ()

revoke

- 2. Click the Register New Application button to open a form for registering your application.

## Advanced tasks

Advanced tasks are best-suited for users who are comfortable working in a Terminal.

## Working with environments

AEN runs on conda, a package management system and environment management system for installing multiple versions of software packages and their dependencies and switching easily between them.

A conda environment usually includes 1 version of Python or R language and some packages.

The ability to have a custom project environment is one of the most powerful features of AEN. Your project environment is integrated so that all of your project applications recognize it and all of your team members have access to it.

This section contains information about:

- *Creating a default conda environment using the Jupyter Notebook application*
- *Creating a default conda environment using the Jupyter Notebook application*
- *Using your conda environment in a notebook*
- *Customizing your conda environment*
- *Installing a conda package using Terminal*
- *Installing a conda package using Notebook*
- *Uninstalling a conda package*

NOTE: This conda environments guide is specific to AEN. For full conda documentation—including cheat sheets, a conda test drive, and command reference—see the [conda documentation](#).

## Creating a default conda environment using the Jupyter Notebook application

You can create, activate, and install packages and deactivate environments from within the Notebook menu bar.

To install from the Notebook menu bar:

1. Click the **Conda** tab and select the plus sign icon.
2. Search for `numpy` in the package search box.
3. Select `numpy` from the search results.

The screenshot shows the Anaconda Jupyter Notebook interface with the 'Conda' tab selected. It displays three conda environments: 'root', 'default' (which is the default), and 'myenv'. Below this, it shows two available packages for search: 'numpy' and 'numpydoc'. At the bottom, it lists 39 installed packages in the 'myenv' environment, including 'anaconda-client', 'certifi', 'cycler', 'decorator', 'ipykernel', and 'ipython'.

Action	Name	Default?	Directory
	root		/opt/wakari/anaconda
	default	✓	/projects/aen_admin/TestProject/envs/default
	myenv		/projects/aen_admin/TestProject/envs/myenv

Name	Version	Channel
<input checked="" type="checkbox"/> numpy	1.13.1	defaults
<input type="checkbox"/> numpydoc	0.7.0	defaults

Name	Version	Build	Available
<input type="checkbox"/> anaconda-client	1.6.3	py36_0	
<input type="checkbox"/> certifi	2016.2.28	py36_0	
<input type="checkbox"/> cycler	1.2.2	py36_0	
<input type="checkbox"/> decorator	4.1.2	py36_0	
<input type="checkbox"/> ipykernel	4.6.1	py36_0	
<input type="checkbox"/> ipython	6.1.0	py36_0	

1. Click the Install button.

The environment is added to the project's `env` directory.

## Creating a default conda environment using Terminal

In AEN, all new environments created with conda automatically include Python, Jupyter Notebooks and pip. You can specify any other packages you want included in your new environment.

**TIP:** By default, conda creates a new environment in your project's `env` directory—so that all team members have access to the environment. For information about limiting your team member's read, write or execute permissions, see [Workbench](#).

To create a new environment within your AEN account, run the command `conda` in a [Terminal](#) application.

**EXAMPLE:** To create a new environment named `WeatherModel` that contains Python, NumPy, pip and Jupyter Notebooks in your project's `env` directory:

1. Log in to AEN.
2. Open a project.
3. On the project home page, click the Terminal application icon to open a Terminal.
4. Create the environment:

```
conda create -n WeatherModel numpy
```

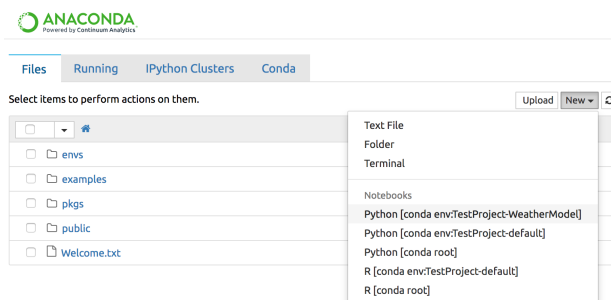
**TIP:** Python, pip and Jupyter Notebooks are automatically installed in each new environment. You only need to specify NumPy in this command.

5. Make the new environment your default:

```
source activate WeatherModel
```

6. To use your new environment with Jupyter Notebooks, open the Notebook application.
7. Click the New button to open a new notebook. In the drop-down menu under Notebooks, the environment you just created is displayed.
8. To activate that environment, select it.

The environment is added to the project's `env` directory.



NOTE: You can deactivate the new environment when you are finished with your notebook by opening the Terminal application and running the command `source deactivate`.

## Using your conda environment in a notebook

Whether you have created an environment using conda in a terminal, or from the **Conda** tab in a notebook, you can use the conda environment in the same way.

When working in a notebook, to select the environment you have created and want to use with that notebook, in the **Kernel** menu, select Change Kernel.

EXAMPLE: If you have an environment named `my_env` in a project named `test1` that includes NumPy and SciPy and you want to use that environment in your notebook, in the **Kernel** menu, select Python [conda env:test1-my\_env].

The notebook code will run in that environment and can import NumPy and SciPy functions.

## Customizing your conda environment

If you need a Python package that AEN doesn't include by default, you can install additional packages into your AEN environment.

TIP: You cannot install packages into the default Anaconda environment. You must create your own environment before installing a new package into that environment.

AEN is built on Anaconda, so you can install additional Python packages using conda or pip—both of which are included with Anaconda.

## Installing a conda package using Terminal

To install a conda package using the Terminal application:

1. Create and activate the environment using the steps in *Creating a default conda environment using the Jupyter Notebook application*.
2. In your Terminal application, run the command `conda install <packagename>`.

NOTE: Be sure to specify the Python version you want when using conda to create the environment, or it will use the same version as root.

EXAMPLE:

```
conda create -n mpy3 python=3 numpy scipy
```

A conda environment named `mpy3`, running on Python 3 and containing NumPy and SciPy is created. All subsequent packages added to this environment will be the Python 3 compatible versions.

## Installing a conda package using Notebook

You can also install the package within your notebook without using the terminal app:

1. From the Notebook application, click the **Conda** tab.
2. Select the environment you wish to use.

3. Search for the package you want to add.
4. Click the Install button.

## Uninstalling a conda package

To uninstall a package using this method, run the command `conda remove <packagename>`.

NOTE: Replace `<packagename>` with the name of the package you are uninstalling.

## Using visualization packages

AEN supports multiple visualization packages for Python and R language.

For Python, the default environment has *Matplotlib* and *Bokeh* installed.

For R language, the default environment has *r-ggplot2* and *r-bokeh* installed.

## Matplotlib

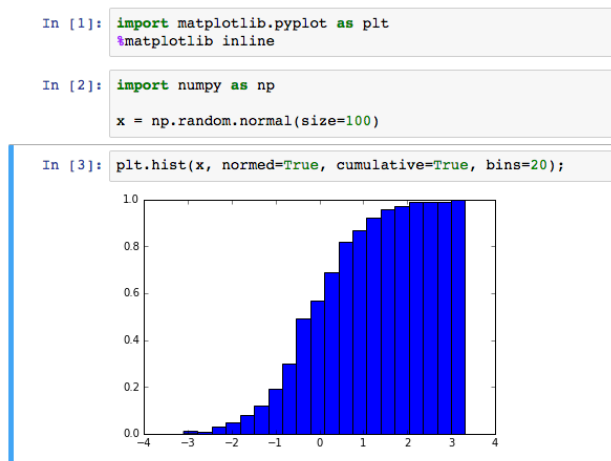
Matplotlib is a Python 2D and 3D plotting and visualization library that produces publication-quality figures in a variety of hardcopy formats and interactive environments across platforms.

To display Matplotlib figures in the output cells of a notebook running the default environment, run:

```
import matplotlib.pyplot as plt
%matplotlib inline
```

Any Matplotlib figures in the notebook are displayed in it's output cells.

EXAMPLE: The following screenshot is of a cumulative density function (CDF) plot using values taken from a normal distribution:





For more information, including a [gallery](#), [examples](#), [documentation](#) and a [list of plotting commands](#), see the [Matplotlib website](#).

## Bokeh

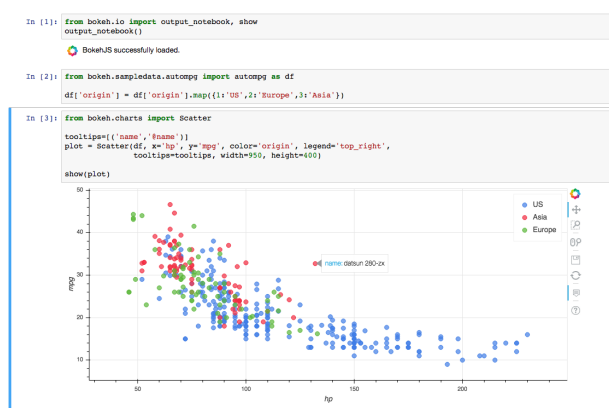
**Bokeh** is an interactive visualization library that targets modern web browsers to provide elegant, concise construction of novel graphics.

To display Bokeh figures in the output cells of a notebook running the default environment, run:

```
from bokeh.io import output_notebook, show
output_notebook()
```

Any Bokeh figures in the notebook are displayed in its output cells.

The following screenshot is of a scatter plot of miles-per-gallon vs. horsepower for 392 automobiles using the `autompg` sample dataset:



## ggplot2

**Ggplot2** is a plotting system for R language which is based on the grammar of graphics. Ggplot2 tries to take only the good parts of base and lattice graphics and none of the bad parts.

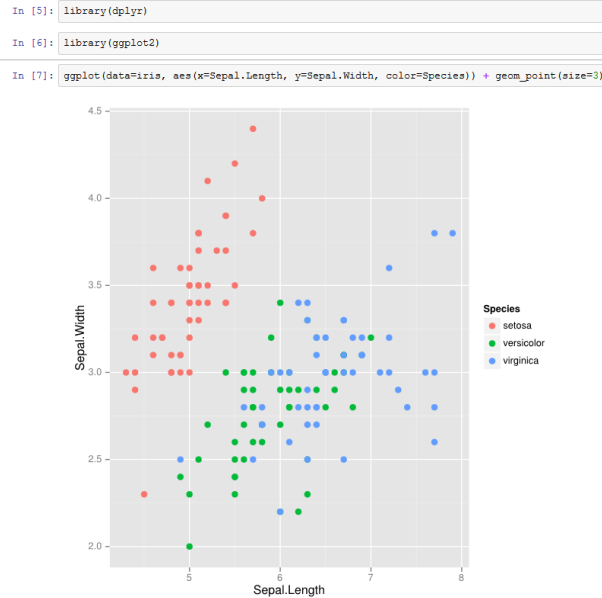
To use ggplot2 with AEN:

1. Open a new Notebook using the R kernel.
2. Load the ggplot2 library with the following code:

```
library(ggplot2)
```

The ggplot2 library is loaded and ready for use in AEN.

The following screenshot is of a scatter plot of sepal width vs sepal length using the `iris` dataset provided by the `dplyr` library:



## Using environment variables

Some Python packages depend on environment variables for correct operation.

EXAMPLE: Theano requires that the directory containing the CUDA compiler is included in the \$PATH environment variable in order for GPU acceleration to be enabled.

To change environment variables for all AEN applications, modify the project runtime configuration file `.projectrc`. For more information, see [Using Compute Resource Configuration](#).

`.projectrc` sets several AEN internal environment variables, sets up the project environment and can set additional user environment variables for that project. This file is sourced when a user opens any AEN application—including Jupyter Notebook—and Jupyter kernels will be able to read the included environment variables.

## Cheat sheet

See the [Anaconda Enterprise Notebooks cheat sheet PDF \(232 KB\)](#) for a single-page summary of the most important information about using AEN.

## Troubleshooting

This troubleshooting guide provides you with ways to deal with issues that may occur with your AEN installation.

### AEN application not working properly

An AEN application is not working as expected.

#### Cause

There are several reasons an application may not work as expected.

## Solution

Most AEN application issues can be resolved by following these steps:

1. Refresh the page.
2. If the issue is not resolved, close and open the application.
3. If the issue is not resolved, *stop and restart your project*.
4. If the issue is not resolved, check that you are using the latest version of your web browser—Chrome, Safari, Edge, or Firefox.
5. Log out of AEN.
6. Restart your browser, and log back in.

If you continue to have issues, then please contact your administrator or enterprise support representative.

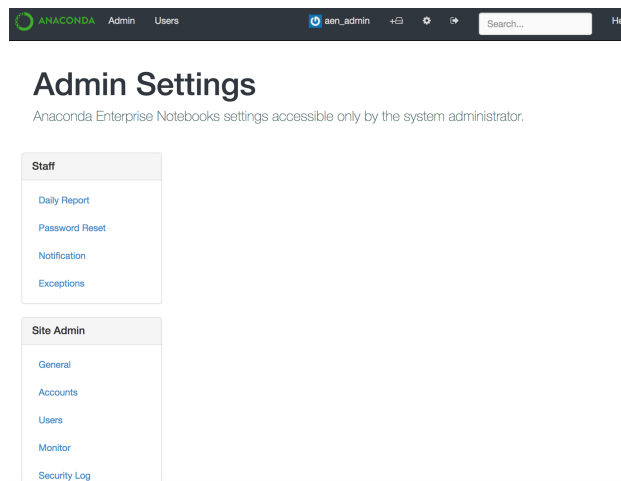
## Admin guide

This administrator guide provides information about the administration of an AEN installation.

Most AEN system management is done from the administrative user interface (admin UI). Some advanced tasks are done *using the command line*.

Any AEN user account can be *upgraded to an administrator account* to have both user and administrator privileges.

Administrators see two additional links in the AEN Navigation bar—Admin and Users:



All of the other navigation bar items are the same as for a user account.

## Concepts

- *System overview*
- *Server node*
- *Gateway node*
- *Compute node(s)*
- *Supervisor and supervisor d*
- *Service Account*
- *Anaconda environments*
- *Projects and permissions*

### System overview

The Anaconda Enterprise Notebooks platform consists of 3 main service groups: AEN server, AEN gateway and AEN compute, which are called “nodes”:

- *Server node*—The administrative front-end to the system where users login, user accounts are stored, and administrators manage the system.
- *Gateway node(s)*—A reverse proxy that authenticates users and directs them to the proper compute node for their project. Users will not notice this node after installation as it automatically routes them.
- *Compute nodes*—Where projects are stored and run.

These services can be run on a single machine or distributed across multiple servers.

Organizationally, each AEN installation has exactly 1 server instance and 1 or more gateway instances. Each compute node can only be connected to a single gateway. The collection of compute nodes served by a single gateway is called a **data center**. You can add data centers to the AEN installation at any time.

EXAMPLE: An AEN deployment with 2 data centers, where 1 gateway has a cluster of 20 physical computers, and the second gateway has 30 virtual machines, must have the following services installed and running:

- 1 AEN server instance
- 2 AEN gateway instances
- 50 AEN compute instances (20 + 30)

Nodes must be configured and maintained separately.

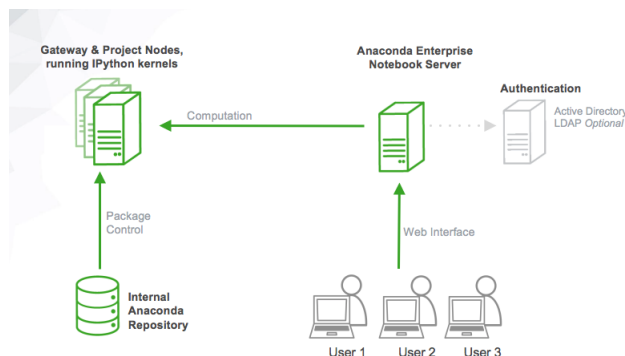
### Server node

The server node controls login, accounts, admin, project creation and management as well as interfacing with the database. It is the main entry point to AEN for all users. The server node handles project setup and ensures that users

The diagram illustrates the Wakari architecture components and their interactions:

- Wakari Server:**
  - Handles user accounts, configuration of the system, LDAP integration, and all authentication and authorization.
  - Connects to an **Active Directory / LDAP** (optional) via a bidirectional arrow.
  - Communicates with the **Wakari Gateway** via **HTTP/HTTPS**.
  - Contains a database icon.
- Wakari Gateway:**
  - Provides a URL: `url: <your server>.com` and `port: 8080`.
  - Communicates with the **Wakari Server** via **HTTP/HTTPS**.
  - Acts as a bridge between the user and the compute resources.
- User 1:**
  - Interacts with the system via **Login to Wakari**, **Create Project**, **Start Project**, **Connect to Notebook**, and **Connect to Terminal**.
- Wakari Compute:**
  - Provides a stack of **Wakari Compute Resources**.
  - Each resource contains a **Wakari Compute** component.
  - Communicates with the **Wakari Gateway** via **HTTP**.
  - Contains a **Project 1..N** component.
- Anaconda Server:**
  - Provides a secure and scalable access to computing resources.
  - Is part of a scale-out architecture where it is easy to add new compute resources.

```
Wakari Server: 8080/80, 8443/443
Wakari Gateway: 8080
Wakari Compute: 5002
Anaconda Server: 8080/80
LDAP:389,636,3268
```



are sent to the correct project data center.

Since AEN is web-based, it uses the standard HTTP port 80 or HTTPS port 443 on the server.

AEN uses MongoDB for its internal data persistency. It is typically run on the same host as the server but can also be *installed* on a separate host.

Server nodes use NGINX to handle the user-facing AEN web interface. NGINX acts as a request proxy for the actual server web-process which runs on a high numbered port that only listens on localhost. NGINX is also responsible for static content.

Server is installed in the `/opt/wakari/wakari-server` directory.

## Server processes

When you *view the status of server processes*, you may see the processes explained below.

supervisord	details
description	Manage wakari-worker, multiple processes of wk-server.
user	wakari
configuration	/opt/wakari/wakari-server/etc/supervisord.conf
log	/opt/wakari/wakari-server/var/log/supervisord.log
control	service wakari-server
ports	none

wk-server	details
description	Handles user interaction and passing jobs on to the wakari gateway. Access to it is managed by NGINX.
user	wakari
command	/opt/wakari/wakari-server/bin/wk-server
configuration	/opt/wakari/wakari-server/etc/wakari/
control	service wakari-server
logs	/opt/wakari/wakari-server/var/log/wakari/server.log
ports	Not used in versions after 4.1.2 *

\* AEN 4.1.2 and earlier use port 5000. This port is used only on localhost. Later versions of AEN use Unix sockets instead. The Unix socket path is: `unix:/opt/wakari/wakari-server/var/run/wakari-server.sock`

wakari-worker	details
description	Asynchronously executes tasks from <code>wk-server</code> .
user	wakari
logs	/opt/wakari/wakari-server/var/log/wakari/worker.log
control	service wakari-server

nginx	details
description	Serves static files and acts as proxy for all other requests passed to <code>wk-server</code> process. *
user	nginx
configuration	/etc/nginx/nginx.conf      /opt/wakari/wakari-server/etc/conf.d/www.enterprise.conf
logs	/var/log/nginx/woc.log /var/log/nginx/woc-error.log
control	service nginx status
port	80

\* In AEN 4.1.2 and earlier the `wk-server` process runs on port 5000 on localhost only. In later versions of AEN the `wk-server` process uses the Unix socket path `unix:/opt/wakari/wakari-server/var/run/wakari-server.sock`.

NGINX runs at least two processes:

- Master process running as root user.
- Worker processes running as nginx user.

## Gateway node

The gateway node serves as an access point for a given group of compute nodes. It acts as a proxy service and manages the authorization and mapping of URLs and ports to services that are running on those nodes. The gateway nodes provide a consistent uniform interface for the user.

NOTE: The gateway may also be referred to as a data center because it serves as the proxy for a collection of compute nodes.

You can put a gateway in each data center in a tiered scale-out fashion.

AEN gateway is installed in the `/opt/wakari/wakari-gateway` directory.

## Gateway processes

When you *view the status of server processes*, you may see the processes explained below.

supervisord	details
description	Manages the <code>wk-gateway</code> process.
user	wakari
configuration	/opt/wakari/wakari-gateway/etc/supervisord.conf
log	/opt/wakari/wakari-gateway/var/log/supervisord.log
control	service wakari-gateway
ports	none

wakari-gateway	details
description	Passes requests from the AEN Server to the Compute nodes.
user	wakari
configuration	/opt/wakari/wakari-gateway/etc/wakari/wk-gateway-config.json
logs	/opt/wakari/wakari-gateway/var/log/wakari/gateway.application.log /opt/wakari/wakari-gateway/var/log/wakari/gateway.log
working dir	/ (root)
port	8089 (webcache)

## Compute node(s)

Compute nodes are where applications such as Jupyter Notebook and Workbench actually run. They are also the hosts that a user sees when using the Terminal app or when using SSH to access a node. Compute nodes contain all user-visible programs.

Compute nodes only need to communicate with a gateway, so they can be completely isolated by a firewall.

Each project is associated with one or more compute nodes that are part of a single data center.

AEN compute nodes are installed in the `/opt/wakari/wakari-compute` directory.

Each compute node in the AEN system requires a compute launcher service to mediate access to the server and gateway.

## Compute processes

When you *view the status of server processes*, you may see the processes explained below.

supervisord	details
description	Manages the wk-compute process.
user	wakari
configuration	/opt/wakari/wakari-compute/etc/supervisord.conf
log	/opt/wakari/wakari-compute/var/log/supervisord.log
control	service wakari-compute
working dir	/opt/wakari/wakari-compute/etc
ports	none



wk-compute	details
de-scription	Launches compute processes.
user	wakari
con-figura-tion	/opt/wakari/wakari-compute/etc/wakari/wk-compute-launcher-config.json /opt/wakari/wakari-compute/etc/wakari/scripts/config.json
logs	/opt/wakari/wakari-compute/var/log/wakari/compute-launcher. application.log /opt/wakari/wakari-compute/var/log/wakari/ compute-launcher.log
work-ing dir	/ (root)
con-trol	service wakari-compute
port	5002 (rfe)

Wk-compute loads each of the following configuration files, in this order:

- /etc/wakari/config.json.
- /etc/wakari/compute-launcher-config.json.
- ./compute-launcher-config.json.
- Any configuration file specified by the `-c` option.

If an option is specified in multiple files, the last one encountered takes precedence.

## Supervisor and supervisord

AEN uses a process control system called “Supervisor” to run its services. Supervisor is run by the AEN Service Account user, usually wakari or aen\_admin.

The Supervisor daemon process is called “supervisord”. It runs in the background and should rarely need to be restarted.

## Service Account

AEN must be installed and executed by a Linux account called the AEN Service Account. The username of the AEN Service Account is called the AEN Functional ID (NFI). The AEN Service Account is created during AEN installation—if it does not exist—and is used to run all AEN services.

The default NFI username is wakari. Another popular choice is aen\_admin.

**WARNING:** The Service Account should only be used for administrative tasks, and should not be used for operating AEN the way an ordinary user would. If the Service Account creates or starts projects, the permissions on the AEN package cache will be reset to match the Service Account, which will interfere with the normal operation of AEN for all other users.

## Anaconda environments

Each project has an associated conda environment containing the packages needed for that project. When a project is first started, AEN clones a default environment with the name “default” into the project directory.

Each release of AEN 4 includes specific tested versions of conda and the conda packages included with AEN. These tested conda packages include Python, R, and other packages, and these tested conda packages include all of the packages in Anaconda.

If you upgrade or install different versions of conda or different versions of any of these conda packages, the new packages will not have been tested as part of the AEN 4 release.

These different packages will usually work, especially if they are newer versions, but they are not tested or guaranteed to work, and in some cases they may break product functionality.

You can use a new conda environment to test a new version of a package before installing it in your existing environments.

If using conda to change the version of a package breaks product functionality, you can use conda to change the version of the package back to the version known to work.

For more information about environments, see [Working with environments](#).

## Projects and permissions

AEN users interact with the system predominantly through *projects*.

Projects are associated with a single data center within the AEN environment. The team of users includes one owner, which is the user that created the project.

Projects live in the `projectRoot` folder on the compute node—by default, `/projects`.

The project directory is created the first time a project is started. The `start-project` script clones it from `/opt/wakari/wakari-compute/lib/node_modules/wakari-compute-launcher/skeleton`.

Project directory permissions are:

```
owner: rwx, user who created the project
group: rwx, group of the owner
other: --x, to allow access to the Public folder
ACL: rwx for any other team members
```

Files and subdirectories within the project directory have the same permissions as the project directory, except:

- The public folder and everything in it are open to anyone.
- Any files hardlinked into the root anaconda environment—`/opt/wakari/anaconda`—are owned by the root or wakari users.

Project file and directory permissions are maintained by the `start-project` script. All files and directories in the project will have their permissions set when the project is started, except for files owned by root or the AEN\_SRVC\_ACCT user—by default, wakari or aen\_admin.

The permissions set for files owned by root or the AEN\_SRVC\_ACCT user are not changed to avoid changing the permissions settings of any linked files in the `/opt/wakari/anaconda` directory.

**CAUTION:** Do not start a project as the AEN\_SRVC\_ACCT user. The permissions system does not correctly manage project files owned by this user.

## Installation

### Installation requirements

- *Hardware requirements*
- *Software requirements*
- *Security requirements*
- *Network requirements*
- *Other requirements*
- *What's next*

### Hardware requirements

AEN server—At least:

- 2+GB RAM.
- 2+CPU cores.
- 20GB storage.

AEN gateway—At least:

- 2 GB RAM.
- 2 CPU cores.

AEN compute (N-machines)—Configured to meet the needs of the projects. At least:

- 2GB RAM.
- 2 CPU cores.
- 20 GB.

NOTE: We recommend putting `/opt/wakari` and `/projects` on the same filesystem. If the project and conda env directories are on separate filesystems then more disk space will be required on compute nodes and performance will be worse.

### Software requirements

- RHEL/CentOS on all nodes. Versions from 6.5 through 7.4 are supported. Other operating systems are supported. However, this document assumes RHEL or CentOS.
- Linux home directories—Jupyter looks in `$HOME` for profiles and extensions.
- Ability to install in AEN directory `/opt/wakari` with at least 10 GB of storage.
- Ability to install in Projects directory `/projects` with at least 20 GB of storage. Size depends on number and size of projects.

NOTE: To install AEN in a different location see *Installing AEN in a custom location*.

## Linux system accounts

Some Linux system accounts (UIDs) are added to the system during installation.

If your organization requires special actions, the following list is available:

- mongod (RHEL) or mongod (Ubuntu/Debian)—created by the RPM or deb package.
- elasticsearch—created by RPM or deb package.
- nginx—created by RPM or deb package.
- AEN\_SRVC\_ACCT—created during installation of AEN, and defaults to wakari.
- ANON\_USER—An account such as “public” or “anonymous” on the compute node.

NOTE: If ANON\_USER is not found, AEN\_SRVC\_ACCT will attempt to create it. If it fails, the project(s) will fail to start.

- ACL directories need the filesystem mounted with Posix ACL support (Posix.1e).

NOTE: You can verify ACL from the command line by running `mount` and `tune2fs -l /path/to/filesystem | grep options`.

## Software prerequisites

- AEN server:
  - Mongo—Greater than or equal to version 2.6.8 and less than or equal to version 3.4.14.
  - NGINX—Greater than or equal to version 1.12.2.
  - Elasticsearch—Greater than or equal to version 1.7.2.
  - Oracle JRE version 7 or 8.
  - bzip2.
- AEN Gateway:
  - bzip2.
- AEN compute:
  - git
  - bzip2
  - bash or zsh
  - X Window System

NOTE: If you don’t want to install the whole X Window System, you must install the following packages to have R plotting support:

```
sudo yum install -y libXrender libXext libXdmc6 libSM libICE libXt \
dejavu-sans-fonts dejavu-serif-fonts dejavu-fonts-common \
fontpackages-filesystem
```

## Security requirements

- Root or sudo access.
- File permissions: `umask 0022` is required during the installation.
- SELinux in permissive or disabled mode.

Edit the following file using either root or sudo access:

```
/etc/sysconfig/selinux
```

Edit the following:

```
# This file controls the state of SELinux on the system.
# SELINUX= can take one of these three values:
#   enforcing - SELinux security policy is enforced.
#   permissive - SELinux prints warnings instead of enforcing.
#   disabled - No SELinux policy is loaded.

SELINUX=enforcing

# SELINUXTYPE= can take one of these two values:
#   targeted - Targeted processes are protected,
#   mls - Multi Level Security protection.

SELINUXTYPE=targeted
```

NOTE: You must reboot for the changes to take effect.

Verify changes with `getenforce`.

## Network requirements

TCP Ports:

Direction	Type	Default Port	Protocol	Optional	Configurable	Comments
Inbound	TCP	80	HTTP or HTTPS	No	Yes	Server
Inbound	TCP	8089	HTTP or HTTPS	No	Yes	Gateway
Inbound	TCP	5002	HTTP	No	Yes	Compute

## Other requirements

As long as the above requirements are met, there are no additional dependencies for AEN.

See also system requirements for Anaconda Repository and Anaconda Scale.

## What's next

*Prepare for installation.*

## Preparing for installation

- *Downloading AEN installers*
- *Gathering IP addresses or FQDNs*
- *Set up variables*
- *What's next*

## Downloading AEN installers

Download the installers and copy them to the corresponding servers.

```
RPM_CDN="https://820451f3d8380952ce65-4cc6343b423784e82fd202bb87cf87cf.ssl.cf1.
↪rackcdn.com"
curl -O $RPM_CDN/aen-server-4.2.2-Linux-x86_64.sh
curl -O $RPM_CDN/aen-gateway-4.2.2-Linux-x86_64.sh
curl -O $RPM_CDN/aen-compute-4.2.2-Linux-x86_64.sh
```

NOTE: The current \$RPM\_CDN server will be confirmed in an email provided by your sales rep.

NOTE: These instructions use *curl* or *wget* to download packages, but you may use other means to move the necessary files into the installation directory.

## Gathering IP addresses or FQDNs

AEN is very sensitive to the IP address or domain name used to connect to the server and gateway nodes. If users will be using the domain name, you should install the nodes using the domain name instead of the IP addresses. The authentication system requires the proper hostnames when authenticating users between the services.

Print this page and fill in the domain names or IP addresses of the nodes below and record the user name and auto-generated password for the administrative user account in the box below after installing the AEN server node:

Node   Name or IP address	Port Number	Username   Password	
AEN server			
AEN gateway			
AEN compute			

NOTE: The values of these IP entries or DNS entries are referred to as <AEN\_SERVER\_IP> or <AEN\_SERVER\_FQDN>, particularly in examples of shell commands. Consider actually assigning those values to environment variables with similar names.

## Set up variables

Certain variables need to have values assigned to them before you start the installation.

## AEN server address

To define an environment variable for the AEN server address—FQDN or IP:

```
export AEN_SERVER=<AEN_SERVER_IP> # <from table above>
```

NOTE: The address—FQDN or IP—specified for the AEN server must be resolvable by your intended AEN users' web clients.

To verify your hostname, run `echo $AEN_SERVER`.

## AEN functional ID

AEN must be installed and executed by a Linux account called the AEN Service Account. The username of the AEN Service Account is called the AEN Functional ID (NFI). The AEN Service Account is created during AEN installation—if it does not exist—and is used to run all AEN services.

The default NFI username is `wakari`. Another popular choice is `aen_admin`.

To set the environment variable `AEN_SRVC_ACCT` to `wakari` or your chosen name before installation, run `export AEN_SRVC_ACCT="aen_admin"`.

This name is now the username of the AEN Service Account and of the AEN administrator account.

When upgrading AEN, set the NFI to the NFI of the current installation.

WARNING: The Service Account should only be used for administrative tasks, and should not be used for operating AEN the way an ordinary user would. If the Service Account creates or starts projects, the permissions on the AEN package cache will be reset to match the Service Account, which will interfere with the normal operation of AEN for all other users.

## AEN functional group

The AEN Functional Group (NFG) may be given any name. Most often, it is set to `aen_admin` or `wakari`. This Linux group includes the AEN service account, so all files and directories that have the owner NFI also have the group NFG.

When upgrading AEN, set the NFG to the NFG of the current installation.

To set the NFG before installation, run:

```
export AEN_SRVC_GRP="<NFG>"
```

NOTE: Replace `<NFG>` with your NFG name.

## AEN install sudo command

During AEN installation the installers perform various operations that require root level privileges. By default, the installers use the `sudo` command to perform these operations.

Before installation, set the `AEN_SUDO_CMD_INSTALL` environment variable to perform root level operations. You can also set it to no command at all if the user running the installer(s) has root privileges and the `sudo` command is not needed or is not available.

EXAMPLES:

```
export AEN_SUDO_CMD_INSTALL=""  
export AEN_SUDO_CMD_INSTALL="sudo2"
```

### AEN sudo command

By default the AEN services uses `sudo -u` to perform operations on behalf of other users—including `mkdir`, `chmod`, `cp` and `mv`.

To override the default `sudo` command when `sudo` is not available on the system, before installing, set the `AEN_SUDO_CMD` environment variable.

AEN must have the ability to perform operations on behalf of other users. Therefore, this environment variable cannot be set to an empty string or to `null`.

**CAUTION:** Any command that replaces `AEN_SUDO_CMD` must support the `-u` command line parameter—similarly to the `sudo` command.

**EXAMPLE:**

```
export AEN_SUDO_CMD="sudo2"
```

The optional environmental variable `AEN_SUDO_SH` is another way to customize AEN sudo operations. When AEN executes any `sudo` command, it will include the value of `AEN_SUDO_SH`, if it is set.

**EXAMPLE:** If your username is “jsmith” and the values are set as:

```
AEN_SUDO_CMD=sudo  
OWNER=jsmith  
AEN_SUDO_SH=sudologger  
PROJECT_HOME=/projects/jsmith/myproj
```

Then AEN will resolve:

```
$AEN_SUDO_CMD -u ${OWNER} $AEN_SUDO_SH rm -rf $PROJECT_HOME
```

As:

```
sudo -u jsmith sudologger rm -rf /projects/jsmith/myproj
```

In this case the `sudologger` utility could be a pass-through utility that logs all `sudo` usage and then executes the remaining parameters.

### Post-installation Sudo configuration

While `root/sudo` privileges are required during installation, `root/sudo` privileges are not required during normal operations after install, if user accounts are managed outside the software. However `root/sudo` privileges are required to start the services, thus in the service config files there may still need to be an `AEN_SUDO_CMD` entry.

For more information, see [Configuring sudo customizations](#).

### AEN remote database settings

By default AEN server uses a local database. To override the default database location, see [Install AEN connected to a remote Mongo DB instance](#).



## What's next

*Install the AEN server.*

## Installing the AEN server

- *Installing the bzip2 package*
- *Downloading prerequisite RPMs*
- *Installing prerequisite RPMs*
- *Setting variables and changing permissions*
- *Running the AEN server installer*
- *Starting NGINX and Elasticsearch*
- *Testing AEN server installation*
- *Updating your license*
- *What's next*

The AEN server is the administrative front end to the system. This is where users log in to the system, where user accounts are stored, and where admins can manage the system.

Server is installed in the `/opt/wakari/wakari-server` directory.

## Installing the bzip2 package

Be sure you have the `bzip2` package installed. If this package is not installed on your system, install it:

```
sudo yum install bzip2
```

## Downloading prerequisite RPMs

To install AEN on a CentOS 6 server:

```
RPM_CDN="https://820451f3d8380952ce65-4cc6343b423784e82fd202bb87cf87cf.ssl.cf1.
↪rackcdn.com"
curl -O $RPM_CDN/nginx-1.12.2-1.el6ngx.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-tools-2.6.8-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-shell-2.6.8-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-server-2.6.8-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-mongos-2.6.8-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-2.6.8-1.x86_64.rpm
curl -O $RPM_CDN/elasticsearch-1.7.2.noarch.rpm
curl -O $RPM_CDN/jre-8u65-linux-x64.rpm
```

To install AEN on a CentOS 7 server:

```
RPM_CDN="https://820451f3d8380952ce65-4cc6343b423784e82fd202bb87cf87cf.ssl.cf1.
↳rackcdn.com"
curl -O $RPM_CDN/nginx-1.12.2-1.el7_4ngx.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-tools-2.6.12-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-shell-2.6.12-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-server-2.6.12-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-mongos-2.6.12-1.x86_64.rpm
curl -O $RPM_CDN/mongodb-org-2.6.12-1.x86_64.rpm
curl -O $RPM_CDN/jre-8u112-linux-x64.rpm
curl -O $RPM_CDN/elasticsearch-1.7.6.noarch.rpm
```

## Installing prerequisite RPMs

Run:

```
sudo yum install -y *.rpm
sudo service mongod start
sudo chkconfig --add elasticsearch
```

## Setting variables and changing permissions

Run:

```
export AEN_SERVER=<FQDN HOSTNAME OR IP ADDRESS> # Use the real FQDN
chmod a+x aen-*.sh # Set installer to be executable
```

NOTE: Change <FQDN HOSTNAME OR IP ADDRESS> to the actual fully qualified domain hostname or IP address.

## Running the AEN server installer

Run:

```
sudo -E ./aen-server-4.2.2-Linux-x86_64.sh -w $AEN_SERVER
<license text>
...
...
PREFIX=/opt/wakari/wakari-server
Logging to /tmp/wakari_server.log
Checking server name
Ready for pre-install steps
Installing miniconda
...
...
Checking server name
Loading config from /opt/wakari/wakari-server/etc/wakari/config.json
Loading config from /opt/wakari/wakari-server/etc/wakari/wk-server-config.json

=====

Created password '<RANDOM_PASSWORD>' for user 'aen_admin'
```

(continues on next page)

(continued from previous page)

```
=====

Starting Wakari daemons...
installation finished.
```

After successfully completing the installation script, the installer creates the administrator account—AEN\_SRVC\_ACCT user—and assigns it a password.

EXAMPLE:

```
Created password '<RANDOM_PASSWORD>' for user 'aen_admin'
```

**TIP:** Record this password. It will be needed in the following steps. It is also available in the installation log file `/tmp/wakari_server.log`.

## Starting NGINX and Elasticsearch

When SELinux is enabled, it blocks NGINX from connecting to the socket created by Gunicorn. If you have SELinux enabled, run these commands to correct these permissions and allow connections between NGINX and Gunicorn:

```
sudo semanage fcontext -a -t httpd_var_run_t "/opt/wakari/wakari-server/var/run/
↳ wakari-server.sock"
sudo restorecon -r /opt/wakari/wakari-server/var/run
```

To start NGINX and Elasticsearch to read the new config file:

```
sudo service nginx start
sudo service elasticsearch start
```

**TIP:** If the AEN web page shows an NGINX 404 error, restart NGINX:

```
sudo nginx -s stop
sudo nginx
```

## Testing AEN server installation

Visit `http://\protect\T1\textdollarAEN_SERVER`.

The License expired page is displayed.

## Updating your license

From the License expired page, follow the onscreen instructions to upload your license file.

After your license is submitted, you will see this page:

No license found!

[Acquire a license](#)

Thank you for using Anaconda Enterprise Notebooks.

After 45 days, or the end of your paid license agreement, you must renew your license.

### Software updates and technical support

Software updates are free of charge during the initial 1-year period after the license purchase. Each subsequent update automatically terminates your rights to use the previous versions of the software. A commercial license qualifies you for unlimited access to technical support.

[Contact support for more information.](#)

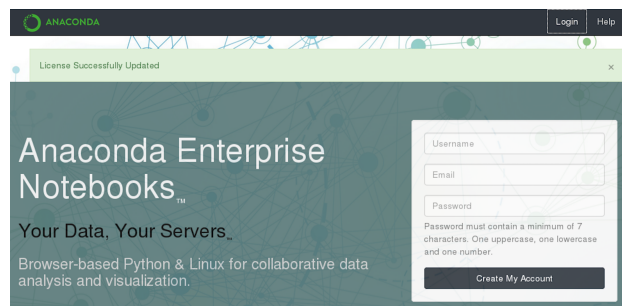
Upload License File

License File

Browse...

No file selected.

Update



## What's next

*Install the AEN gateway.*

## Installing the AEN gateway

- *Setting variables and changing permissions*
- *Running the AEN gateway installer*
- *Registering your gateway*
- *What's next*

The gateway is a reverse proxy that authenticates users and automatically directs them to the proper AEN compute node for their project. Users will not notice this node as it automatically routes them.

Gateway is installed in the `/opt/wakari/wakari-gateway` directory.

## Setting variables and changing permissions

Run:

```
export AEN_SERVER=<FQDN HOSTNAME OR IP ADDRESS> # Use the real FQDN
export AEN_GATEWAY_PORT=8089
```

(continues on next page)

(continued from previous page)

```
export AEN_GATEWAY=<FQDN HOSTNAME OR IP ADDRESS> # will be needed shortly
chmod a+x aen-*.sh # Set installer to be executable
```

NOTE: Change <FQDN HOSTNAME OR IP ADDRESS> to the actual fully qualified domain hostname or IP address.

NOTE: You must perform the entire procedure before closing the terminal to ensure the variable export persists. If the terminal is closed before successful installation, export the variables to continue with the installation.

## Running the AEN gateway installer

Run:

```
sudo -E ./aen-gateway-4.2.2-Linux-x86_64.sh -w $AEN_SERVER
<license text>
...
...

PREFIX=/opt/wakari/wakari-gateway
Logging to /tmp/wakari_gateway.log
...
...
Checking server name
Please restart the Gateway after running the following command
to connect this Gateway to the AEN Server
...
```

## Registering your gateway

The gateway needs to register with the AEN server.

This needs to be authenticated, so the NFI user's credentials created during the AEN server install must be used.

To write the configuration file `/opt/wakari/wakari-gateway/etc/wakari/wk-gateway-config.json`, run the following as `sudo` or `root`:

```
sudo /opt/wakari/wakari-gateway/bin/wk-gateway-configure \
--server http://$AEN_SERVER --host $AEN_GATEWAY \
--port $AEN_GATEWAY_PORT --name Gateway --protocol http \
--summary Gateway --username $AEN_SRVC_ACCT \
--password '<NFI USER PASSWORD>'
```

NOTE: replace <NFI USER PASSWORD> with the password of the NFI user that was generated during *server installation*.

## Setting permissions

Run:

```
sudo chown $AEN_SRVC_ACCT /opt/wakari/wakari-gateway/etc/wakari/wk-gateway-config.json
```

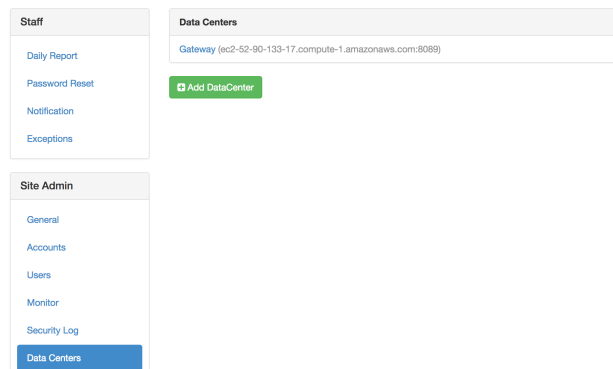
### Starting the gateway

Run:

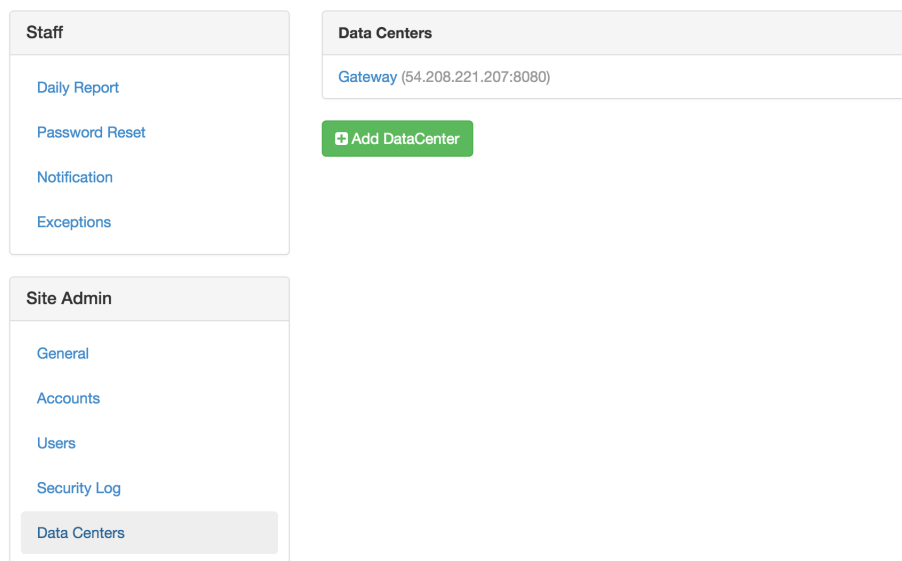
```
sudo service wakari-gateway start
```

### Verifying your gateway registration

1. Log into the AEN server using the Chrome or Firefox browser and the AEN\_SRVC\_ACCT user.
2. In the AEN navigation bar, click Admin to open the Admin Settings page.
3. In the **Site Admin** menu, select Data Centers:



4. Click your data center:



5. Verify that your data center is registered and the status is {"status": "ok", "messages": []}:

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Datacenter Gateway

Provider

wk\_server.plugins.providers.enterprise

Client ID

59c119cd3f94c30fe45ff5db

Client Secret

50cc629d-4e8e-44a5-9a2e-a46fee7c1921

Redirect URIs

http://ec2-52-90-133-17.compute-1.amazonaws.com:8089/login/authorized

wk-gateway-config.json

```
{
  "CDN": "http://ec2-204-236-198-47.compute-1.amazonaws.com/static/",
  "SUBDOMAIN_ROUTING": false,
  "client_id": "59c119cd3f94c30fe45ff5db",
  "client_secret": "50cc629d-4e8e-44a5-9a2e-a46fee7c1921",
  "WAKARI_SERVER": "http://ec2-204-236-198-47.compute-1.amazonaws.com",
  "port": 8089
}
```

status

```
{"status": "ok", "messages": []}
```

Back

Remove

## What's next

*Install the AEN compute node(s).*

## Installing the AEN compute node(s)

- *Setting variables and changing permissions*
- *Running the AEN compute installer*
- *Restart the AEN Server*
- *Configuring your compute node(s)*
- *What's next*

Compute nodes are where projects are stored and run.

Adding multiple AEN compute machines allows you to scale-out horizontally to increase capacity. Projects can be created on individual compute nodes to spread the load.

Repeat this procedure on each compute machine.

## Setting variables and changing permissions

Run:

```
export AEN_SERVER=<FQDN HOSTNAME OR IP ADDRESS> # Use the real FQDN
chmod a+x aen-*.sh # Set installer to be executable
```

NOTE: Change <FQDN HOSTNAME OR IP ADDRESS> to the actual fully qualified domain hostname or IP address.

NOTE: You must perform the entire procedure before closing the terminal to ensure the variable export persists.

### Running the AEN compute installer

Run:

```
sudo -E ./aen-compute-4.2.2-Linux-x86_64.sh -w $AEN_SERVER
...
...
PREFIX=/opt/wakari/wakari-compute
Logging to /tmp/wakari_compute.log
Checking server name
...
...
Initial clone of root environment...
Starting Wakari daemons...
installation finished.
Do you wish the installer to prepend the wakari-compute install location
to PATH in your /root/.bashrc ? [yes|no]
[no] >>> yes
```

### Restart the AEN Server

Once configured, restart the AEN server:

```
sudo service wakari-server restart
```

### Configuring your compute node(s)

Once installed, you must configure the compute launcher on your server:

1. In your browser, go to your AEN server.
2. Log in as the AEN\_SRVC\_ACCT user.
3. In the AEN navigation bar, click Admin to open the Admin Settings page.
4. In the **Providers** menu, select Enterprise Resources:
5. Click the Add Resource button to open the new resource form.
6. Select the data center to associate this compute node with.



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Providers

[Enterprise Resources](#)

Resources

Add Resource

Gateway

ec2-54-210-232-251.compute-1.amazonaws.com

remove

Resources / new

Data Center

Gateway 59c119cd3f94c30fe45ff5db

Name

Compute Node1

URL

http://ec2-54-210-232-251.compute-1.amazonaws.com:5002

Description

Configuring Compute Node

☒ Public

Uncheck this if you want to control exactly who has access to this compute node

Add Resource

7. In the URL box, type: `http://$AEN_COMPUTE:5002`.

NOTE: If the compute launcher is located on the same box as the gateway, we recommended that you type `http://localhost:5002` instead.

8. Type a Name and Description for the compute node.
9. Click the Add Resource button to save the changes.

Your AEN compute node is configured.

## What's next

*Configure conda to use your local on-site AEN repository.*

## Configuring conda to use your local on-site AEN repository

You can configure AEN to use a local on-site Anaconda Repository server instead of Anaconda.org.

To configure AEN to use a local on-site Repository, you must:

1. *Edit condarc on the compute node.*
2. *Configure the Anaconda client.*

## Editing condarc on the compute node

NOTE: If there are channels that you haven't mirrored, you must remove them from the configuration.

Edit the file `.condarc` to match the following:

```
#/opt/wakari/anaconda/.condarc
channels:
  - defaults

create_default_packages:
  - anaconda-client
  - ipykernel

# Default channels is needed for when users override the system .condarc
# with ~/.condarc. This ensures that "defaults" maps to your Anaconda Repository and
↪not
# repo.continuum.io
default_channels:
  - http://<your Anaconda Repository name>:8080/conda/anaconda
  - http://<your Anaconda Repository name>:8080/conda/wakari
  - http://<your Anaconda Repository name>:8080/conda/r-channel

# Note: You must add the "conda" subdirectory to the end
channel_alias: http://<your Anaconda Repository name>:8080/conda
```

NOTE: Replace `<your Anaconda Repository name>` with the actual name or IP address of your local Anaconda Repository installation.

## Configuring the Anaconda client

Anaconda client lets users work with Repository from the command-line—including searching for packages, logging in, uploading packages, and more.

To set the default configuration of anaconda-client for all users on your compute node:

```
sudo /opt/wakari/anaconda/bin/anaconda config --set url http://<your Anaconda_
↳Repository>:8080/api -s
```

NOTE: Sudo is required because the configuration file is written to the root file system: `/etc/xdg/binstar/config.yaml`.

NOTE: Replace `<your Anaconda Repository>` with the actual name or IP address of your local Anaconda Repository installation.

## What's next

Review the *optional configuration* tasks to see if any apply to your system.

## Optional configuration

### Using configuration files

- *AEN configuration keys*
- *Checking configuration file syntax*

The default locations for each component's configuration files are:

- Server—`/opt/wakari/wakari-server/etc/wakari/config.json`.
- Gateway—`/opt/wakari/wakari-gateway/etc/wakari/config.json`.
- Compute—`/opt/wakari/wakari-compute/etc/wakari/config.json`.

Additionally, service-specific configuration files may also be present in the following locations:

- Server—`/opt/wakari/wakari-server/etc/wakari/wk-server-config.json`.
- Gateway—`/opt/wakari/wakari-gateway/etc/wakari/wk-gateway-config.json`.
- Compute—`/opt/wakari/wakari-compute/etc/wakari/wk-compute-config.json`.

Each service loads each of the configuration files in the following order and updates the AEN configuration at each step:

1. `/etc/wakari/config.json`.
2. `/etc/wakari/wk-gateway-config.json`.
3. `/opt/wakari/wakari-SERVICE/etc/wakari/config.json`.
4. `/opt/wakari/wakari-SERVICE/etc/wakari/wk-SERVICE-config.json`.
5. `./config.json`.
6. `./wk-gateway-config.json`.

### AEN configuration keys

The following is a list of AEN supported configuration keys:

Table 25: Server Configuration Keys

Key	Default	Description
CDN	\$WAKARI_SERVER/ static/	The location of static assets.
MONGO_DB	wakari	The name of the AEN database in mongodb.
MONGO_URL	mongodb:// localhost/	The URL of your AEN server's mon- godb instance. Format: mongodb:// <username>:<password>@<host>:<port>/
WAKARI_SERVER		The URL of this AEN server.
DEFAULT_PRIVACY	public	The default project privacy setting—can be either public or private.
SESSION_COOKIE_NAME	wk. enterprise. session	The Cookie name used to maintain Anaconda Enterprise Note- books Enterprise login sessions.
PERMANENT_SESSION	True	Sets cookie session to permanent. This will keep the session open after the browser is closed. The session will still expire af- ter the number of minutes set in the SESSION_LIFETIME key.
SESSION_LIFETIME	120	Time in minutes until the session expires. The counter resets with each request.
USE_SES	false	Sets whether AEN will use Amazon SES to send emails.
SMTP		Sets the SMTP email settings.
- host		A SMTP subkey—the SMTP mail server hostname.
- user		SMTP subkey—the username for SMTP server authentication.
- password		SMTP subkey—the password for SMTP server authentication.
- from_addr		SMTP subkey—the From address for emails sent through SMTP.
verify_gateway_certificate	true	A boolean setting that indicates whether your AEN server should verify the gateway SSL certificate.
accounts	wk_server. plugins .accounts.cloud	The account provider class. For LDAP, this should be set to wk_server.plugins.accounts.ldap_accounts.
uniqueEmail	true	A boolean setting that indicates whether unique user email ad- dresses are required. See <a href="#">note below</a> about updating the database when setting uniqueEmail.
has_internet	true	Boolean for retrieving the avatar from the gravatar URL. If false a local default is used instead.
LDAP	389	LDAP configurations.
- SERVER		LDAP subkey—A list of LDAP servers. At least one server name must be listed. The primary server should be listed first. All secondary or fail-over servers should be listed after the pri- mary.
- PORT	389	LDAP subkey—The LDAP port on the LDAP server.
- AUTH_TYPE		LDAP subkey—LDAP Authentication types. simple—no encryption not secure.“TLS”—encrypted secure requires the TLS_CERT to be set.
- TLS_CERT		LDAP subkey—the full path to the TLS certificate file. The cer- tificate file must also be provided by the Enterprise.
- BASEDN		LDAP subkey—the LDAP Base DN value.
- OU		LDAP subkey—a list of Organizational Units. Some Enterprises group users by OUs in their LDAP server records. AEN will loop over the list of OUs when authenticating a user. The OU value is a list of lists to support multiple OUs where each OU is a single name or a hierarchy of names.
ANON_USER	anonymous	Username—such as public or anonymous— assigned users who are not logged in to access projects. To disable public access use the special value disabled. For more information, <a href="#">see</a> <a href="#">Configuring sudo customizations</a> .
<b>4.1. Anaconda Enterprise 4</b>		<b>1005</b>
SEARCH_ENABLED	true	Boolean indicating whether ElasticSearch is enabled
SEARCH_SERVER	'localhost:9200'	IP address or domain name and port of ElasticSearch server

NOTE: If you set `uniqueEmail` to `false`, you must drop the existing index in the database. EXAMPLE: If the index name is `email_1`, run `db.users.dropIndex("email_1")`.

Table 26: Gateway Configuration Keys

Key	Default	Description
WAKARI_SERVER		The URL of the AEN WAKARI_SERVER.
port	8089	The Port number used by the gateway application. Must be a non-privileged port ( $\geq 1024$ ).
client_id		The client ID assigned to this gateway by the server during <code>wk-gateway-configure</code> .
client_secret		The Client secret assigned to this gateway by the server during <code>wk-gateway-configure</code> .
httpTimeout	600	Timeout in seconds. The default is 10 minutes to allow project creation.
logLevel	info	Log verbosity. One of: 'error' 'warn' 'info' 'debug'.
https		Enable SSL encryption. For more information, see <a href="#">Configuring SSL</a> .
- key		A https subkey-Path to gateway key.
- cert		A https subkey-Path to gateway cert.
- ca		A https subkey-Required if cert was signed by a private root CA or signed by an intermediate authority. It must contain separate values for the paths to the CA root, any intermediates and the certificate for the Server.
- passphrase		A https subkey-Passphrase required to decrypt SSL certs.

Table 27: Compute Node Configuration Keys

Key	Default	Description
WAKARI_SERVER		The URL of the AEN WAKARI_SERVER.
MANAGE_ACCOUNTS	true	A boolean setting that indicates whether AEN should manage system user accounts. Set to false for LDAP installations.
identicalGID	false	<b>To make the AEN compute service create groups with the same uid. Set to true</b> /projects folder resides on an NFSv3 volume. For more information, see <a href="#">Group and user permissions for NFS</a> .
port	2227	The port number used by the compute-launcher application. Note that individual applications use dynamic ports.
projectRoot	/projects	The location of project file storage.
logLevel	info	Log verbosity. One of: 'error' 'warn' 'info' 'debug'
logMaxSize	10000000	Max size in bytes of the logfile. Default is 10 MB. If the size is exceeded then a new file is created and a counter will become a suffix of the log file.
logMaxFiles	30	Limit the number of files created when the size of the logfile is exceeded
appIdleTime	172800000 (48 hours)	The amount of idle time before applications will be auto-terminated (in msec).
idleCheckInterval	13600000 (1 hour)	The frequency of idle checks.
numericUsernames	false	A boolean setting that indicates whether numeric usernames are permitted.
httpTimeout	600	The time before a timeout—in seconds. The default is 10 minutes—600 seconds—to allow time for project creation.
ANON_USER	anonymous	Username such as public or anonymous for users who are not logged in to access projects. To disable public access use the special value disabled. For more information, see <a href="#">Configuring sudo customizations</a> .
projDirsAsHome	false	A boolean setting. When false AEN apps use /home/<username> as HOME. When true AEN apps use /projects/<username> as HOME.

Table 28: Server Internal Configuration Keys - Do not change

Key	Default	Description
PROVIDERS	["wk_server. plugins providers. enterprise"]	A list of compute provider classes.
MONGO_ACTION_LOG_SIZE	262144000	The size of the Mongo action log in bytes.
SITE_ADMINS		A list of site administrator email addresses—used for crash notifications and LDAP password reset requests.
FROM_EMAIL_ADDR		The From address for notification emails sent by AEN.
uniqueUserName	true	A boolean setting that indicates whether unique usernames are required.

Table 29: Gateway Internal Configuration Keys - Do not change

Key	Default	Description
CDN	\$WAKARI_SERVER/ static/	The location of static assets.
SUBDOMAIN_ROUTING	false	A boolean that indicates whether subdomains are being used.
refreshTokenExpiration	60000	Idle time in milliseconds before the Gateway session expires.

Table 30: Compute Node Internal Configuration Keys - Do not change

Key	Default	Description
CDN	\$WAKARI_SERVER/ static/	The location of static assets.
USE_SES	false	Sets whether AEN will use Amazon SES to send emails.
multiUser	true	A boolean that indicates whether multi-user support is enabled.
multiProject	true	A boolean that indicates whether multi-project support is enabled.
ANACONDA_ROOT	/opt/wakari/ anaconda	The location of your Anaconda installation.
appLogs	/opt/wakari/ wakari- compute/var/ log/wakari/ compute-launcher-apps	The directory where application logs are stored.
appPIDs	/opt/wakari/ wakari-compute/ var/run/ compute-launcher-apps	The directory where application PID files are stored.
applicationLog	/opt/wakari/ wakari-compute/ var/log/ wakari/ compute-launcher. application. log	The path to the compute launcher log.
accessLog	opt/wakari/ wakari-compute/ var/log/ wakari/ compute-launcher. access.log	Path to compute launcher access log

## Checking configuration file syntax

To verify that the configuration file contains valid JSON, run:

```
root@server # python -m json.tool /opt/wakari/wakari-server/etc/wakari/*.json
root@gateway # python -m json.tool /opt/wakari/wakari-gateway/etc/wakari/*.json
root@compute # python -m json.tool /opt/wakari/wakari-compute/etc/wakari/*.json
```

If the file is correct, the contents are displayed.

If there is a syntax error in the file, a “No JSON object could be decoded” message is displayed instead.



To fix any errors, edit the configuration file and verify that it contains the correct JSON syntax.

## Increasing HTTP timeout between gateway and compute nodes

The default HTTP timeout is 600 seconds (10 minutes).

This setting works for HTTP timeout only, not HTTPS.

To modify the HTTP timeout setting:

1. Open the `/opt/wakari/wakari-compute/etc/wakari/wk-compute-launcher-config.json` file and modify the `httpTimeout` key:

```
"httpTimeout": 600
```

2. Update the gateway node by modifying the `httpTimeout` key in the `/opt/wakari/wakari-gateway/etc/wakari/wk-gateway-config.json` file to match the above settings.
3. Restart the AEN compute service:

```
sudo service wakari-compute restart
```

## Installing AEN in a custom location

To install AEN in a custom location:

1. Make the custom install folder owned by `$AEN_SRVC_ACCT`. EXAMPLE: `/data/aen/`.
2. Make a symlink from `/opt/wakari` to `/data/aen`.
3. Run the installers.
4. Move the folder from `/projects` to your chosen custom location. EXAMPLE: `/data/aen/projects`.
5. Make a symlink from `/projects` to `/data/aen/projects`.

NOTE: We recommend putting `/opt/wakari` and `/projects` on the same filesystem. If the project and conda environment directories are on separate filesystems then more disk space will be required on compute nodes and performance will be worse.

## Changing where projects are stored

NOTE: We recommend putting `/opt/wakari` and `/projects` on the same filesystem. If the project and conda env directories are on separate filesystems then more disk space will be required on compute nodes and performance will be worse.

To make aen-compute service use a different directory than `/projects` to store your AEN projects:

1. Modify the `/opt/wakari/wakari-compute/etc/wakari/wk-compute-launcher-config.json` file:

```
"projectRoot" : "/nfs/storage/services/wakari/projects",
```

NOTE: The directory `/nfs/storage/services/wakari/projects` specified as `projectRoot` must already exist for this command to resolve properly.

2. Restart the AEN compute service:

```
sudo service wakari-compute restart
```

### Group and user permissions for NFS

To install AEN with multiple compute nodes and a `/projects` folder on an NFSv3 volume, manually pre-create both the anonymous user and the `$AEN_SRVC_ACCOUNT` user on all nodes. Each of these users must have the same user identity number (UID) and group identity number (GID) on all nodes.

By default AEN creates local users with a different GID on each node. To make the AEN compute service create groups with the same GID:

1. In the `/opt/wakari/wakari-compute/etc/wakari/wk-compute-launcher-config.json` file, change the `identicalGID` key value to `true`:

```
, "identicalGID": true
```

If you don't see the `identicalGID` key, add it.

NOTE: You must add the comma at the beginning of the line. If you add this line as the last key, you must remove any comma at the end of the line.

2. Restart the AEN compute service:

```
sudo service wakari-compute restart
```

### Using numeric usernames

1. In the `/opt/wakari/wakari-compute/etc/wakari/wk-compute-launcher-config.json` file, change the `numericUsernames` key value to `true`.

```
, "numericUsernames": true
```

If you don't see the `numericUsernames` key, add it.

NOTE: You must add the comma at the beginning of the line. If you add this line as the last key, you must remove any comma at the end of the line.

2. Restart the AEN compute service:

```
sudo service wakari-compute restart
```

### Using project directories as home directories

The `projDirsAsHome` option changes the AEN home directories from the standard `/home/<username>` location to the project directories and the location `/projects/<username>/<project_name>/<username>/`. This ensures that AEN and AEN apps will not be affected by configuration files in a user's home directory, such as `.bashrc` or configuration files in subdirectories such as `.ipython` and `.jupyter`.

### Package cache locations

AEN version 4.1.3 stores the cache of packages in `/home/<username>`, while AEN versions 4.2.0 and higher store the cache of packages in `/projects/<username>/<project_name>/<username>/`. By moving the

package cache to the same filesystem as the project, AEN versions 4.2.0 and higher can use hardlinks and save disk space and time when creating or cloning environments.

These package cache locations are not affected by the `projDirsAsHome` option.

After upgrading from AEN 4.1.3 to AEN 4.2.0 or higher, existing projects will still use the package cache in `/home/<username>`. Do not remove this cache, or the existing projects will break.

When users create new projects or install packages, the newly installed packages will use the new cache location.

If you wish to remove the older package cache in `/home/<username>`:

- Upgrade AEN to 4.2.0 or higher.
- Use `conda remove` to remove every non-default package in every project.
- Use `conda install` to replace them. The replaced packages will link to the new package cache in `/projects/<username>/<project_name>/<username>/`.
- You can now safely remove the older package cache.

## Enabling `projDirsAsHome`

NOTE: The `projDirsAsHome` option should be enabled immediately after performing the installation process and before any users have logged in to AEN. This ensures that users will not have home directories in different places due to some creating their home directories when the option was disabled and others creating their home directories when the option was enabled.

1. In the `/opt/wakari/wakari-compute/etc/wakari/wk-compute-launcher-config.json` file, add the `projDirsAsHome` key value and set it to `true`.

```
, "projDirsAsHome": true
```

NOTE: You must add the comma at the beginning of the line. If you add this line as the last key, you must remove any comma at the end of the line.

2. Restart the AEN compute service:

```
sudo service wakari-compute restart
```

## Setting up a default project environment

AEN includes a full installation of the Anaconda Python distribution—along with several additional packages—located within the root conda environment in `/opt/wakari/anaconda`.

The first time any new AEN project is started, this default project environment is cloned into the new project's workspace.

To configure a different set of packages than the default:

1. Create a new conda environment in the `/opt/wakari/anaconda/envs/default` directory.

EXAMPLE: Using a Python 3.4 base environment, run:

```
sudo -u $AEN_SRV_ACCT /opt/wakari/anaconda/bin/conda \
  create -p /opt/wakari/anaconda/envs/default python=3.4
```

2. Use `conda` to install any additional packages into the environment.
3. After the environment is created, clone it to ensure that it works correctly:

```
sudo -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda \  
    create -p /opt/wakari/testenv --clone /opt/wakari/anaconda/envs/default  
sudo -u $AEN_SRVC_ACCT rm -rf /opt/wakari/testenv
```

For more information and examples about creating a default project environment with Microsoft R Open (MRO), see *Using MRO in AEN*.

## Converting an existing project

1. Run the following command to clone the environment:

```
sudo -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda \  
    create -n /projects/owner/project/envs/<ENV_NAME> \  
    --clone /opt/wakari/anaconda/envs/default
```

NOTE: Replace `/projects/owner/project/envs/<ENV_NAME>` with the path to the new environment you would like to create within the project.

2. Open the *Compute Resource Configuration application* for your project and set the project environment path there as well.

## Using MRO in AEN

In AEN 4.2.2 and higher, you can choose to create environments with the Microsoft R Open (MRO) interpreter by installing the `mro-base` package, or create environments with the R interpreter by installing the `r-base` package. Unless you request a change, conda will continue to use the existing interpreter in each environment. In AEN `r-base` is the default.

EXAMPLE: To create a custom environment called `mro_env` with MRO and R Essentials:

```
.. code-block:: bash  
  
sudo -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda \  
    create -c https://repo.continuum.io/pkgs/main \  
    -n mro_env r-essentials
```

NOTE: Conda 4.4 and higher include the `main` channel by default. Earlier versions of conda do not.

## Making a default project environment with MRO

You can also create an environment with MRO and make this the default AEN project environment.

The first time a new project is started, the default project environment is cloned into the new project's workspace.

1. Create a new conda environment in the `/opt/wakari/anaconda/envs/default` directory.

The command is similar to the one used in the previous example to create a custom environment.

```
sudo -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda \  
    create -c https://repo.continuum.io/pkgs/main \  
    -p /opt/wakari/anaconda/envs/default r-essentials
```

2. Use conda to install any additional packages into the environment.
3. After the environment is created, clone it to check that it works correctly, and then clean up the clone.

```
sudo -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda \
    create -p /opt/wakari/testenv --clone /opt/wakari/anaconda/envs/default
sudo -u $AEN_SRVC_ACCT rm -rf /opt/wakari/testenv
```

NOTE: To convert existing projects, see *Converting an existing project*.

## Install AEN connected to a remote Mongo DB instance

To install AEN with a remote database:

1. Connect to the Mongodb instance and create the user for AEN:

```
> user = { user: "<username>",
  pwd: "<super-secure-password>",
  roles: [
    { role: "dbOwner", db: "<db_name>" },
    { role: "dbOwner", db: "<db_name>_mq" }
  ]
}
> db.createUser(user)
Successfully added user: { ... }
```

2. Before installing AEN-server export the database URL and name:

```
$ export MONGO_URL="mongodb://<username>:<password>@<host>:<port>/"
$ export MONGO_DB="<database_name>"
```

3. Continue the installation process: *Install the AEN server*.

## Migrate from local to remote MongoDB

To configure your remote database to work with an already installed AEN server:

1. Stop the server, gateway and compute nodes:

```
sudo service wakari-server stop
sudo service wakari-gateway stop
sudo service wakari-compute stop
```

2. Open the `/opt/wakari/wakari-server/etc/wakari/config.json` file and create the `MONGO_URL` key. For the value parameter, add the database information.

The final file should read:

```
{
  "MONGO_URL": "mongodb://MONGO-USER:MONGO-PASSWORD@MONGO-URL:MONGO-PORT",
  "MONGO_DB": "MONGO-DB-NAME",
  "WAKARI_SERVER": "http://YOUR-IP",
  "USE_SES": false,
  "CDN": "http://YOUR-IP/static/",
  "ANON_USER": "anonymous"
}
```

For more information about configuration keys, see *Using configuration files*.

3. Migrate the data from the former database into the new one. For more information, see the [MongoDB documentation website](#).
4. After migration, restart the nodes:

```
sudo service wakari-server start
sudo service wakari-gateway start
sudo service wakari-compute start
```

### Running SELinux in enforcing mode

To run SELinux in Enforcing mode, a few ports must be set up using the `semanage port` command.

The `semanage` command relies on `polycoreutils-python`. To install `polycoreutils-python`, if needed, run:

```
sudo yum -y install polycoreutils-python
```

Enable ports 9200 and 9300 for Elasticsearch:

```
sudo semanage port -a -t http_port_t -p tcp 9200
sudo semanage port -a -t http_port_t -p tcp 9300
```

### Changing server hostnames

It is possible to change the domain names (hostnames) of the various AEN nodes by updating the configuration files.

NOTE: After the configuration files are updated, the associated nodes need to be restarted.

To edit the information for all of the data centers that you are changing the base domain name for:

1. Go to the Site Admin section of the Admin Settings page.
2. In the Data Centers section, click the Edit button.
3. Make any necessary updates.

NOTE: This must include the service port if it is different from the default—80 for HTTP and 443 for HTTPS.

4. In the Enterprise Resources sub-section of the Providers section, edit each compute node that has a changed domain name.

NOTE: These URLs should include the protocol, hostname and port.

### Authenticating with LDAP

Anaconda Enterprise Notebooks performs local authentication against accounts in the AEN database by default.

To configure AEN to authenticate against accounts in an LDAP (Lightweight Directory Access Protocol) server, follow the instructions below.

### Installing OpenLDAP libraries

The system needs OpenLDAP libraries to be installed and accessible by AEN. AEN uses the OpenLDAP libraries to establish an LDAP connection to your LDAP servers.

To install OpenLDAP on CentOS or Redhat:

```
sudo yum install openldap
```

To install OpenLDAP on Ubuntu or Debian, follow the official [OpenLDAP installation instructions](#).

## Configuring OpenLDAP

1. Open the `/opt/wakari/wakari-server/etc/wakari/wk-server-config.json` file.
2. Add the following LDAP settings:

```
{
  "accounts": "wk_server.plugins.accounts.ldap2",
  "LDAP" : {
    "URI": "ldap://openldap.EXAMPLE.COM",
    "BIND_DN": "cn=Bob Jones,ou=Users,DC=EXAMPLE,DC=COM",
    "BIND_AUTH": "secretpass",
    "USER_SEARCH": { "base": "DC=EXAMPLE,DC=COM",
                     "filter": "(| (& (ou=Payroll)
                                   (uid=%(username)s))
                               (& (ou=Facilities)
                                   (uid=%(username)s)))"
                   },
    "KEY_MAP": { "username": "uid",
                 "email": "mail",
                 "name": "cn"
               }
  }
}
```

- **URI**—The IP address or hostname of your OpenLDAP server. For SSL/TLS, use the `ldaps://` prefix and specify a `TLS_CACERT` as described in the SSL/TLS configuration section below.
- **BIND\_DN**—The full directory path of the user you want AEN server to bind as.
- **BIND\_AUTH**—The password of the **BIND\_DN** user.
- **USER\_SEARCH**:
  - **base**—The level at which you want to start the search.
  - **filter**—The default is to search for the `sAMAccountName` attribute, and use its value for the AEN server username field.
- **KEY\_MAP**—Maps user attributes in AEN server to LDAP user attributes.

EXAMPLE: The `mail` attribute in LDAP maps to the `email` attribute in AEN server.

NOTE: Map the `uid` attribute in LDAP to the `username` attribute in AEN server to preserve username capitalization.

3. Restart AEN server to load new settings.
4. Log in with the admin account. This creates the admin user in the local database.
5. As soon as LDAP is installed, LDAP authentication takes over, so you need to add your admin account again:

```
/opt/wakari/wakari-server/bin/wk-server-admin superuser --add "jsmith"
```

## Configuring Active Directory

Microsoft Active Directory is a server program that provides directory services and uses the open industry standard Lightweight Directory Access Protocol (LDAP).

To enable Active Directory support:

1. Open the `/opt/wakari/wakari-server/etc/wakari/wk-server-config.json` file.
2. Add the following LDAP settings:

```
{
  "accounts": "wk_server.plugins.accounts.ldap2",
  "LDAP" : {
    "URI": "ldap://<ad.EXAMPLE.COM>",
    "BIND_DN": "CN=Bind User,CN=Users,DC=EXAMPLE,DC=COM",
    "BIND_AUTH": "secretpass",
    "USER_SEARCH": { "base": "CN=Users,DC=EXAMPLE,DC=COM",
                     "filter": "sAMAccountName=%(username)s"
                   },
    "KEY_MAP": { "username": "sAMAccountName",
                 "email": "mail",
                 "name": "cn"
               }
  }
}
```

- URI—The IP address or hostname of your Active Directory server. Replace `<ad.EXAMPLE.COM>` with the actual URI. For SSL/TLS, use the `ldaps://` prefix and specify a `TLS_CACERT` as described in the SSL/TLS configuration section below.
- BIND\_DN—The full directory path of the user you want AEN server to bind as.
- BIND\_AUTH—The password of the BIND\_DN user.
- USER\_SEARCH:
  - base—the level at which you want to start the search.
  - filter—default is to search for the `sAMAccountName` attribute, and use its value for the AEN server `username` field.
- KEY\_MAP—Maps user attributes in AEN server to LDAP user attributes.

EXAMPLE: The `mail` attribute in LDAP maps to the `email` attribute in AEN server.

NOTE: Map the `sAMAccountName` attribute in LDAP to the `username` attribute in AEN server to preserve username capitalization.

3. Restart AEN server to load new settings.
4. Log in with the admin account. This creates the admin user in the local database.
5. As soon as LDAP is installed, LDAP authentication takes over, so you need to add your admin account again:

```
/opt/wakari/wakari-server/bin/wk-server-admin superuser --add "jsmith"
```

## Configuring SSL/TLS

AEN uses system-wide LDAP settings, including SSL/TLS support.



- On Redhat/CentOS systems, these settings are located in the `/etc/openldap/ldap.conf` file.
- On Ubuntu/Debian systems, these settings are located in the `/etc/ldap/ldap.conf` file.

Typically, the only configuration necessary is updating the file to read:

```
TLS_CACERT /path/to/CA.cert
```

NOTE: `CA.cert` is the Certificate Authority used to sign the LDAP server's SSL certificate. In the case of a self-signed SSL certificate, this is the path to the SSL certificate itself.

## Testing LDAP configuration

Test your LDAP configuration using `flask-ldap-login-check`:

```
/opt/wakari/wakari-server/bin/flask-ldap-login-check \
  wk_server.wsgi:app \
  -u [username] \
  -p [password]
```

NOTE: `username` is the username of a valid user and `password` is that user's `BIND_AUTH` password.

## Configuring sudo customizations

If your organization's IT security policy does not allow root access or has restrictions on the use of `sudo`, after AEN installation, you may customize AEN to meet their requirements.

Your organization may choose to implement any or all of the following:

- *Remove root access* for AEN service account (Note: this restricts AEN from managing user accounts).
- *Configurable sudo command*.
- *Restrict sudo access to all processes*.

These customizations must be done in a terminal window after copying the files to the server node.

## Removing all root access from the service account

Because root access is required for `useradd`, the following process restricts AEN from managing user accounts.

1. Modify the `/etc/sudoers.d/wakari_sudo` file to read:

```
Defaults:wakari !requiretty, visiblepw
Runas_Alias    OP = ALL,!root
wakari ALL=(OP) NOPASSWD: ALL
```

NOTE: If you used a service account name other than `wakari`, enter that name instead of `wakari`.

2. Modify the `/opt/wakari/wakari-compute/etc/wakari/config.json` file to read:

```
"MANAGE_ACCOUNTS": false,
```

Using this option means that your IT department must create and manage all user accounts at the OS level.

After an OS-level account exists, you may create on the main AEN web page an AEN account using the same name. The password you choose is not linked in any way to the OS-level password for the account.

Alternatively, you can configure the system to *use LDAP for authenticating users*.

### Allowing public users to have access to your AEN projects

A public account is visible to anyone who can access the AEN server. The name of this account can be configured to any name you wish. For example, `public` or `anonymous`. To disable this feature use the special value `disabled`.

1. In the `/opt/wakari/wakari-compute/etc/wakari/wk-compute-launcher-config.json` file, modify the `ANON_USER` line to read:

```
"ANON_USER": "public"
```

2. Restart AEN compute node:

```
sudo service wakari-compute restart
```

3. In the `/opt/wakari/wakari-server/etc/wakari/wk-server-config.json` file, modify the `ANON_USER` line to read:

```
"ANON_USER": "public"
```

4. Restart AEN server:

```
sudo service wakari-server restart
```

For more information about configuration keys, see *Using configuration files*.

### Using a sudo alternative

You can use a sudo alternative as long as it supports the same execution semantics as the original sudo. The alternative must be configured to give the service account permission to run commands on behalf of AEN users.

1. In your terminal window, open the `/opt/wakari/wakari-compute/etc/wakari/config.json` file.
2. Modify the `AEN_SUDO_CMD` line to read:

```
"AEN_SUDO_CMD": "/path/to/alternative/sudo",
```

NOTE: If the alternate sudo command is available on `PATH`, then the full path is not required.

### Restricting sudo access to a single gatekeeper

By default, `sudoers` is configured to allow AEN to run any command as a particular user which allows the platform to initiate processes as the logged-in end user. If more restrictive control is required, it should be implemented using a suitable `sudoers` policy. If that is not possible or practical, it is also possible to route all AEN ID-changing operations through a single gatekeeper.

This gatekeeper wraps the desired executable and provides an alternate way to log, monitor, or control which processes can be initiated by AEN on behalf of a user.

CAUTION: Gatekeeper is a special case configuration and should only be used if required.

To configure an AEN gatekeeper:

1. Modify the `/etc/sudoers.d/wakari_sudo` file to contain:

```
Defaults:wakari !requiretty, visiblepw
Runas_Alias    OP = ALL,!root
wakari ALL=(OP) NOPASSWD: /path/to/gatekeeper
```

2. In the `/opt/wakari/wakari-compute/etc/wakari/config.json` file, modify the `AEN_SUDO_SH` line to read:

```
"AEN_SUDO_SH": "/path/to/gatekeeper"
```

EXAMPLE: The gatekeeper can be as simple as a script with contents such as:

```
#!/bin/bash
first_cmd=$1
if [ 'bash' == $1 ]; then
    shift
    export HOME=~
    export SHELL=/bin/bash
    export PATH=$PATH:/opt/wakari/anaconda/bin
    bash "$@"
else
    exec $@
fi
```

## Configuring SSL

The server node uses NGINX to proxy all incoming http(s) requests to the server running on a local port, and uses NGINX for SSL termination. The default setup uses http—non-SSL—since cert files are required to configure SSL and each enterprise will have their own cert files.

The `www.enterprise.conf` file is the default `nginx.conf` file used for AEN. It is copied to the `/etc/nginx/conf.d` directory during server installation.

NOTE: This section describes setting up SSL after your gateway node has been installed and registered with the server node.

## Copying the required files

To configure SSL on AEN, you will need the following files:

- Server certificate and key
- Server CA bundle
- Gateway certificate and key
- Gateway CA bundle

Configure SSL on AEN:

1. Copy the Gateway certificate and key to `/opt/wakari/wakari-gateway/etc/` on the Gateway as `gateway.crt` and `gateway.key`.
2. Copy the Gateway CA bundle to `/opt/wakari/wakari-server/etc/` on the Server.
3. Copy the Server certificate and key to `/etc/nginx` on the Server as `server.crt` and `server.key`.
4. Copy the Server CA bundle to `/opt/wakari/wakari-gateway/etc/` on the Gateway.

If you have a certificate that was signed by a private root CA and/or an intermediate authority:

- The Gateway CA bundle must contain the full chain: root CA, any intermediate authority and the certificate.

```
cat gateway.crt intermediate.crt root.crt >> gateway-crt-int-root.crt
```

- The Server CA bundle must be separated into individual files for the root CA, any intermediate and the certificate.

## Configuring SSL on the server node

The `www.enterprise.https.conf` is an NGINX configuration file for SSL. It is set up to use the `server.crt` and `server.key` cert files.

**CAUTION:** You must change these values to point to the signed cert files for your domain.

**NOTE:** Self-signed certs or those signed by a private root CA require additional configuration.

Perform the following steps as root:

1. Stop NGINX:

```
service nginx stop
```

2. Move the `/etc/nginx/conf.d/www.enterprise.conf` file to a backup directory.
3. Copy the `/opt/wakari/wakari-server/etc/nginx/conf.d/www.enterprise.https.conf` file to `/etc/nginx/conf.d`.  
**NOTE:** `/etc/nginx/conf.d` may have `www.enterprise.conf` or `www.enterprise.https.conf` but it may not have both.
4. Edit the `/etc/nginx/conf.d/www.enterprise.https.conf` file and change the `server.crt` and `server.key` values to the names of the real cert and key files if they are different.
5. Restart NGINX by running:

```
service nginx start
```

6. Update the `WAKARI_SERVER` and `CDN` settings to use `https` instead of `http` in the following configuration files:

```
/opt/wakari/wakari-server/etc/wakari/config.json  
/opt/wakari/wakari-gateway/etc/wakari/wk-gateway-config.json  
/opt/wakari/wakari-compute/etc/wakari/config.json
```

7. Copy the gateway certificate, `gateway.crt` to `/opt/wakari/wakari-server/etc/`.
8. In an editor, open `/opt/wakari/wakari-server/etc/wakari/wk-server-config.json` and add:

```
"verify_gateway_certificate": "/opt/wakari/wakari-server/etc/gateway.crt"
```

9. Restart AEN services on the server by running:

```
service wakari-server restart
```

**NOTE:** This step may return an error since the gateway has not yet been configured for SSL.

10. In AEN, verify that the browser uses `https`. On the Admin Settings page, under Data Centers, click Gateway, then select `https`:

# Admin Settings

Anaconda Enterprise Notebooks settings accessible only by the administrator

The screenshot shows two side-by-side panels from the Anaconda Enterprise Admin Settings interface.

- Staff Panel:** Contains three links: "Daily Report", "Password Reset", and "Notification".
- Data Centers / Register a datacenter Panel:**
  - Has a "Name" field with the value "Gateway 1".
  - Has two checkboxes: "Subdomain Routing" (unchecked) and "Https" (checked).

## Configuring SSL on the gateway

1. For all types of SSL certificates, in `/opt/wakari/wakari-gateway/etc/wakari/wk-gateway-config.json`, add:

```
{
  EXISTING_CONFIGURATION,
  "https": {
    "key": "/opt/wakari/wakari-gateway/etc/gateway.key",
    "cert": "/opt/wakari/wakari-gateway/etc/gateway.crt"
  }
}
```

2. For a server certificate signed by a private root CA or signed by an intermediate authority, add:

```
{
  EXISTING_CONFIGURATION,
  "https": {
    "key": "/opt/wakari/wakari-gateway/etc/gateway.key",
    "cert": "/opt/wakari/wakari-gateway/etc/gateway.crt",
    "ca": ["/opt/wakari/wakari-gateway/etc/server.crt"]
  }
}
```

**NOTE:** When the certificate chain has more than one intermediate cert signed by a higher root CA authority, you must manually break up the certs in the chain into individual files, and enumerate them in the `ca` key:

```
{
  EXISTING_CONFIGURATION,
  "https": {
```

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```

    "key": "/opt/wakari/wakari-gateway/etc/gateway.key",
    "cert": "/opt/wakari/wakari-gateway/etc/gateway.crt",
    "ca": ["/opt/wakari/wakari-gateway/etc/server1.crt",
           "/opt/wakari/wakari-gateway/etc/server2.crt",
           "/opt/wakari/wakari-gateway/etc/server3.crt"]
  }
}

```

3. For a gateway certificate that is encrypted using a passphrase, add:

```

{
  EXISTING_CONFIGURATION,
  "https": {
    "key": "/opt/wakari/wakari-gateway/etc/gateway.key",
    "cert": "/opt/wakari/wakari-gateway/etc/gateway.crt",
    "passphrase": "mysecretpassphrase"
  }
}

```

NOTE: Alternatively, the passphrase can be passed using an environment variable or entered when the wakari-gateway service is manually started.

#### EXAMPLES:

```

# using an environment variable
AEN_GATEWAY_SSL_PASSPHRASE='mysecretpassphrase' wk-gateway

```

```

# starting wakari-gateway manually
sudo service wakari-gateway start --ask-for-passphrase
Passphrase?

```

4. Restart the gateway:

```

sudo service wakari-gateway restart

```

## Configuring SSL on compute nodes

Anaconda Enterprise does not support direct SSL on Compute Nodes. If you need SSL on Compute Nodes, you must install each Compute Node on the same server as a Gateway using `http://localhost:5002` for the URL value while adding it as a resource, and you must use a Gateway for each and every Compute Node.

## Security reminder

The permissions on the cert files must be set correctly to prevent them from being read by others. Since NGINX is run by the root user, only the root user needs read access to the cert files.

EXAMPLE: If the cert files are called `server.crt` and `server.key`, then use the root account to set permissions:

```

chmod 600 server.key
chmod 600 server.crt

```

## Enabling or disabling the Strict-Transport-Security header

By default, Strict-Transport-Security (STS) is enabled in the `www.enterprise.https.conf` file:

```
add_header Strict-Transport-Security max-age=31536000;
```

It can remain enabled if either of the following is true:

- The gateway is running on a different host than the server.
- or
- SSL has been enabled for the gateway.

You must comment out this line if both of the following are true:

- The gateway is running on the same host as the server.
- and
- SSL has not been enabled for the gateway.

Leaving STS enabled when these conditions are true will cause a mismatch in protocols between the server and gateway, causing your apps to fail to launch correctly.

## Configuring single sign-on

AEN's single sign-on (SSO) capability creates a new authentication provider that defers to your Anaconda Repository for login and authentication cookies.

To enable SSO:

1. Deploy AEN and Repository on the same machine.
2. In the `/opt/wakari/wakari-server/etc/wakari/config.json` file, add:

```
{
  EXISTING_CONFIGURATION,
  "SECRET_KEY": "<repo signing secret>",
  "REPO_LOGIN_URL":
    "http://example_repo.com:8080/account/login?next=http://example_repo.com/"
}
```

3. Copy the `SECRET_KEY` from the Repository configuration file.
4. In the `/opt/wakari/wakari-server/etc/wakari/wk-server-config.json` file, modify:

```
{
  EXISTING_CONFIGURATION,
  "accounts": "wk_server.plugins.accounts.repo",
}
```

5. If you are using Repository version 2.33.3 through 2.33.10, set `USE_SERVER_BASED_SESSIONS: false` in the Repository configuration.

This setting affects the network security properties of AEN and Repository. Specifically, if `USE_SERVER_BASED_SESSIONS` is set to false, and if a new cross-site scripting (XSS) vulnerability is discovered, it could expose an additional server fixation vulnerability. Please discuss this with your Anaconda representative and be sure the feature is compatible with your network requirements before setting `USE_SERVER_BASED_SESSIONS: false`.

6. To activate the changes restart `wakari-server`:

```
sudo service wakari-server restart
```

SSO is enabled.

### Adding a third-party extension

Anaconda officially supports and tests functionality of the default environment(s) only for those extensions that ship with AEN.

It is possible to add third-party and custom extensions from `conda-forge` or `pip`, but doing so may cause instability in your default project environments or kernels.

**CAUTION:** Anaconda does not officially support third-party extensions. This section is informational only.

### Installing unofficial Jupyter Notebook extensions for AEN

**TIP:** Always back up and verify your complete system before installing extensions.

The `jupyter-contrib-nbextensions` extensions are installed on a compute node.

The default `conda` executable directory for AEN is `/opt/wakari/anaconda/bin/conda`. If you are installing a Jupyter extension, it must be installed in the `wakari-compute` directory.

**EXAMPLE:** Run:

```
/opt/wakari/anaconda/bin/conda install -p /opt/wakari/wakari-compute/ -c conda-forge_
↪ jupyter_contrib_nbextension
```

For more information, see [Unofficial Jupyter Notebook Extensions](#).

### Configure search indexing

For search indexing to work correctly, verify that the AEN Compute node can communicate with the AEN Server.

```
curl -m 5 $AEN_SERVER > /dev/null
```

There must be at least one `inotify` watch available for the number of subdirectories within the project root filesystem. Some Linux distributions default to a low number of watches, which can prevent the search indexer from monitoring project directories for changes.

```
cat /proc/sys/fs/inotify/max_user_watches
```

If necessary, increase the number of max user watches with the following command:

```
echo fs.inotify.max_user_watches=100000 | sudo tee -a /etc/sysctl.conf && sudo sysctl_
↪ -p
```

There must be at least one `inotify` user instance available per project.

```
cat /proc/sys/fs/inotify/max_user_instances
```

If necessary, this can be increased with the following command:



```
echo fs.inotify.max_user_instances=1000 | sudo tee -a /etc/sysctl.conf && sudo sysctl_
↪-p
```

## Create custom Jupyter kernel for Pyspark

These instructions add a custom Jupyter Notebook option to allow users to select PySpark as the kernel.

### Install Spark

The easiest way to install Spark is with [Cloudera CDH](#).

You will use YARN as a resource manager. After installing Cloudera CDH, [install Spark](#). Spark comes with a PySpark shell.

### Create a notebook kernel for PySpark

You may create the kernel as an administrator or as a regular user. Read the instructions below to help you choose which method to use.

#### 1. As an administrator

Create a new kernel and point it to the root env in each project. To do so create a directory 'pyspark' in `/opt/wakari/wakari-compute/share/jupyter/kernels/`.

Create the following kernel.json file:

```
{ "argv": [ "/opt/wakari/anaconda/bin/python",
  "-m", "ipykernel", "-f", "connection_file", "--profile", "pyspark"],
  "display_name": "PySpark", "language": "python" }
```

You may choose any name for the 'display\_name'.

This configuration is pointing to the python executable in the root environment. Since that environment is under admin control, users cannot add new packages to the environment. They will need an admin to help update the environment.

#### 2. As an administrator without IPython profile

To have an admin level PySpark kernel without the user .ipython space:

```
{ "argv":
  [ "/opt/wakari/wakari-compute/etc/ipython/pyspark.sh", "-f", "{connection_file}" ],
  "display_name": "PySpark", "language": "python" }
```

NOTE: The pyspark.sh script is defined in *Without IPython profile* section below.

#### 3. As a regular user

Create a new directory in the user's home directory: `.local/share/jupyter/kernels/pyspark/`. This way the user will be using the default environment and able to upgrade or install new packages.

Create the following kernel.json file:

```
{ "argv": [ "/projects/<username>/<project_name>/envs/default/bin/python",  
  "-m", "ipykernel", "-f", "connection_file", "--profile", "pyspark"],  
  "display_name": "PySpark", "language": "python" }
```

NOTE: Replace “<username>” with the correct user name and “<project\_name>” with the correct project name.

You may choose any name for the ‘display\_name’.

### Create an IPython profile

The above profile call from the kernel requires that we define a particular PySpark profile. This profile should be created for each user that logs in to AEN to use the PySpark kernel.

In the user’s home, create the directory and file ~/.ipython/profile\_pyspark/startup/00-pyspark-setup.py with the file contents:

```
import os  
import sys  
  
# The place where CDH installed spark, if the user installed Spark locally it can be_  
↪ changed here.  
# Optionally we can check if the variable can be retrieved from environment.  
  
os.environ["SPARK_HOME"] = "/usr/lib/spark"  
  
os.environ["PYSPARK_PYTHON"] = "/opt/wakari/anaconda/bin/python"  
  
# And Python path  
os.environ["PYLIB"] = os.environ["SPARK_HOME"] + "/python/lib"  
sys.path.insert(0, os.environ["PYLIB"] + "/py4j-0.9-src.zip") #10.4-src.zip"  
sys.path.insert(0, os.environ["PYLIB"] + "/pyspark.zip")  
  
os.environ["PYSPARK_SUBMIT_ARGS"] = "--name yarn pyspark-shell"
```

Now log in using the user account that has the PySpark profile.

### Without IPython profile

If it is necessary to avoid creating a local profile for the users, a script can be made to be called from the kernel. Create a bash script that will load the environment variables:

```
sudo -u $AEN_SRVC_ACCT mkdir /opt/wakari/wakari-compute/etc/ipython  
sudo -u $AEN_SRVC_ACCT touch /opt/wakari/wakari-compute/etc/ipython/pyspark.sh  
sudo -u $AEN_SRVC_ACCT chmod a+x /opt/wakari/wakari-compute/etc/ipython/pyspark.sh
```

The contents of the file should look like:

```
#!/usr/bin/env bash  
# setup environment variable, etc.  
  
export PYSPARK_PYTHON="/opt/wakari/anaconda/bin/python"  
export SPARK_HOME="/usr/lib/spark"
```

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```
# And Python path
export PYLIB=$SPARK_HOME:/python/lib
export PYTHONPATH=$PYTHONPATH:$PYLIB:/py4j-0.9-src.zip
export PYTHONPATH=$PYTHONPATH:$PYLIB:/pyspark.zip

export PYSARK_SUBMIT_ARGS="--name yarn pyspark-shell"

# run the ipykernel
exec /opt/wakari/anaconda/bin/python -m ipykernel $@
```

## Using PySpark

When creating a new notebook in a project, now there will be the option to select PySpark as the kernel. When creating such a notebook you'll be able to import pyspark and start using it:

```
from pyspark import SparkConf
from pyspark import SparkContext
```

NOTE: You can always add those lines and any other command you may use frequently in the PySpark setup file 00-pyspark-setup.py as shown above.

## Upgrading AEN

- *Before you upgrade*
- *Upgrading the AEN server node*
- *Upgrading the AEN gateway node*
- *Upgrading AEN compute nodes*
- *After upgrading*

CAUTION: These instructions are for upgrading AEN to the current version 4.2.2 from 4.2.1 ONLY. Each version must be upgraded iteratively from the previous version. Do not skip versions.

Upgrade instructions for previous versions:

- *AEN 4.2.1 upgrade instructions*
- *AEN 4.2.0 upgrade instructions*
- *AEN 4.1.3 upgrade instructions*
- *AEN 4.1.2 upgrade instructions*
- *AEN 4.1.1 upgrade instructions.*
- *AEN 4.1.0 upgrade instructions.*
- *AEN 4.0.0 upgrade instructions.*

For upgrades from versions before those listed above, please contact your enterprise support representative.

NOTE: Named Service Account functionality is available with AEN 4.0.0+ for new installations only. It is not available for upgraded installations. Contact your enterprise support representative for more information.

An AEN platform update requires that each instance of the 3 node types be upgraded individually:

- AEN Server
- AEN Gateway
- AEN Compute

The upgrade process requires that all AEN service instances be stopped, upgraded, and then restarted.

NOTE: Any commands that call for the root user can also be done using `sudo`.

If you encounter any difficulty during the upgrade process, see [Troubleshooting](#) which provides guidance on:

- processes
- configuration files
- log files
- ports

If you are unable to resolve an installation or upgrade problem, please contact your enterprise support representative.

### Before you upgrade

CAUTION: Make a tested backup of your installation before starting the upgrade. Upgrading to a higher version of AEN is not reversible. Any errors during the upgrade procedure may result in partial or complete data loss and require restoring data from backups.

CAUTION: Terminate all AEN applications and stop all projects before starting the upgrade process.

Before upgrading each service on each host:

1. Suspend the services on each of the nodes:

```
sudo service wakari-server stop
sudo service wakari-gateway stop
sudo service wakari-compute stop
```

2. Set the AEN Functional ID (“NFI”) and AEN Functional Group (“NFG”) to the NFI and NFG of the current installation:

```
export AEN_SRVC_ACCT="wakari"
export AEN_SRVC_GRP="wakari"
```

NOTE: The default NFI is `wakari`, but `aen_admin` or any other name may be used instead.

For more information on NFI and NFG, see the [installation instructions](#).

3. Install `wget`:

```
yum install wget
```

### Upgrading the AEN server node

NOTE: If you are using LDAP-based authentication, back up the `/opt/wakari/wakari-server/etc/wakari/wk-server-config.json` configuration file. After the server has been upgraded, copy that file back into the same location as before the upgrade.

Complete the following steps on the server host:

## 1. Stop the Elasticsearch service:

```
sudo service elasticsearch stop
```

## 2. Remove any previous index:

```
sudo rm -rf /var/lib/elasticsearch/*
```

**NOTE:** You can choose to keep the old index, but if you detect any issues with the search capabilities after the upgrade, you will need to run the following to start with a clean index:

```
sudo service wakari-server stop
sudo service elasticsearch stop
sudo rm -rf /var/lib/elasticsearch/*
sudo service elasticsearch start
sudo service wakari-server start
```

## 3. Upgrade the server:

```
pushd /tmp
wget http://j.mp/aen-server-update-4_2_2

sudo -E -u $AEN_SRVC_ACCT /opt/wakari/miniconda/bin/conda install \
    -p /opt/wakari/wakari-server \
    --file aen-server-update-4_2_2

sudo -E -u $AEN_SRVC_ACCT /opt/wakari/miniconda/bin/conda install \
    -p /opt/wakari/wakari-server \
    --no-deps \
    wakari-enterprise-server-conf-update=2.0.9

popd
```

## 4. Start Elasticsearch:

```
sudo service elasticsearch start
```

Or, if you do not want to use the search features, edit your server's `/opt/wakari/wakari-server/etc/wakari/config.json` file by adding the line `"SEARCH_ENABLED": false`.

## 5. Restart the NGINX server:

AEN server version `>= 4.1.3` uses Unix sockets for communication with NGINX. Restart NGINX to load this new configuration:

```
sudo service nginx restart
```

Alternatively, you can restart NGINX with:

```
sudo nginx -s stop
sudo nginx
```

## 6. Start the server:

```
sudo service wakari-server start
```

## 7. Check that the server is running properly:

```
sudo service wakari-server status
```

8. If you see NGINX errors, please check the configuration at `/opt/wakari/wakari-server/etc/nginx/conf.d/www.enterprise.conf:18`.
9. Connect to AEN server using your web browser with the correct protocol (http or https), hostname and port number.

## Upgrading the AEN gateway node

Complete the following steps on each gateway host:

1. Upgrade the gateway:

```
pushd /tmp
wget http://j.mp/aen-gateway-update-4_2_2

sudo -E -u $AEN_SRVC_ACCT /opt/wakari/miniconda/bin/conda install \
    -p /opt/wakari/wakari-gateway \
    --file aen-gateway-update-4_2_2

sudo -E -u $AEN_SRVC_ACCT /opt/wakari/miniconda/bin/conda install \
    -p /opt/wakari/wakari-gateway \
    --no-deps \
    wakari-enterprise-gateway-conf-update=2.0.9

popd
```

2. Start the gateway:

```
sudo service wakari-gateway start
```

3. Check that the gateway is running properly:

```
sudo service wakari-gateway status
```

4. Connect to the gateway using your web browser with the correct http/https, hostname and port number.

## Upgrading AEN compute nodes

Complete the following steps on each host where an AEN compute service is running:

1. Check for any `wakari-indexer` processes running:

```
ps aux | grep wakari-indexer
```

NOTE: If you stopped all the projects, you will not see any `wakari-indexer` processes running.

Terminate any remaining `wakari-indexer` processes:

```
sudo killall wakari-indexer
```

NOTE: The processes killed with `killall` are run by the `$AEN_SRVC_ACCT` user, so they can be killed as root with `sudo killall` or killed as the `$AEN_SRVC_ACCT` user with `sudo -u $AEN_SRVC_ACCT killall`. Example commands show the `sudo killall` option.

2. Check for any AEN applications processes running—Workbench, Viewer, Terminal or Notebook:

```
ps aux | grep wk-app-gateone
ps aux | grep wk-app-workbench
ps aux | grep wk-app-viewer
ps aux | grep wk-app-terminal
ps aux | grep jupyter-notebook
```

NOTE: If you stopped all the projects, you will not see any AEN app processes running.

Terminate any remaining AEN application processes by running one or more of the following:

```
sudo killall wk-app-gateone
sudo killall wk-app-workbench
sudo killall wk-app-viewer
sudo killall wk-app-terminal
sudo killall jupyter-notebook
```

3. Verify the contents of `/opt/wakari/anaconda/.condarc`. Modify it to contain the following entries, and possibly others if you customized the `.condarc` file.

NOTE: Modify the file as the `AEN_SRVC_ACCT` user (or be sure to keep the same ownership).

```
channels:
- https://conda.anaconda.org/t/<TOKEN>/anaconda-nb-extensions
- r
- https://conda.anaconda.org/wakari
- defaults

create_default_packages:
- anaconda-client
- ipykernel
```

NOTE: Contact your enterprise support representative to get your token for the Anaconda channel referenced above. Replace `<TOKEN>` with the actual token from your enterprise support representative.

4. Upgrade *Anaconda* in the root environment:

```
pushd /tmp
wget http://j.mp/aen-anaconda-update-4_2_2

sudo -E -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda install \
    -p /opt/wakari/anaconda \
    --file aen-anaconda-update-4_2_2

popd
```

5. Upgrade each compute service:

```
pushd /tmp
wget http://j.mp/aen-compute-update-4_2_2

sudo -E -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda install \
    -p /opt/wakari/wakari-compute \
    --file aen-compute-update-4_2_2

sudo -E -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda install \
    --no-deps \
    -p /opt/wakari/wakari-compute \
    wakari-enterprise-compute-conf-update=2.0.13

popd
```

NOTE: When upgrading the wakari-compute environment, you may see ImportError warnings with some nbextensions. As long as the Validating message is OK, the ImportError warnings are harmless—a consequence of the post-link presence on those packages.

6. Initialize the root environment to prime the package cache:

```
sudo -E -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda create \  
    -p /opt/wakari/testenv \  
    --clone root
```

7. Test the offline cloning step:

```
sudo -E -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda create \  
    -p /opt/wakari/testenvoffline \  
    --clone root --offline
```

8. Remove the test environments:

```
sudo rm -rf /opt/wakari/testenv  
sudo rm -rf /opt/wakari/testenvoffline
```

9. Install necessary dependencies:

NOTE: Skip this step if you already have these dependencies installed from previous installations.

```
sudo yum groupinstall "X Window System" -y  
sudo yum install git -y
```

NOTE: If you don't want to install the whole X Window System, you must install the following packages to have R plotting support:

```
sudo yum install -y libXrender libXext libXdmcp libSM libICE libXt \  
dejavu-sans-fonts dejavu-serif-fonts dejavu-fonts-common \  
fontpackages-filesystem
```

10. Start the compute service:

```
sudo service wakari-compute start
```

11. Verify the compute service is running properly:

```
sudo service wakari-compute status
```

12. Restart the AEN Server with:

```
sudo service wakari-server restart
```

13. Repeat this upgrade procedure for all compute nodes in your Data Center.

## After upgrading

1. Restart the projects and start using AEN applications.
2. If you have a *customized default environment*, you may choose to upgrade it depending on the needs of your users.

Upgrade the customized default environment at `/opt/wakari/anaconda/envs/default` with the `$AEN_SRVC_ACCT` user:



```
pushd /tmp
wget http://j.mp/aen-anaconda-update-4_2_2

sudo -E -u $AEN_SRVC_ACCT /opt/wakari/anaconda/bin/conda install \
    -p /opt/wakari/anaconda/envs/default \
    --file aen-anaconda-update-4_2_2

popd
```

To upgrade the customized default environments for every user and every project at `/projects/<USER>/<PROJECT>/envs/default`, run these commands for **every** user as that user:

```
pushd /tmp
wget http://j.mp/aen-anaconda-update-4_2_2

sudo -E -u <USER> /opt/wakari/anaconda/bin/conda install \
    -p /projects/<USER>/<PROJECT>/envs/default \
    --file aen-anaconda-update-4_2_2

popd
```

NOTE: Replace `<USER>` with the user's name. Replace `<PROJECT>` with the project name.

NOTE: Upgrading the default environment at `/opt/wakari/anaconda/envs/default` does NOT automatically upgrade the default environment in the users pre-existing projects. For pre-existing projects, the upgrade, if requested, should be done on a per-user basis.

NOTE: These commands update packages listed in `aen-anaconda-update-4_2_2` and do not update any other package.

3. If you did not stop all your projects before upgrading, then the first time you start an application you will see an error page requesting that you restart the application.
4. Restart the application to complete the upgrade.
5. If you still see old applications or icons after restart, reload the page to reset the browser cache.

## Uninstalling AEN

Each AEN node must be uninstalled separately.

- *Uninstalling a server node*
- *Uninstalling a gateway node*
- *Uninstalling a compute node*
- *OPTIONAL: Removing projects from compute nodes*

Begin by setting the AEN Functional ID (NFI). The NFI is the username of the AEN Service Account which is used to run all AEN services and is also the username of the AEN Admin account. The NFI may be any name. The default NFI is `wakari`. The NFI is also often set to `aen_admin`. The NFI (and AEN Functional Group or NFG) are described in *the installation instructions*.

Set the NFI with this command:

```
export AEN_SRVC_ACCT="aen_admin"
```

Replace the name `aen_admin` with the NFI that was set in your installation of Anaconda Enterprise Notebooks.

## Uninstalling a server node

To remove a server node, run the following commands as root or sudo on the server node's host system:

1. Stop the server processes:

```
service wakari-server stop
```

2. Stop MongoDB:

```
service mongod stop
```

3. Remove AEN server software, AEN database files and NGINX configuration:

```
rm -Rf /opt/wakari/wakari-server
rm -Rf /opt/wakari/miniconda
rm -Rf /var/lib/mongo/wakari*
rm -Rf /etc/nginx/conf.d/www.enterprise.conf
```

NOTE: Remove `/etc/nginx/conf.d/www.enterprise.https.conf` if SSL is enabled on the Server node.

4. Restart MongoDB and NGINX:

```
service mongod restart
service nginx restart
```

5. Check for any outstanding server processes and stop them:

```
ps -ef | grep -e wakari-server -e wk-server
```

6. Remove the AEN Service Account:

```
userdel $AEN_SRVC_ACCT
```

7. Check for and remove any references to “aen” or “wakari” from the root user's `.condarc` file:

```
grep -i aen ~/.condarc
grep -i wakari ~/.condarc
```

## Uninstalling a gateway node

To uninstall a gateway node, run the following commands as root or sudo on the gateway host system:

1. Stop the gateway processes:

```
service wakari-gateway stop
```

2. Remove gateway software:

```
rm -Rf /opt/wakari/wakari-gateway
```

3. Check for any outstanding gateway processes and stop them:

```
ps -ef | grep -e wakari-gateway -e wk-gateway
```

4. Remove the AEN Service Account:

```
userdel $AEN_SRVC_ACCT
```

5. Check for and remove any references to “aen” or “wakari” from the root user’s `.condarc` file:

```
grep -i aen ~/.condarc
grep -i wakari ~/.condarc
```

## Uninstalling a compute node

To remove a compute node, run the following commands as root or sudo on each compute node host system:

1. Stop the compute processes:

```
service wakari-compute stop
```

2. Remove the compute software:

```
rm -Rf /opt/wakari/wakari-compute
rm -Rf /opt/wakari/miniconda
rm -Rf /opt/wakari/anaconda
```

3. Check for any outstanding compute processes and stop them:

```
ps -ef | grep -e wakari-compute -e wk-compute
```

4. Remove the AEN Service Account:

```
userdel $AEN_SRVC_ACCT
```

5. Check for and remove any references to “aen” or “wakari” from the root user’s `.condarc` file:

```
grep -i aen ~/.condarc
grep -i wakari ~/.condarc
```

## OPTIONAL: Removing projects from compute nodes

**CAUTION:** This is an extreme measure and is not necessary in most instances. We recommend you create and verify a backup before doing this or any other file removal.

To remove all AEN projects from all of your compute nodes:

```
rm -Rf /projects
```

This is a step-by-step guide to installing an Anaconda Enterprise Notebooks system comprised of a front-end server, a gateway and compute machines.

If you have any questions about these instructions or you encounter any issues while installing AEN, please contact your sales representative or Priority Support team.

When you have completed the installation process, review the *optional configuration tasks* to see if any are appropriate for your system.

### Distributed install

In a distributed install the server and gateway run on separate hosts.

### Single-box install

In a single-box install, both the server and the gateway need separate external ports since they are independent services that are running on the same host in the single-box installation.

Both port 80 and port 8089 must be open on the firewall for a single-box install.

The compute node only receives connections from the gateway and server nodes and typically runs on port 80 or port 443.

### User management

#### Adding or removing an administrative user

An administrator can make any other user an administrator—or remove their administrator permissions—by using administrator commands in the Terminal application.

A user can also be designated as a superuser or as staff, giving them greater administrative privileges within the system.

#### Designating a user as an administrator/superuser

To designate a user as an administrator and superuser:

```
/opt/wakari/wakari-server/bin/wk-server-admin superuser --add <username>
```

NOTE: Replace <username> with the actual username.

EXAMPLE: To give administrative privileges to the user named “jsmith” and set them as a superuser, run:

```
/opt/wakari/wakari-server/bin/wk-server-admin superuser --add jsmith
```

#### Removing an administrator/superuser

To remove a user’s administrative privileges:

```
/opt/wakari/wakari-server/bin/wk-server-admin superuser --remove <username>
```

NOTE: Replace <username> with the actual username.

#### Allowing and restricting new user registration

When Open Registration is enabled, anyone who has access to the URL of your AEN server can create their own account.

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select Accounts.

The screenshot shows the Anaconda Admin Settings interface. On the left, there are two sidebars. The top sidebar, titled 'Staff', contains links for 'Daily Report', 'Password Reset', 'Notification', and 'Exceptions'. The bottom sidebar, titled 'Site Admin', contains links for 'General' and 'Accounts'. The main content area is titled 'Cloud Registration' and contains a checkbox labeled 'Open Registration' with the text 'Allow new user signups' below it. A green 'Update' button is located at the bottom of this section.

3. To open user registration, select the Open Registration checkbox. To close registration, clear the checkbox.
4. Click the Update button.

### Resetting a user password

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Staff** menu, select Password Reset:

—  
Anaconda Enterprise Notebooks settings accessible only by the system administrator.

The screenshot shows the Anaconda Admin Settings interface with the 'Password Reset' section selected. The left sidebar is the same as in the previous screenshot. The main content area is titled 'Password Reset' and contains a text input field with the value 'guest'. Below the input field is a button labeled 'Generate URL'.

3. Enter the username of the user whose password needs to be reset.
4. Click the Generate URL button.

A password reset link is generated that you can email to the user.

Alternatively you may use the command line interface:

1. Use ssh to log into the server as root.
2. Run:

```
/opt/wakari/wakari-server/bin/wk-server-admin reset-password -u SOME_USER -p SOME_
↪PASSWORD
```

NOTE: Replace SOME\_USER with the username and SOME\_PASSWORD with the password.

3. Log into AEN as the user.

## Managing permissions

This page explains the admin commands used to manage user permissions.

### Checking file ownership

To verify that all files in the `/opt/wakari/anaconda` directory are owned by the `wakari` user or group:

```
root@server # find /opt/wakari/anaconda \! -user wakari -print
root@server # find /opt/wakari/anaconda \! -group wakari -print
```

### Fixing file ownership settings

To fix the ownership settings of any files that are listed in the output:

```
chown -R wakari:wakari /opt/wakari/anaconda
```

### Setting a file owner and permissions

To set a file owner and set its permissions:

```
chown wakari:wakari /opt/wakari/wakari-server/bin/wk-*
chmod 700 /opt/wakari/wakari-server/bin/wk-*
```

### Verifying that POSIX ACLs are enabled

The `acl` option must be enabled on the file system that contains the project root directory.

NOTE: By default, the project root directory is `/projects`.

To determine the project root directory where a custom `projectRoot` is configured:

```
root@compute # grep projectRoot /opt/wakari/wakari-compute/etc/wakari/config.json
```

The `mount` options or default options listed by `tune2fs` should indicate that the `acl` option is enabled.

EXAMPLE:

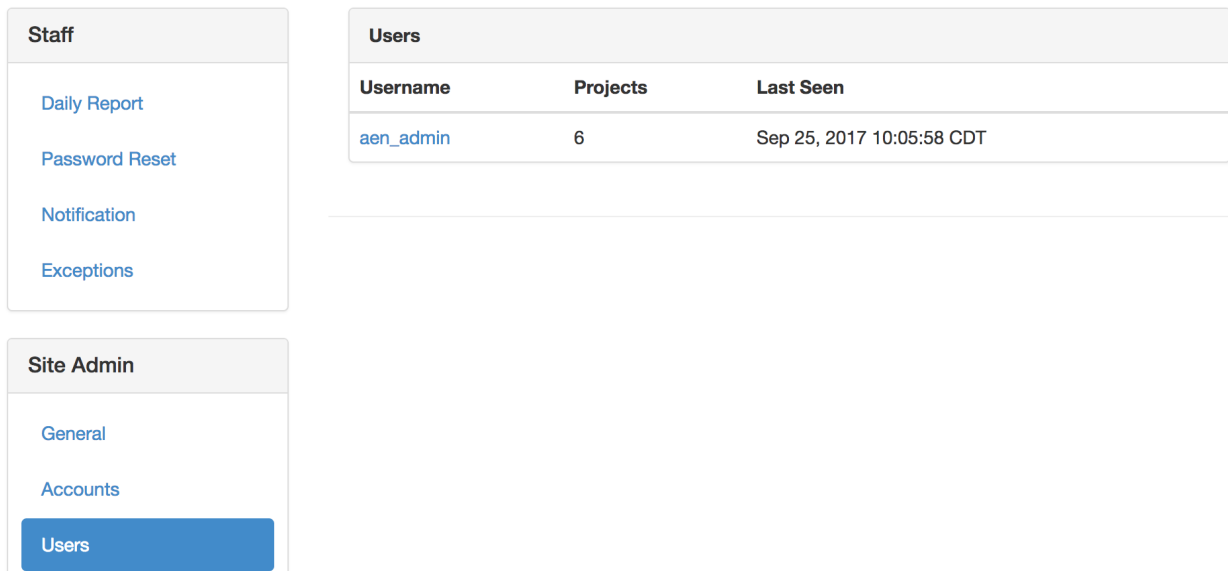
```

root@compute # fs=`df /projects | tail -1 | cut -d " " -f 1`
root@compute # mount | grep $fs
/dev/vda on / type ext4 (rw)
root@compute # tune2fs -l $fs | grep options
Default mount options:    user_xattr acl

```

## Viewing a list of users

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select Users:



The screenshot shows the AEN Admin Settings page. On the left, there are two sidebars. The top sidebar is titled 'Staff' and contains links for 'Daily Report', 'Password Reset', 'Notification', and 'Exceptions'. The bottom sidebar is titled 'Site Admin' and contains links for 'General', 'Accounts', and 'Users' (which is highlighted in blue). On the right, there is a table titled 'Users' with three columns: 'Username', 'Projects', and 'Last Seen'. The table contains one row with the username 'aen\_admin', 6 projects, and a last seen time of 'Sep 25, 2017 10:05:58 CDT'.

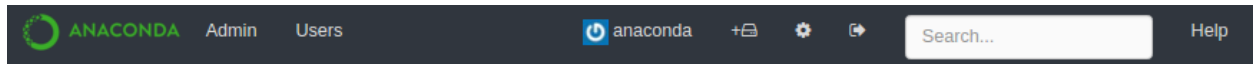
Username	Projects	Last Seen
aen_admin	6	Sep 25, 2017 10:05:58 CDT

The Users section lists the all users who are signed up, the number of projects they have created and the last time they logged on to AEN.

## Viewing a list of currently active users

In the AEN navigation bar, click Users.

Click a username to open the user's profile page.



# Users

List of currently active users in the system.

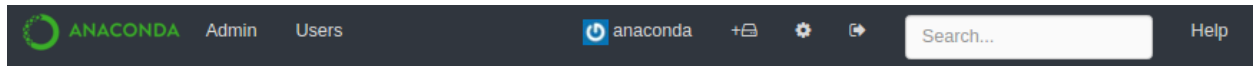
 anaconda
 andrew
 bokeh
 christine
 guest
 hubert
 ivan
 paula
 simon
 tanya
 wakari



## Viewing a user profile

A user's profile page includes a summary of the projects created by that user and a list of projects on which the user is a team member.

1. In the AEN navigation bar, click Users to see a list of users who are currently logged into the system.
2. On the Users page, click the username of the user whose profile page you want to view.



## Users

List of currently active users in the system.

 anaconda
 andrew
 bokeh
 christine
 guest
 hubert
 ivan
 paula
 simon
 tanya
 wakari

## Sending a system message

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Staff** menu, select Notification:

Staff

[Daily Report](#)

[Password Reset](#)

[Notification](#)

[Exceptions](#)

Site Admin

[General](#)

[Accounts](#)

[Users](#)

[Security Log](#)

[Data Centers](#)

[Task Queue](#)

[License](#)

Providers

[Enterprise Resources](#)

Notification Settings

☒ **Off**

No email notification will be sent

☐ **SES - Amazon Simple Email Service**

This requires a .boto file in the wakari home dir

☐ **SMTP Email Server**

SMTP Settings

SMTP Hostname

SMTP Username *(optional)*

SMTP Password *(optional)*

SMTP From Address *(optional)*

Update

The Notification Settings section allows you to create a system message that can be relayed to users.

By default, notifications are off.

3. To turn on email notifications, select the radio button for the type of email service to use:

- SES to use Amazon Simple Email Service (SES).
- SMTP Email Server.

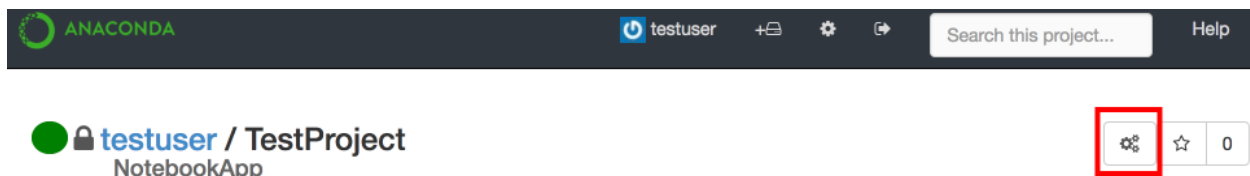
4. If you select SMTP Email Server, complete the SMTP Settings.

NOTE: If you get an error message after changing the SMTP settings, you may need to restart the server.

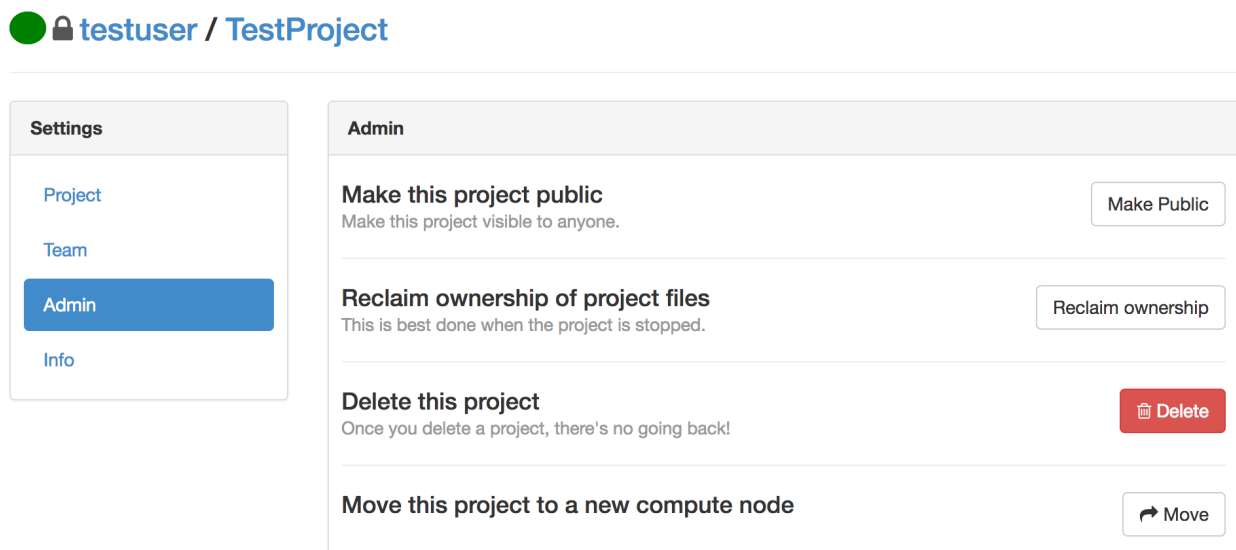
## Moving a project to another compute node

If you have multiple compute nodes available and want to move a project from one to another, the project must exist on both nodes.

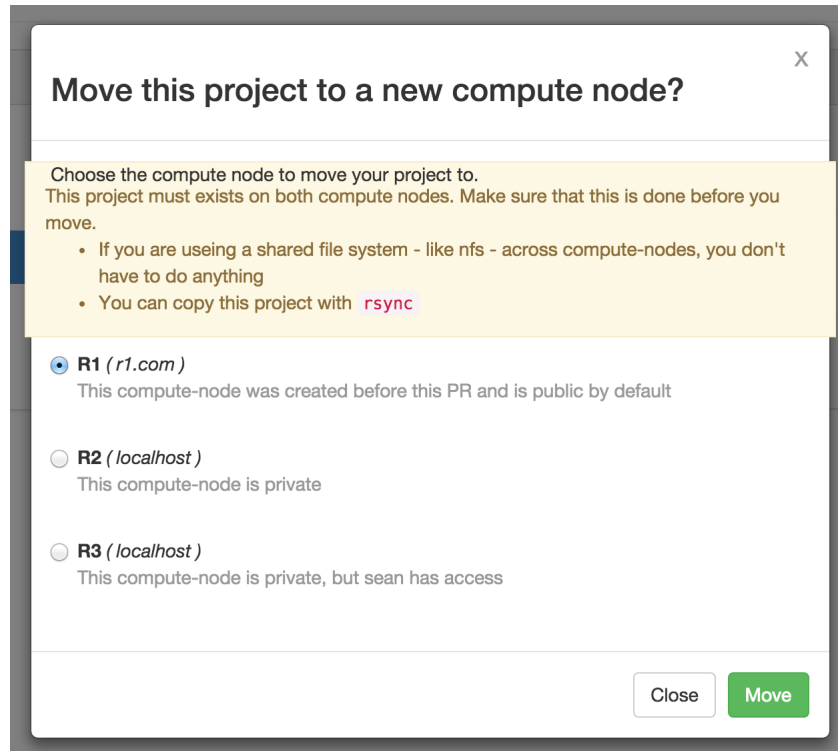
1. Verify that the project has been created on both compute nodes. You can use `rsync` for this job unless you have a shared file system like `nfs`.
2. On the project home page, click the Project Settings icon to open the Project Settings page.



3. In the **Settings** menu, select Admin.



4. Click the Move button.
5. In the move dialog box, click to choose the compute node destination, and click the Move button.



## Deleting a user

To remove a user from the AEN database:

```
/opt/wakari/wakari-server/bin/wk-server-admin remove-user <username>
```

NOTE: Replace <username> with the actual username.

NOTE: Changing the owner of a project requires that both the previous owner and the new owner are still AEN users. Before deleting a user, *change the owner* of that user's projects.

## Deleting a project

To remove a project from the AEN database:

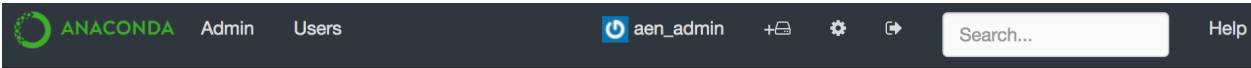
```
/opt/wakari/wakari-server/bin/wk-server-admin remove-project <username> <projectname>
```

NOTE: Replace <username> with the actual username and <projectname> with the actual project name you are removing.

System management

Opening the Admin dashboard

If you have administrator privileges, you see two additional links in the AEN navigation bar—Admin and Users:  
To open the Admin dashboard, click the Admin link.



# Admin Settings

Anaconda Enterprise Notebooks settings accessible only by the system administrator.

Staff

[Daily Report](#)  
[Password Reset](#)  
[Notification](#)  
[Exceptions](#)

Site Admin

[General](#)  
[Accounts](#)  
[Users](#)  
[Monitor](#)  
[Security Log](#)

Backing up and restoring AEN

- *Document purpose*
- *Important notes*
- *Server component steps*
  - *Backup*

- \* *Mongo database*
- \* *AEN Server config files (including License file)*
- \* *Nginx config (if needed)*
- \* *SSL certificates (if needed)*
- *Restore*
  - \* *Reinstall AEN-Server*
  - \* *Restore Mongo database*
  - \* *AEN Server config files (including License file)*
  - \* *Nginx config (if needed)*
  - \* *SSL certificates (if needed)*
  - \* *Restart server*
- *Gateway component steps*
  - *Backup*
    - \* *Config files*
    - \* *Custom .condarc file (if needed)*
    - \* *SSL certificates (if needed)*
  - *Restore*
    - \* *Reinstall AEN-Gateway*
    - \* *Config files*
    - \* *Custom .condarc file (if needed)*
    - \* *SSL certificates (if needed)*
    - \* *Restart gateway*
- *Compute component steps*
  - *Backup*
    - \* *Config files*
    - \* *Custom Changes (rare)*
    - \* *Create user list*
    - \* *Project files*
    - \* *Full Anaconda (option 1)*
    - \* *Partial Anaconda (option 2)*
  - *Restore*
    - \* *Reinstall AEN-Compute*
    - \* *Config files*
    - \* *Custom changes (rare)*
    - \* *Create users*

- \* *Project files*
- \* *Full Anaconda (option 1)*
- \* *Partial Anaconda (option 2)*
- \* *Custom environments (if needed)*
- \* *Restart compute node*

## Document purpose

This document lays out the steps to backup and restore Anaconda Enterprise Notebooks (AEN) for Disaster Recovery. It is not intended to provide High Availability. Each of the components (Server, Gateway and Compute) has its own instructions and each may be done individually as needed. The steps primarily involve creating tar files of important configuration files and data.

This document is written for a system administrator who is comfortable with basic Linux command line navigation and usage.

To migrate to a new cluster, use these backup and restore instructions to back up the system from the old cluster and restore it to the new cluster.

## Important notes

Review the [Concepts](#) page to become familiar with the different components and how they work together.

Root or sudo access is required for some commands.

**CAUTION:** All commands **MUST** be run by \$AEN\_SRVC\_ACCT (the account used to run AEN) except for those commands explicitly indicated to run as root or sudo. If the commands are not run by the correct user, the installation will not work, and a full uninstallation and reinstallation will be required!

These instructions assume that the fully qualified domain name (FQDN) has not changed for any of the component nodes. If any of the FQDNs are not the same, additional steps will be needed.

## Server component steps

### Backup

#### Mongo database

This will create a single tar file called `aen_mongo_backup.tar` that includes only the database named “wakari” that is used by AEN. It also generates a log of the database backup.

NOTE: These commands must be run by \$AEN\_SRVC\_ACCT.

```
mongodump -db wakari -o aen_main >> mongo_backup.log
tar -cvf aen_mongo_backup.tar aen_main
```

#### AEN Server config files (including License file)

Create a tar file of all of the configuration files, including any license files.

NOTE: This command must be run by \$AEN\_SRVC\_ACCT.

```
tar -cvf aen_server_config.tar -C /opt/wakari/ wakari-server/etc/wakari/
```

### Nginx config (if needed)

Make a copy of the nginx configuration file if it has been customized. The default configuration for the AEN server is a symlink.

NOTE: This command must be run by \$AEN\_SRVC\_ACCT.

```
/etc/nginx/conf.d/www.enterprise.conf -> /opt/wakari/wakari-server/etc/nginx/conf.d/  
↪www.enterprise.conf
```

### SSL certificates (if needed)

Make a copy of the SSL certificates files (certfiles) for the server, including the key file, and a copy of the certfile for the gateway, which is needed for verification if using self-signed or private CA signed certs.

## Restore

### Reinstall AEN-Server

See *the instructions for installing the current version of AEN-Server*.

It is not necessary to upload the license, because it will be restored with the config files.

NOTE: The new installation will generate a new password for the local \$AEN\_SRVC\_ACCT account.

### Restore Mongo database

This assumes that mongo was reinstalled as part of the reinstallation of the server component. Untar the mongo database and restore it.

NOTE: These commands must be run by \$AEN\_SRVC\_ACCT.

```
tar -xvf aen_mongo_backup.tar  
mongorestore --drop aen_main
```

NOTE: The --drop option resets the \$AEN\_SRVC\_ACCT user password and restores the database to the exact state it was in at the time of backup. Please see the [MongoDB documentation](#) for more information about mongorestore options for Mongo 2.6.

NOTE: AEN uses Mongo 2.6 by default. If you are using a different version, consult the documentation for your version.

### AEN Server config files (including License file)

Untar the tar file of all of the configuration files, including any license files.

NOTE: This command must be run by \$AEN\_SRVC\_ACCT.



```
tar -xvf aen_server_config.tar -C /opt/wakari/
```

Make sure the files are in `/opt/wakari/wakari-server/etc/wakari/` and are owned by the `$AEN_SRVC_ACCT`.

### Nginx config (if needed)

Make sure any modifications to the nginx configuration are either in `/etc/nginx/conf.d` or in `/opt/wakari/wakari-server/etc/nginx/conf.d/` with a proper symlink.

NOTE: This command must be run by `$AEN_SRVC_ACCT`.

```
/etc/nginx/conf.d/www.enterprise.conf -> /opt/wakari/wakari-server/etc/nginx/conf.d/  
↪www.enterprise.conf
```

### SSL certificates (if needed)

Move any SSL certificate files to the locations indicated in the config files.

### Restart server

Restart the server application.

NOTE: This command must be run as root or with `sudo`.

```
service wakari-server restart
```

## Gateway component steps

### Backup

### Config files

Create a tar file of all of the configuration files.

NOTE: This command must be run by `$AEN_SRVC_ACCT`.

```
tar -cvf aen_gateway_config.tar -C /opt/wakari/ wakari-gateway/etc/wakari/
```

### Custom .condarc file (if needed)

Make a copy of any `/opt/wakari/miniconda/.condarc` if it has been modified.

### SSL certificates (if needed)

Make a copy of SSL certificate files for the gateway (including the key file) and the certfile for the server (needed for verification if using self-signed or private CA signed certs).

### Restore

### Reinstall AEN-Gateway

### Setting variables and changing permissions

NOTE: These commands must be run by \$AEN\_SRVC\_ACCT.

Run:

```
export AEN_SERVER=<FQDN HOSTNAME OR IP ADDRESS> # Use the real FQDN
export AEN_GATEWAY_PORT=8089
export AEN_GATEWAY=<FQDN HOSTNAME OR IP ADDRESS> # will be needed shortly
chmod a+x aen-*.sh # Set installer to be executable
```

NOTE: Change <FQDN HOSTNAME OR IP ADDRESS> to the actual fully qualified domain hostname or IP address.

NOTE: You must perform the entire procedure before closing the terminal to ensure the variable export persists. If the terminal is closed before successful installation, export the variables to continue with the installation.

### Running the AEN gateway installer

Run:

```
sudo -E ./aen-gateway-4.2.2-Linux-x86_64.sh -w $AEN_SERVER
<license text>
...
...

PREFIX=/opt/wakari/wakari-gateway
Logging to /tmp/wakari_gateway.log
...
...
Checking server name
Please restart the Gateway after running the following command
to connect this Gateway to the AEN Server
...
```

### Config files

Untar the configuration files.

NOTE: This command must be run by \$AEN\_SRVC\_ACCT.

```
tar -xvf aen_gateway_config.tar -C /opt/wakari
```

Verify that the files are in /opt/wakari/wakari-gateway/etc/wakari/ and are owned by the \$AEN\_SRVC\_ACCT.

### Custom .condarc file (if needed)

Move the custom .condarc file to /opt/wakari/miniconda/.condarc.

## SSL certificates (if needed)

Move any SSL certificate files to the locations indicated in the config files.

## Restart gateway

Restart the gateway application.

NOTE: This command must be run as root or with sudo.

```
service wakari-gateway restart
```

## Compute component steps

### Backup

### Config files

Create a tar file of all of the configuration files.

NOTE: This command must be run by \$AEN\_SRVC\_ACCT.

```
tar -cvf aen_compute_config.tar -C /opt/wakari/ wakari-compute/etc/wakari
```

## Custom Changes (rare)

Manually backup any custom changes that were applied to the code. One change might be additional files in the skeleton folder:

```
/opt/wakari/wakari-compute/lib/node_modules/wakari-compute-launcher/skeleton
```

## Create user list

AEN uses POSIX access control lists (ACLs) for project sharing, so the backup must preserve the ACL information. This is done with a script that creates a file named `users.lst` containing a list of all users that have access to projects on a given compute node. Download and run the script.

NOTE: These commands must be run by \$AEN\_SRVC\_ACCT.

```
wget https://s3.amazonaws.com/continuum-airgap/misc/wk-compute-get-acl-users.py
chmod 755 wk-compute-get-acl-users.py
./wk-compute-get-acl-users.py
```

## Project files

Create a tar of the projects directory with ACLs enabled. The default projects base location is `/projects`.

NOTE: This command must be run as root or with sudo.

```
tar --acls -cpvf projects.tar -C <projects base location>/*
```

### Full Anaconda (option 1)

If any changes have been made to the default Anaconda installation (additional packages installed or packages removed), it is necessary to backup the entire Anaconda installation.

NOTE: This command must be run by \$AEN\_SRVC\_ACCT.

```
tar -cvf aen_anaconda.tar -C /opt/wakari/anaconda/*
```

If no changes have been made to the default installation of Anaconda, you may just backup the `.condarc` file and any custom environments.

### Partial Anaconda (option 2)

#### Custom `.condarc` file

Make a copy of `/opt/wakari/anaconda/.condarc`.

#### Custom environments (if needed)

Create a tar file of any custom shared environments.

NOTE: This command must be run by \$AEN\_SRVC\_ACCT.

```
tar -cvf aen_compute_envs.tar -C /opt/wakari/ anaconda/envs
```

NOTE: If no custom shared environments have been created, the `envs` folder will not be present.

### Restore

#### Reinstall AEN-Compute

#### Setting variables and changing permissions

NOTE: These commands must be run by \$AEN\_SRVC\_ACCT.

Run:

```
export AEN_SERVER=<FQDN HOSTNAME OR IP ADDRESS> # Use the real FQDN
chmod a+x aen-*.sh # Set installer to be executable
```

NOTE: Change `<FQDN HOSTNAME OR IP ADDRESS>` to the actual fully qualified domain hostname or IP address.

NOTE: You must perform the entire procedure before closing the terminal to ensure the variable export persists.

## Running the AEN compute installer

Run:

```
sudo -E ./aen-compute-4.2.2-Linux-x86_64.sh -w $AEN_SERVER
...
...
PREFIX=/opt/wakari/wakari-compute
Logging to /tmp/wakari_compute.log
Checking server name
...
...
Initial clone of root environment...
Starting Wakari daemons...
installation finished.
Do you wish the installer to prepend the wakari-compute install location
to PATH in your /root/.bashrc ? [yes|no]
[no] >>> yes
```

## Config files

Untar the config files.

NOTE: This command must be run by \$AEN\_SRVC\_ACCT.

```
tar -xvf aen_compute_config.tar -C /opt/wakari
```

NOTE: Verify that they are located in /opt/wakari/wakari-compute/etc/wakari and are owned by the \$AEN\_SRVC\_ACCT.

## Custom changes (rare)

Manually restore any custom changes you saved in the backup section. If there are changes in the skeleton directory, these files must be world readable or projects will refuse to start.

## Create users

NOTE: Only create users with these instructions if your Linux machine is not bound to LDAP.

In order for the ACLs to be set properly on restore, all users that have permissions to the files must be available on the machine. Ask your system administrator for the proper way to do this for your system, such as using the “useradd” tool. A list of users that are needed was created in the backup process as a file named `users.lst`.

A process similar to the following `useradd` example will be suitable for most Linux systems.

NOTE: This command must be run by \$AEN\_SRVC\_ACCT.

```
xargs -0 -n 1 useradd --user-group < users.lst
```

## Project files

Create the projects directory in the location specified in `projectRoot` in `wk-compute-launcher-config.json`.

NOTE: By default this directory is `/projects`.

Then untar the projects directory with ACLs.

NOTE: This command must be run as root or with `sudo`:

```
tar --acls -xpvf projects.tar -C <projects base location>
```

### Full Anaconda (option 1)

If you did a full backup of the full Anaconda installation, untar this file to `/opt/wakari/anaconda`.

NOTE: This command must be run by `$AEN_SRVC_ACCT`.

```
tar -xvf aen_anaconda.tar -C /opt/wakari
```

### Partial Anaconda (option 2)

Restore the custom `.condarc` file.

If you did a partial backup of the Anaconda installation, move the copy of the `.condarc` file to `/opt/wakari/anaconda/.condarc`.

### Custom environments (if needed)

Untar any custom environments that were created to `/opt/wakari/anaconda/envs`.

NOTE: This command must be run by `$AEN_SRVC_ACCT`.

```
tar -xvf aen_compute_envs.tar -C /opt/wakari
```

### Restart compute node

Restart the compute-launcher application.

NOTE: This command must be run as root or with `sudo`.

```
service wakari-compute restart
```

### Viewing a list of admin commands

A user who is promoted to administrator can access administrator commands to perform advanced administrator tasks.

NOTE: Utility files are owned by, and should only be executed by, the AEN user who owns the files.

To display a list of all administrator commands:

```
ls -al /opt/wakari/wakari-server/bin/wk-*
```

## Viewing help for admin commands

To view help information for command, run the command followed by `-h` or `--help`.

EXAMPLE: To view help for the `remove-user` command:

```
/opt/wakari/wakari-server/bin/wk-server-admin remove-user -h
/opt/wakari/wakari-server/bin/wk-server-admin remove-project -h
```

## Running daily reports

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Staff** menu, select Daily Report:

**Staff**

Daily Report
Password Reset
Notification
Exceptions

**Site Admin**

General
Accounts
Users
Monitor
Security Log
Data Centers
Task Queue
License

**Providers**

Enterprise Resources

## Report

Today
Yesterday
This Week
This Month

**From:**  
Sun Sep 24 15:09:03 2017  
**Until:**  
Mon Sep 25 15:09:03 2017  
**Date Range**  
1 day, 0:00:00

### Users

	New	Total
<b>Users</b>	0	1
<b>Projects</b>	0	6

### New User Emails

Username	Email
----------	-------

### Actions

Count	Action
82	<a href="#">oauth.authenticate</a>

The Report section displays the following:

- Users—The number of users and projects.
- New User Emails—If *open registration is enabled*, the user names and emails for new users.
- Actions—The actions—projects created, projects updated, user authentications and added users—that have occurred in during the selected time frame—today, yesterday, this week, or this month.

## Viewing system errors

When an error occurs, a red dot is displayed in the AEN navigation bar next to the Admin link. The red dot is removed when all exceptions are marked as “read.”

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Staff** menu, select Exceptions:

The screenshot shows the Anaconda Cloud Admin interface. On the left, the 'Staff' menu is expanded, showing 'Daily Report', 'Password Reset', 'Notification', and 'Exceptions' (which is selected). Below 'Staff' is the 'Site Admin' menu with 'General', 'Accounts', 'Users', 'Security Log', 'Data Centers', 'Task Queue', and 'License'. At the bottom is the 'Providers' menu with 'Enterprise Resources'. The main content area is titled 'Exceptions' and has a 'Mark all as read' button in the top right. The list of exceptions shows several 'jinja2.exceptions.UndefinedError' messages, with the first one highlighted by a red square. Below these are several 'elasticsearch.exceptions.ConnectionError' messages.

Exceptions	Mark all as read
<input checked="" type="radio"/> jinja2.exceptions.UndefinedError: 'wk_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'	Mark all as read
<input type="radio"/> jinja2.exceptions.UndefinedError: 'wk_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'	
<input type="radio"/> jinja2.exceptions.UndefinedError: 'wk_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'	
<input type="radio"/> jinja2.exceptions.UndefinedError: 'wk_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'	
<input type="radio"/> jinja2.exceptions.UndefinedError: 'wk_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'	
<input type="radio"/> jinja2.exceptions.UndefinedError: 'wk_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'	
<input type="radio"/> jinja2.exceptions.UndefinedError: 'wk_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'	
<input type="radio"/> jinja2.exceptions.UndefinedError: 'wk_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'	
<input type="radio"/> jinja2.exceptions.UndefinedError: 'wk_server.blueprints.accounts.forms.LoginForm object' has no attribute 'email'	
<input type="radio"/> elasticsearch.exceptions.ConnectionError:	
<input type="radio"/> elasticsearch.exceptions.ConnectionError:	
<input type="radio"/> elasticsearch.exceptions.ConnectionError:	
<input type="radio"/> elasticsearch.exceptions.ConnectionError:	



The Exceptions section lists all errors that have occurred while AEN is running.

3. To see the details of an error, click the radio button next to the error. This also marks the error as “read.”
4. To mark all errors as read without reviewing each one, click the Mark all as read button.

## Viewing security errors

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select Security Log:

Staff

Daily Report

Password Reset

Notification

Exceptions

Site Admin

General

Accounts

Users

Monitor

Security Log

Security Log

View	Actor	Action	Date
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 25, 2017 09:46:09 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 25, 2017 09:39:17 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 25, 2017 09:22:04 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 25, 2017 09:10:31 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 25, 2017 08:45:50 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 25, 2017 08:43:12 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 25, 2017 08:10:30 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 25, 2017 08:09:38 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 24, 2017 23:52:06 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 24, 2017 23:51:58 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 24, 2017 23:51:58 CDT
	<a href="#">aen_admin</a>	oauth.authenticate	Sep 24, 2017 23:51:58 CDT

The Security Log section lists all errors that have occurred that could potentially affect AEN security.

3. To view a user’s profile page, click their username in the Actor column.
4. To see the details of an error, click the Eye icon next to the error.

The error details are displayed:

5. To close the error details, click the Back link.

Public Profile

Account Settings

Security Log

Applications

oauth.authenticate	
_id	59c907f03f94c30fe45ffb9e
action	oauth.authenticate
actor_id	59c069b1ae55d1b3fe9fa45e
actor_username	aen_admin
client_id	59c119cd3f94c30fe45ff5db
remote_addr	None
time	2017-09-25 13:43:12.479000+00:00
token_id	59c907f03f94c30fe45ffb9d

[⏪ Back](#)

Managing data centers

- 1. In the AEN navigation bar, click Admin to open the Admin Settings page.
- 2. In the **Site Admin** menu, select Data Centers:

Staff

Daily Report

Password Reset

Notification

Exceptions

Site Admin

General

Accounts

Users

Monitor

Security Log

Data Centers

Data Centers

Gateway (ec2-52-90-133-17.compute-1.amazonaws.com:8089)

+ Add DataCenter

The Data Centers section displays current data center information.

## Adding a data center

1. Click the Add DataCenter button to display the the Register a datacenter form.
2. In the Name box, type a Name for the new data center:

**Data Centers / Register a datacenter**

**Name**

☐ Subdomain Routing  
☐ Https

**Base Domain Name**

**summary**

**Provider**

3. Select the Subdomain Routing and/or Https checkboxes.
4. In the Base Domain Name box, type the base domain name.
5. In the Summary box, type a description of the data center.
6. In the Provider list, select a provider.
7. Click the Submit button.

## Managing enterprise resources

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Providers** menu, select Enterprise Resources:

Staff

[Daily Report](#)  
[Password Reset](#)  
[Notification](#)  
[Exceptions](#)

Site Admin

[General](#)  
[Accounts](#)  
[Users](#)  
[Monitor](#)  
[Security Log](#)  
[Data Centers](#)  
[Task Queue](#)  
[License](#)

Providers

[Enterprise Resources](#)

Resources

Add Resource

Gateway

[ec2-54-210-232-251.compute-1.amazonaws.com](#)

remove

The Resources section lists your existing cloud and local resources.

### Adding a resource

1. Click the Add Resource button to open the new resource form.
2. Complete the form:

**Resources / new**

**Data Center**  
Gateway 59c119cd3f94c30fe45ff5db

**Name**  
Compute Node1

**URL**  
http://ec2-54-210-232-251.compute-1.amazonaws.com:5002

**Description**  
Configuring Compute Node

☒ **Public**  
Uncheck this if you want to control exactly who has access to this compute node

Add Resource

3. Click the Add Resource button.

### Viewing or changing the resource details

1. Click a resource name to open the Local Resource form.
2. If necessary, change the resource details:

**Data Center**

Gateway 59c119cd3f94c30fe45ff5db

**Name**

ec2-54-210-232-251.compute-1.amazonaws.com

**URL**

http://ec2-54-210-232-251.compute-1.amazonaws.com:5002

**Description**

☒ **Public**  
Uncheck this if you want to control exactly who has access to this compute node

Update

**status**

{"status": "ok", "messages": []}

3. Click the Update button.

### Making a node public or private

1. Click the resource name to open the Local Resource form.
2. Select or clear the Public checkbox:

**Data Center**  
Gateway 59c119cd3f94c30fe45ff5db

**Name**  
ec2-54-210-232-251.compute-1.amazonaws.com

**URL**  
http://ec2-54-210-232-251.compute-1.amazonaws.com:5002

**Description**

☒ **Public**  
Uncheck this if you want to control exactly who has access to this compute node

**Update**

**status**  
{ "status": "ok", "messages": [] }

3. Click the Update button.

## Removing a resource

Click the Remove button next to the resource you want to remove.

NOTE: When you remove a resource assigned to a project, the project becomes orphaned. To fix an orphaned project, *move the project to a valid Compute Resource*.

## Managing services

The tasks on this page assume that the 3 AEN nodes are installed in the following locations:

- Server—`/opt/wakari/wakari-server/`.
- Gateway—`/opt/wakari/wakari-gateway/`.
- Compute-Launcher—`/opt/wakari/wakari-compute/`.

- *Checking the status of server node processes*
- *Checking the status of gateway node processes*
- *Checking the status of compute node processes*
- *Starting AEN services*
- *Verifying that AEN services are set to start with the system*
- *Stopping AEN services*
- *Restarting AEN services*
- *Identifying extraneous processes*
- *Removing extraneous processes*

## Checking the status of server node processes

1. Run:

```
# service wakari-server status
wk-server          RUNNING      pid 20758, uptime 5 days, 0:30:23
worker             RUNNING      pid 20757, uptime 5 days, 0:30:23
```

OR

```
root@server # ps -Hu wakari
PID TTY          TIME CMD
20756 ?              00:02:26 .supervisord
20757 ?              00:05:58 mtq-worker
20758 ?              00:00:08 wk-server
```

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```
20765 ?      00:02:00      wk-server
20766 ?      00:01:55      wk-server
20767 ?      00:02:20      wk-server
20770 ?      00:02:02      wk-server
```

**2. Run:**

```
root@server # service nginx status
nginx (pid 26303) is running...
```

For more information on server processes, see *Server processes*.

**Checking the status of gateway node processes****Run:**

```
# service wakari-gateway status
wk-gateway          RUNNING      pid 1137, uptime 5 days, 1:59:28
```

**OR**

```
root@gateway # ps -Hu wakari
  PID TTY          TIME CMD
 1136 ?            00:01:59 .supervisord
 1137 ?            00:00:02  wk-gateway
```

For more information on gateway processes, see *Gateway processes*.

**Checking the status of compute node processes****Run:**

```
# service wakari-compute status
wk-compute          RUNNING      pid 22050, uptime 3 days, 1:03:19
```

**OR**

```
root@compute # ps -Hu wakari
  PID TTY          TIME CMD
 1150 ?            00:02:01 .supervisord
 1152 ?            00:00:01  wk-compute
```

For more information on compute node processes, see *Compute processes*.

**Starting AEN services**

Services should start automatically both when they are first installed and at any point when the system is restarted.

If you need to manually start an AEN service, you must start each node independently, because they may be running on separate machines.

NOTE: The process is basically the same for each node, but the path to the correct commands vary.

To manually start a service:

- On the server node, run:

```
service wakari-server start
```

- On the gateway node, run:

```
service wakari-gateway start
```

- On a compute node, run:

```
service wakari-compute start
```

### Verifying that AEN services are set to start with the system

To verify that AEN services are set up to start automatically:

1. Run the following command on each node:

```
chkconfig --list | grep wakari
```

2. If services are missing, add them:

```
chkconfig --add [wakari-server|wakari-gateway|wakari-compute]
```

3. *Restart the services.*

### Stopping AEN services

CAUTION: Do not stop or kill supervisord without first stopping wk-compute and any other processes that use it.

You must stop services on each node independently, because they may be running on separate machines.

To stop an AEN service:

- On the server node, run:

```
service wakari-server stop
```

- On the gateway node, run:

```
service wakari-gateway stop
```

- On a compute node, run:

```
service wakari-compute stop
```

Compute nodes may have running processes that are not automatically stopped. To stop them, run:

```
sudo /opt/wakari/wakari-compute/bin/wk-compute-apps kill-all
```

### Restarting AEN services

- On the server node, run:

```
service wakari-server restart
```

- On the gateway node, run:

```
service wakari-gateway restart
```

- On a compute node, run:

```
service wakari-compute restart
```

## Identifying extraneous processes

To get a complete list of the processes running under the wakari user account, run `ps -Hu wakari`.

EXAMPLE:

```
root@server # ps -Hu wakari
  PID TTY          TIME CMD
 20756 ?            00:02:26 .supervisord
 20757 ?            00:05:58 mtq-worker
 20758 ?            00:00:08 wk-server
 20765 ?            00:02:00 wk-server
 20766 ?            00:01:55 wk-server
 20767 ?            00:02:20 wk-server
 20770 ?            00:02:02 wk-server

root@server # ps -f -C nginx
UID      PID  PPID  C  STIME TTY          TIME CMD
root    26303    1   0  12:18 ?        00:00:00 nginx: master process /usr/sbin/nginx -c /
→etc/nginx/nginx.conf
nginx   26305 26303   0  12:18 ?        00:00:00 nginx: worker process

root@gateway # ps -Hu wakari
  PID TTY          TIME CMD
 1136 ?            00:01:59 .supervisord
 1137 ?            00:00:02 wk-gateway

root@compute # ps -Hu wakari
  PID TTY          TIME CMD
 1150 ?            00:02:01 .supervisord
 1152 ?            00:00:01 wk-compute
```

- wk-server, wk-gateway and wk-compute should have PIDs reported by supervisorctl.
- The nginx master process should have a PID reported by service nginx status.
- If you have installed more than one AEN node on a single machine, the processes from all of the installed nodes should be displayed for that machine.
- On compute node(s), any AEN applications currently being run by users will be present.

EXAMPLE:

```
root@compute # ps -Hu wakari
  PID TTY          TIME CMD
 1150 ?            00:00:00 .supervisord
 1152 ?            00:00:00 wk-compute
```

(continues on next page)

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```
1340 ?      00:00:00 bash
1341 ?      00:00:00 notebookwrapper
```

## Removing extraneous processes

If extra `wk-server`, `wk-gateway`, `wk-compute`, or `supervisord` processes are present, use the `kill` command to remove them to prevent issues with AEN.

You can safely *restart* any process that you remove in error.

## Making sure NGINX and MongoDB are running

In order for AEN to run, the dependencies `mongodb` and `nginx` must be up and running. If either of these fail to start, AEN will not be served on port 80.

Check if `nginx` and `mongod` are both running (RHEL 6x):

```
$ sudo service nginx status
nginx (pid 25956) is running...

$ sudo service mongod status
mongod (pid 25928) is running...
```

If either of these failed to start, tail the log files. The default location of log files is:

```
$ tail -n 50 /var/log/mongodb/mongod.log

# nginx errors reported in error.log
$ tail -n 50 /var/log/nginx/error.log
```

## Viewing, terminating, and relaunching applications

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select Monitor:

The Monitor menu lists started applications by user and project.

The list includes columns for the application name, current running status, running node and last seen date.

3. Use the buttons to terminate or relaunch an application.
4. To view an application's logs, click the Logs button with the document icon.

## Viewing the task queue

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select Task Queue:

Staff

[Daily Report](#)  
[Password Reset](#)  
[Notification](#)  
[Exceptions](#)

Running Apps								
User	Project	Application	Status	Node	Last Seen	Terminate	Relaunch	Logs
aen_admin	asd	notebook	running	localhost	Jul 24, 2017 15:15:24 CDT	<a href="#">Terminate</a>	<a href="#">Relaunch</a>	<a href="#">Logs</a>
aen_admin	Test	notebook	running	localhost	Jul 25, 2017 11:54:05 CDT	<a href="#">Terminate</a>	<a href="#">Relaunch</a>	<a href="#">Logs</a>

Site Admin

[General](#)  
[Accounts](#)  
[Users](#)  
[Monitor](#)

Staff

[Daily Report](#)  
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## Task Queue

Workers

ip-172-31-10-196.4053 | [high](#) [default](#) [low](#)

Queues

[high](#)  
Backlog: 0  
Failed: 1

[default](#)  
Backlog: 0  
Failed: 3

Site Admin

[General](#)  
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[Task Queue](#)

The Workers section lists the workers in the task queue and whether each worker is set at high, default or low priority.

The Queues section provides information on the default and high priority queues.

3. To view all the tasks in a particular queue, in the Queues section, click the queue name.

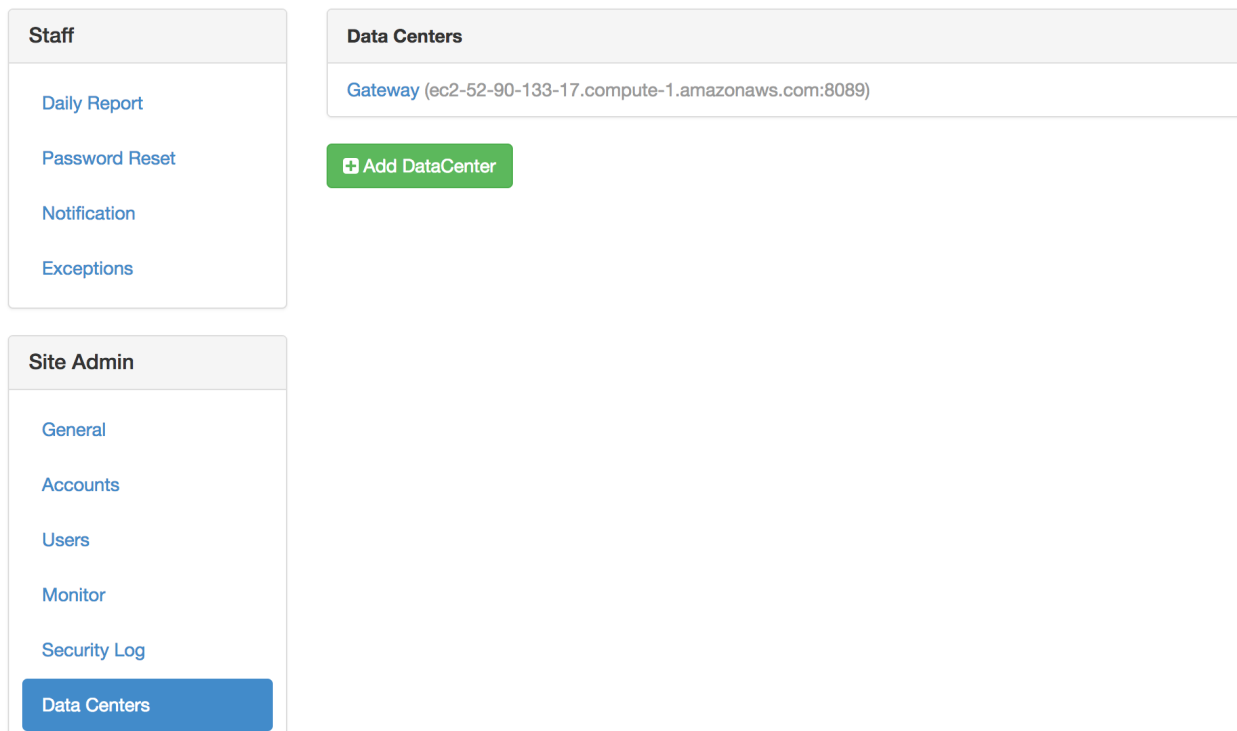
### Checking node connections

When the AEN nodes cannot communicate with each other as intended, it can cause issues with you AEN platform installation.

- *Verifying server to gateway connectivity*
- *Verifying gateway to compute node connectivity*
- *Verifying gateway to server connectivity*

### Verifying server to gateway connectivity

1. On the server, in the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select Data Centers:



- For each data center in the list, check connectivity from the server to that gateway.

EXAMPLE: The gateway in this example is `http://gateway.example.com:8089`:

```
root@server # curl --connect-timeout 5 http://gateway.example.com:8089 > /dev/null
```

## Verifying gateway to compute node connectivity

- On the server, in the AEN navigation bar, click Admin to open the Admin Settings page.
- In the **Providers** menu, select Enterprise Resources:

The screenshot displays the Anaconda Enterprise Admin Settings interface. On the left, there is a navigation menu with three main sections: **Staff**, **Site Admin**, and **Providers**. The **Staff** section includes links for Daily Report, Password Reset, Notification, and Exceptions. The **Site Admin** section includes links for General, Accounts, Users, Monitor, Security Log, Data Centers, Task Queue, and License. The **Providers** section has a button for Enterprise Resources. On the right, the **Resources** section is visible, featuring a green '+ Add Resource' button and a table with one entry. The entry is for a gateway with the URL `ec2-54-210-232-251.compute-1.amazonaws.com` and a red 'remove' button next to it.

Staff	Resources
<a href="#">Daily Report</a> <a href="#">Password Reset</a> <a href="#">Notification</a> <a href="#">Exceptions</a>	<div> <div>+ Add Resource</div> </div> <div> <div>Gateway</div> <div> <a href="#">ec2-54-210-232-251.compute-1.amazonaws.com</a> <div>remove</div> </div> </div>

Site Admin
<a href="#">General</a> <a href="#">Accounts</a> <a href="#">Users</a> <a href="#">Monitor</a> <a href="#">Security Log</a> <a href="#">Data Centers</a> <a href="#">Task Queue</a> <a href="#">License</a>

Providers
<a href="#">Enterprise Resources</a>

- Open each compute node in the Resources section.
- Verify that the contents of the URL field begin with either `http` or `https`.

**Data Center**

Gateway 59c119cd3f94c30fe45ff5db

**Name**

ec2-54-210-232-251.compute-1.amazonaws.com

**URL**

http://ec2-54-210-232-251.compute-1.amazonaws.com:5002

**Description**

☒ **Public**  
Uncheck this if you want to control exactly who has access to this compute node

Update

**status**

{"status": "ok", "messages": []}



5. Check connectivity to that URL from the corresponding gateway.

EXAMPLE: The gateway in this example is `http://gateway.example.com:8089`:

```
root@gateway # curl --connect-timeout 5 http://compute.example.com:5002 > /dev/
↪null
```

## Verifying gateway to server connectivity

The gateway-to-server path is used by the gateway configuration command `wk-gateway-configure`.

1. Verify that the gateway is linked to the correct server in the configuration file.
2. Verify that the full server URL is specified.
3. Check connectivity to the server:

```
root@gateway # grep WAKARI_SERVER /opt/wakari/wakari-gateway/etc/wakari/wk-
↪gateway-config.json
"WAKARI_SERVER": "http://wakari.example.com",

root@gateway # curl --connect-timeout 5 http://wakari.example.com > /dev/null
root@gateway # curl --connect-timeout 5 http://error.example.com > /dev/null
curl: (7) Failed to connect to error.example.com port 80: Connection refused
```

4. If a connection fails:
  1. Ensure that gateways (data centers) and compute nodes (Enterprise Resources) are correctly configured on the server.
  2. Verify that processes are listening on the configured ports:

```
$ sudo netstat -nplt
Active Internet connections (only servers)
Proto Recv-Q Send-Q Local Address   Foreign Address State  PID/Program
tcp        0      0 *:80            :::*           LISTEN 26409/nginx
tcp        0      0 *:22            :::*           LISTEN 986/sshd
tcp        0      0 127.0.0.1:25    :::*           LISTEN 1063/master
tcp        0      0 *:5000          :::*           LISTEN 26192/python
tcp        0      0 127.0.0.1:27017 :::*           LISTEN 29261/mongod
tcp        0      0 *:22            :::*           LISTEN 986/sshd
tcp        0      0 127.0.0.1:25    :::*           LISTEN 1063/master
```

3. Check the firewall setting and logs on both hosts to ensure that packets are not being blocked or discarded.

## Verifying and tuning search indexing

For search indexing to work correctly, a compute node must be able to communicate with the server. To verify this:

1. Run:

```
curl -m 5 $AEN_SERVER > /dev/null
```

2. Verify that there are sufficient inotify watches available for the number of subdirectories within the project root file system:

```
cat /proc/sys/fs/inotify/max_user_watches
```

NOTE: Some Linux distributions default to a low number of watches, which may prevent the search indexer from monitoring project directories for changes.

3. If necessary, increase the number of watches:

```
echo fs.inotify.max_user_watches=100000 | sudo tee -a /etc/sysctl.conf && sudo  
→ sysctl -p
```

4. Verify that there are sufficient inotify user instances available—at least one per project:

```
cat /proc/sys/fs/inotify/max_user_instances
```

5. If necessary, increase the number of inotify user instances:

```
echo fs.inotify.max_user_instances=1000 | sudo tee -a /etc/sysctl.conf && sudo  
→ sysctl -p
```

### Changing the AEN server URL

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select General:
3. In the Wakari Server box, type the main URL where the site can be viewed.
4. Click the Update button.

### Changing the static URL for JavaScript files

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select General:
3. In the Static URL box, type the static URL where JavaScript files can be accessed.
4. Click the Update button.

### Changing the AEN account type

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select General:

Staff

[Daily Report](#)  
[Password Reset](#)  
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Site Admin

General

[Accounts](#)  
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[Data Centers](#)  
[Task Queue](#)  
[License](#)

Providers

General Admin Settings

**Wakari Server**  
Set the main URL where this site will be accessed

**Static URL**  
Set static URL where the js can be accessed

**Default Project Access**  
This will be the default when a user creates a project

☐ Public  
Anyone can see this project. Collaborators have write access

☒ Private  
No one can see this project except collaborators.

**Account Type**

Update

Config Files

Staff	General Admin Settings
<a href="#">Daily Report</a>	<b>Wakari Server</b> Set the main URL where this site will be accessed <input type="text" value="http://anaconda-enterprise.trl"/>
<a href="#">Password Reset</a>	<b>Static URL</b> Set static URL where the js can be accessed <input type="text" value="http://anaconda-enterprise.trl/static/"/>
<a href="#">Notification</a>	<b>Default Project Access</b> This will be the default when a user creates a project  <input type="radio"/> <b>Public</b> Anyone can see this project. Collaborators have write access  <input checked="" type="radio"/> <b>Private</b> No one can see this project except collaborators.
<a href="#">Exceptions</a>	<b>Account Type</b> <input type="text" value="wk_server.plugins.accounts.cloud"/>
	<input type="button" value="Update"/>
Site Admin	Config Files
<a href="#">General</a>	
<a href="#">Accounts</a>	
<a href="#">Users</a>	
<a href="#">Monitor</a>	
<a href="#">Security Log</a>	
<a href="#">Data Centers</a>	
<a href="#">Task Queue</a>	
<a href="#">License</a>	
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Providers

General Admin Settings

**Wakari Server**  
Set the main URL where this site will be accessed

**Static URL**  
Set static URL where the js can be accessed

**Default Project Access**  
This will be the default when a user creates a project

☐ Public  
Anyone can see this project. Collaborators have write access

☒ Private  
No one can see this project except collaborators.

**Account Type**

Update

Config Files

3. In the Account Type box, select the account type—cloud or LDAP.
4. Click the Update button.

### Changing the default for project access

1. In the AEN navigation bar, click Admin to open the Admin Settings page.
2. In the **Site Admin** menu, select General:

Staff	General Admin Settings
<a href="#">Daily Report</a>	<b>Wakari Server</b> Set the main URL where this site will be accessed
<a href="#">Password Reset</a>	<input type="text" value="http://anaconda-enterprise.trl"/>
<a href="#">Notification</a>	<b>Static URL</b> Set static URL where the js can be accessed
<a href="#">Exceptions</a>	<input type="text" value="http://anaconda-enterprise.trl/static/"/>
<b>Site Admin</b>	<b>Default Project Access</b> This will be the default when a user creates a project
<b>General</b>	<input type="radio"/> <b>Public</b> Anyone can see this project. Collaborators have write access
<a href="#">Accounts</a>	<input checked="" type="radio"/> <b>Private</b> No one can see this project except collaborators.
<a href="#">Users</a>	<b>Account Type</b>
<a href="#">Monitor</a>	<input type="text" value="wk_server.plugins.accounts.cloud"/>
<a href="#">Security Log</a>	<input type="button" value="Update"/>
<a href="#">Data Centers</a>	
<a href="#">Task Queue</a>	
<a href="#">License</a>	
<b>Providers</b>	<b>Config Files</b>

3. Under Default Project Access, select the default access type for new projects: Public or Private.
4. Click the Update button.

## Changing the owner of a project

To change the owner of a project:

1. Collect the project name, the user name of the previous owner, and the user name of the new owner.
2. Run the `wakari-server` executable command `wk-server-admin`:

```
/opt/wakari/wakari-server/bin/wk-server-admin project-owner --project PROJECT --  
↪old OLD_OWNER --new NEW_OWNER --delete --keep-owner
```

- **PROJECT**: The project name.
- **OLD\_OWNER**: The user name of the previous owner.
- **NEW\_OWNER**: The user name of the new owner.
- **--delete**: An optional flag that deletes the old project directory in the `projects` directory of **OLD\_OWNER**. If this flag is not used, the old project directory is preserved but no longer used.
- **--keep-owner**: An optional flag that makes **OLD\_OWNER** a collaborator of the project after it is transferred to **NEW\_OWNER**. If this flag is not used, **OLD\_OWNER** will no longer have collaborator access to the project.

**NOTE:** The **OLD\_OWNER** user must still exist when the project's owner is changed. Before deleting any user, be sure to change the owner of the user's projects.

## Editing configuration files

1. In the AEN navigation bar, click **Admin** to open the Admin Settings page.
2. In the **Site Admin** menu, select **General**.
3. In the **Config Files** section, change the configuration settings for your AEN installation. For more information on configuration files, see [Using configuration files](#).
4. Click the **Update** button.

## Managing your AEN license

1. In the AEN navigation bar, click **Admin** to open the Admin Settings page.
2. In the **Site Admin** menu, select **License**:

The **Current License** section displays information regarding your AEN license, including the name of the product, vendor, license holder's name, end and issued dates, company name, license type, and contact email.

Staff	General Admin Settings
<a href="#">Daily Report</a>	<b>Wakari Server</b> Set the main URL where this site will be accessed <input type="text" value="http://anaconda-enterprise.trl"/>
<a href="#">Password Reset</a>	<b>Static URL</b> Set static URL where the js can be accessed <input type="text" value="http://anaconda-enterprise.trl/static/"/>
<a href="#">Notification</a>	<b>Default Project Access</b> This will be the default when a user creates a project  <input type="radio"/> <b>Public</b> Anyone can see this project. Collaborators have write access  <input checked="" type="radio"/> <b>Private</b> No one can see this project except collaborators.
<a href="#">Exceptions</a>	<b>Account Type</b> <input type="text" value="wk_server.plugins.accounts.cloud"/>
	<input type="button" value="Update"/>
Site Admin	Config Files
<a href="#">General</a>	
<a href="#">Accounts</a>	
<a href="#">Users</a>	
<a href="#">Monitor</a>	
<a href="#">Security Log</a>	
<a href="#">Data Centers</a>	
<a href="#">Task Queue</a>	
<a href="#">License</a>	
Providers	



Staff

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[Task Queue](#)
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Current License

You have **166 days** remaining on your current license.

Renew your license

<b>product</b>	Anaconda Enterprise Notebooks
<b>vendor</b>	Continuum Analytics, Inc.
<b>name</b>	Continuum Development
<b>end_date</b>	2018-03-10
<b>issued</b>	2017-03-10
<b>company</b>	Continuum Analytics
<b>type</b>	undefined
<b>email</b>	dev@continuum.io

Upload New License

License File

Choose File

No file chosen

Update

## Renewing your AEN license

1. Click the Renew your license button.
2. In the Upload New License section, click the Choose File button.
3. Select the new license file.
4. Click the Open button.
5. Click the Update button.

Your renewed license information is displayed.

## Cheat sheet

The Admin dashboard includes three menus in the left column: **Staff**, **Site Admin** and **Providers**.

### Staff menu

- Daily Report—See the number of users and projects.
- Password Reset—Reset a user password.
- Notification—Send system messages to users via SES or SMTP.

- Exceptions—If errors are raised while AEN is running, a red dot appears in the AEN navigation bar. Review errors and mark them as read.

### Site Admin menu

- General—Change the configuration settings for your AE Notebook server installation.
- Accounts—Turns on or off Open Registration.
- Users—View usernames, number of projects and last logins.
- Monitor—View status of applications with related data, terminate or restart
- Security Log—View errors that could affect security.
- Data Centers—View current data centers and add a new data center.
- Task Queue—View workers in the task queue and priority.
- License—View current AEN license or upload a new license.

### Providers menu

Enterprise Resources—View, add or remove local or cloud services and designate public or private to control access to a compute node.

### Troubleshooting

This troubleshooting guide provides you with ways to deal with issues that may occur with your AEN installation.

- *General troubleshooting steps*
- *Browser error: too many redirects*
- *Browser error: too many redirects when starting project apps*
- *Exception: exceptions.TypeError: 'NoneType' object has no attribute '\_\_getitem\_\_'*
- *Error: unix:///opt/wakari/wakari-server/etc/supervisor.sock no such file*
- *Error: “Data Center Not Found” when deleting a project*
- *Forgotten administrator password*
- *Log files being deleted*
- *Error: This socket is closed*
- *Service error 502: Cannot connect to the application manager*
- *502 communication error on Amazon web services (AWS)*
- *Invalid username*
- *Notebook Error: Cannot download notebook as PDF via LaTeX*
- *Unresponsive wk-server thread without error messages*
- *Unresponsive wk-gateway thread without error messages*

- *Error starting projects*
- *Changes in .condarc file are ignored*

## General troubleshooting steps

1. Clear browser cookies. When you change the AEN configuration or upgrade AEN, cookies remaining in the browser can cause issues. Clearing cookies and logging in again can help to resolve problems.
2. *Make sure NGINX and MongoDB are running.*
3. Make sure that AEN services are *set to start at boot*, on all nodes.
4. *Make sure that services are running* as expected. If any services are not running or are missing, *restart them*.
5. *Check for and remove extraneous processes.*
6. *Check the connectivity between nodes.*
7. *Check the configuration file syntax.*
8. *Check file ownership.*
9. *Verify that POSIX ACLs are enabled.*

## Browser error: too many redirects

### Cause

Browser cookies are out of date.

### Solution

1. Log out.
2. Clear the browser's cookies.
3. Clear the browser cache.
4. Log in.

## Browser error: too many redirects when starting project apps

Browser shows “Too many redirects” when the user tries to start an application.

### Cause

The project's Compute Resource is invalid or was deleted.

### Solution

*Move the project to a valid Compute Resource.*

### Exception: `exceptions.TypeError: 'NoneType' object has no attribute '__getitem__'`

This exception appears on the Admin > Exceptions page when a project does not have a Compute Resource assigned.

#### Cause

The project's Compute Resource is invalid or was deleted.

#### Solution

*Move the project to a valid Compute Resource.*

### Error: `unix:///opt/wakari/wakari-server/etc/supervisor.sock no such file`

This is a supervisorctl error.

#### Cause

supervisord is not running on the Server.

#### Solution

Ensure that supervisord is included in the crontab. Then restart supervisord manually.

### Error: “Data Center Not Found” when deleting a project

#### Cause

The data center has been removed.

#### Solution

As root, run:

```
/opt/wakari/wakari-server/bin/wk-server-admin remove-project --db-only <user>  
↪ <project>
```

### Forgotten administrator password

1. Use ssh to log into the server as root.
2. Run:

```
/opt/wakari/wakari-server/bin/wk-server-admin reset-password -u SOME_USER -p SOME_  
↪ PASSWORD
```

NOTE: Replace SOME\_USER with the administrator username and SOME\_PASSWORD with the password.

3. Log into AEN as the administrator user with the new password.

Alternatively you may add an administrator user:

1. Use ssh to log into the server as root.
2. Run:

```
/opt/wakari/wakari-server/bin/wk-server-admin add-user SOME_USER --admin -p SOME_
-PASSWORD -e YOUR_EMAIL
```

NOTE: Replace SOME\_USER with the username, replace SOME\_PASSWORD with the password, and replace YOUR\_EMAIL with your email address.

3. Log into AEN as the administrator user with the new password.

## Log files being deleted

Log files are being deleted.

NOTE: Locations of AEN log files for each process and application are shown in the node sections in [Concepts](#).

## Cause

AEN installers log into `/tmp/wakari\_server, gateway, compute}.log`. If the log files grow too large, they might be deleted.

## Solution

To set the logs to be more or less verbose, Jupyter Notebooks uses `Application.log_level`.

To make the logs less verbose than the default, but still informative, set `Application.log_level` to `ERROR`.

## Error: This socket is closed

You receive the “This socket is closed” error message when you try to start an application.

## Cause

When the `supervisord` process is killed, information sent to the standard output `stdout` and the standard error `stderr` is held in a pipe that will eventually fill up.

Once full, attempting to start any application will cause the “This socket is closed” error.

## Solution

To prevent this issue:

- Follow the instructions in [Managing services](#) to stop and restart processes.
- Do not stop or kill `supervisord` without first stopping `wk-compute` and any other processes that use it.

To resolve the “This socket is closed” error:

1. Stop wk-compute by running `sudo kill -9`.
2. Restart the supervisord and wk-compute processes:

```
sudo /etc/init.d/wakari-compute stop
sudo /etc/init.d/wakari-compute start
```

### Service error 502: Cannot connect to the application manager

Gateway node displays “Service Error 502: Can not connect to the application manager.”

#### Cause

A compute node is not responding because the wk-compute process has stopped.

#### Solution

Stop and then restart the supervisord and wk-compute processes:

```
sudo /etc/init.d/wakari-compute stop
sudo /etc/init.d/wakari-compute start
```

### 502 communication error on Amazon web services (AWS)

You receive the “502 Communication Error: This gateway could not communicate with the Wakari server” error message.

#### Cause

An AEN gateway cannot communicate with the Wakari server on AWS. There may be an issue with the IP address of the Wakari server.

#### Solution

Configure your AEN gateway to use the DNS hostname of the server. On AWS this is the DNS hostname of the Amazon Elastic Compute Cloud (EC2) instance.

### Invalid username

#### Cause

The username does not follow 1 or more of these rules:

- Must be at least 3 characters and no more than 25 characters.
- The first character must be a letter (A-Z) or a digit (0-9).

- Other characters can be a letter, digit, period (.), underscore (\_) or hyphen (-).
- The [POSIX standard](#) specifies that these characters are the portable filename character set, and that portable usernames have the same character set.

## Solution

Follow the above rules for usernames.

## Notebook Error: Cannot download notebook as PDF via LaTeX

### Cause

LaTeX is not properly installed.

### CentOS/6 Solution

1. Install TeXLive from the [TUG site](#). Follow the described steps. The installation may take some time.
2. Add the installation to the PATH in the file `/etc/profile.d/latex.sh`. Add the following, replacing the year and architecture as needed:

```
PATH=/usr/local/texlive/2017/bin/x86_64-linux:$PATH
```

3. Restart the compute node.

### CentOS/7 Solution

1. Install the missing packages running the command:

```
yum install texlive texlive-xetex texlive-xetexconfig texlive-xetex-def texlive-  
↪adjustbox texlive-upquote texlive-ulem
```

## Unresponsive `wk-server` thread without error messages

### Cause

Two things can cause the `wk-server` thread to freeze without error messages:

- LDAP freezing
- MongoDB freezing

If LDAP or MongoDB are configured with a long timeout, Gunicorn can time out first and kill the LDAP or MongoDB process. Then the LDAP or MongoDB process dies without logging a timeout error.

## Solution

1. Check for frozen LDAP or MongoDB server processes.
2. You may also wish to configure the Gunicorn timeout to more than 30 seconds.

### Unresponsive `wk-gateway` thread without error messages

#### Cause

If TLS is configured with a passphrase protected private key, `wk-gateway` will freeze without any error messages.

#### Solution

Update the TLS configuration so that it does not use a passphrase protected private key.

### Error starting projects

Project's status page shows "There was an error starting this project".

#### Cause

Lack of disk space in compute nodes prevents projects from starting.

#### Solution

1. Verify that the project node meets the *system requirements*.
2. Check if there is enough free space on the compute node's partition where `/projects` lives:

```
df -h /projects
```

3. Free up some disk space to meet the system requirements.
4. Restart the project.

### Changes in `.condarc` file are ignored

Changes applied to `.condarc` are ignored by conda.

#### Cause

Conda loads its configuration by merging multiple files together.

#### Solution

Check if you are applying the changes to the correct file.

To show the merged state that conda is currently using:

```
conda config --show
```

To show all config files that conda is currently reading:



```
conda config --show-sources
```

## Frequently asked questions

- *What is AEN?*
- *Can notebooks be shared with anyone?*
- *Can I disable the option, “publish your notebook to anaconda.org”?*
- *How can I check the version number of my AEN server?*
- *Can I use AEN to access CSV or Amazon S3 data?*
- *Can I install other Python packages?*
- *Can I create a Python environment from the command line?*
- *Can I connect to GitHub with AEN?*
- *Can I print or print preview my Jupyter Notebooks?*
- *Is there a set amount of storage on AEN?*
- *How do I get help, give feedback, suggest features or report a bug?*

## What is AEN?

For information on AEN, see *Anaconda Enterprise Notebooks 4*.

## Can notebooks be shared with anyone?

Yes. When you share a Jupyter Notebook through AEN, it can be viewed and run without the need to install anything special, regardless of what libraries were used to create the notebook. Each notebook also includes the python environment that it needs to run in.

AEN allows users to clone a shared Jupyter Notebook into their AEN account to make whatever changes or modifications they want. The notebook’s Python environment is also cloned, so it runs in the same environment as the shared Jupyter Notebook unless it is changed.

## Can I disable the option, “publish your notebook to anaconda.org”?

Yes. The upload button in the notebook app executes the option “publish your notebook to anaconda.org”. To disable it, log in as the AEN\_SRVC\_ACCT and run these commands:

```
source activate /opt/wakari/wakari-compute
jupyter-nbextension disable nb_anacondacloud --py --sys-prefix
jupyter-serverextension disable nb_anacondacloud --py --sys-prefix
```

### How can I check the version number of my AEN server?

Go to this URL in a browser: `http://$AEN_SERVER/admin/list`

NOTE: Replace `$AEN_SERVER` with the domain name or the domain name and port number of your AEN server.

### Can I use AEN to access CSV or Amazon S3 data?

Yes. If your data is in CSV files, upload the CSV files to your AEN account using the upload controls in the File Browser of the Workbench Application or the File Transfer Application.

To access data stored on Amazon S3, use the Boto interface from AEN. See the public data files in AEN for examples of how to use Boto to pull your data from Amazon S3 into AEN. For more information, see [Boto documentation](#).

You can also use IOPro to simplify and optimize the conversion of your data into Python arrays.

### Can I install other Python packages?

Yes, by creating a custom environment for your packages within your project.

For more information, see [Using the NBConda extension](#).

### Can I create a Python environment from the command line?

Yes, you can use the `conda create` command to create custom Python environments with whatever packages you choose. All AEN environments are shared with all the team members of a project.

EXAMPLE: In this example, `myenv` is a new environment containing the NumPy package.

```
conda create -n myenv numpy
```

NOTE: Python, Jupyter Notebooks and PIP are installed by default in all new AEN environments.

To use your new environment, activate it by running `source activate myenv`.

### Can I connect to GitHub with AEN?

Yes, you have full access to GitHub through an AEN Terminal application.

To generate an SSH key from your AEN account and add it to your GitHub account:

1. [Generate a GitHub SSH key](#).
2. Copy your key by running `cat ~/.ssh/id_rsa.pub`.
3. Select and copy the contents of the `id_rsa.pub` file to the clipboard.
4. Follow [GitHub's instructions](#) to go to your GitHub account and paste it from your clipboard into the appropriate box in your GitHub settings.

### Can I print or print preview my Jupyter Notebooks?

Yes, you can print your notebooks using your browser's regular printing capabilities.

You can also preview the printed page by clicking the **File** menu and selecting Print Preview.

## Is there a set amount of storage on AEN?

No, there is no set limit for storage in AEN. You are limited only by the size of the disk where AEN is installed.

If you need more storage, contact your system administrator.

## How do I get help, give feedback, suggest features or report a bug?

See *Help and support*.

### Help and support

Priority support is included with the purchase of an Anaconda subscription.

Contact your administrator first if you are having problems. Your administrator has a service level agreement where your issue will be responded to within a specific response time, depending on type and severity.

### Training and consulting

Training and consulting is available for AEN and any other Anaconda product.

For more information, please contact your account representative or [email the sales team](#).

### Providing feedback

Your feedback is very important to us!

Please, send us any [product feedback](#) while you are thinking about it.

TIP: Be sure to select AEN as the Platform Component Name.

### Submitting feature requests

We'd love to hear your ideas for consideration in future releases!

Your ideas help us build a better product. Your administrator can submit a support ticket for you.

NOTE: You can also request new features by using the [product feedback](#) form.

### Reporting a bug

If you think you have found a bug, please contact your administrator immediately. They will open a support ticket for your issue.

### Additional resources

The following resources are useful for getting started with Jupyter Notebooks:

- [Jupyter Notebook quick start guide](#)
- [Jupyter Notebook user documentation](#)

- [GitHub](#) shows the most popular Jupyter notebooks of the [month](#), [week](#), and [day](#).

### Release notes

#### v4.2.2 March 1, 2018

##### Administrator-facing changes:

- Add admin command to change project owner
- Server: Add ability to disable public projects
- Gateway: Add support for SSL private key passphrase
- Docs: Add backup and restore runbook to the docs
- Docs: Emphasize backups before upgrading process
- Docs: Recommend putting AEN and projects folder on the same filesystem
- Docs: Add RHEL version 7.4 to supported versions
- Docs: Add troubleshooting instructions to fix problems when downloading notebook as PDF via LaTeX

##### User-facing changes:

- Upgrade bokeh to version 0.12.7
- Upgrade holoviews to version 1.8.3
- Upgrade numba to version 0.35.0
- Upgrade scikit-learn to version 0.19.0

##### Internal fixes:

- Fix bug in init scripts when requiretty is enabled
- Fix bugs related to AEN\_SUDO\_SSH option
- Fix bug in fix\_ownership function when directories contain spaces
- Docs: Fix error in Active Directory configuration example
- Server: Fix bug when updating user/group in supervisor configuration files in post-install for server and gateway
- Server: Fix bug Admin reports on user totals are inconsistent
- Server: Fix error in login screen when open registration and LDAP are enabled
- Server: Fix bug in Last seen date
- Server: Fix bug Monitor Report blank
- Server: Load JS files from local CDN
- Server: Fix error when terminating or relaunching an application from Monitor
- Server: Fix error creating projects when using Internet Explorer 11
- Compute: Fix 404 errors when using pivottablesjs
- Remove Wakari Cloud leftovers

### v4.2.1 December 18, 2017

Administrator-facing changes:

- None

User-facing changes:

- None

Internal fixes:

- Fix undetected “ca” key when using self-signed certificates signed by a private CA
- Fix login redirects when using SSL
- Add verify gateway SSL certificate for get and post requests

### v4.2.0 November 22, 2017

Administrator-facing changes:

- Feature/allow remote MongoDB
- Allow for configuration for login timeout and set default
- Add verbose option to conda create clone
- Avoid duplicate name for resources / compute-nodes
- Allow renaming main and message queue databases
- PAM-based authentication module
- Change wakari logos to Anaconda logos
- Replace ‘wakari’ wording
- New config option to move the user’s home directory into the user’s project directory
- Make logging less verbose in AEN
- Documentation for PySpark kernel installation
- Improve SSL documentation

User-facing changes:

- New config option to move the user’s home directory into the user’s project directory
- Package cache was moved from user’s home directory into the user’s project directory
- Change wakari logos to Anaconda logos
- Fix error for deleting tags to work
- Define shell prompt in `.projectrc` template
- Replace ‘wakari’ wording

Internal fixes:

- Move server unix socket from `/tmp` to `/opt/wakari/wakari-server/var/run`
- Make project deletion synchronous for consistency
- Avoid storing `csrf` token in the user profile

- Expire gateway session when server logs out
- Allow log rotation in the three components
- Fix permissions on static files
- Change log level to debug in gateway
- Do not log private keys in gateway
- Save request remote address when logging action
- Unify logs formatting and timezone in compute nodes with Winston
- Several fixes and documentation improvements

### v4.1.3 August 16, 2017

- Upgrade conda to version 4.3.24
- Upgrade anaconda to version 4.4.0
- Admin application monitor
- Block access to package list view
- Add placeholders in password reset form
- Change static content location
- Fix error when checking for package updates in notebook application
- Replace slashes in project tags
- Fix submit errors in password reset form
- Replace/remove “wakari” word from multiple places
- Fix missing commands missing sudo in start-project
- Improve gateway and compute node validators
- Check if bzip2 is installed during server setup process
- Include port number in host header
- Forbid creation of empty tags
- Repair “Create Account” link in login page
- Use UTC for server logs
- Mark datacenters as trusted by default
- Disable heart beating
- Compute resource: Show full path to log file
- Improve init scripts
- Allow deleting all projects
- mtq: Implement exponential backoff on connection error to mongodb
- In the general admin display, do not show the bind password for LDAP
- The accelerate package has been removed from the installation
- Other minor bugfixes

### **v4.1.2 March 29, 2017**

This is mainly a maintenance release improving internal machinery and upgrading the root packages.

- Upgrade conda to version 4.3.14
- Upgrade Anaconda to 4.3.1
- Upgrade r-base to 3.2.2
- Fixed AEN nb\_conda to be compatible with conda 4.3.x series
- Several documentation fixes
- Other minor bugfixes

### **v4.1.1 December 15, 2016**

- Added CentOS 7 support
- Support dots in usernames
- More usernames validation
- Fixed creation (through nb\_conda) of single letter environment names
- Environment names (through nb\_conda) validation
- Fixed uploading of notebook using nb\_anacondacloud
- Fixed attaching of environments in published notebooks through nb\_anacondacloud
- Several documentation fixes
- Other bugfixes

### **v4.1.0 October 21, 2016**

- Added JupyterLab application
- Removed GateOne terminal application
- Included additional notebook extensions (nbpresent and nb\_anaconda\_theme)
- Updated to conda 4.2.9 in default project environments
- Added HTTP timeout setting for gateway and compute launcher
- Changed default gateway port to 8089
- Added support for all-numeric usernames
- Add R channel to default conda configuration file
- Other bugfixes

### **v4.0.0 June 30, 2016**

- Customized installation with:
  - AEN Functional ID and Group
  - AEN (installation and run) `sudo` commands

- Removal of root access from the AEN service account
- Configurable sudo command
- Restriction of sudo access to all the processes
- Upgrade Jupyter to 4.2
- Upgrade the anaconda-nb-extensions to the latest versions
- Upgrade Anaconda to 4.0
- Deprecate wakari-publisher
- Security enhancements
- SSL configuration documented between all AEN Server components
- Several bugfixes
- Overall documentation revision and general improvement

### v0.10.0 February 2, 2016

- New projects dashboard
- Capability to star and tag a project
- Sticky searches
- New Jupyter Notebook extensions
- Updates to all packages. Highlights: bokeh 0.11, ipython/jupyter 4.1.

### v0.9.1 October 19, 2015

- New Search capability to find projects and files within a project.
- Added “Related Projects” list to the project view, based on code similarity.
- New UI for fine-grained access control of project files in the Workbench app
- Viewer app now renders plain text files correctly
- Updated LDAP configuration docs
- Updates to all packages. Highlights: bokeh 0.10, ipython/jupyter 4.0.

**Note** ElasticSearch, and an Oracle JRE, must be installed on the server in order to use the new search features. Indexing of project files will begin when the project is started (or paused and re-started). If search features are not desired, set `"SEARCH_ENABLED": false` in the server configuration file to avoid errors.

### v0.8.0 August 21, 2015

#### New Features

- Updated packages based on Anaconda 2.3, and removed older packages no longer in Anaconda.
- Updated IPython to version 3.2.1
- Documentation is now installed with the server (use the Help link in the top navigation bar)



- Added the ability for the administrator to define a customized default project environment.
- The server has been updated to use python 2.7.10.
- Init scripts are now provided for each Anaconda Enterprise Notebooks service.
- Added relevant links to some error pages

### Problems Resolved in this Release

- Project status indicators (e.g. starting, pausing) now automatically update.
- If an access is unauthorized, the server now returns a 403 (Unauthorized) status code and prompts the user to log in.
- Modified nginx configuration to support running the server on non-standard ports.
- The server installation no longer uses a default password for the wakari user. A random password is generated and displayed during installation.
- Prevent double-click from attempting to create a project twice
- Removed an obsolete script reference that was causes a 404 error to be logged in the browser console when opening the Terminal app.
- The installer scripts no longer fail if the database already contains the 'wakari' user.
- Updated example notebooks to work with latest Bokeh release.
- Fixed terminal app key bindings to allow Mac command key to work normally
- Installers now indicate where the installation logs are stored
- LDAP user attributes containing binary data are now ignored.

### Documentation Updates

- Updated and consolidated Troubleshooting guide.
- Simplified some steps in the installation procedure.
- Updated notebooks in the Examples directory for use with the latest IPython Notebook and Bokeh.
- Added a section on project permissions to the Troubleshooting guide.
- Added notes on how to remove a project if the datacenter has already been removed.

### v0.7.0 June 12, 2015

#### New Features

- Updated Bokeh to v0.9
- Ability to list packages installed on the server
- Administrators now have full access to all projects.
- Added automated checking and display of connection status between server, data centers, and compute resources.

- When creating a new project, an environment for the project is automatically created as a clone of the root Anaconda environment.

### Problems Resolved in this Release

- Problem with checking in files with revision control extension
- Revision control extension can't handle notebook names with spaces
- Problem moving files from one compute node to another if configured for LDAP
- Should default to UTF-8 encoding and warn user if no locale is detected
- Adding a compute resource via the command line admin tool does not work
- The installer now sets `umask 0022` to ensure correct file permissions

### Documentation Updates

- Added a *Troubleshooting* section to the documentation.
- Added notes on how to configure crontab to start the Anaconda Enterprise Notebooks services at startup
- Example SSL config file now has correct log paths
- Added instructions on how to ensure that POSIX ACL support is enabled on the projects directory.
- Fixed syntax problem in sample LDAP config.json
- Added section on how to use self-signed or private CA certificates

### v0.6.3 March 27, 2015

- Updated LDAP module
- LDAP user filtering
- Added Notebook locking
- Added Notebook integrated revision control system
- Move projects between compute nodes
- User-specific binding to compute nodes (private compute nodes)
- Improved installation process and dependency checking
- Incorporated support for SSL for Server and Gateway nodes
- Improved Gateway error handling
- Fixed package dependencies for update process
- Documentation updates

## Previous versions

Previous version documentation is provided for users who have not yet upgraded to the current version of AEN.

- *AEN 4.2.1*
- *AEN 4.2.0*
- *AEN 4.1.3*
- *AEN 4.1.2*
- *AEN 4.1.1*
- *AEN 4.1.0*
- *AEN 4.0*

## Anaconda Enterprise Notebooks (AEN 4.2.1)

### User guide (AEN 4.2.1)

### Concepts (AEN 4.2.1)

### Getting started (AEN 4.2.1)

### Basic tasks (AEN 4.2.1)

### Working with projects (AEN 4.2.1)

### Searching for a project or file (AEN 4.2.1)

### Adding and removing team members on a project (AEN 4.2.1)

### Controlling access to your project (AEN 4.2.1)

### Starting and stopping a project (AEN 4.2.1)

### Making a project public or private (AEN 4.2.1)

### Tagging a project (AEN 4.2.1)

### Starring a project (rating) (AEN 4.2.1)

### Claim ownership of a project (AEN 4.2.1)

### Changing a project's summary or description (AEN 4.2.1)

### Viewing a project's status (AEN 4.2.1)

Viewing related projects (AEN 4.2.1)

Viewing top-rated projects (AEN 4.2.1)

Using tags to find a project (AEN 4.2.1)

Viewing your top collaborators (AEN 4.2.1)

Sharing projects and notebooks (AEN 4.2.1)

Deleting a project (AEN 4.2.1)

Using AEN applications (AEN 4.2.1)

Using Workbench (AEN 4.2.1)

Using Viewer (AEN 4.2.1)

Using JupyterLab (AEN 4.2.1)

Using Terminal (AEN 4.2.1)

Using Jupyter Notebook (AEN 4.2.1)

Using Jupyter Notebook extensions (AEN 4.2.1)

Using the Synchronize Environments extension (AEN 4.2.1)

Using the Locking extension (AEN 4.2.1)

Using the Revision Control Mechanism extension (AEN 4.2.1)

Using the NBConda extension (AEN 4.2.1)

Using the Conda Notebook extension (AEN 4.2.1)

Using the Anaconda Cloud extension (AEN 4.2.1)

Using the Notebook Present extension (AEN 4.2.1)

Using Compute Resource Configuration (AEN 4.2.1)

Managing your account (AEN 4.2.1)

Advanced tasks (AEN 4.2.1)

**Working with environments (AEN 4.2.1)**

**Using visualization packages (AEN 4.2.1)**

**Using environment variables (AEN 4.2.1)**

**Cheat sheet (AEN 4.2.1)**

**Troubleshooting (AEN 4.2.1)**

**Admin guide (AEN 4.2.1)**

**Concepts (AEN 4.2.1)**

**Installation (AEN 4.2.1)**

**Installation requirements (AEN 4.2.1)**

**Preparing for installation (AEN 4.2.1)**

**Installing the AEN server (AEN 4.2.1)**

**Installing the AEN gateway (AEN 4.2.1)**

**Installing the AEN compute node(s) (AEN 4.2.1)**

**Configuring conda to use your local on-site AEN repository (AEN 4.2.1)**

**Optional configuration (AEN 4.2.1)**

**Using configuration files (AEN 4.2.1)**

**Increasing HTTP timeout between gateway and compute nodes (AEN 4.2.1)**

**Changing where projects are stored (AEN 4.2.1)**

**Creating groups with the same uid (AEN 4.2.1)**

**Using numeric usernames (AEN 4.2.1)**

**Using project directories as home directories (AEN 4.2.1)**

**Setting up a default project environment (AEN 4.2.1)**

**Install AEN connected to a remote Mongo DB instance (AEN 4.2.1)**

Running SELinux in enforcing mode (AEN 4.2.1)

Changing server hostnames (AEN 4.2.1)

Authenticating with LDAP (AEN 4.2.1)

Configuring sudo customizations (AEN 4.2.1)

Configuring SSL (AEN 4.2.1)

Configuring single sign-on (AEN 4.2.1)

Adding a third-party extension (AEN 4.2.1)

Configure search indexing (AEN 4.2.1)

Create custom Jupyter kernel for Pyspark (AEN 4.2.1)

Upgrading AEN (AEN 4.2.1)

Uninstalling AEN (AEN 4.2.1)

User management (AEN 4.2.1)

Adding or removing an administrative user (AEN 4.2.1)

Allowing and restricting new user registration (AEN 4.2.1)

Resetting a user password (AEN 4.2.1)

Managing permissions (AEN 4.2.1)

Viewing a list of users (AEN 4.2.1)

Viewing a list of currently active users (AEN 4.2.1)

Viewing a user profile (AEN 4.2.1)

Sending a system message (AEN 4.2.1)

Moving a project to another compute node (AEN 4.2.1)

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### Getting started (AEN 4.1.2)

### User guide (AEN 4.1.2)

After you've run through the *Getting started guide*, you're ready to learn the details of using Anaconda Enterprise Notebooks.

### Basic

These topics all use the web browser to manage your projects. They are suited for a beginning user.

### Projects (AEN 4.1.2)

### Using applications (AEN 4.1.2)

### Workbench Application (AEN 4.1.2)

### Viewer Application (AEN 4.1.2)

### JupyterLab Application (AEN 4.1.2)

### Terminal Application (AEN 4.1.2)

### Jupyter Notebook Application (AEN 4.1.2)

### Compute Resource Config Application (AEN 4.1.2)

### Team Collaboration (AEN 4.1.2)

### Account Administration (AEN 4.1.2)

### Advanced

If you are comfortable entering commands on the command line, there is a lot more you can do with Anaconda Enterprise Notebooks.

### Anaconda Environments (AEN 4.1.2)

### Data (AEN 4.1.2)

### Visualization (AEN 4.1.2)

### Project environment variables (AEN 4.1.2)

### Help & support

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**Start/Shutdown (AEN 4.1.2)**

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**Third Party Extensions (AEN 4.1.2)**

**Troubleshooting (AEN 4.1.2)**

**Compute-nodes (AEN 4.1.2)**

**Installation (AEN 4.1.2)**

### **Install Steps**

Carry out the procedures linked from the table below to perform a complete install of all Anaconda Enterprise Notebooks components.

**Installation preparation (AEN 4.1.2)**

**Install AEN Server (AEN 4.1.2)**

**Install AEN Gateway (AEN 4.1.2)**

**Install AEN Compute (AEN 4.1.2)**

The following optional install procedures may need to be performed, depending on how you set up your Data Center:

**Optional configuration (AEN 4.1.2)**

**Sudo configuration (AEN 4.1.2)**

**LDAP configuration (AEN 4.1.2)**

**SSL (AEN 4.1.2)**

**wakari\_https.conf (AEN 4.1.2)**

**Single sign on (AEN 4.1.2)**

Additional post-install information:

**Upgrading Anaconda Enterprise Notebooks (AEN 4.1.2)**

**Uninstall (AEN 4.1.2)**

**Release notes (AEN 4.1.2)**

**Anaconda Enterprise Notebooks (AEN 4.1.1)**

**Backup/Restore (AEN 4.1.1)**

**Compute-nodes (AEN 4.1.1)**

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**Troubleshooting (AEN 4.1.1)**

**Installation customization (AEN 4.1.1)**

**Installation Instructions (AEN 4.1.1)**

**Installation Runbook (AEN 4.1.1)**

**Updating Anaconda Enterprise Notebooks (AEN 4.1.1)**

**Configuration (AEN 4.1.1)**

**Release notes (AEN 4.1.1)**

**SSL (AEN 4.1.1)**

**SSO (AEN 4.1.1)**

**Uninstall (AEN 4.1.1)**

**wakari\_https.conf (AEN 4.1.1)**

**Additional Resources (AEN 4.1.1)**

**Account Administration (AEN 4.1.1)**

**Anaconda Environments (AEN 4.1.1)**

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**Data (AEN 4.1.1)**

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**JupyterLab Application (AEN 4.1.1)**

**Jupyter Notebook Application (AEN 4.1.1)**

**Project environment variables (AEN 4.1.1)**

**Projects (AEN 4.1.1)**

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**Installation Instructions (AEN 4.1.0)**

**Installation Runbook (AEN 4.1.0)**

**Updating Anaconda Enterprise Notebooks (AEN 4.1.0)**

**Configuration (AEN 4.1.0)**

**Release notes (AEN 4.1.0)**

**SSL (AEN 4.1.0)**

**SSO (AEN 4.1.0)**

**Uninstall (AEN 4.1.0)**

**wakari\_https.conf (AEN 4.1.0)**

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**Account Administration (AEN 4.1.0)**

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project\_permissions.py (AEN 4.0)

repair\_team\_members.py (AEN 4.0)

SSL (AEN 4.0)

SSO (AEN 4.0)

Uninstall (AEN 4.0)

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Jupyter Notebook Application (AEN 4.0)



**You want to use Jupyter Notebook (AEN 4.0)**

**Projects (AEN 4.0)**

**Sharing in Anaconda Enterprise Notebooks (AEN 4.0)**

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**Terminal Application (AEN 4.0)**

**User guide (AEN 4.0)**

**Viewer Application (AEN 4.0)**

**Visualization (AEN 4.0)**

**Workbench Application (AEN 4.0)**

**Anaconda Enterprise Notebooks for Teams (AEN 4.0)**

## 4.1.3 Using Anaconda Distribution with AE4

Anaconda Distribution includes two options for package and environment management on local systems, the [Conda](#) command line program, and the [Anaconda Navigator](#) graphical interface. If Anaconda Enterprise users will use either of these options, there are a few items you might want to configure:

### Configuring firewall settings

If platform users will use Navigator **online**, you may need to whitelist the necessary sites in your network's firewall settings so that Navigator can reach these sites:

- <https://repo.anaconda.com> (or for older versions of Navigator and Conda, <https://repo.continuum.io> )
- <https://conda.anaconda.org> for conda-forge and other channels on Anaconda Cloud ([anaconda.org](https://anaconda.org))
- <https://vscode-update.azurewebsites.net/> for updating Visual Studio Code
- [google-public-dns-a.google.com](https://google-public-dns-a.google.com) (8.8.8.8:53) to check internet connectivity with [Google Public DNS](#)

If platform users will use Navigator **offline**, conda environment creation will be limited to the packages available in their package cache. Using Navigator in offline mode is equivalent to using the `create`, `install`, `remove`, and `update` conda commands with the `--offline` flag so that conda does not connect to the internet. If your users will use Navigator offline, you may want to [change the Navigator icons](#) that link to the web.

**NOTE:** If Navigator detects that internet access is not available, it automatically enables offline mode. Users can also select **Anaconda Navigator > Preferences** and check the `Enable offline mode` option to work in offline mode any time, even when internet access is available.

## Configuring conda

If platform users will use conda to install packages, they can configure conda to search a specific set of channels for packages.

*As an Administrator*, you can also [configure conda at the system level](#), which will override any user-level configuration.

## Configuring Navigator

By default, Navigator includes icons linking to the GitHub, YouTube, and Twitter pages of Anaconda Inc. *Users* can change or remove these links by editing the configuration file located here: `HOME_DIR/.anaconda/navigator/anaconda-navigator-config.yml`.

The configuration file uses key-value pairs in the form `key: value`, such as `github_url: https://github.com`. Each of the three values `github_url`, `youtube_url` and `twitter_url` may be set to any URL or `null`. If the value is `null`, Navigator does not display that icon.

*As an Administrator*, you can create a configuration file for Navigator to enable users to access the Enterprise repository and set additional parameters that are not exposed in the preferences dialog. This main configuration file stores *all user preferences* for Navigator, and is located here: `~/anaconda/navigator/anaconda-navigator.ini`.

The configuration file includes `main` and `home` sections, each containing sets of key-value pairs in `.ini` format.

You can use it to customize the following options in the `main` section:

- `default_anaconda_api_url`: This points to the internal Anaconda Repository API endpoint.

**NOTE:** This URL must end with `/api`— it is not simply the homepage of your instance. This API reads the configuration data from your instance to set UI behavior and text, such as the **Sign in to...** link in the the top right corner of the Navigator window.

- `default_ssl_certificate` — This can be set to `True`, `False`, or a path to an existing and valid SSL certificate file.

**NOTE:** If your Anaconda Repository instance requires an SSL cert/RSA key to access it, that information must exist in a text file on the user's machine, *and pointed to via the path specified here* in the `.ini` file. The format for the text file should resemble the following:

```
-----BEGIN CERTIFICATE-----
```

**<actual cert here>**

```
-----END CERTIFICATE-----
```

```
-----BEGIN RSA PRIVATE KEY-----
```

**<actual key here>**

```
-----END RSA PRIVATE KEY-----
```

- `twitter_url` — This can be configured to point to your company's account, or be set to `None` to display no icon.
- `youtube_url` — This can be configured to point to your company's account, or be set to `None` to display no icon.
- `github_url` — This can be configured to point to your company's account, or be set to `None` to display no icon.

And set this option in the `home` section:

- `vscode_enable` — This can be set to `True` or `False`, based on whether you want to enable or disable VSCode from appearing on the Home tab and making queries to the Microsoft endpoint from within the application.

For example:

```
```.ini
[main]
default_anaconda_api_url = https://www.your-domain.com:8443/api
default_ssl_certificate = /path/to/certificate/file.pem

# Custom URLs
twitter_url = https://twitter.com/your-company
youtube_url = https://www.youtube.com/c/your-company
github_url = https://github.com/your-company

[home]
vscode_enable = False
```.
```

After making your changes, save and close the `.ini` file, then launch Navigator to update the `.condarc` and `anaconda-client` configurations to reflect the customized settings you've specified within it.

## 4.2 Anaconda Individual Edition

*The Most Trusted Distribution for Data Science*

Anaconda® is a package manager, an environment manager, a Python/R data science distribution, and a collection of *over 7,500+ open-source packages*. Anaconda is free and easy to install, and it offers [free community support](#).

Get the [Anaconda Cheat Sheet](#) and then [download Anaconda](#).

Want to install conda and use conda to install just the packages you need? Get [Miniconda](#).

### Anaconda Navigator or conda?

After you install Anaconda or Miniconda, if you prefer a desktop graphical user interface (GUI) then use [Navigator](#). If you prefer to use Anaconda prompt (or terminal on Linux or macOS), then use that and conda. You can also switch between them.

You can install, remove, or update any Anaconda package with a few clicks in Navigator, or with a single conda command in Anaconda Prompt (terminal on Linux or macOS).

- **To try Navigator**, after installing Anaconda, click the Navigator icon on your operating system's program menu, or in Anaconda prompt (or terminal on Linux or macOS), run the command `anaconda-navigator`.
- **To try conda**, after installing Anaconda or Miniconda, take the [30-minute conda test drive](#) and download a [conda cheat sheet](#).

### Packages available in Anaconda

- Over [250 packages](#) are automatically installed with Anaconda.
- Over 7,500 additional open-source packages (including R) can be individually installed from the Anaconda repository with the `conda install` command.
- Thousands of other packages are available from [Anaconda Cloud](#).
- You can download other packages using the `pip install` command that is installed with Anaconda. [Pip packages](#) provide many of the features of conda packages and in some cases they can work together. However, the preference should be to install the conda package if it is available.
- You can also make your own [custom packages](#) using the `conda build` command, and you can share them with others by uploading them to [Anaconda Cloud](#), PyPI, or other repositories.

### Previous versions

Previous versions of Anaconda are available in the [archive](#). For a list of packages included in each previous version, see [Old package lists](#).

Anaconda2 includes Python 2.7 and Anaconda3 includes Python 3.7. However, it does not matter which one you download, because you can create new environments that include any version of Python packaged with conda. See [Managing Python with conda](#).

## 4.2.1 Installation

Review the system requirements listed below before installing Anaconda Individual Edition. If you don't want the hundreds of packages included with Anaconda, you can [install Miniconda](#), a mini version of Anaconda that includes just conda, its dependencies, and Python.

---

**Tip:** Looking for Python 3.5 or 3.6? See our [FAQ](#).

---

### System requirements

- License: Free use and redistribution under the terms of the [End User License Agreement - Anaconda® Individual Edition](#).
- Operating system: Windows 8 or newer, 64-bit macOS 10.13+, or Linux, including Ubuntu, RedHat, CentOS 6+, and others.
- If your operating system is older than what is currently supported, you can find older versions of the Anaconda installers in our [archive](#) that might work for you. See [Using Anaconda on older operating systems](#) for version recommendations.

- System architecture: Windows- 64-bit x86, 32-bit x86; MacOS- 64-bit x86; Linux- 64-bit x86, 64-bit Power8/Power9.
- Minimum 5 GB disk space to download and install.

On Windows, macOS, and Linux, it is best to install Anaconda for the local user, which does not require administrator permissions and is the most robust type of installation. However, if you need to, you can install Anaconda system wide, which does require administrator permissions.

## Installing on Windows

1. Download the Anaconda installer.
2. RECOMMENDED: *Verify data integrity with SHA-256*. For more information on hashes, see [What about cryptographic hash verification?](#)
3. Double click the installer to launch.

---

**Note:** To prevent permission errors, do not launch the installer from the *Favorites* folder.

---

---

**Note:** If you encounter issues during installation, temporarily disable your anti-virus software during install, then re-enable it after the installation concludes. If you installed for all users, uninstall Anaconda and re-install it for your user only and try again.

---

4. Click Next.
5. Read the licensing terms and click “I Agree”.
6. Select an install for “Just Me” unless you’re installing for all users (which requires Windows Administrator privileges) and click Next.
7. Select a destination folder to install Anaconda and click the Next button. See [FAQ](#).

---

**Note:** Install Anaconda to a directory path that does not contain spaces or unicode characters.

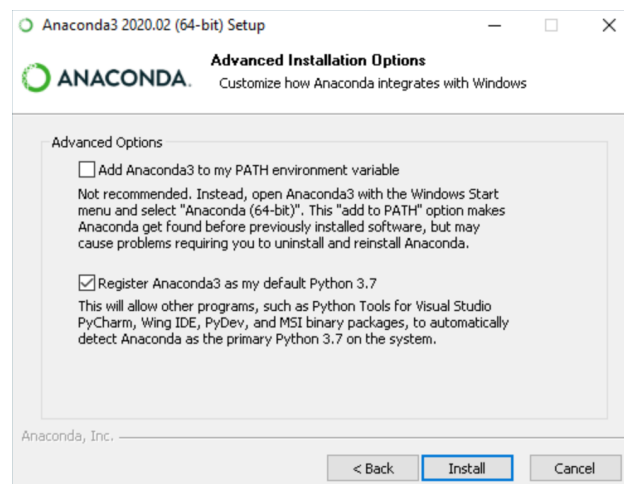
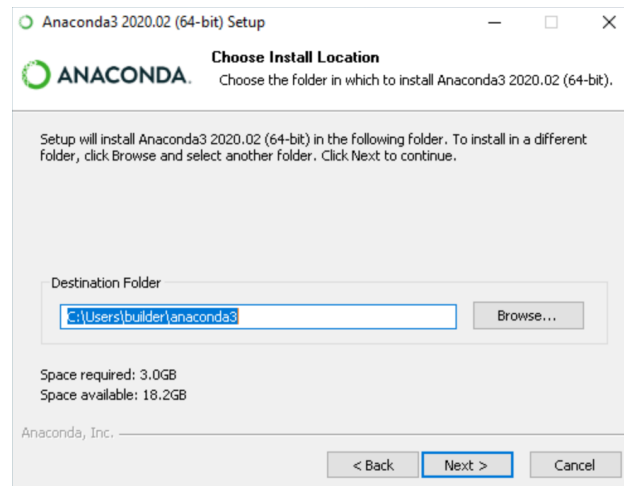
---

---

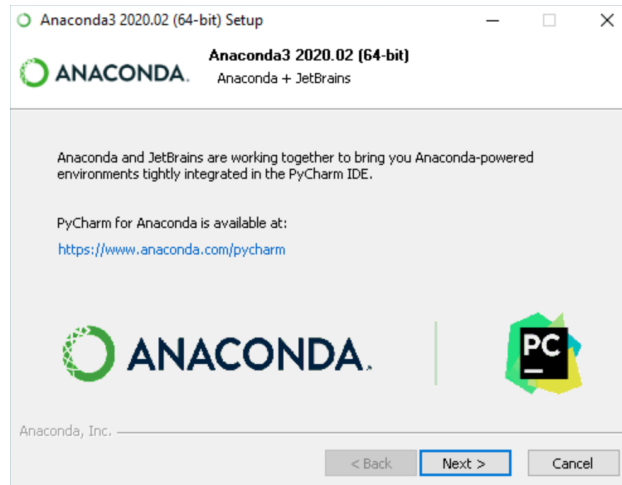
**Note:** Do not install as Administrator unless admin privileges are required.

---

8. Choose whether to add Anaconda to your PATH environment variable. We recommend not adding Anaconda to the PATH environment variable, since this can interfere with other software. Instead, use Anaconda software by opening Anaconda Navigator or the Anaconda Prompt from the Start Menu.

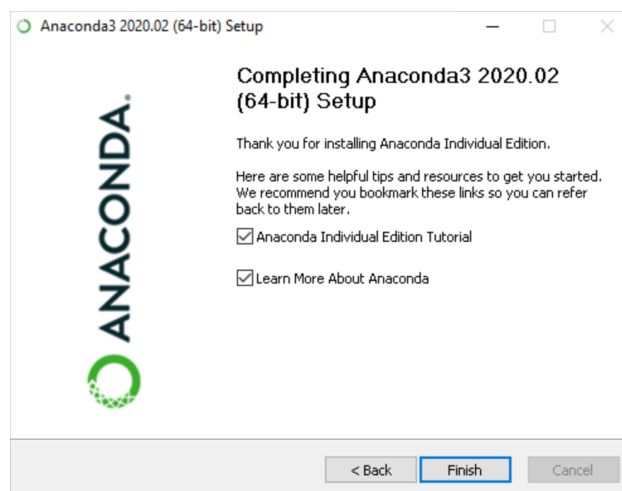


9. Choose whether to register Anaconda as your default Python. Unless you plan on installing and running multiple versions of Anaconda or multiple versions of Python, accept the default and leave this box checked.
10. Click the Install button. If you want to watch the packages Anaconda is installing, click Show Details.
11. Click the Next button.
12. Optional: To install PyCharm for Anaconda, click on the link to <https://www.anaconda.com/pycharm>.



Or to install Anaconda without PyCharm, click the Next button.

13. After a successful installation you will see the “Thanks for installing Anaconda” dialog box:



14. If you wish to read more about Anaconda Cloud and how to get started with Anaconda, check the boxes “Learn more about Anaconda Cloud” and “Learn how to get started with Anaconda”. Click the Finish button.

15. *Verify your installation.*

---

**Note:** If you are behind a company proxy, you may need to do some additional set up. See how to set up your *proxy*.

---

### Problems?

See *troubleshooting*.

### What's next?

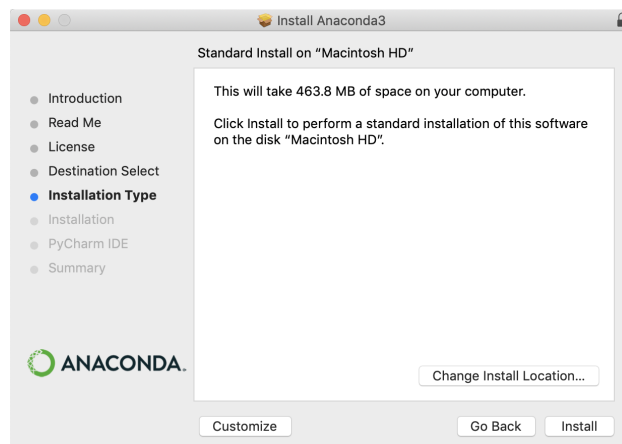
Get started programming quickly with Anaconda in the *Getting started with Anaconda* guide.

### Installing on macOS

You can install Anaconda using either the graphical installer (“wizard”) or the command line (“manual”) instructions below. If you are unsure, choose the graphical install.

#### macOS graphical install

1. Download the graphical *macOS installer* for your version of Python.
2. RECOMMENDED: *Verify data integrity with SHA-256*. For more information on hashes, see *What about cryptographic hash verification?*
3. Double-click the downloaded file and click continue to start the installation.
4. Answer the prompts on the Introduction, Read Me, and License screens.
5. Click the Install button to install Anaconda in your ~/opt directory (recommended):

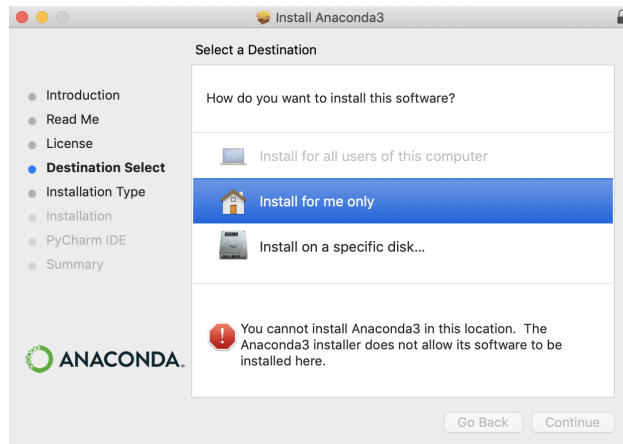


6. OR, click the Change Install Location button to install in another location (not recommended).



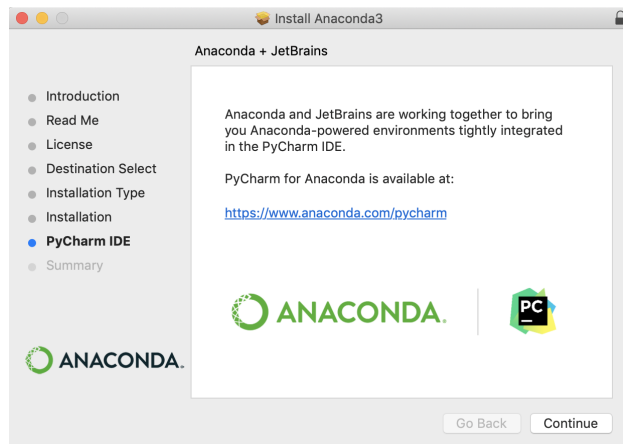
On the Destination Select screen, select Install for me only.

**Note:** If you get the error message “You cannot install Anaconda in this location,” reselect Install for me only.



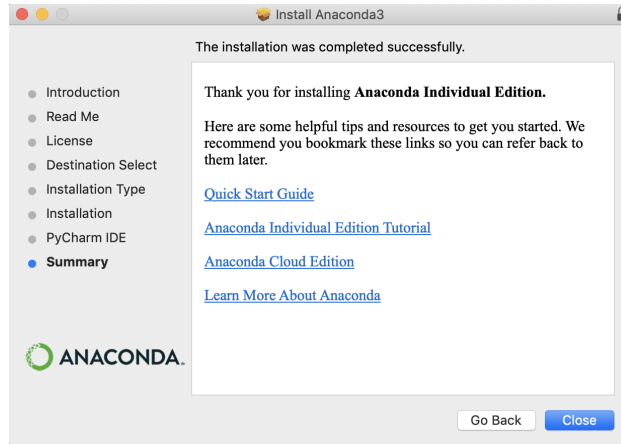
7. Click the continue button.

8. Optional: To install PyCharm for Anaconda, click on the link to <https://www.anaconda.com/pycharm>.



Or to install Anaconda without PyCharm, click the Continue button.

9. A successful installation displays the following screen:



10. *Verify your installation.*

## Using the command-line install

Use this method if you prefer to use a terminal window.

1. In your browser, download the command-line version of the [macOS installer](#) for your system.
2. RECOMMENDED: *Verify data integrity with SHA-256*. For more information on hash verification, see [cryptographic hash validation](#).
  - Open a terminal and run the following:

```
shasum -a 256 /path/filename
```

---

**Note:** Replace `/path/filename` with your installation's path and filename.

---

3. Install for Python 3.7 or 2.7:
  - For Python 3.7 enter the following:

```
bash ~/Downloads/Anaconda3-2020.02-MacOSX-x86_64.sh
```

- For Python 2.7, open the Terminal.app or iTerm2 terminal application and then enter the following:

```
bash ~/Downloads/Anaconda2-2019.10-MacOSX-x86_64.sh
```

---

**Note:** Include the `bash` command regardless of whether or not you are using the Bash shell.

---

---

**Note:** Replace `~/Downloads` with your actual path and `Anaconda3-2020.02-MacOSX-x86_64.sh` with actual name of the file you downloaded.

---

4. The installer prompts “In order to continue the installation process, please review the license agreement.” Click Enter to view the license terms.
5. Scroll to the bottom of the license terms and enter yes to agree to them.
6. The installer prompts you to Press Enter to confirm the location, Press CTRL-C to cancel the installation or specify an alternate installation directory. If you confirm the default location, it will display `PREFIX=/home/<user>/anaconda<2 or 3>` and continue the installation.

---

**Note:** Unlike the graphical install, installing the shell file will place it in `~/anaconda<2 or 3>` by default, not `~/opt`. This is due to limitations with installing .pkg files on macOS Catalina.

---

Installation may take a few minutes to complete.

---

**Note:** We recommend you accept the default install location. Do not choose the path as `/usr` for the Anaconda/Miniconda installation.

---

7. The installer prompts “Do you wish the installer to initialize Anaconda3 by running `conda init`?” We recommend “yes”.

---

**Note:** If you enter “no”, then conda will not modify your shell scripts at all. In order to initialize after the installation process is done, first run `source <path to conda>/bin/activate` and then run `conda init`.

---

---

**Note:** If you are on macOS Catalina, the new default shell is `zsh`. You will instead need to run `source <path to conda>/bin/activate` followed by `conda init zsh`.

---

8. The installer displays “Thank you for installing Anaconda!”
9. Optional: The installer describes the partnership between Anaconda and JetBrains and provides a link to install PyCharm for Anaconda at <https://www.anaconda.com/pycharm>.
10. Close and open your terminal window for the Anaconda installation to take effect.
11. To control whether or not each shell session has the base environment activated or not, run `conda config --set auto_activate_base False` or `True`. To run conda from anywhere without having the base environment activated by default, use `conda config --set auto_activate_base False`. This only works if you have run `conda init` first.

---

**Note:** `conda init` is available in conda versions 4.6.12 and later.

---

12. *Verify your installation.*

## Problems?

See [troubleshooting](#).

## What's next?

Get started programming quickly with Anaconda in the *Getting started with Anaconda* guide.

## Installing on Linux

### Prerequisites

To use GUI packages with Linux, you will need to install the following extended dependencies for Qt:

Debian	<code>apt-get install libgl1-mesa-glx libegl1-mesa libxrandr2 libxrandr2 libxss1 libxcursor1 libxcomposite1 libasound2 libxi6 libxtst6</code>
Red-Hat	<code>yum install libXcomposite libXcursor libXi libXtst libXrandr alsa-lib mesa-libEGL libXdamage mesa-libGL libXScrnSaver</code>
Arch-Linux	<code>pacman -Sy libxau libxi libxss libxtst libxcursor libxcomposite libxdamage libxfixes libxrandr libxrender mesa-libgl alsa-lib libglvnd</code>
OpenSUSE/SLES	<code>zypper install libXcomposite1 libXi6 libXext6 libXau6 libX11-6 libXrandr2 libXrender1 libXss1 libXtst6 libXdamage1 libXcursor1 libxcb1 libasound2 libX11-xcb1 Mesa-libGL1 Mesa-libEGL1</code>
Gen-too	<code>emerge x11-libs/libXau x11-libs/libxcb x11-libs/libX11 x11-libs/libXext x11-libs/libXfixes x11-libs/libXrender x11-libs/libXi x11-libs/libXcomposite x11-libs/libXrandr x11-libs/libXcursor x11-libs/libXdamage x11-libs/libXScrnSaver x11-libs/libXtst media-libs/alsa-lib media-libs/mesa</code>

## Installation

For x86 systems.

1. In your browser, download the [Anaconda installer for Linux](#).
2. RECOMMENDED: *Verify data integrity with SHA-256*. For more information on hashes, see [What about cryptographic hash verification?](#)
  - Open a terminal and run the following:

```
sha256sum /path/filename
```

3. Enter the following to install Anaconda for Python 3.7:

```
bash ~/Downloads/Anaconda3-2020.02-Linux-x86_64.sh
```

OR Enter the following to install Anaconda for Python 2.7:

```
bash ~/Downloads/Anaconda2-2019.10-Linux-x86_64.sh
```

---

**Note:** Include the bash command regardless of whether or not you are using Bash shell.

---

---

**Note:** If you did not download to your Downloads directory, replace `~/Downloads/` with the path to the file you downloaded.

---

4. The installer prompts “In order to continue the installation process, please review the license agreement.” Click Enter to view license terms.
5. Scroll to the bottom of the license terms and enter “Yes” to agree.
6. The installer prompts you to click Enter to accept the default install location, CTRL-C to cancel the installation, or specify an alternate installation directory. If you accept the default install location, the installer displays “PREFIX=/home/<user>/anaconda<2 or 3>” and continues the installation. It may take a few minutes to complete.

---

**Note:** We recommend you accept the default install location. Do not choose the path as /usr for the Anaconda/Miniconda installation.

---

7. The installer prompts “Do you wish the installer to initialize Anaconda3 by running conda init?” We recommend “yes”.

---

**Note:** If you enter “no”, then conda will not modify your shell scripts at all. In order to initialize after the installation process is done, first run `source <path to conda>/bin/activate` and then run `conda init`. See [FAQ](#).

---

8. The installer finishes and displays “Thank you for installing Anaconda<2 or 3>!”
9. The installer provides a link to install PyCharm for Anaconda at <https://www.anaconda.com/pycharm>.
10. Close and open your terminal window for the installation to take effect, or you can enter the command `source ~/.bashrc`.
11. To control whether or not each shell session has the base environment activated or not, run `conda config --set auto_activate_base False` or `True`. To run conda from anywhere without having the base environment activated by default, use `conda config --set auto_activate_base False`. This only works if you have run `conda init` first.

---

**Note:** `conda init` is available in conda versions 4.6.12 and later.

---

12. [Verify your installation](#).

---

**Note:** If you install multiple versions of Anaconda, the system defaults to the most current version as long as you haven’t altered the default install path.

---

## Problems?

See [troubleshooting](#).

## What’s next?

Get started programming quickly with Anaconda in the [Getting started with Anaconda](#) guide.

## Installing on Linux POWER

### Prerequisites

To use GUI packages with Linux, you will need to install the following extended dependencies for Qt:

Red-Hat	<code>yum install libXcomposite libXcursor libXi libXtst libXrandr alsa-lib mesa-libEGL libXdamage mesa-libGL libXScrnSaver</code>
Open-Suse/SLES	<code>zypper install libXcomposite1 libXi6 libXext6 libXau6 libX11-6 libXrandr2 libXrender1 libXss1 libXtst6 libXdamage1 libXcursor1 libxcb1 libasound2 libX11-xcb1 Mesa-libGL1 Mesa-libEGL1</code>

### Installation

1. In your browser, download the [Anaconda installer for POWER8 and POWER9](#).
2. RECOMMENDED: *Verify data integrity with SHA-256*. For more information on hashes, see [What about cryptographic hash verification?](#)

- Open a terminal and run the following:

```
sha256sum /path/filename
```

3. Enter the following to install Anaconda for Python 3.7:

```
bash ~/Downloads/Anaconda3-2020.02-Linux-ppc64le.sh
```

OR enter the following to install Anaconda for Python 2.7:

```
bash ~/Downloads/Anaconda2-2019.10-Linux-ppc64le.sh
```

---

**Note:** Include the `bash` command regardless of whether or not you are using Bash shell.

---

---

**Note:** If you did not download to your Downloads directory, replace `~/Downloads/` with the path to the file you downloaded.

---

4. The installer prompts “In order to continue the installation process, please review the license agreement.” Click Enter to view license terms.
5. Scroll to the bottom of the license terms and enter “Yes” to agree to them.
6. The installer prompts you to click Enter to accept the default install location, CTRL-C to cancel the installation, or specify an alternate installation directory. If you accept the default install location, the installer displays “PREFIX=/home/<user>/anaconda<2 or 3>” and continues the installation. It may take a few minutes to complete.

---

**Note:** We recommend you accept the default install location. Do not choose the path as `/usr` for the Anaconda/Miniconda installation.

---

7. The installer prompts “Do you wish the installer to initialize Anaconda3 by running `conda init`?” We recommend “yes”.

---

**Note:** If you enter “no”, then conda will not modify your shell scripts at all. In order to initialize after the installation process is done, first run `source <path to conda>/bin/activate` and then run `conda init`.

---

---

**Note:** If you enter “No”, you must manually add the path to Anaconda or conda will not work. See [FAQ](#).

---

8. The installer finishes and displays “Thank you for installing Anaconda<2 or 3>!”
9. The installer provides a link to install PyCharm for Anaconda at <https://www.anaconda.com/pycharm>.
10. Close and open your terminal window for the installation to take effect, or you can enter the command `source ~/.bashrc`.
11. To control whether or not each shell session has the base environment activated or not, run `conda config --set auto_activate_base False` or `True`. To run conda from anywhere without having the base environment activated by default, use `conda config --set auto_activate_base False`. This only works if you have run `conda init` first.

---

**Note:** `conda init` is available in conda versions 4.6.12 and later.

---

12. [Verify your installation](#).
13. After your install completes, start using Anaconda with the instructions in [Getting started with Anaconda](#).

---

**Note:** Anaconda on Power8 or Power9 only supports little endian mode.

---

---

**Note:** If you install multiple versions of Anaconda, the system defaults to the most current version as long as you haven’t altered the default install path.

---

## Problems?

See [troubleshooting](#).

## What’s next?

Get started programming quickly with Anaconda in the [Getting started with Anaconda](#) guide.

## Installing in silent mode

### Windows

Download the installer:

- [Miniconda installer for Windows](#)
- [Anaconda installer for Windows](#)

---

**Note:** The following instructions are for Miniconda. For Anaconda, substitute Anaconda for Miniconda in all of the commands.

---

To run the the Windows installer for Miniconda in silent mode, use the `/S` argument. The following optional arguments are supported:

- `/InstallationType=[JustMe|AllUsers]`—Default is JustMe.
- `/AddToPath=[0|1]`—Default is 1
- `/RegisterPython=[0|1]`—Make this the system's default Python. 0 indicates JustMe, which is the default. 1 indicates AllUsers.
- `/S`—Install in silent mode.
- `/D=<installation path>`—Destination installation path. Must be the last argument. Do not wrap in quotation marks. Required if you use `/S`.

All arguments are case-sensitive.

EXAMPLE: The following command installs Miniconda for the current user without registering Python as the system's default:

```
start /wait "" Miniconda3-latest-Windows-x86_64.exe /InstallationType=JustMe /
↪RegisterPython=0 /S /D=%UserProfile%\Miniconda3
```

## Linux & macOS

---

**Note:** The following instructions are for Miniconda. For Anaconda, substitute anaconda for miniconda in all of the commands. Also, substitute the [Anaconda installer](#) for the [Miniconda installer](#) in the wget step.

---

To run the silent installation of Miniconda for macOS or Linux, specify the `-b` and `-p` arguments of the bash installer. The following arguments are supported:

- `-b`—Batch mode with no PATH modifications to `~/ .bashrc`. Assumes that you agree to the license agreement. Does not edit the `.bashrc` or `.bash_profile` files.
- `-p`—Installation prefix/path.
- `-f`—Force installation even if prefix `-p` already exists.

EXAMPLE:

```
wget https://repo.anaconda.com/miniconda/Miniconda3-latest-Linux-x86_64.sh -O ~/
↪miniconda.sh
bash ~/miniconda.sh -b -p $HOME/miniconda
```

The installer will not prompt you for anything, including setup of your shell to activate conda. To add this activation in your current shell session:

```
eval "$(/Users/jsmith/anaconda/bin/conda shell.YOUR_SHELL_NAME hook)"
```

With this activated shell, you can then install conda's shell functions for easier access in the future:

```
conda init
```

If you'd prefer that conda's base environment not be activated on startup, set the `auto_activate_base` parameter to false:



```
conda config --set auto_activate_base false
```

## Installing for multiple users

The default Anaconda installation option is “Just Me”, which gives an independent installation of Anaconda that will not be shared with other users on the same system. The other option is to install for all users.

### All users

If you have administrator access, you can choose to install for “All Users”. This is a good option for a multi-user system where you want to allow users to import Python libraries and run Python applications.

This option does not give write permissions by default so the users will not be able to install packages in the root environment. It allows an administrator to protect what is in the root environment. If packages are needed in the root environment, you can elevate the privileges to administrator from the Command Prompt and run install commands.

## Multi-user Anaconda installation on Windows

1. Download the [Anaconda installer](#).
2. Double click the installer to launch.
3. Click Next to continue.
4. Read the licensing terms and click “I Agree”.
5. Select an install for “All Users” (this requires administrator privileges on the computer) and click Next.
6. Click “Yes” to allow the installer to make changes to your computer.
7. Select a destination folder that is accessible to the users, the default is C:\ProgramData\Anaconda.
8. After your install is complete, open Computer Management, navigate to Local Users and Groups. Create a new group for your Anaconda users. Add users to this new group, Anaconda-Users.
9. Navigate to your Anaconda directory and then go to the Properties. Uncheck the box for Attributes: Read-only and save changes. Go to the Security tab and click Edit. From there you can add Anaconda-Users and set permissions. Your group will need read and write privileges.

## Multi-user Anaconda installation on Linux

To set up a multi-user Anaconda or Miniconda installation on Linux operating systems:

---

**Note:** sudo access is required.

---

1. [Install Anaconda](#).
2. After installation is complete, create a new group: `sudo group add mygroup`
3. Change the group ownership to “mygroup” on the entire directory where Anaconda is installed: `sudo chgrp -R mygroup /opt/anaconda2`. Replace `/opt/anaconda2` with the actual path to your installed Anaconda file.
4. Set read and write permission for the owner, root, and the mygroup only: `sudo chmod 770 -R /opt/anaconda2`

5. Add users to a group: `sudo adduser username mygroup`. Users added to the “mygroup” group now have the ability to access Anaconda, install packages, and create environments.

This is another option for all-user installation. It installs Anaconda at `C:\Anaconda`, which is not a protected directory and can have write permissions set for users. This is a good option if your username has spaces in it because the Anaconda installer cannot install in paths that contain spaces.

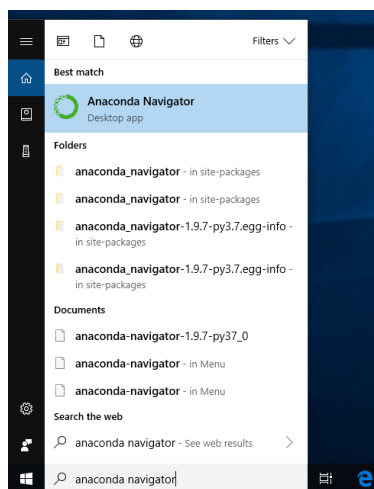
### Verifying your installation

You can confirm that Anaconda is installed and working with Anaconda Navigator or `conda`.

### Anaconda Navigator

Anaconda Navigator is a graphical user interface that is automatically installed with Anaconda. Navigator will open if the installation was successful. If Navigator does not open, review our [help resources](#).

- Windows: Click Start, search or select Anaconda Navigator from the menu.



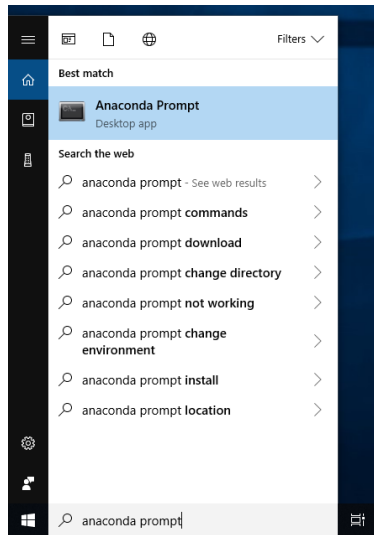
- macOS: Click Launchpad, select Anaconda Navigator. Or, use `Cmd+Space` to open Spotlight Search and type “Navigator” to open the program.
- Linux: See next section.

### Conda

If you prefer using a command line interface (CLI), you can use `conda` to verify the installation using Anaconda Prompt on Windows or terminal on Linux and macOS.

To open Anaconda Prompt:

- Windows: Click Start, search, or select Anaconda Prompt from the menu.



- macOS: Cmd+Space to open Spotlight Search and type “Navigator” to open the program.
- Linux–CentOS: Open Applications - System Tools - terminal.
- Linux–Ubuntu: Open the Dash by clicking the upper left Ubuntu icon, then type “terminal”.

After opening Anaconda Prompt or the terminal, choose any of the following methods to verify:

- Enter `conda list`. If Anaconda is installed and working, this will display a list of installed packages and their versions.
- Enter the command `python`. This command runs the Python shell. If Anaconda is installed and working, the version information it displays when it starts up will include “Anaconda”. To exit the Python shell, enter the command `quit()`.
- Open Anaconda Navigator with the command `anaconda-navigator`. If Anaconda is installed properly, Anaconda Navigator will open.

## Problems?

If you encounter any errors, see the following resources:

- [Navigator troubleshooting](#)
- [Troubleshooting guide](#) for general troubleshooting
- [Help and support](#) for resources such as free community support and bug reports

## Anaconda installer file hashes

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by running a local program to generate their SHA-256 cryptographic hashes and checking the output to be sure it matches the hashes (or “checksums”) below. We do not suggest MD5 verification as SHA-256 provides greater security.

If the SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, the hash you generated, and the hash on the site.

	Python 2	Python 3
64-bit Windows	<i>64-bit Windows, Py2</i>	<i>64-bit Windows, Py3</i>
32-bit Windows	<i>32-bit Windows, Py2</i>	<i>32-bit Windows, Py3</i>
macOS graphical installer	<i>macOS, Py2</i>	<i>macOS, Py3</i>
macOS command line installer	<i>macOS, Py2</i>	<i>macOS, Py3</i>
64-bit Linux	<i>64-bit Linux, Py2</i>	<i>64-bit Linux, Py3</i>
32-bit Linux	<i>32-bit Linux, Py2</i>	<i>32-bit Linux, Py3</i>

## Information for all files on a single page

### Hashes for all files

Name	Size	Time modified	SHA256 hash
Anaconda3-2020.07-Linux-ppc64le.sh	290.4 MiB	2020-07-23 12:16:47	0df7c3784973ab46a9ef9848aced01311
Anaconda3-2020.07-Linux-x86_64.sh	550.1 MiB	2020-07-23 12:16:50	38ce717758b95b3bd0b1797cc6ccfb76f
Anaconda3-2020.07-MacOSX-x86_64.pkg	462.3 MiB	2020-07-23 12:16:42	e095c487d2837e4c984d0fcd2217be42c
Anaconda3-2020.07-MacOSX-x86_64.sh	454.1 MiB	2020-07-23 12:16:44	3980c2a57fde5de2ccfd0d7973f95ac1
Anaconda3-2020.07-Windows-x86.exe	397.3 MiB	2020-07-23 12:16:51	19803e5ccc357b57051cf7fa272e6b499
Anaconda3-2020.07-Windows-x86_64.exe	467.5 MiB	2020-07-23 12:16:46	66acb9bdf7d2d5925df8762311a85ad72
Anaconda3-2020.02-Linux-ppc64le.sh	276.0 MiB	2020-03-11 10:32:32	d6d1827a38b988cbbe714d6e0357c9e25
Anaconda3-2020.02-Linux-x86_64.sh	521.6 MiB	2020-03-11 10:32:37	2b9f088b2022edb474915d9f69a803d64
Anaconda3-2020.02-MacOSX-x86_64.pkg	442.2 MiB	2020-03-11 10:32:57	4f7cc14b5b1d7aec3d9a5e781dede065e
Anaconda3-2020.02-MacOSX-x86_64.sh	430.1 MiB	2020-03-11 10:32:34	d237e6c976eb9c58368ca156a51bd913d
Anaconda3-2020.02-Windows-x86.exe	423.2 MiB	2020-03-11 10:32:58	d13381d6145c47755b198662af8a5f412
Anaconda3-2020.02-Windows-x86_64.exe	466.3 MiB	2020-03-11 10:32:35	83c2f53c7174253adcc2de7d1293a7408
Anaconda2-2019.10-Linux-ppc64le.sh	295.3 MiB	2019-10-15 09:26:13	0521743829c1b3c301542a20fa0daecda
Anaconda2-2019.10-Linux-x86_64.sh	477.4 MiB	2019-10-15 09:26:03	8b2e7dea2da7d8cc18e822e8ec1804052
Anaconda2-2019.10-MacOSX-x86_64.pkg	635.7 MiB	2019-10-15 09:27:30	d82b6aa37b41782b7823ff712b0899374
Anaconda2-2019.10-MacOSX-x86_64.sh	408.8 MiB	2019-10-15 09:27:31	463cbd0b90c47d02ec341377110653870
Anaconda2-2019.10-Windows-x86.exe	355.6 MiB	2019-10-15 09:26:15	b4731acd02f96923922d995bb16984d71
Anaconda2-2019.10-Windows-x86_64.exe	412.8 MiB	2019-10-15 09:26:08	3e09c8e95e10f077be1e1d26f26df8d6a
Anaconda3-2019.10-Linux-ppc64le.sh	320.3 MiB	2019-10-15 09:26:11	118c579f625555e1b116f0c3fd3842772
Anaconda3-2019.10-Linux-x86_64.sh	505.7 MiB	2019-10-15 09:26:05	46d762284d252e51cd58a8ca6c8adc9da
Anaconda3-2019.10-MacOSX-x86_64.pkg	653.5 MiB	2019-10-15 09:27:33	8b2192cbd586939d68bac00b0f9cbd2bf
Anaconda3-2019.10-MacOSX-x86_64.sh	424.2 MiB	2019-10-15 09:27:31	4f77299ff4170cda64fdfcc27ac609a37
Anaconda3-2019.10-Windows-x86.exe	409.6 MiB	2019-10-15 09:26:10	05e6738919673a6d57b5895b8b4df0b7e
Anaconda3-2019.10-Windows-x86_64.exe	461.5 MiB	2019-10-15 09:27:17	9e632439ed40620b8518f11469ded7316
Anaconda2-2019.07-Linux-ppc64le.sh	298.2 MiB	2019-07-25 09:36:29	ee7f61dab233cdd0acb376ad55e977b16

Table 31 – continued from previous page

Name	Size	Time modified	SHA256 hash
Anaconda2-2019.07-Linux-x86_64.sh	476.1 MiB	2019-07-25 09:36:01	189e16e7adf9ba4b7b7d06ecdc10ce4ad
Anaconda2-2019.07-MacOSX-x86_64.pkg	634.1 MiB	2019-07-25 09:37:04	7f8a0defa2905bd5e3ca679d6772c896b
Anaconda2-2019.07-MacOSX-x86_64.sh	407.8 MiB	2019-07-25 09:37:45	3e63919eed116826e683ed7d480d06517
Anaconda2-2019.07-Windows-x86.exe	360.5 MiB	2019-07-25 09:36:49	1bd676a51ccdee57c2c01a2bc87fa8b1b
Anaconda2-2019.07-Windows-x86_64.exe	427.2 MiB	2019-07-25 09:36:11	fb7493a5c40d28ab47e54c57f025186dc
Anaconda3-2019.07-Linux-ppc64le.sh	326.0 MiB	2019-07-25 09:36:56	e788094f7a18bfe14038accb26c8809a8
Anaconda3-2019.07-Linux-x86_64.sh	516.8 MiB	2019-07-25 09:36:20	69581cf739365ec7fb95608eef694ba95
Anaconda3-2019.07-MacOSX-x86_64.pkg	653.1 MiB	2019-07-25 09:38:03	bc1a4cb642b775159125521d1dbcf8bd1
Anaconda3-2019.07-MacOSX-x86_64.sh	435.4 MiB	2019-07-25 09:37:06	dcbbdbab37c5b5f3873fe24d2617a4325
Anaconda3-2019.07-Windows-x86.exe	418.4 MiB	2019-07-25 09:37:26	3d26ddf9ddb2287822a14ac1da3359a0d
Anaconda3-2019.07-Windows-x86_64.exe	485.8 MiB	2019-07-25 09:37:53	37e753801a881649ceb608449b66ff9da
Anaconda2-2019.03-Linux-ppc64le.sh	291.3 MiB	2019-04-04 16:00:36	3ab35c11b50ff26965266655d7dc76cf2
Anaconda2-2019.03-Linux-x86_64.sh	629.5 MiB	2019-04-04 16:00:35	cedfee5b5a3f62fcdac0a1d2d12396d0f
Anaconda2-2019.03-MacOSX-x86_64.pkg	624.3 MiB	2019-04-04 16:01:08	4e335d60fc9dcfb31caee809143352e28
Anaconda2-2019.03-MacOSX-x86_64.sh	530.2 MiB	2019-04-04 16:00:34	414917d00deaeeaf38719992e6437470f
Anaconda2-2019.03-Windows-x86.exe	492.5 MiB	2019-04-04 16:00:43	76be4b3d1f7a1207b786cbb54b3ed5261
Anaconda2-2019.03-Windows-x86_64.exe	586.9 MiB	2019-04-04 16:00:53	96c21ae0d152755e8f4ac4a593da4063e
Anaconda3-2019.03-Linux-ppc64le.sh	314.5 MiB	2019-04-04 16:00:58	b4ecfca3b6d6c284a3f9370f6a5ccfac1
Anaconda3-2019.03-Linux-x86_64.sh	654.1 MiB	2019-04-04 16:00:31	45c851b7497cc14d5ca060064394569f7
Anaconda3-2019.03-MacOSX-x86_64.pkg	637.4 MiB	2019-04-04 16:00:33	1d89450ec2b8236404bab5a47aaa9c69f
Anaconda3-2019.03-MacOSX-x86_64.sh	541.6 MiB	2019-04-04 16:00:27	b232f0b16181f48667d2ca89c04a4ee4b
Anaconda3-2019.03-Windows-x86.exe	545.7 MiB	2019-04-04 16:00:28	03d94f55c4c5e1187382ff414c78e6624
Anaconda3-2019.03-Windows-x86_64.exe	661.7 MiB	2019-04-04 16:00:30	d2c90169879f40816eac91bec585a1f9f
Anaconda2-2018.12-Linux-ppc64le.sh	289.7 MiB	2018-12-21 13:14:33	4ff037544f9191e24887176b44b04100
Anaconda2-2018.12-Linux-x86.sh	518.6 MiB	2018-12-21 13:13:15	e086c041695c0e50642aee8f4e7adad31
Anaconda2-2018.12-Linux-x86_64.sh	628.2 MiB	2018-12-21 13:13:10	1821d4b623ed449e0acb6df3ecbabd394
Anaconda2-2018.12-MacOSX-x86_64.pkg	640.7 MiB	2018-12-21 13:14:30	f07fb39c41f9cc7839adababdece209d9
Anaconda2-2018.12-MacOSX-x86_64.sh	547.1 MiB	2018-12-21 13:14:31	5c590b1b3c3dc2eedd52edce0caabbce66
Anaconda2-2018.12-Windows-x86.exe	458.6 MiB	2018-12-21 13:16:27	d75d51c8f9a7c345128805a55db3856f6
Anaconda2-2018.12-Windows-x86_64.exe	560.6 MiB	2018-12-21 13:16:17	7571d334eac3b9bd4f3e199fc5f493f06
Anaconda3-2018.12-Linux-ppc64le.sh	313.6 MiB	2018-12-21 13:13:03	f636f747d5b581ea05e5f20edb1c9ae5d
Anaconda3-2018.12-Linux-x86.sh	542.7 MiB	2018-12-21 13:13:14	7895052814921d45ed0585d1fb19f8edd
Anaconda3-2018.12-Linux-x86_64.sh	652.5 MiB	2018-12-21 13:13:06	1019d0857e5865f8a6861eaf15bfe535b
Anaconda3-2018.12-MacOSX-x86_64.pkg	652.7 MiB	2018-12-21 13:14:32	e40e076194df57f3fce8734acd5b2e3f6
Anaconda3-2018.12-MacOSX-x86_64.sh	557.0 MiB	2018-12-21 13:13:13	4ccd3944d994fd47e5701c341725a63e9
Anaconda3-2018.12-Windows-x86.exe	509.7 MiB	2018-12-21 13:13:12	3f2955c1874ca452b985627a10859f690
Anaconda3-2018.12-Windows-x86_64.exe	614.3 MiB	2018-12-21 13:14:34	09d84a789013d5e2bfb0148bdd9f5d69a
Anaconda2-5.3.1-Linux-x86.sh	507.6 MiB	2018-11-19 13:37:35	a38017dfa59141c63ec9882a15bd35e7c
Anaconda2-5.3.1-Linux-x86_64.sh	617.8 MiB	2018-11-19 13:37:31	f0650ad2f9ca4ae3f3162d7204a32950b
Anaconda2-5.3.1-MacOSX-x86_64.pkg	628.4 MiB	2018-11-19 13:37:38	7dc614e281df33f09fa006b245a955b94
Anaconda2-5.3.1-MacOSX-x86_64.sh	539.0 MiB	2018-11-19 13:37:43	df81e9d5d7d4c6595609a8d353eab8010
Anaconda2-5.3.1-Windows-x86.exe	458.1 MiB	2018-11-19 13:38:32	59680be839aa8b58477a24519a7575756
Anaconda2-5.3.1-Windows-x86_64.exe	580.1 MiB	2018-11-19 13:37:47	63b8a687cddcf462f9f61993d07ba8838
Anaconda3-5.3.1-Linux-x86.sh	527.3 MiB	2018-11-19 13:38:49	5dab8b2c95595df7fa55b88643f837213
Anaconda3-5.3.1-Linux-x86_64.sh	637.0 MiB	2018-11-19 13:38:46	d4c4256a8f46173b675dd6a62d12f566e
Anaconda3-5.3.1-MacOSX-x86_64.pkg	634.0 MiB	2018-11-19 13:38:54	ee9fb23d4beb30e5ed9d27d5703b46a02
Anaconda3-5.3.1-MacOSX-x86_64.sh	543.7 MiB	2018-11-19 13:38:57	23c373abce2463d4df495f5a1c7e8b0fa
Anaconda3-5.3.1-Windows-x86.exe	509.5 MiB	2018-11-19 13:39:54	a028d0550bf307c69af7c3210f487e230
Anaconda3-5.3.1-Windows-x86_64.exe	632.5 MiB	2018-11-19 13:38:59	295fed5940369d4ea1e2c6d04d418619d

Table 31 – continued from previous page

Name	Size	Time modified	SHA256 hash
Anaconda2-5.3.0-Linux-ppc64le.sh	285.7 MiB	2018-09-27 16:00:22	b71cdf75ca10875d49170eb64a02920f4
Anaconda2-5.3.0-Linux-x86.sh	507.5 MiB	2018-09-27 16:00:27	58d4229ad7097e1f3387d7f6582dcf2bb
Anaconda2-5.3.0-Linux-x86_64.sh	617.6 MiB	2018-09-27 16:00:25	50eeaab24bfa2472bc6485fe8f0e612ed
Anaconda2-5.3.0-MacOSX-x86_64.pkg	628.3 MiB	2018-09-27 15:59:12	834c221b413bdcbbce434f0a3008511f5
Anaconda2-5.3.0-MacOSX-x86_64.sh	538.9 MiB	2018-09-27 16:00:31	bea3eb7667d265c8fe678ddde8432ac1f
Anaconda2-5.3.0-Windows-x86.exe	457.2 MiB	2018-09-27 15:59:15	f18bdb9a38e5c444a3cb79c5c6bc927fb
Anaconda2-5.3.0-Windows-x86_64.exe	579.0 MiB	2018-09-27 15:59:14	30bf9131df2314c00a9cd5e5f0b7d6184
Anaconda3-5.3.0-Linux-ppc64le.sh	305.1 MiB	2018-09-27 16:01:33	550dd67626172a42eb0dd02a08bc78a67
Anaconda3-5.3.0-Linux-x86.sh	527.2 MiB	2018-09-27 16:01:37	c15ffac2ae35179a15dc5872e5bb405b4
Anaconda3-5.3.0-Linux-x86_64.sh	636.9 MiB	2018-09-27 16:01:35	cfbf5fe70dd1b797ec677e63c61f8efc9
Anaconda3-5.3.0-MacOSX-x86_64.pkg	633.9 MiB	2018-09-27 15:59:18	013e9968f437f91f7a1dfdfef4c7d6f9d3
Anaconda3-5.3.0-MacOSX-x86_64.sh	543.6 MiB	2018-09-27 16:01:41	bc073b6e6d3b2ef29d01a2caf1de7c206
Anaconda3-5.3.0-Windows-x86.exe	508.7 MiB	2018-09-27 16:00:05	1dceb687efbf5a609a66d19dc2528ef78
Anaconda3-5.3.0-Windows-x86_64.exe	631.4 MiB	2018-09-27 15:59:20	1083d05ecec45707940a6c7afb375a5f3
Anaconda2-5.2.0-Linux-ppc64le.sh	269.6 MiB	2018-05-30 13:04:31	a8fcac3f0884520c35103e76549fcc45d
Anaconda2-5.2.0-Linux-x86.sh	488.7 MiB	2018-05-30 13:05:30	402758c24767e9eb3b77312c388725a05
Anaconda2-5.2.0-Linux-x86_64.sh	603.4 MiB	2018-05-30 13:04:33	cb0d7a08b0e2cec4372033d3269979b4e
Anaconda2-5.2.0-MacOSX-x86_64.pkg	616.8 MiB	2018-05-30 13:05:32	f7695a3571eb8e8ae71fe9f413c36f57c
Anaconda2-5.2.0-MacOSX-x86_64.sh	527.1 MiB	2018-05-30 13:05:34	d7d46e566306da5979cd5632079497fe6
Anaconda2-5.2.0-Windows-x86.exe	443.4 MiB	2018-05-30 13:04:17	2b81916c477e64db917821bb48a97000f
Anaconda2-5.2.0-Windows-x86_64.exe	564.0 MiB	2018-05-30 13:04:16	e5ff95332d08a7b006a5bb723e0a5124c
Anaconda3-5.2.0-Linux-ppc64le.sh	288.3 MiB	2018-05-30 13:05:40	024c811526fffc40ed6fa243a25795fbab
Anaconda3-5.2.0-Linux-x86.sh	507.3 MiB	2018-05-30 13:05:46	f3527d085d06f35b6aeb96be2a9253ff9
Anaconda3-5.2.0-Linux-x86_64.sh	621.6 MiB	2018-05-30 13:05:43	09f53738b0cd3bb96f5b1bac488e5528d
Anaconda3-5.2.0-MacOSX-x86_64.pkg	613.1 MiB	2018-05-30 13:07:00	dae8befc73d32b480faef31fa6fb73332
Anaconda3-5.2.0-MacOSX-x86_64.sh	523.3 MiB	2018-05-30 13:07:03	c8089121dc89ffe8f9a0c01205bab75a1
Anaconda3-5.2.0-Windows-x86.exe	506.3 MiB	2018-05-30 13:04:19	64305a4c0041aaf4a3fd0fee4466d7b7f
Anaconda3-5.2.0-Windows-x86_64.exe	631.3 MiB	2018-05-30 13:04:18	2672f6537e2c8a79ae9540cf3c49b18bb
Anaconda2-5.1.0-Linux-ppc64le.sh	267.3 MiB	2018-02-15 09:08:49	ff9baa4d3710bb24bc3a6a40c0f4ef691
Anaconda2-5.1.0-Linux-x86.sh	431.3 MiB	2018-02-15 09:08:51	5af0c7a09a5f3aaf3666c0b362246d342
Anaconda2-5.1.0-Linux-x86_64.sh	533.0 MiB	2018-02-15 09:08:50	5f26ee92860d1dffdc20910ff2cf7557
Anaconda2-5.1.0-MacOSX-x86_64.pkg	588.0 MiB	2018-02-15 09:08:52	edbe9ef1ee5cfe62e131d7650e07c031a
Anaconda2-5.1.0-MacOSX-x86_64.sh	505.9 MiB	2018-02-15 09:08:53	b686e01aeadb33526d9c154a0ac6f691d
Anaconda2-5.1.0-Windows-x86.exe	419.8 MiB	2018-02-15 09:08:55	fa78c71d88b01e6367f0c3cbd23da1f82
Anaconda2-5.1.0-Windows-x86_64.exe	522.6 MiB	2018-02-15 09:08:54	3674c8d8c233dbea30842f14dc76cc3fe
Anaconda3-5.1.0-Linux-ppc64le.sh	285.7 MiB	2018-02-15 09:08:56	58d1d093450dabefef9279694c9345afe
Anaconda3-5.1.0-Linux-x86.sh	449.7 MiB	2018-02-15 09:08:58	0e940272517d8f8a6f26316a19e4be2bd
Anaconda3-5.1.0-Linux-x86_64.sh	551.2 MiB	2018-02-15 09:08:57	7e6785caad25e33930bc03fac4994a434
Anaconda3-5.1.0-MacOSX-x86_64.pkg	594.7 MiB	2018-02-15 09:09:06	d6bf6309ccaafa84314d85ca7421fddc16
Anaconda3-5.1.0-MacOSX-x86_64.sh	511.3 MiB	2018-02-15 09:10:24	be705b3c3a0ca29ee32ce7658890bb5ed
Anaconda3-5.1.0-Windows-x86.exe	435.5 MiB	2018-02-15 09:10:28	7a05da21fd592991d181ac8467faac513
Anaconda3-5.1.0-Windows-x86_64.exe	537.1 MiB	2018-02-15 09:10:26	7d192e58915d7e7fbfd0c987ddc4db38a
Anaconda2-5.0.1-Linux-x86.sh	413.2 MiB	2017-10-24 12:13:07	88c8d698fff16af15862daca10e94a0a4
Anaconda2-5.0.1-Linux-x86_64.sh	507.7 MiB	2017-10-24 12:13:52	23c676510bc87c95184ecaeb327c0b2c8
Anaconda2-5.0.1-MacOSX-x86_64.pkg	562.8 MiB	2017-10-23 20:01:12	22350fe830e6786a263d7727e537f066b
Anaconda2-5.0.1-MacOSX-x86_64.sh	486.5 MiB	2017-10-23 19:51:04	e3a9a5c84cb89ff079b0781ba773a3433
Anaconda2-5.0.1-Windows-x86.exe	403.4 MiB	2017-10-24 12:08:14	1a50fac8644f2128e318337b218299e53
Anaconda2-5.0.1-Windows-x86_64.exe	499.8 MiB	2017-10-23 21:57:22	c43f94c51623850b0c1a826710fe9c8e5
Anaconda3-5.0.1-Linux-x86.sh	431.0 MiB	2017-10-23 18:07:51	991a4b656fcb0236864fbb27ff03bb7f3

Table 31 – continued from previous page

Name	Size	Time modified	SHA256 hash
Anaconda3-5.0.1-Linux-x86_64.sh	525.3 MiB	2017-10-23 17:52:55	55e4db1919f49c92d5abbf27a4be5986a
Anaconda3-5.0.1-MacOSX-x86_64.pkg	568.9 MiB	2017-10-23 20:01:19	50c28594c785f5828990c950534684885
Anaconda3-5.0.1-MacOSX-x86_64.sh	491.0 MiB	2017-10-23 19:51:10	f438a0af923bc1edc7bca53f496c59a66
Anaconda3-5.0.1-Windows-x86.exe	420.4 MiB	2017-10-24 12:37:10	9edc3012324c9c8c9aa5257688bd79327
Anaconda3-5.0.1-Windows-x86_64.exe	514.8 MiB	2017-10-24 12:37:59	0b1ec18b7425f8c8518d6dc2fc0bc8ec2
Anaconda2-5.0.0.1-Linux-x86.sh	411.9 MiB	2017-10-02 10:50:13	00fbd979c815ede0bbad48fb4ef62cda3
Anaconda2-5.0.0.1-Linux-x86_64.sh	506.3 MiB	2017-10-02 10:50:12	18730808d863a5c194ab3f59dd395c1a6
Anaconda3-5.0.0.1-Linux-x86.sh	429.8 MiB	2017-10-02 10:50:15	407576899d3aa546bc3c2c4a13cbc18ab
Anaconda3-5.0.0.1-Linux-x86_64.sh	524.0 MiB	2017-10-02 10:50:14	092c92427f44687d789a41922ce8426fb
Anaconda2-5.0.0-Linux-ppc64le.sh	282.3 MiB	2017-09-26 16:25:07	e0512f3c81251e5dcd48fcf02fe2044a6
Anaconda2-5.0.0-Linux-x86.sh	411.4 MiB	2017-09-26 14:48:02	a3ed8769d20d55a41c04cf7c04e81c959
Anaconda2-5.0.0-Linux-x86_64.sh	505.7 MiB	2017-09-26 14:37:21	58a7117f89c40275114bf7e824a613a96
Anaconda2-5.0.0-MacOSX-x86_64.pkg	561.3 MiB	2017-09-26 16:25:08	3ee5cfe80d51685d6f374f83a9b76fa7e
Anaconda2-5.0.0-MacOSX-x86_64.sh	485.3 MiB	2017-09-26 16:25:09	d85198c63657924fae11b6ea5961f50d8
Anaconda2-5.0.0-Windows-x86.exe	402.2 MiB	2017-09-26 16:25:09	078551cfb0df72779897026724f375671
Anaconda2-5.0.0-Windows-x86_64.exe	498.2 MiB	2017-09-26 14:30:49	5fb73395cdf003613f5d44844da9870db
Anaconda3-5.0.0-Linux-ppc64le.sh	296.3 MiB	2017-09-25 14:39:31	3574d423084e604a9d85a9f38ea481e0f
Anaconda3-5.0.0-Linux-x86.sh	429.3 MiB	2017-09-26 14:48:02	634d2dfa97d19f2cc15e941cb4d059bc8
Anaconda3-5.0.0-Linux-x86_64.sh	523.4 MiB	2017-09-26 14:37:22	67f5c20232a3e493ea3f19a8e273e0618
Anaconda3-5.0.0-MacOSX-x86_64.pkg	567.2 MiB	2017-09-26 16:25:10	06d959384869290845bc61346bb33a18d
Anaconda3-5.0.0-MacOSX-x86_64.sh	489.9 MiB	2017-09-26 16:25:11	23df1e3a38a6b4aaa0ab559d0c1e51be7
Anaconda3-5.0.0-Windows-x86.exe	415.8 MiB	2017-09-26 16:25:12	a0d5d8e328b1d3a1ed921cadeecda659c
Anaconda3-5.0.0-Windows-x86_64.exe	510.0 MiB	2017-09-26 14:14:53	53bd80727099b5767b9f20f99e908f9c1
Anaconda2-4.4.0.1-Linux-ppc64le.sh	271.4 MiB	2017-07-26 16:10:02	e14acab146181699e47ca108fc624eceb
Anaconda3-4.4.0.1-Linux-ppc64le.sh	285.6 MiB	2017-07-26 16:08:42	d7c367c9c4ffffec37c31c6570218c9944
Anaconda2-4.4.0-Linux-ppc64le.sh	276.6 MiB	2017-05-17 15:45:20	c19edfd9a3bd2fcb37ddb0c3aa09339c9
Anaconda2-4.4.0-Linux-x86.sh	415.0 MiB	2017-05-26 18:23:30	452aa91ac83d3b6a68b79cea3042170ec
Anaconda2-4.4.0-Linux-x86_64.sh	485.2 MiB	2017-05-26 18:22:48	2d30b91ed4d215b6b4a15162a3389e905
Anaconda2-4.4.0-MacOSX-x86_64.pkg	438.0 MiB	2017-05-26 18:36:08	e5acf026892eaeabb055e6317af96f295d
Anaconda2-4.4.0-MacOSX-x86_64.sh	375.4 MiB	2017-05-26 18:35:52	ab95aef1110c2a385fd39a17e5f11dfba
Anaconda2-4.4.0-Windows-x86.exe	354.4 MiB	2017-05-26 17:52:15	0dec861f8839fdf2cbe4fa306c127f69
Anaconda2-4.4.0-Windows-x86_64.exe	430.7 MiB	2017-05-26 17:53:22	7a8ec1a36f385ebf28a1a8cf63b8b03ac
Anaconda3-4.4.0-Linux-ppc64le.sh	290.7 MiB	2017-05-17 15:45:50	605251829edecdc0c39df8db856d4f09e4
Anaconda3-4.4.0-Linux-x86.sh	428.7 MiB	2017-05-26 18:23:45	b0e492206d43067314b25963bc7d1f012
Anaconda3-4.4.0-Linux-x86_64.sh	499.0 MiB	2017-05-26 18:23:04	3301b37e402f3ff3df216fe0458f1e6a4
Anaconda3-4.4.0-MacOSX-x86_64.pkg	442.5 MiB	2017-05-26 18:36:17	c5fc645f11505ac3ef710023b4072b7fb
Anaconda3-4.4.0-MacOSX-x86_64.sh	380.4 MiB	2017-05-26 18:35:59	10fe58f09ae524df2548d17b8bb1e75db
Anaconda3-4.4.0-Windows-x86.exe	362.2 MiB	2017-05-26 17:54:21	37afe00b8305cc09b7bd8dd07f65cec3f
Anaconda3-4.4.0-Windows-x86_64.exe	437.6 MiB	2017-05-26 17:55:34	ea582602541e748053df5505144604262
Anaconda2-4.3.1-Linux-x86.sh	387.7 MiB	2017-03-06 16:12:31	4519ac724d5120d21bb80289c5509c0d1
Anaconda2-4.3.1-Linux-x86_64.sh	462.0 MiB	2017-03-06 16:12:14	e9b8f2645df6b1527ba56d61343162e07
Anaconda2-4.3.1-MacOSX-x86_64.pkg	419.4 MiB	2017-03-06 16:26:18	f5d950451c038f9a7ca80d4036b6a8152
Anaconda2-4.3.1-MacOSX-x86_64.sh	358.2 MiB	2017-03-06 16:26:02	35261360f2b01793f441b29715a94052d
Anaconda2-4.3.1-Windows-x86.exe	339.0 MiB	2017-03-06 16:18:12	fc363cea3c321c17b43a0bf2137aa845f
Anaconda2-4.3.1-Windows-x86_64.exe	413.7 MiB	2017-03-06 16:18:59	c0e13a756a856d7b7757b10d65bee577d
Anaconda3-4.3.1-Linux-x86.sh	399.3 MiB	2017-03-06 16:12:47	7b70bdba282a18ddbdc167afe8131f753
Anaconda3-4.3.1-Linux-x86_64.sh	474.3 MiB	2017-03-06 16:12:24	4447b93d2c779201e5fb50cfc45de0ec9
Anaconda3-4.3.1-MacOSX-x86_64.pkg	424.1 MiB	2017-03-06 16:26:27	ca608d58b1acf77b5c77d10e937b9084e
Anaconda3-4.3.1-MacOSX-x86_64.sh	363.4 MiB	2017-03-06 16:26:09	a42267203e207cb5e0f539e0d879ead12

Table 31 – continued from previous page

Name	Size	Time modified	SHA256 hash
Anaconda3-4.3.1-Windows-x86.exe	348.1 MiB	2017-03-06 16:19:46	adf322f49542cf509d4f72152cea24e54
Anaconda3-4.3.1-Windows-x86_64.exe	422.1 MiB	2017-03-06 16:20:48	65ce6d7c09884935fee9eb8d318b30e95
Anaconda2-4.3.0.1-Windows-x86.exe	338.1 MiB	2017-02-02 14:19:05	863702665aa2b55ede2103a8ca7d26435
Anaconda2-4.3.0.1-Windows-x86_64.exe	412.8 MiB	2017-02-02 14:20:08	2198e28e9e8e3c43ab72a8371e5b2d0a9
Anaconda3-4.3.0.1-Windows-x86.exe	347.2 MiB	2017-02-02 14:21:02	7f8ffce6b2c3a968ce19171c9dc332dec
Anaconda3-4.3.0.1-Windows-x86_64.exe	421.2 MiB	2017-02-02 14:22:10	b5954bf7da9a92d351d905dfdfa0e7bee
Anaconda2-4.3.0-Linux-x86.sh	386.8 MiB	2017-01-27 14:14:15	b80d471839e8cf7b100e59308720cc13c
Anaconda2-4.3.0-Linux-x86_64.sh	461.1 MiB	2017-01-27 14:15:08	7c52e6e99aabb24a49880130615a48e68
Anaconda2-4.3.0-MacOSX-x86_64.pkg	418.4 MiB	2017-01-27 14:26:23	3e1d1026d2c0b87213a8b4a5f28431060
Anaconda2-4.3.0-MacOSX-x86_64.sh	357.3 MiB	2017-01-27 14:26:08	834ac0287062929ab5930661735ee617f
Anaconda2-4.3.0-Windows-x86.exe	338.1 MiB	2017-01-27 14:17:06	a98767acefdeda02fe8d3ef9dadda1a34
Anaconda2-4.3.0-Windows-x86_64.exe	412.8 MiB	2017-01-27 14:17:59	1117839746a8eabf7ed26ff311fc74e44
Anaconda3-4.3.0-Linux-x86.sh	398.4 MiB	2017-01-27 14:14:29	f7ce2eeec3e42c2ba1ee3b9fcd670478f
Anaconda3-4.3.0-Linux-x86_64.sh	473.4 MiB	2017-01-27 14:15:21	e9169c3a5029aa820393ac92704eb9ee0
Anaconda3-4.3.0-MacOSX-x86_64.pkg	423.1 MiB	2017-01-27 14:26:32	f4522ac099ba292940bb47429e8e53eb9
Anaconda3-4.3.0-MacOSX-x86_64.sh	362.6 MiB	2017-01-27 14:26:15	c53059b810c5e7a9a5ef9c46a7ed76675
Anaconda3-4.3.0-Windows-x86.exe	347.2 MiB	2017-01-27 14:18:45	4a5dfea30b926074b4d6e0f1cea3e9765
Anaconda3-4.3.0-Windows-x86_64.exe	421.2 MiB	2017-01-27 14:19:41	324568dbef777a6ac8a25c1e8ae1975ff
Anaconda2-4.2.0-Linux-x86.sh	365.0 MiB	2016-09-27 15:50:20	618b720f309fe8da4f235415f11b6ce3d
Anaconda2-4.2.0-Linux-x86_64.sh	446.0 MiB	2016-09-27 15:49:54	beee286d24fb37dd6555281bba39b3deb
Anaconda2-4.2.0-MacOSX-x86_64.pkg	403.9 MiB	2016-10-17 19:33:11	4a74d34c3a3a82df31673ab49497816b0
Anaconda2-4.2.0-MacOSX-x86_64.sh	346.4 MiB	2016-09-27 15:50:02	a8b3ef86233635d9dcc3499dc38498076
Anaconda2-4.2.0-Windows-x86.exe	324.1 MiB	2016-09-27 15:54:50	a97ca79cb771568d051ef7773d25c0dda
Anaconda2-4.2.0-Windows-x86_64.exe	381.0 MiB	2016-09-27 15:55:47	6254b150edee53000c94e9abfc9c51a2d
Anaconda3-4.2.0-Linux-x86.sh	373.9 MiB	2016-09-27 15:50:34	1a8320635f2f06ec9d8610e77d6d0f9cb
Anaconda3-4.2.0-Linux-x86_64.sh	455.9 MiB	2016-09-27 15:50:04	73b51715a12b6382dd4df3dd1905b531b
Anaconda3-4.2.0-MacOSX-x86_64.pkg	407.1 MiB	2016-10-17 19:33:47	44fe57910aa10967c4afe41ab5663cb49
Anaconda3-4.2.0-MacOSX-x86_64.sh	349.5 MiB	2016-09-27 15:50:07	95448921601e1952e01a17ba9767cd362
Anaconda3-4.2.0-Windows-x86.exe	333.4 MiB	2016-09-27 15:56:30	e7b79a9886da3f840b52882c47ecab3ed
Anaconda3-4.2.0-Windows-x86_64.exe	391.4 MiB	2016-09-27 15:57:21	84e30c99833e142a27fc9ee2c748b03f1
Anaconda2-4.1.1-Linux-x86.sh	324.6 MiB	2016-07-08 11:19:57	1ab001c7a469345a90d549ebf4afa3376
Anaconda2-4.1.1-Linux-x86_64.sh	399.6 MiB	2016-07-08 11:19:56	9413b1d3ca9498ba6f53913df9c43d685
Anaconda2-4.1.1-MacOSX-x86_64.pkg	345.0 MiB	2016-07-08 11:19:59	879385461cc65bd9dbf9639bbf4471ecf
Anaconda2-4.1.1-MacOSX-x86_64.sh	295.8 MiB	2016-07-08 11:20:00	3b2fb323eb26c1c58788f63c41e164c20
Anaconda2-4.1.1-Windows-x86.exe	286.0 MiB	2016-07-08 11:20:01	4708d73952a0a8040bf1594ea42027a30
Anaconda2-4.1.1-Windows-x86_64.exe	341.2 MiB	2016-07-08 11:20:01	7be13a69df254b86e47612c726b0b2ba9
Anaconda3-4.1.1-Linux-x86.sh	329.1 MiB	2016-07-08 11:20:02	931626363f4030c7a1e8897549b1d3589
Anaconda3-4.1.1-Linux-x86_64.sh	406.3 MiB	2016-07-08 11:20:02	4f5c95feb0e7efeadd3d348dcef117d77
Anaconda3-4.1.1-MacOSX-x86_64.pkg	347.9 MiB	2016-07-08 11:21:15	b5e8cf44958d0aa03a7cc2da15fa835b1
Anaconda3-4.1.1-MacOSX-x86_64.sh	298.7 MiB	2016-07-08 11:21:17	7c3c06e9281c41f1213d357cb5f233fd9
Anaconda3-4.1.1-Windows-x86.exe	293.8 MiB	2016-07-08 11:21:18	224e3dd90850651ae0d1c9216b4c317d1
Anaconda3-4.1.1-Windows-x86_64.exe	352.9 MiB	2016-07-08 11:21:17	b4889513dc574f9d6f96db089315d69d2
Anaconda2-4.1.0-Linux-x86.sh	324.4 MiB	2016-06-28 11:28:28	54c06cd1b11cb687db6ba3613df443c05
Anaconda2-4.1.0-Linux-x86_64.sh	398.8 MiB	2016-06-28 11:28:28	3b7e504ca0132fb555d1f10e174cae070
Anaconda2-4.1.0-MacOSX-x86_64.pkg	344.2 MiB	2016-06-28 11:28:29	a97840be50d8c86b28caf8be1786bbe74
Anaconda2-4.1.0-MacOSX-x86_64.sh	295.1 MiB	2016-06-28 11:28:30	8b2c2a32f5e0da75cf8c81c568124cc1e
Anaconda2-4.1.0-Windows-x86.exe	285.1 MiB	2016-06-28 11:28:31	c4ad4eefdfbf6d838424c62c8b524352d
Anaconda2-4.1.0-Windows-x86_64.exe	340.2 MiB	2016-06-28 11:28:30	7a62880ff9bb7f747d70f518f024dfd17
Anaconda3-4.1.0-Linux-x86.sh	328.4 MiB	2016-06-28 11:28:32	7764093f337a43e4962b12d01508c1a38



Table 31 – continued from previous page

Name	Size	Time modified	SHA256 hash
Anaconda3-4.1.0-Linux-x86_64.sh	405.0 MiB	2016-06-28 11:28:31	11d32cf4026603d3b327dc4299863be6b
Anaconda3-4.1.0-MacOSX-x86_64.pkg	346.7 MiB	2016-06-28 11:28:32	83772b5fcd3d6deb945316ec96ecc7b0c
Anaconda3-4.1.0-MacOSX-x86_64.sh	297.6 MiB	2016-06-28 11:28:33	4c45c8d75665fa5194ebe4e355d3427f5
Anaconda3-4.1.0-Windows-x86.exe	292.6 MiB	2016-06-28 11:28:34	4f444ed9400505e822bb475e986800fa
Anaconda3-4.1.0-Windows-x86_64.exe	351.4 MiB	2016-06-28 11:28:33	9acde60b591233452dba23ac15800f39f
Anaconda2-4.0.0-Linux-x86.sh	332.3 MiB	2016-03-29 11:14:57	41341c840cea4185ef5bd82520c1de72b
Anaconda2-4.0.0-Linux-x86_64.sh	392.5 MiB	2016-03-29 11:14:55	ae312143952ca00e061a656c2080e0e4f
Anaconda2-4.0.0-MacOSX-x86_64.pkg	339.2 MiB	2016-03-29 11:14:57	242691c7dc9e20143d7620fd9e0cc344f
Anaconda2-4.0.0-MacOSX-x86_64.sh	290.2 MiB	2016-03-29 11:14:59	aa7ba6e1a40e08e672660c00c3151f012
Anaconda2-4.0.0-Windows-x86.exe	281.0 MiB	2016-03-29 11:15:00	f8185ad2fe89356ab001e55a463b663bc
Anaconda2-4.0.0-Windows-x86_64.exe	334.6 MiB	2016-03-29 11:14:59	213c7d94bdb6f0931edd31bb14ae33ab5
Anaconda3-4.0.0-Linux-x86.sh	336.9 MiB	2016-03-29 11:15:03	e1469fa0d24de12f33661ce3d7a06d779
Anaconda3-4.0.0-Linux-x86_64.sh	398.4 MiB	2016-03-29 11:15:02	36a558a1109868661a5735f5f32607643
Anaconda3-4.0.0-MacOSX-x86_64.pkg	341.5 MiB	2016-03-29 11:16:08	32a089b1be465a8b03c837041bbfbc76
Anaconda3-4.0.0-MacOSX-x86_64.sh	292.7 MiB	2016-03-29 11:16:21	704a776c0cf3fcc6a6e0c5a1e6b6043728
Anaconda3-4.0.0-Windows-x86.exe	283.1 MiB	2016-03-29 11:16:22	b5a31a9d130a40c3110c0592a6c8fbd43
Anaconda3-4.0.0-Windows-x86_64.exe	345.4 MiB	2016-03-29 11:16:22	39bf467cd142c1f8fdb7d673fdea273d8
Anaconda2-2.5.0-Linux-x86.sh	330.4 MiB	2016-02-03 15:41:54	4911047df51c46661f551d6022aee21a7
Anaconda2-2.5.0-Linux-x86_64.sh	390.9 MiB	2016-02-03 15:41:18	e10abf459cde4a838bd6fc5ca03023c34
Anaconda2-2.5.0-MacOSX-x86_64.pkg	367.9 MiB	2016-02-03 15:55:31	0f546ed4f388299824e98a31ca9e3fe98
Anaconda2-2.5.0-MacOSX-x86_64.sh	316.1 MiB	2016-02-03 15:41:22	e7aa3b41210ee7ccf3c12e5b5ea43190d
Anaconda2-2.5.0-Windows-x86.exe	296.2 MiB	2016-02-03 15:45:21	a0336729f0400ff12fe18a7d5e20c3f9b
Anaconda2-2.5.0-Windows-x86_64.exe	348.6 MiB	2016-02-03 15:46:14	4423b43eb23184b4239abc426a564760d
Anaconda3-2.5.0-Linux-x86.sh	334.4 MiB	2016-02-03 15:42:07	22ac26c8bde7c4153ea859f6f6d8aca93
Anaconda3-2.5.0-Linux-x86_64.sh	395.6 MiB	2016-02-03 15:41:27	addadcb927f15cb0b5b6e36890563d335
Anaconda3-2.5.0-MacOSX-x86_64.pkg	369.8 MiB	2016-02-03 15:56:04	b1a6945f0f025086806624c59de5d92e5
Anaconda3-2.5.0-MacOSX-x86_64.sh	318.3 MiB	2016-02-03 15:41:27	9bb0f926927db210f8c2a8de881213d1a
Anaconda3-2.5.0-Windows-x86.exe	296.3 MiB	2016-02-03 15:46:53	4a3441aaaa269d06f39e1430155f9f25a
Anaconda3-2.5.0-Windows-x86_64.exe	361.1 MiB	2016-02-03 15:47:40	4728044d77da715e48d4c95d7f2e3c2a0
Anaconda2-2.4.1-Linux-x86.sh	248.5 MiB	2015-12-08 15:00:50	2388cc714567afe7697bf43b4063ff0ea
Anaconda2-2.4.1-Linux-x86_64.sh	265.0 MiB	2015-12-08 15:00:49	2de682c96edf8cca2852071a84ff86002
Anaconda2-2.4.1-MacOSX-x86_64.pkg	245.8 MiB	2015-12-08 15:00:50	1e2445aaf9faf84e801404bf89091fbf4
Anaconda2-2.4.1-MacOSX-x86_64.sh	212.0 MiB	2015-12-08 15:00:51	f4bd45a21e0dff106e36d11cfd532f2b5
Anaconda2-2.4.1-Windows-x86.exe	287.8 MiB	2015-12-08 15:00:52	65fb15559b0ddb5055c110ecdb84823a6
Anaconda2-2.4.1-Windows-x86_64.exe	354.2 MiB	2015-12-08 15:00:51	cfbe5539cb7f2e5807ec3d2fa2e59db3a
Anaconda3-2.4.1-Linux-x86.sh	253.2 MiB	2015-12-08 15:00:53	00d13413f5b8129e863dabcc2296a181c
Anaconda3-2.4.1-Linux-x86_64.sh	270.7 MiB	2015-12-08 15:00:53	0735e69199fc37135930ea2fd4fb6ad0a
Anaconda3-2.4.1-MacOSX-x86_64.pkg	247.6 MiB	2015-12-08 15:00:54	95e9f2d370f7816ed72b862c9413c973e
Anaconda3-2.4.1-MacOSX-x86_64.sh	213.9 MiB	2015-12-08 15:00:54	22a3267638da9b7d64210d7da90d8762d
Anaconda3-2.4.1-Windows-x86.exe	299.1 MiB	2015-12-08 15:00:56	dfe50d13473547b5230f6194dfe6bdf9
Anaconda3-2.4.1-Windows-x86_64.exe	363.7 MiB	2015-12-08 15:00:55	21d155a4b43805042499b8d008835bcd
Anaconda2-2.4.0-Linux-x86.sh	279.9 MiB	2015-11-02 16:22:19	478a8fdde3a6e4040a68c57d7bdd6fab1
Anaconda2-2.4.0-Linux-x86_64.sh	288.4 MiB	2015-11-02 16:22:19	49d19834da06b1b82b6fa85bc647d2e78
Anaconda2-2.4.0-MacOSX-x86_64.pkg	274.3 MiB	2015-11-02 16:22:20	d6842135062f3c3d2f8bd33318133376d
Anaconda2-2.4.0-MacOSX-x86_64.sh	239.5 MiB	2015-11-02 16:22:20	53c9123c9d508555100805fdb44d98455
Anaconda2-2.4.0-Windows-x86.exe	321.4 MiB	2015-11-02 16:22:21	2a05db81a0fe4155bc2dd83a689294d3a
Anaconda2-2.4.0-Windows-x86_64.exe	388.0 MiB	2015-11-02 16:22:21	7a40484e58e91f62d91961c8607de586d
Anaconda3-2.4.0-Linux-x86.sh	277.4 MiB	2015-11-02 16:22:22	f6080c6493cefc603cfeb67aaf6c3c4c6
Anaconda3-2.4.0-Linux-x86_64.sh	285.2 MiB	2015-11-02 16:22:22	fb4e480059e991f2fa632b5a9bcd284c

Table 31 – continued from previous page

Name	Size	Time modified	SHA256 hash
Anaconda3-2.4.0-MacOSX-x86_64.pkg	267.4 MiB	2015-11-02 16:22:23	791f045258bd39bbcdabb4c5425dce082e
Anaconda3-2.4.0-MacOSX-x86_64.sh	233.8 MiB	2015-11-02 16:22:23	f0cd785dbed0bab28dfc08a391c9de1b0
Anaconda3-2.4.0-Windows-x86.exe	316.4 MiB	2015-11-02 16:22:25	a69a9fe00ce337b0cfd7d024b79ba5141
Anaconda3-2.4.0-Windows-x86_64.exe	392.3 MiB	2015-11-02 16:22:24	beaa1b803dd30022c6aca1c6f05182bea
Anaconda-2.3.0-Linux-x86.sh	309.6 MiB	2015-07-01 13:35:09	73fdbbbb3e38207ed18e5059f71676d18d
Anaconda-2.3.0-Linux-x86_64.sh	323.9 MiB	2015-07-01 13:35:08	7c02499e9511c127d225992cfe1cd815e
Anaconda-2.3.0-MacOSX-x86_64.pkg	283.7 MiB	2015-07-01 13:35:09	f920ae6211d9da3288b5e160100543667
Anaconda-2.3.0-MacOSX-x86_64.sh	249.9 MiB	2015-07-01 13:35:10	c4bb59a57bf44dde80612041bbbcfd2e5
Anaconda-2.3.0-Windows-x86.exe	277.4 MiB	2015-07-01 13:35:11	3b60dddfb84533539e767889706bd64298
Anaconda-2.3.0-Windows-x86_64.exe	334.7 MiB	2015-07-01 13:35:10	70b4a84e78c721bd46f3de39c75acb37d
Anaconda3-2.3.0-Linux-x86.sh	322.6 MiB	2015-07-01 13:35:13	4cc10d65c303191004ada2b6d75562c8e
Anaconda3-2.3.0-Linux-x86_64.sh	336.7 MiB	2015-07-01 13:35:12	3be5410b2d9db45882c7de07c554cf4f1
Anaconda3-2.3.0-MacOSX-x86_64.pkg	292.8 MiB	2015-07-01 13:35:13	0b936ab3067bbf32b5a52768f31ff437f
Anaconda3-2.3.0-MacOSX-x86_64.sh	257.4 MiB	2015-07-01 13:35:14	6a0c94a49f41f9fda0138c8e966bd7b0a
Anaconda3-2.3.0-Windows-x86.exe	281.1 MiB	2015-07-01 13:35:15	02d5f84da308f96d1a252a6669f3ca91e
Anaconda3-2.3.0-Windows-x86_64.exe	336.4 MiB	2015-07-01 13:35:14	bd693b61cf191666ae0473327f3c15bcf
Anaconda-2.2.0-Linux-x86.sh	303.2 MiB	2015-03-25 15:19:54	6437d5b08a19c3501f2f5dc3ae1ae16f9
Anaconda-2.2.0-Linux-x86_64.sh	317.3 MiB	2015-03-25 15:20:08	ca2582cb2188073b0f348ad42207211a2
Anaconda-2.2.0-MacOSX-x86_64.pkg	279.7 MiB	2015-03-25 15:27:27	65784323db94b0c297e998bc81db5978e
Anaconda-2.2.0-MacOSX-x86_64.sh	247.1 MiB	2015-03-25 15:17:33	20570e2f3911e38a78d8f888f3ff445d6
Anaconda-2.2.0-Windows-x86.exe	274.2 MiB	2015-03-25 15:28:48	247e8e7e386224a3df736ffe607596546
Anaconda-2.2.0-Windows-x86_64.exe	331.2 MiB	2015-03-25 15:30:13	1e01d7e1560668f4c05d1cfafcb59b79d
Anaconda3-2.2.0-Linux-x86.sh	313.3 MiB	2015-03-25 15:20:07	223655cd256aa912dfc83ab24570e47bb
Anaconda3-2.2.0-Linux-x86_64.sh	326.9 MiB	2015-03-25 15:20:14	4aac68743e7706adb93f042f970373a6e
Anaconda3-2.2.0-MacOSX-x86_64.pkg	288.8 MiB	2015-03-25 15:28:12	16a5154267d7d52d3e7e0d12ec3405077
Anaconda3-2.2.0-MacOSX-x86_64.sh	254.5 MiB	2015-03-25 15:17:44	81a2089ea6127717f146454e99ea0be2b
Anaconda3-2.2.0-Windows-x86.exe	277.7 MiB	2015-03-25 15:31:19	20c46fff048fb313aaf1a49171c1a7b96
Anaconda3-2.2.0-Windows-x86_64.exe	332.6 MiB	2015-03-25 15:32:30	28c5a13b27a9dbd57c7c633316c5f4beb
Anaconda-2.1.0-Linux-x86.sh	321.2 MiB	2014-09-25 10:50:30	fd70c08719e6b5caae45b7c8402c6975a
Anaconda-2.1.0-Linux-x86_64.sh	337.4 MiB	2014-09-25 10:50:15	191fbf290747614929d0bdd576e330c94
Anaconda-2.1.0-MacOSX-x86_64.pkg	275.0 MiB	2014-09-25 11:33:13	d8001bae990e7024b81e74c6b06d0f488
Anaconda-2.1.0-MacOSX-x86_64.sh	241.0 MiB	2014-09-25 10:53:13	128fd4f53e0895e0d23f33e924ae32e01
Anaconda-2.1.0-Windows-x86.exe	310.2 MiB	2014-09-25 11:05:03	c39193c9018a9c1e9e8f3c1d2692ac635
Anaconda-2.1.0-Windows-x86_64.exe	367.0 MiB	2014-09-25 11:07:11	d9d7c8ed1c914312848407f08fff3d193
Anaconda3-2.1.0-Linux-x86.sh	317.7 MiB	2014-09-25 10:50:35	657cb599004c21e37ce693515ea33922e
Anaconda3-2.1.0-Linux-x86_64.sh	332.8 MiB	2014-09-25 10:50:20	af3225ccbe8df0ffba918939e009aa5774
Anaconda3-2.1.0-MacOSX-x86_64.pkg	277.3 MiB	2014-09-25 11:40:54	2780df02f400e44c0adcd209825fddf95
Anaconda3-2.1.0-MacOSX-x86_64.sh	243.5 MiB	2014-09-25 10:53:23	efdb7e9d1e539cbcd62dc3874b0de6a14
Anaconda3-2.1.0-Windows-x86.exe	308.7 MiB	2014-09-25 11:09:01	8ffa252aa2b4f63889888ae85a81626ce
Anaconda3-2.1.0-Windows-x86_64.exe	363.3 MiB	2014-09-25 11:11:03	ea4059469b1820069f62bd6c256def625
Anaconda-2.0.1-Linux-x86.sh	309.1 MiB	2014-06-12 15:02:41	e8fffc63f31673b5ce41a95796a1f729dd
Anaconda-2.0.1-Linux-x86_64.sh	327.9 MiB	2014-06-12 15:02:33	074204fa26872b4a946123071d15b8390
Anaconda-2.0.1-MacOSX-x86_64.pkg	244.3 MiB	2014-06-12 15:02:50	d6a0ce0422daa004929a4aef6b485d94f
Anaconda-2.0.1-MacOSX-x86_64.sh	214.4 MiB	2014-06-12 15:02:56	4ecda163c6f46e70cc6a1fe62dece4c6e
Anaconda-2.0.1-Windows-x86.exe	287.3 MiB	2014-06-12 15:03:27	be5a341bc3f9bf8386c686cfc9ad253f3
Anaconda-2.0.1-Windows-x86_64.exe	343.7 MiB	2014-06-12 15:03:07	5b27e7de356312da711a19ae6a4438c1c
Anaconda3-2.0.1-Linux-x86.sh	287.7 MiB	2014-06-12 15:00:00	21293fabbd3d5cfbb1afe0c9a8b39e0bc
Anaconda3-2.0.1-Linux-x86_64.sh	304.8 MiB	2014-06-12 14:59:53	3c3b834793e461f3316ad1d9a9178c678
Anaconda3-2.0.1-MacOSX-x86_64.pkg	230.7 MiB	2014-06-12 15:00:05	0d53815a83a50bdcfcb5ada686f582730

Table 31 – continued from previous page

Name	Size	Time modified	SHA256 hash
Anaconda3-2.0.1-MacOSX-x86_64.sh	203.3 MiB	2014-06-12 15:00:09	7a08509d4e45efcc7055a6d06d8406a77
Anaconda3-2.0.1-Windows-x86.exe	265.7 MiB	2014-06-12 15:00:27	b08803296d7439413d590fd1f967b2012
Anaconda3-2.0.1-Windows-x86_64.exe	319.8 MiB	2014-06-12 15:00:15	e2b6d3d6a9e378fc0d0dd63342417c02b
Anaconda-2.0.0-Linux-x86.sh	298.4 MiB	2014-05-28 16:50:36	efb9d3987134d484d88a9d915437b1bd5
Anaconda-2.0.0-Linux-x86_64.sh	316.9 MiB	2014-05-28 16:50:30	3aa27ddf4a0ba5046ba52b97da99e20eb
Anaconda-2.0.0-MacOSX-x86_64.pkg	236.2 MiB	2014-05-28 16:50:41	e2eb3805451a26235b2ed7f3e63535fc3
Anaconda-2.0.0-MacOSX-x86_64.sh	206.1 MiB	2014-05-28 16:50:45	ad6271ad21403166bf54d0734ba8c7f7e
Anaconda-2.0.0-Windows-x86.exe	278.2 MiB	2014-05-28 16:51:02	d86cc7100b4c04ec25768267b81798f70
Anaconda-2.0.0-Windows-x86_64.exe	334.4 MiB	2014-05-28 16:50:53	60078f8677e62e435e5a53f1084e6f39d
Anaconda3-2.0.0-Linux-x86.sh	277.5 MiB	2014-05-27 16:35:55	439761159d5604e182951650a478dd53c
Anaconda3-2.0.0-Linux-x86_64.sh	294.4 MiB	2014-05-27 16:26:59	57ce4f97e300cf94c5724f72d992e9eec
Anaconda3-2.0.0-MacOSX-x86_64.pkg	222.9 MiB	2014-05-27 16:30:16	4d4189ec0c514d344389e216b3ad4eeac
Anaconda3-2.0.0-MacOSX-x86_64.sh	195.3 MiB	2014-05-27 17:02:53	776a1cf8a8e898b41bb6558c093632cc9
Anaconda3-2.0.0-Windows-x86.exe	256.9 MiB	2014-05-27 16:59:13	37986ce4c104ed3c82838de74b3a4de17
Anaconda3-2.0.0-Windows-x86_64.exe	310.9 MiB	2014-05-27 17:01:42	a8046fc82da7463ef53cdeaba97c72433
Anaconda-1.9.2-Linux-x86.sh	411.8 MiB	2014-04-08 17:33:09	1f7c850d0b98c011a717b3b757d82077a
Anaconda-1.9.2-Linux-x86_64.sh	484.0 MiB	2014-04-08 17:32:38	7181d399833a2549a9584255bb477487f
Anaconda-1.9.2-MacOSX-x86_64.pkg	281.0 MiB	2014-04-10 10:05:32	2fff6dca12507f675b04ed1f303d0ee99
Anaconda-1.9.2-MacOSX-x86_64.sh	245.4 MiB	2014-04-08 17:34:03	be4611ca671f80b984fa330d4ecf82244
Anaconda-1.9.2-Windows-x86.exe	311.8 MiB	2014-04-08 17:39:25	fe005aeacd1345b856c73d640856b79ed
Anaconda-1.9.2-Windows-x86_64.exe	367.3 MiB	2014-04-08 17:41:16	ef9cfb69c831210fc9000ee5482d2d98b
Anaconda-1.9.1-Linux-x86.sh	411.8 MiB	2014-02-20 13:34:56	9aa39c05f723fee18c54a9cc172998619
Anaconda-1.9.1-Linux-x86_64.sh	483.9 MiB	2014-02-20 13:35:16	f6455e06a72b8cc11c8a96fb88a85518a
Anaconda-1.9.1-MacOSX-x86_64.pkg	280.9 MiB	2014-02-20 15:44:04	2aa707b162e71d488495085fd13232f8
Anaconda-1.9.1-MacOSX-x86_64.sh	245.3 MiB	2014-02-20 13:02:05	7e4358adbbae2db9e17d1e0e4263b9a01
Anaconda-1.9.1-Windows-x86.exe	311.7 MiB	2014-02-20 15:08:42	46cbe29a30cfcd56018f7f69a35525708
Anaconda-1.9.1-Windows-x86_64.exe	367.3 MiB	2014-02-20 15:10:34	d0c3c2faca03b3820ff8fc39688f500bd
Anaconda-1.9.0-Linux-x86.sh	545.3 MiB	2014-02-10 10:23:30	16471e90b3deb7be1b3d449d8883983d8
Anaconda-1.9.0-Linux-x86_64.sh	618.8 MiB	2014-02-10 10:23:05	855f1265e4c0b40d50f5a3a0fe7bae05b
Anaconda-1.9.0-MacOSX-x86_64.pkg	279.8 MiB	2014-02-10 10:23:46	b74134e7626f10fc4d86209a3ebbb19de
Anaconda-1.9.0-MacOSX-x86_64.sh	244.4 MiB	2014-02-10 10:23:47	722fe4d4406e88c5023e7ee21dc1401bb
Anaconda-1.9.0-Windows-x86.exe	308.6 MiB	2014-02-10 10:24:52	2c8c58cf21e537e930535df5a0e8fd4b6
Anaconda-1.9.0-Windows-x86_64.exe	365.1 MiB	2014-02-10 10:24:18	265c7e849688164f7a7fe9df541be0186
Anaconda-1.8.0-Linux-x86.sh	393.0 MiB	2013-11-04 15:37:29	2c08a5cd6ccaa9dc84063b0ee9b007aa8
Anaconda-1.8.0-Linux-x86_64.sh	465.7 MiB	2013-11-04 15:37:12	69f42966d918f4197040e4dd126d2e3cc
Anaconda-1.8.0-MacOSX-x86_64.pkg	263.0 MiB	2013-11-04 13:57:20	fb92afc7750bc58ac12f3cbd65c18ee0f
Anaconda-1.8.0-MacOSX-x86_64.sh	228.8 MiB	2013-11-04 13:10:16	5844ca595b5930399a1213db64ab53e9b
Anaconda-1.8.0-Windows-x86.exe	290.0 MiB	2013-11-04 13:54:14	719bc0987be80b46f9c6b745822777fa1
Anaconda-1.8.0-Windows-x86_64.exe	342.1 MiB	2013-11-04 13:55:59	434c2b325a368958b66d52cee4cc710f5
Anaconda-1.7.0-Linux-x86.sh	381.0 MiB	2013-09-08 17:02:26	af372a27a1887e11061485e2a854c5357
Anaconda-1.7.0-Linux-x86_64.sh	452.6 MiB	2013-09-08 17:01:59	6115cfaf55a0746b4ae4128be839c99db
Anaconda-1.7.0-MacOSX-x86_64.pkg	256.7 MiB	2013-09-09 12:15:34	d277f7e162c77043e416d03a754389a0d
Anaconda-1.7.0-MacOSX-x86_64.sh	223.3 MiB	2013-09-09 11:52:45	046b592245bc2c11e733acb9700dc5094
Anaconda-1.7.0-Windows-x86.exe	280.6 MiB	2013-09-08 17:10:23	b434776dfeac98f37328c6e538f5a1a53
Anaconda-1.7.0-Windows-x86_64.exe	330.1 MiB	2013-09-08 17:12:00	59a3667fd33f8de1ed476d7ff07917d72
Anaconda-1.6.2-Windows-x86.exe	244.4 MiB	2013-07-09 13:44:58	0873576bbd979e3b7859808bcc2311ed
Anaconda-1.6.2-Windows-x86_64.exe	289.9 MiB	2013-07-09 13:46:28	641fc25c1d13e49cc030df5f4040170d1
Anaconda-1.6.1-Linux-x86.sh	247.1 MiB	2013-07-02 11:59:07	745b9452fd18720deefb465a6687c0d66
Anaconda-1.6.1-Linux-x86_64.sh	317.6 MiB	2013-07-02 11:57:42	81d1819ba08069343f228b9c819cdba0e

Table 31 – continued from previous page

Name	Size	Time modified	SHA256 hash
Anaconda-1.6.1-MacOSX-x86_64.pkg	197.3 MiB	2013-07-02 17:30:12	7c79819dd40a14e52439664c3e88e89ec
Anaconda-1.6.1-MacOSX-x86_64.sh	170.0 MiB	2013-07-02 11:59:25	bbc15de34208ce8af5aceedee1334636
Anaconda-1.6.1-Windows-x86.exe	244.4 MiB	2013-07-02 12:02:59	a823dc7688cec49499bb5922783377c26
Anaconda-1.6.1-Windows-x86_64.exe	289.9 MiB	2013-07-02 12:04:26	8cad320d4d6981644fbd1741bd5589d19
Anaconda-1.6.0-Linux-x86.sh	241.6 MiB	2013-06-21 14:23:39	d6aeedfcb39d648fd5bd72c4d0b3063
Anaconda-1.6.0-Linux-x86_64.sh	309.5 MiB	2013-06-21 14:23:51	20f5b70193af4b0b8f10aa0e66aabca55
Anaconda-1.6.0-MacOSX-x86_64.sh	169.0 MiB	2013-06-21 14:26:14	e03317888c36c07451a349577b426f435
Anaconda-1.6.0-Windows-x86.exe	244.9 MiB	2013-06-21 14:36:46	3dc2588557455484b3b38feb14fa95d94
Anaconda-1.6.0-Windows-x86_64.exe	290.4 MiB	2013-06-21 14:38:20	6e95dc3612ed430ded28bb48fa1671b32
Anaconda-1.5.1-MacOSX-x86_64.sh	166.2 MiB	2013-05-09 14:26:20	6d3c86a2fdbaeec2a6c251d5c9034a32
Anaconda-1.5.0-Linux-x86.sh	238.8 MiB	2013-05-08 09:18:43	ca7e356dc1b8c8ef27dfb74b32c77563d
Anaconda-1.5.0-Linux-x86_64.sh	306.7 MiB	2013-05-08 09:18:36	f4cdc194f076e1b438c8a34e7e5f53e70
Anaconda-1.5.0-MacOSX-x86_64.sh	166.2 MiB	2013-05-08 09:18:44	c69609f0f48f33ca5a12d425a9e4d0fc9
Anaconda-1.5.0-Windows-x86.exe	236.0 MiB	2013-05-08 09:18:44	d3dd92fa00d999a94638513daf2d4aedd
Anaconda-1.5.0-Windows-x86_64.exe	280.4 MiB	2013-05-08 09:20:08	7edbe2e51b71c69e7e7a1ec01d8d83954
Anaconda-1.4.0-Linux-x86.sh	220.5 MiB	2013-03-09 16:46:53	065284c5de369c9b89dcae79e7169ce9b
Anaconda-1.4.0-Linux-x86_64.sh	286.9 MiB	2013-03-09 16:46:38	85ae8a0a6e3a41cf7845be3def36ed405
Anaconda-1.4.0-MacOSX-x86_64.sh	156.4 MiB	2013-03-09 16:46:57	e5d5dae6e93bb7df528abc19f5ed3a69c
Anaconda-1.4.0-Windows-x86.exe	210.1 MiB	2013-03-09 16:55:45	e590e45d36d3f164fcacf58cda6a3cb092
Anaconda-1.4.0-Windows-x86_64.exe	241.4 MiB	2013-03-09 16:57:09	6ff0a3bf82fdf5c6f0568d12ff030237e

## Anaconda with Python 2 on 64-bit Windows

To verify the file integrity using MD5 or SHA-256, see [cryptographic hash verification](#).

### Hashes for Anaconda2-2019.10-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1571149568.292862
time file was last modified, in human readable format	2019-10-15 09:26:08
exact file size, in bytes	432851808
file size, in human friendly format	412.8 MiB
md5	b152e6f36032ed414ad88cca9ace331a
sha256	3e09c8e95e10f077be1e1d26f26df8d6a13356449e06d7d47ddc066fbaf43

### Hashes for Anaconda2-2019.07-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1564065371.0114431
time file was last modified, in human readable format	2019-07-25 09:36:11
exact file size, in bytes	447973832
file size, in human friendly format	427.2 MiB
md5	4813b22808b4042ed54120fd0e44327a
sha256	fb7493a5c40d28ab47e54c57f025186dc26309183b21c8a0df733837e86b1

### Hashes for Anaconda2-2019.03-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1554411653.82107
time file was last modified, in human readable format	2019-04-04 16:00:53
exact file size, in bytes	615389640
file size, in human friendly format	586.9 MiB
md5	042809940fb2f60d979eac02fc4e6c82
sha256	96c21ae0d152755e8f4ac4a593da4063e0f3796064dbe25dbbad163e926f9

### Hashes for Anaconda2-2018.12-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1545419777.6148324
time file was last modified, in human readable format	2018-12-21 13:16:17
exact file size, in bytes	587793280
file size, in human friendly format	560.6 MiB
md5	10ff4176a94fcff86e6253b0cc82c782
sha256	7571d334eac3b9bd4f3e199fc5f493f0601890620c22e6d487246bde90497

### Hashes for Anaconda2-5.3.1-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1542656267.7349658
time file was last modified, in human readable format	2018-11-19 13:37:47
exact file size, in bytes	608275536
file size, in human friendly format	580.1 MiB
md5	ff29ffcd1f767cde91bab71110c00294
sha256	63b8a687cddcf462f9f61993d07ba88389c413265d3035a1b1bdb2c481592

### Hashes for Anaconda2-5.3.0-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1538081954.248261
time file was last modified, in human readable format	2018-09-27 15:59:14
exact file size, in bytes	607139640
file size, in human friendly format	579.0 MiB
md5	19fb5f9eedf834b4329dcdeac9824516
sha256	30bf9131df2314c00a9cd5e5f0b7d6184c3aec38e4068eaaafc962f6201811

## Hashes for Anaconda2-5.2.0-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1527703456.9154801
time file was last modified, in human readable format	2018-05-30 13:04:16
exact file size, in bytes	591413392
file size, in human friendly format	564.0 MiB
md5	595e427e4b625b6eab92623a28dc4e21
sha256	e5ff95332d08a7b006a5bb723e0a5124c4c4c9a9e4289afdd05941791a79e

## Hashes for Anaconda2-5.1.0-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1518707334.896789
time file was last modified, in human readable format	2018-02-15 09:08:54
exact file size, in bytes	548001744
file size, in human friendly format	522.6 MiB
md5	b16d6d6858fc7decf671ac71e6d7cfdb
sha256	3674c8d8c233dbea30842f14dc76cc3feaf4badf7d9dfe4145aa5b6679fab

## Hashes for Anaconda2-5.0.1-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.



exact time file was last modified, as Unix time stamp	1508813842.7920458
time file was last modified, in human readable format	2017-10-23 21:57:22
exact file size, in bytes	524040968
file size, in human friendly format	499.8 MiB
md5	b8d9bc02edd61af3f7ece3d07e726e91
sha256	c43f94c51623850b0c1a826710fe9c8e50b0d73708874c9cf9b6ef03806ba

### Hashes for Anaconda2-5.0.0-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1506454249.0
time file was last modified, in human readable format	2017-09-26 14:30:49
exact file size, in bytes	522426032
file size, in human friendly format	498.2 MiB
md5	8323b1d5f0b1c3fdb5b85efbb099beeb0
sha256	5fb73395cdf003613f5d44844da9870dbdc2a35cede0f928b02c38b5ee2eb

### Hashes for Anaconda2-4.4.0-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1495839202.0
time file was last modified, in human readable format	2017-05-26 17:53:22
exact file size, in bytes	451651872
file size, in human friendly format	430.7 MiB
md5	0f60aa52ef3a5d6170aeb6f7e3651f91
sha256	7a8ec1a36f385ebf28a1a8cf63b8b03ac0f7744e1531f5d359ce6a6d90391



### Hashes for Anaconda2-4.3.1-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1488838739.0
time file was last modified, in human readable format	2017-03-06 16:18:59
exact file size, in bytes	433804976
file size, in human friendly format	413.7 MiB
md5	bfd41f4de09a690f8b3525d3fb79bd2f
sha256	c0e13a756a856d7b7757b10d65bee577d8c9826317050eecec42d2e48d2ea

### Hashes for Anaconda2-4.3.0.1-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1486066808.0
time file was last modified, in human readable format	2017-02-02 14:20:08
exact file size, in bytes	432863736
file size, in human friendly format	412.8 MiB
md5	56b181af1959de40e67fb5ef50612ae2
sha256	2198e28e9e8e3c43ab72a8371e5b2d0a9aa6574391aebbc94bf768a50a57

### Hashes for Anaconda2-4.3.0-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1485548279.0
time file was last modified, in human readable format	2017-01-27 14:17:59
exact file size, in bytes	432864904
file size, in human friendly format	412.8 MiB
md5	2c02e21e542d61760c3e19bf0b3086fe
sha256	1117839746a8eabf7ed26ff311fc74e44a58e319555e306f241e04b32363a

### Hashes for Anaconda2-4.2.0-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1475009747.0
time file was last modified, in human readable format	2016-09-27 15:55:47
exact file size, in bytes	399546128
file size, in human friendly format	381.0 MiB
md5	0a30d509568724dac0ae193e139b9c37
sha256	6254b150edee53000c94e9abfc9c51a2d2e5ef3453d8e7cc7ef0a848d6d3b

### Hashes for Anaconda2-4.1.1-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1467994801.0
time file was last modified, in human readable format	2016-07-08 11:20:01
exact file size, in bytes	357765440
file size, in human friendly format	341.2 MiB
md5	1db0244dbf02579f452d1b19ce245144
sha256	7be13a69df254b86e47612c726b0b2ba9ffa35c060b4d28edb348004c1f72

## Hashes for Anaconda2-4.1.0-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1467131310.0
time file was last modified, in human readable format	2016-06-28 11:28:30
exact file size, in bytes	356677104
file size, in human friendly format	340.2 MiB
md5	6c1066a240b28dbb33e9293a97cd40f5
sha256	7a62880ff9bb7f747d70f518f024dfd1795a26d4130a20d1ff30043d05ec7

## Hashes for Anaconda2-4.0.0-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1459268099.0
time file was last modified, in human readable format	2016-03-29 11:14:59
exact file size, in bytes	350807856
file size, in human friendly format	334.6 MiB
md5	6b2ad997c42fbf58bb1b54baa5619e4f
sha256	213c7d94bdb6f0931edd31bb14ae33ab557cee52c4ac949300e512397a29e

## Hashes for Anaconda2-2.5.0-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1454535974.0
time file was last modified, in human readable format	2016-02-03 15:46:14
exact file size, in bytes	365581384
file size, in human friendly format	348.6 MiB
md5	57e42190411054333781c1208822659d
sha256	4423b43eb23184b4239abc426a564760d6ddf0187ce451468546b88931de4

### Hashes for Anaconda2-2.4.1-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1449608451.0
time file was last modified, in human readable format	2015-12-08 15:00:51
exact file size, in bytes	371393960
file size, in human friendly format	354.2 MiB
md5	733ce916c4c392367c611efd493410b0
sha256	cfb5e5539cb7f2e5807ec3d2fa2e59db3a419caa1ef8f0497516dd0c861f92

### Hashes for Anaconda2-2.4.0-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1446502941.0
time file was last modified, in human readable format	2015-11-02 16:22:21
exact file size, in bytes	406819096
file size, in human friendly format	388.0 MiB
md5	00a09d300d13c9f4754165920396625d
sha256	7a40484e58e91f62d91961c8607de586d3ef14645319c0395683e5f718255

## Hashes for Anaconda-2.3.0-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1435775710.0
time file was last modified, in human readable format	2015-07-01 13:35:10
exact file size, in bytes	350951272
file size, in human friendly format	334.7 MiB
md5	93d3d5d2aae82c175cd9ef4a570c2ab0
sha256	70b4a84e78c721bd46f3de39c75acb37d1980a3afa23cf3cef387569606f7

## Hashes for Anaconda-2.2.0-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1427315413.0
time file was last modified, in human readable format	2015-03-25 15:30:13
exact file size, in bytes	347294944
file size, in human friendly format	331.2 MiB
md5	27230171e315bcdee370ef97ef622158
sha256	1e01d7e1560668f4c05d1cfafeb59b79da1b352671dc913a5ec8b766dde12

## Hashes for Anaconda-2.1.0-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1411661231.0
time file was last modified, in human readable format	2014-09-25 11:07:11
exact file size, in bytes	384818768
file size, in human friendly format	367.0 MiB
md5	a80eea69583fcee6d3d0f6a63a900b2e
sha256	d9d7c8ed1c914312848407f08fff3d19350c20d754c8872d36ef45ce7541c

### Hashes for Anaconda-2.0.1-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1402603387.0
time file was last modified, in human readable format	2014-06-12 15:03:07
exact file size, in bytes	360443904
file size, in human friendly format	343.7 MiB
md5	b498d9bf6b266bc09507d2ef9d4b7b55
sha256	5b27e7de356312da711a19ae6a4438c1c857b9c4e357c4aa3275d014db73c

### Hashes for Anaconda-2.0.0-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1401313853.0
time file was last modified, in human readable format	2014-05-28 16:50:53
exact file size, in bytes	350647728
file size, in human friendly format	334.4 MiB
md5	9ec65c4cc0d640ff36f89193cb9e7b7d
sha256	60078f8677e62e435e5a53f1084e6f39df7f4874892b77d04fbd819033c4

### Hashes for Anaconda-1.9.2-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1396996876.0
time file was last modified, in human readable format	2014-04-08 17:41:16
exact file size, in bytes	385184016
file size, in human friendly format	367.3 MiB
md5	a610322f6752413c9b02abf72f960ff9
sha256	ef9c9b69c831210fc9000ee5482d2d98ba609d4f9e05746f93f569045ba

### Hashes for Anaconda-1.9.1-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1392930634.0
time file was last modified, in human readable format	2014-02-20 15:10:34
exact file size, in bytes	385134224
file size, in human friendly format	367.3 MiB
md5	b8a404c9f5bfd2452316db3710d2b8ef
sha256	d0c3c2faca03b3820ff8fc39688f500bd140f207aab7553c50005484ff755

### Hashes for Anaconda-1.9.0-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.



exact time file was last modified, as Unix time stamp	1392049458.0
time file was last modified, in human readable format	2014-02-10 10:24:18
exact file size, in bytes	382872112
file size, in human friendly format	365.1 MiB
md5	3c5e322e71428167e4d38725e1d92be0
sha256	265c7e849688164f7a7fe9df541be018675772f2e91be39d116e6d0e07181

### Hashes for Anaconda-1.8.0-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1383594959.0
time file was last modified, in human readable format	2013-11-04 13:55:59
exact file size, in bytes	358748424
file size, in human friendly format	342.1 MiB
md5	dccc94b5e1b77e56385a318c5c91b6d1
sha256	434c2b325a368958b66d52cee4cc710f5ea40e45657854a9b2b54dd50b9c

### Hashes for Anaconda-1.7.0-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1378678320.0
time file was last modified, in human readable format	2013-09-08 17:12:00
exact file size, in bytes	346131087
file size, in human friendly format	330.1 MiB
md5	c4e6987a83b00da8d36fc4e559df7d01
sha256	59a3667fd33f8de1ed476d7ff07917d726be51de239deaf7ce13ab277bb41



### Hashes for Anaconda-1.6.2-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1373395588.0
time file was last modified, in human readable format	2013-07-09 13:46:28
exact file size, in bytes	303973708
file size, in human friendly format	289.9 MiB
md5	80bc3fe5f8d2f83110eee775946ed3b8
sha256	641fc25c1d13e49cc030df5f4040170d123072e54b439e7097531a61cc385

### Hashes for Anaconda-1.6.1-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1372784666.0
time file was last modified, in human readable format	2013-07-02 12:04:26
exact file size, in bytes	303973712
file size, in human friendly format	289.9 MiB
md5	3e63a96cc45f665bf53fa38b18491f94
sha256	8cad320d4d6981644fbd1741bd5589d198f5e4ca1e1f66a10d57c704ee485

### Hashes for Anaconda-1.6.0-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1371843500.0
time file was last modified, in human readable format	2013-06-21 14:38:20
exact file size, in bytes	304462009
file size, in human friendly format	290.4 MiB
md5	d215a5aca9515f1875cf131b0c35d78d
sha256	6e95dc3612ed430ded28bb48fa1671b32a185c976eba905796707f9b5b44e

### Hashes for Anaconda-1.5.0-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1368022808.0
time file was last modified, in human readable format	2013-05-08 09:20:08
exact file size, in bytes	294062717
file size, in human friendly format	280.4 MiB
md5	058a62bb0fba53870b92798453e718a
sha256	7edbe2e51b71c69e7e7a1ec01d8d83954ada9e885e08adfffd624b9e1b10

### Hashes for Anaconda-1.4.0-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1362869829.0
time file was last modified, in human readable format	2013-03-09 16:57:09
exact file size, in bytes	253175221
file size, in human friendly format	241.4 MiB
md5	7e4ff5278e86cc88852abb5da453ae7a
sha256	6ff0a3bf82fdf5c6f0568d12ff030237ee90825bb0ea60e4cf3833db84753

## Anaconda with Python 3 on 64-bit Windows

To verify the file integrity using MD5 or SHA-256, see [cryptographic hash verification](#).

### Hashes for Anaconda3-2020.07-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1595524606.6399345
time file was last modified, in human readable format	2020-07-23 12:16:46
exact file size, in bytes	490200880
file size, in human friendly format	467.5 MiB
md5	7c718535a7dd89fa46b147626ada9e46
sha256	66acb9bdf7d2d5925df8762311a85ad72f57dfd340447bf00636d35a28456

### Hashes for Anaconda3-2020.02-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1583940755.8850853
time file was last modified, in human readable format	2020-03-11 10:32:35
exact file size, in bytes	488908696
file size, in human friendly format	466.3 MiB
md5	6b02c1c91049d29fc65be68f2443079a
sha256	83c2f53c7174253adcc2de7d1293a7408c37b295abbbb8feca32cb8428a26

### Hashes for Anaconda3-2019.10-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1571149637.6830847
time file was last modified, in human readable format	2019-10-15 09:27:17
exact file size, in bytes	483964816
file size, in human friendly format	461.5 MiB
md5	fa fcdbf5feb6dc3081bf07cbb8af1dbe
sha256	9e632439ed40620b8518f11469ded7316eccb489d0dfc41770f72ca2b2202

### Hashes for Anaconda3-2019.07-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1564065473.5581777
time file was last modified, in human readable format	2019-07-25 09:37:53
exact file size, in bytes	509439656
file size, in human friendly format	485.8 MiB
md5	56edfc7280fb8def19922a0296b45633
sha256	37e753801a881649ceb608449b66ff9daa35a393409c6e651e56a60c5043b

### Hashes for Anaconda3-2019.03-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1554411630.4340134
time file was last modified, in human readable format	2019-04-04 16:00:30
exact file size, in bytes	693800272
file size, in human friendly format	661.7 MiB
md5	bfb4da8555ef5b1baa064ef3f0c7b582
sha256	d2c90169879f40816eac91bec585a1f9f788016fe0a8215ca066299e4b653

### Hashes for Anaconda3-2018.12-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1545419674.9961112
time file was last modified, in human readable format	2018-12-21 13:14:34
exact file size, in bytes	644094168
file size, in human friendly format	614.3 MiB
md5	8d068f924a77e8d015906e81e91b31ab
sha256	09d84a789013d5e2bfb0148bdd9f5d69a6baa2127edabb9a8e50e77c6fc57

### Hashes for Anaconda3-5.3.1-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1542656339.6522474
time file was last modified, in human readable format	2018-11-19 13:38:59
exact file size, in bytes	663195528
file size, in human friendly format	632.5 MiB
md5	3e4d013223d8a71d0fa4d58fe5b31023
sha256	295fed5940369d4ea1e2c6d04d418619d9942c19d925921cheb941bbc5bd7

### Hashes for Anaconda3-5.3.0-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1538081960.392536
time file was last modified, in human readable format	2018-09-27 15:59:20
exact file size, in bytes	662059680
file size, in human friendly format	631.4 MiB
md5	1807a3c595ed2dab9fc7662f2cdf79fd
sha256	1083d05eeec45707940a6c7afb375a5f330d7a24a9de1e6f8d86b4f4e49be

### Hashes for Anaconda3-5.2.0-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1527703458.8495667
time file was last modified, in human readable format	2018-05-30 13:04:18
exact file size, in bytes	661987080
file size, in human friendly format	631.3 MiB
md5	62244c0382b8142743622fdc3526eda7
sha256	2672f6537e2c8a79ae9540cf3c49b18bb9ba35caec649191b5fa1e759f15b

### Hashes for Anaconda3-5.1.0-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1518707426.6260371
time file was last modified, in human readable format	2018-02-15 09:10:26
exact file size, in bytes	563168960
file size, in human friendly format	537.1 MiB
md5	83a8b1edcb21fa0ac481b23f65b604c6
sha256	7d192e58915d7e7fbfd0c987ddc4db38a22d5fc47a22db71ac5873ef9ba8a

### Hashes for Anaconda3-5.0.1-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1508866679.6710148
time file was last modified, in human readable format	2017-10-24 12:37:59
exact file size, in bytes	539829832
file size, in human friendly format	514.8 MiB
md5	3dde7dbbef158db6dc44fce495671c92
sha256	0b1ec18b7425f8c8518d6dc2fc0bc8ec2f06ba57f15727aee4731a4f98278

### Hashes for Anaconda3-5.0.0-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1506453293.0
time file was last modified, in human readable format	2017-09-26 14:14:53
exact file size, in bytes	534742736
file size, in human friendly format	510.0 MiB
md5	fee3fad608d0006afa5c7bca4de3d02b
sha256	53bd80727099b5767b9f20f99e908f9c19cea7572c14f9538dc1c8ca7ab5e



### Hashes for Anaconda3-4.4.0-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1495839334.0
time file was last modified, in human readable format	2017-05-26 17:55:34
exact file size, in bytes	458893576
file size, in human friendly format	437.6 MiB
md5	aa200a1c059a551e0ba9a5314a9554a5
sha256	ea582602541e748053df550514460426202fb4507edf9af4d7d706bc41044

### Hashes for Anaconda3-4.3.1-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1488838848.0
time file was last modified, in human readable format	2017-03-06 16:20:48
exact file size, in bytes	442630816
file size, in human friendly format	422.1 MiB
md5	16f337426454eac463fd0d41c6d2bbb8
sha256	65ce6d7c09884935fee9eb8d318b30e95f75f6efe8a8ba221df282cf22c39

### Hashes for Anaconda3-4.3.0.1-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.



exact time file was last modified, as Unix time stamp	1486066930.0
time file was last modified, in human readable format	2017-02-02 14:22:10
exact file size, in bytes	441680784
file size, in human friendly format	421.2 MiB
md5	07ea8c5a2306ac8fabf3902bd6623787
sha256	b5954bf7da9a92d351d905dfdfa0e7bee1cfd8c74ed0532a29416849a92b

### Hashes for Anaconda3-4.3.0-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1485548381.0
time file was last modified, in human readable format	2017-01-27 14:19:41
exact file size, in bytes	441681320
file size, in human friendly format	421.2 MiB
md5	137043b3f9860519967759fc8ea76514
sha256	324568dbef777a6ac8a25c1e8ae1975ffbd95bb621dc91cb3869606cc5924

### Hashes for Anaconda3-4.2.0-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1475009841.0
time file was last modified, in human readable format	2016-09-27 15:57:21
exact file size, in bytes	410431504
file size, in human friendly format	391.4 MiB
md5	0ca5ef4dcfe84376aad073bbb3f8db00
sha256	84e30c99833e142a27fc9ee2c748b03f16c8b1a3ced765024d5db4e68bfbf

### Hashes for Anaconda3-4.1.1-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1467994877.0
time file was last modified, in human readable format	2016-07-08 11:21:17
exact file size, in bytes	370055720
file size, in human friendly format	352.9 MiB
md5	a3be394f8274c391148efdfbc63e8ca4
sha256	b4889513dc574f9d6f96db089315d69d293f8b17635da4d2e6eee118dc105

### Hashes for Anaconda3-4.1.0-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1467131313.0
time file was last modified, in human readable format	2016-06-28 11:28:33
exact file size, in bytes	368509992
file size, in human friendly format	351.4 MiB
md5	50fe73c084b91e55837f4d090809a35e
sha256	9acde60b591233452dba23ac15800f39f2de9b7a180a89916dffa3b6edb326

### Hashes for Anaconda3-4.0.0-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1459268182.0
time file was last modified, in human readable format	2016-03-29 11:16:22
exact file size, in bytes	362171448
file size, in human friendly format	345.4 MiB
md5	a6b7a787c6c574867cee3f2d12ecfc50
sha256	39bf467cd142c1f8fdb7d673fdea273d87ec011af1dbf4b4804c2b0994c61

### Hashes for Anaconda3-2.5.0-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1454536060.0
time file was last modified, in human readable format	2016-02-03 15:47:40
exact file size, in bytes	378634984
file size, in human friendly format	361.1 MiB
md5	6572ceba288b6f145e9b3d0c02a5281c
sha256	4728044d77da715e48d4c95d7f2e3c2a02c4ea7de9d2c69accc851bf294500

### Hashes for Anaconda3-2.4.1-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1449608455.0
time file was last modified, in human readable format	2015-12-08 15:00:55
exact file size, in bytes	381329960
file size, in human friendly format	363.7 MiB
md5	17c562ff74676f004ba8dd029718c09c
sha256	21d155a4b43805042499b8d008835bcd9c3a45fe53d1183de9e0a937170

### Hashes for Anaconda3-2.4.0-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1446502944.0
time file was last modified, in human readable format	2015-11-02 16:22:24
exact file size, in bytes	411312288
file size, in human friendly format	392.3 MiB
md5	bc74a4fb4e8455e8e7c61b7f100e3bac
sha256	beaa1b803dd30022c6aca1c6f05182beaea3cd8a17130f73906851269dfe0

### Hashes for Anaconda3-2.3.0-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1435775714.0
time file was last modified, in human readable format	2015-07-01 13:35:14
exact file size, in bytes	352774600
file size, in human friendly format	336.4 MiB
md5	ad4abc78581f6fa68b7f7fc342003f6c
sha256	bd693b61cf191666ae0473327f3c15bcf32b7d09961a0aa0284c10e7ea724

### Hashes for Anaconda3-2.2.0-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1427315550.0
time file was last modified, in human readable format	2015-03-25 15:32:30
exact file size, in bytes	348764152
file size, in human friendly format	332.6 MiB
md5	cd7dae4fd482c94156b4d60bf21d8771
sha256	28c5a13b27a9dbd57c7c633316c5f4beb0cd32cf19b148debd1a81eac86f3

### Hashes for Anaconda3-2.1.0-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1411661463.0
time file was last modified, in human readable format	2014-09-25 11:11:03
exact file size, in bytes	380970064
file size, in human friendly format	363.3 MiB
md5	5d559802f3c699a885c66ea6064f5440
sha256	ea4059469b1820069f62bd6c256def6259d801d7382be70523e081c5adbec

### Hashes for Anaconda3-2.0.1-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1402603215.0
time file was last modified, in human readable format	2014-06-12 15:00:15
exact file size, in bytes	335317304
file size, in human friendly format	319.8 MiB
md5	139c6d32c484e0886c6cbe530b9fbd4c
sha256	e2b6d3d6a9e378fc0d0dd63342417c02bdf6a9676040e05ff8017396d6449

## Hashes for Anaconda3-2.0.0-Windows-x86\_64.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1401228102.0
time file was last modified, in human readable format	2014-05-27 17:01:42
exact file size, in bytes	325992440
file size, in human friendly format	310.9 MiB
md5	35fb9536ccb1aca93ec34714e8e69a5b
sha256	a8046fc82da7463ef53cdeaba97c72433c37b211c50fa87f1bc19bdfe5163

## Anaconda with Python 2 on 32-bit Windows

To verify the file integrity using MD5 or SHA-256, see [cryptographic hash verification](#).

## Hashes for Anaconda2-2019.10-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1571149575.2411845
time file was last modified, in human readable format	2019-10-15 09:26:15
exact file size, in bytes	372892232
file size, in human friendly format	355.6 MiB
md5	0057a4b9d432ef0b78badee4f74a54a0
sha256	b4731acd02f96923922d995bb16984d71b4a934b7af6737984dd9eb5d8cc6

## Hashes for Anaconda2-2019.07-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1564065409.7452314
time file was last modified, in human readable format	2019-07-25 09:36:49
exact file size, in bytes	378051296
file size, in human friendly format	360.5 MiB
md5	38d96b86f4266a125bf3180c225292d9
sha256	1bd676a51ccdee57c2c01a2bc87fa8b1bd48cf7a6c0b16c44a241374f798f

### Hashes for Anaconda2-2019.03-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1554411643.769616
time file was last modified, in human readable format	2019-04-04 16:00:43
exact file size, in bytes	516464832
file size, in human friendly format	492.5 MiB
md5	4b055a00f4f99352bd29db7a4f691f6e
sha256	76be4b3d1f7a1207b786cbb54b3ed526126ee0d4facf41e662b4136224581

### Hashes for Anaconda2-2018.12-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.



exact time file was last modified, as Unix time stamp	1545419787.3302794
time file was last modified, in human readable format	2018-12-21 13:16:27
exact file size, in bytes	480837024
file size, in human friendly format	458.6 MiB
md5	f123fda0ec8928bb7d55d1ca72c0d784
sha256	d75d51c8f9a7c345128805a55db3856f6999dd6aa11f31c0009c640fe0e8d

### Hashes for Anaconda2-5.3.1-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1542656312.8510244
time file was last modified, in human readable format	2018-11-19 13:38:32
exact file size, in bytes	480313024
file size, in human friendly format	458.1 MiB
md5	7286587bcfb6a5a164d70fe02c1968d5
sha256	59680be839aa8b58477a24519a7575756bead26b300eb7aae8c82086781bd

### Hashes for Anaconda2-5.3.0-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1538081955.8443325
time file was last modified, in human readable format	2018-09-27 15:59:15
exact file size, in bytes	479430240
file size, in human friendly format	457.2 MiB
md5	45a5880d1a56aa8e444b43edcc5e6aa2
sha256	f18bdb9a38e5c444a3cb79c5c6bc927fbcd863683b4197713337216af7300



## Hashes for Anaconda2-5.2.0-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1527703457.7225163
time file was last modified, in human readable format	2018-05-30 13:04:17
exact file size, in bytes	464889960
file size, in human friendly format	443.4 MiB
md5	4a3729b14c2d3fccd3a050821679c702
sha256	2b81916c477e64db917821bb48a97000fad78cd1041022b343cec3cebf9e9

## Hashes for Anaconda2-5.1.0-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1518707335.7558289
time file was last modified, in human readable format	2018-02-15 09:08:55
exact file size, in bytes	440226936
file size, in human friendly format	419.8 MiB
md5	a09347a53e04a15ee965300c2b95dfde
sha256	fa78c71d88b01e6367f0c3cbd23da1f82e86e02088b0d281437789bfefba59

## Hashes for Anaconda2-5.0.1-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1508864894.4238315
time file was last modified, in human readable format	2017-10-24 12:08:14
exact file size, in bytes	422964800
file size, in human friendly format	403.4 MiB
md5	623e8d9ca2270cb9823a897dd0e9bfce
sha256	1a50fac8644f2128e318337b218299e53e92ee20ddaf47911ff2be22255c6

### Hashes for Anaconda2-5.0.0-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1506461109.7266462
time file was last modified, in human readable format	2017-09-26 16:25:09
exact file size, in bytes	421720568
file size, in human friendly format	402.2 MiB
md5	bd3ed48229db828cef4c6b371a8759d1
sha256	078551cfb0df72779897026724f375671e12a5fd384cabeaede5cc325cac1

### Hashes for Anaconda2-4.4.0-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1495839135.0
time file was last modified, in human readable format	2017-05-26 17:52:15
exact file size, in bytes	371653096
file size, in human friendly format	354.4 MiB
md5	51f14d30b08b82cd5e44bbb6b0d63349
sha256	0decd861f8839fdf2cbe4fa306c127f69e50b54374e56d7960ba5217087bf

### Hashes for Anaconda2-4.3.1-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1488838692.0
time file was last modified, in human readable format	2017-03-06 16:18:12
exact file size, in bytes	355485664
file size, in human friendly format	339.0 MiB
md5	4f5ed9917f8c2d2ae2e027e45a85fe8b
sha256	fc363cea3c321c17b43a0bf2137aa845fef349c534fcf511dc285ebb8ae57

### Hashes for Anaconda2-4.3.0.1-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1486066745.0
time file was last modified, in human readable format	2017-02-02 14:19:05
exact file size, in bytes	354548480
file size, in human friendly format	338.1 MiB
md5	4bfff7044ecf0229a0974ba8429520cad
sha256	863702665aa2b55ede2103a8ca7d26435efef614e9d201909c21ec572878f

### Hashes for Anaconda2-4.3.0-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1485548226.0
time file was last modified, in human readable format	2017-01-27 14:17:06
exact file size, in bytes	354550816
file size, in human friendly format	338.1 MiB
md5	ffd6296dc4b359684c54ce6f3d10e144
sha256	a98767acefdeda02fe8d3ef9dadda1a3439fec110ede9bf5d0e359be76ac1

### Hashes for Anaconda2-4.2.0-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1475009690.0
time file was last modified, in human readable format	2016-09-27 15:54:50
exact file size, in bytes	339829096
file size, in human friendly format	324.1 MiB
md5	f4f12af8811759e56464eef5a484963d
sha256	a97ca79cb771568d051ef7773d25c0dda407c63e7ec91305f35dff790aeda

### Hashes for Anaconda2-4.1.1-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1467994801.0
time file was last modified, in human readable format	2016-07-08 11:20:01
exact file size, in bytes	299852168
file size, in human friendly format	286.0 MiB
md5	b319d6867c67723ba74aef4f9dd35f82
sha256	4708d73952a0a8040bf1594ea42027a30e9bacb4d6760cc5d3e4414b6bfd9

## Hashes for Anaconda2-4.1.0-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1467131311.0
time file was last modified, in human readable format	2016-06-28 11:28:31
exact file size, in bytes	298958864
file size, in human friendly format	285.1 MiB
md5	ec44ea5c92542ca0112a6be79aff79bf
sha256	c4ad4eefdfbf6d838424c62c8b524352d8b8e4752382b0a09e9d8b7e9e44b

## Hashes for Anaconda2-4.0.0-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1459268100.0
time file was last modified, in human readable format	2016-03-29 11:15:00
exact file size, in bytes	294659856
file size, in human friendly format	281.0 MiB
md5	9fb16479d7eb3dd63cf4ad6704622c8a
sha256	f8185ad2fe89356ab001e55a463b663bcb9e7699ab7f7c1775a98d5332db

## Hashes for Anaconda2-2.5.0-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1454535921.0
time file was last modified, in human readable format	2016-02-03 15:45:21
exact file size, in bytes	310590880
file size, in human friendly format	296.2 MiB
md5	506c08af8932332303561e822f285d9b
sha256	a0336729f0400ff12fe18a7d5e20c3f9b45f14cd07fe654029daa1ec611e2

### Hashes for Anaconda2-2.4.1-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1449608452.0
time file was last modified, in human readable format	2015-12-08 15:00:52
exact file size, in bytes	301790720
file size, in human friendly format	287.8 MiB
md5	0e6cdba39322c28240f4dceaf7bf72f8
sha256	65fb15559b0ddb5055c110ecdb84823a6fbc8d3938932fbfa0110bb6d3395

### Hashes for Anaconda2-2.4.0-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1446502941.0
time file was last modified, in human readable format	2015-11-02 16:22:21
exact file size, in bytes	337056800
file size, in human friendly format	321.4 MiB
md5	5a5225bd2f74a5be9ef840ae8e62c82a
sha256	2a05db81a0fe4155bc2dd83a689294d3ac7fa1d1a68a5ec6bdafaac9140d4

## Hashes for Anaconda-2.3.0-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1435775711.0
time file was last modified, in human readable format	2015-07-01 13:35:11
exact file size, in bytes	290903240
file size, in human friendly format	277.4 MiB
md5	7efff6446dcb06e4c44607539c953689
sha256	3b60ddfb84533539e767889706bd64298a73d07a7bfe944a3c5c7f951e395

## Hashes for Anaconda-2.2.0-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1427315328.0
time file was last modified, in human readable format	2015-03-25 15:28:48
exact file size, in bytes	287557144
file size, in human friendly format	274.2 MiB
md5	32246b48658d4c3faeef425cec64a131
sha256	247e8e7e386224a3df736ffe607596546f4bdd64b44a945fd831db5603782

## Hashes for Anaconda-2.1.0-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.



exact time file was last modified, as Unix time stamp	1411661103.0
time file was last modified, in human readable format	2014-09-25 11:05:03
exact file size, in bytes	325285048
file size, in human friendly format	310.2 MiB
md5	4b4303ff83c94f6af128fe43c202756b
sha256	c39193c9018a9c1e9e8f3c1d2692ac635133e9b68e72d7864c75841086337

### Hashes for Anaconda-2.0.1-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1402603407.0
time file was last modified, in human readable format	2014-06-12 15:03:27
exact file size, in bytes	301248280
file size, in human friendly format	287.3 MiB
md5	579ed15c9599cc49bc073dbbe8870021
sha256	be5a341bc3f9bf8386c686cfc9ad253f3074670c96f130b345b731370ce89

### Hashes for Anaconda-2.0.0-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1401313862.0
time file was last modified, in human readable format	2014-05-28 16:51:02
exact file size, in bytes	291661544
file size, in human friendly format	278.2 MiB
md5	c3b147e0d5f6d708e884ee03d8856040
sha256	d86cc7100b4c04ec25768267b81798f70a8563a2bdb6dacfe6ec7e45bfbb



## Hashes for Anaconda-1.9.2-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1396996765.0
time file was last modified, in human readable format	2014-04-08 17:39:25
exact file size, in bytes	326939720
file size, in human friendly format	311.8 MiB
md5	7217cfa5c5b45de3e683ff09a10ce35b
sha256	fe005aeacd1345b856c73d640856b79ed94a6694245ea8df8cbf94aa7bac7

## Hashes for Anaconda-1.9.1-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1392930522.0
time file was last modified, in human readable format	2014-02-20 15:08:42
exact file size, in bytes	326889840
file size, in human friendly format	311.7 MiB
md5	5404da4f89dca1a4f5c9efd5ae6fbc5a
sha256	46cbe29a30cfcd56018f7f69a35525708f2d14211a613e7344f91ad4171a8

## Hashes for Anaconda-1.9.0-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1392049492.0
time file was last modified, in human readable format	2014-02-10 10:24:52
exact file size, in bytes	323587016
file size, in human friendly format	308.6 MiB
md5	02496bcd853574628adfbeldefe5c40f
sha256	2c8c58cf21e537e930535df5a0e8fd4b6d60d4dbe87f13b5964bf2f5f4d27

### Hashes for Anaconda-1.8.0-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1383594854.0
time file was last modified, in human readable format	2013-11-04 13:54:14
exact file size, in bytes	304130696
file size, in human friendly format	290.0 MiB
md5	3b3bbbc639556499d62342f653443553a
sha256	719bc0987be80b46f9c6b745822777fa1f0cb7386ff746fa8e71763bfd997

### Hashes for Anaconda-1.7.0-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1378678223.0
time file was last modified, in human readable format	2013-09-08 17:10:23
exact file size, in bytes	294250542
file size, in human friendly format	280.6 MiB
md5	91a6398f63a8cc6fa3db3a1e9195b3bf
sha256	b434776dfeac98f37328c6e538f5a1a53199e0c6ca2ef3a39cb3cd2e64db2

## Hashes for Anaconda-1.6.2-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1373395498.0
time file was last modified, in human readable format	2013-07-09 13:44:58
exact file size, in bytes	256262643
file size, in human friendly format	244.4 MiB
md5	5d9ca457b14fe9af5f8f5e338f9db9e2
sha256	0873576bbd979e3b7859808bccc2311edaea3d34f4d6ed1f6b44b1ba1cf1a

## Hashes for Anaconda-1.6.1-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1372784579.0
time file was last modified, in human readable format	2013-07-02 12:02:59
exact file size, in bytes	256262655
file size, in human friendly format	244.4 MiB
md5	3cdf41952ad09f00ab03cca5a289fe50
sha256	a823dc7688cec49499bb5922783377c262cbf456830ff8db7c0d4018a2321

## Hashes for Anaconda-1.6.0-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1371843406.0
time file was last modified, in human readable format	2013-06-21 14:36:46
exact file size, in bytes	256780921
file size, in human friendly format	244.9 MiB
md5	156a48269ae6b2bfc0bede9c3ff719cc
sha256	3dc2588557455484b3b38feb14fa95d941de732e06678365860cd4961c19f

### Hashes for Anaconda-1.5.0-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1368022724.0
time file was last modified, in human readable format	2013-05-08 09:18:44
exact file size, in bytes	247436755
file size, in human friendly format	236.0 MiB
md5	871f9f4f2321ceded8d25ff83f24e70da
sha256	d3dd92fa00d999a94638513daf2d4aeced15a387b820eb08b1907387a4f2e8

### Hashes for Anaconda-1.4.0-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1362869745.0
time file was last modified, in human readable format	2013-03-09 16:55:45
exact file size, in bytes	220256092
file size, in human friendly format	210.1 MiB
md5	797f4a28462db075de4d21e7977f32a5
sha256	e590e45d36d3f164fcacf58cda6a3cb09252a502af5942e0909324b394710f

## Anaconda with Python 3 on 32-bit Windows

To verify the file integrity using MD5 or SHA-256, see [cryptographic hash verification](#).

### Hashes for Anaconda3-2020.07-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1595524611.9741752
time file was last modified, in human readable format	2020-07-23 12:16:51
exact file size, in bytes	416619544
file size, in human friendly format	397.3 MiB
md5	aa7dcf4d02baa25d14baf5728e29d067
sha256	19803e5ccc357b57051cf7fa272e6b499dfedf13790778dc24af302f894e3b

### Hashes for Anaconda3-2020.02-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1583940778.6121256
time file was last modified, in human readable format	2020-03-11 10:32:58
exact file size, in bytes	443796296
file size, in human friendly format	423.2 MiB
md5	64ae8d0e5095b9a878d4522db4ce751e
sha256	d13381d6145c47755b198662af8a5f412836adecdb68627bc297be6738a3b

### Hashes for Anaconda3-2019.10-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1571149570.2669535
time file was last modified, in human readable format	2019-10-15 09:26:10
exact file size, in bytes	429475496
file size, in human friendly format	409.6 MiB
md5	0e71632df6a17f625c1103b34f66e8ba
sha256	05e6738919673a6d57b5895b8b4df0b7e3f4d7ed0e30faf9c99f1b7d3399e9

### Hashes for Anaconda3-2019.07-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1564065446.9519494
time file was last modified, in human readable format	2019-07-25 09:37:26
exact file size, in bytes	438674400
file size, in human friendly format	418.4 MiB
md5	861c83778458be287f4739ef89413cce
sha256	3d26ddf9ddb2287822a14ac1da3359a0db6ceb302b57edb9fcc69061f3927

### Hashes for Anaconda3-2019.03-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1554411628.9449463
time file was last modified, in human readable format	2019-04-04 16:00:28
exact file size, in bytes	572204080
file size, in human friendly format	545.7 MiB
md5	f1f636e5d34d129b6b996ff54f4a05b1
sha256	03d94f55c4c5e1187382ff414c78e66244893170fa7aacd0deb71536b7a92

### Hashes for Anaconda3-2018.12-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1545419592.008293
time file was last modified, in human readable format	2018-12-21 13:13:12
exact file size, in bytes	534439744
file size, in human friendly format	509.7 MiB
md5	dc26da1eeae5cc78121b1d3f80a6e9c
sha256	3f2955c1874ca452b985627a10859f6906eb21d4f6a4c055b78049cf6822b

### Hashes for Anaconda3-5.3.1-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1542656394.173735
time file was last modified, in human readable format	2018-11-19 13:39:54
exact file size, in bytes	534242616
file size, in human friendly format	509.5 MiB
md5	52d9041d33c0134dd3824e6c15b458c4
sha256	a028d0550bf307c69af7c3210f487e23004fcb6384f94523e216cc8021390



### Hashes for Anaconda3-5.3.0-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1538082005.3295457
time file was last modified, in human readable format	2018-09-27 16:00:05
exact file size, in bytes	533359800
file size, in human friendly format	508.7 MiB
md5	72e4f7bf75eb46c60f496d326631fddd
sha256	1dceb687efbf5a609a66d19dc2528ef78a54439a74c98b239041744174c6a

### Hashes for Anaconda3-5.2.0-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1527703459.8546116
time file was last modified, in human readable format	2018-05-30 13:04:19
exact file size, in bytes	530914888
file size, in human friendly format	506.3 MiB
md5	285387e7b6ea81edba98c011922e235a
sha256	64305a4c0041aaf4a3fd0fee4466d7b7f238fddd9e44a4c8c10f5fa059e82

### Hashes for Anaconda3-5.1.0-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.



exact time file was last modified, as Unix time stamp	1518707428.264113
time file was last modified, in human readable format	2018-02-15 09:10:28
exact file size, in bytes	456610264
file size, in human friendly format	435.5 MiB
md5	7a2291ab99178a4cdec530861494531f
sha256	7a05da21fd592991d181ac8467faac51345fb64acca6553609b53c9825e5e

### Hashes for Anaconda3-5.0.1-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1508866630.5278003
time file was last modified, in human readable format	2017-10-24 12:37:10
exact file size, in bytes	440867256
file size, in human friendly format	420.4 MiB
md5	9d2fffb0aac1f8a72ef4a5c535f3891f2
sha256	9edc3012324c9c8c9aa5257688bd793277ee25bc99cfffcd8da6610b5f45585

### Hashes for Anaconda3-5.0.0-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1506461112.5017715
time file was last modified, in human readable format	2017-09-26 16:25:12
exact file size, in bytes	436033392
file size, in human friendly format	415.8 MiB
md5	4a48ded89f15b4a2e39ffa69f3532df2
sha256	a0d5d8e328b1d3a1ed921cadeecda659c49b6042980558f5c5f491e884bf8

### Hashes for Anaconda3-4.4.0-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1495839261.0
time file was last modified, in human readable format	2017-05-26 17:54:21
exact file size, in bytes	379794600
file size, in human friendly format	362.2 MiB
md5	c7a66350b79354773dabbbef6f58a3af
sha256	37afe00b8305cc09b7bd8dd07f65cec3f4e1534966c275eb55df7c91fb660

### Hashes for Anaconda3-4.3.1-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1488838786.0
time file was last modified, in human readable format	2017-03-06 16:19:46
exact file size, in bytes	365005040
file size, in human friendly format	348.1 MiB
md5	27fa7486dfe82cf31642eb355b9a184f
sha256	adf322f49542cf509d4f72152cea24e54edfb4ff279ba3ab19582a5f27461

### Hashes for Anaconda3-4.3.0.1-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1486066862.0
time file was last modified, in human readable format	2017-02-02 14:21:02
exact file size, in bytes	364057456
file size, in human friendly format	347.2 MiB
md5	5dd0a8b09a5eb6c9d002dc26d6f31492
sha256	7f8ffce6b2c3a968ce19171c9dc332dec61741113f7cac4b52953596f9e20

### Hashes for Anaconda3-4.3.0-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1485548325.0
time file was last modified, in human readable format	2017-01-27 14:18:45
exact file size, in bytes	364059456
file size, in human friendly format	347.2 MiB
md5	ae7ec9752cf81c01983fcf0ddf8d7cc2
sha256	4a5dfea30b926074b4d6e0f1cea3e9765799fd33532b4347fa0d3d9aaacf

### Hashes for Anaconda3-4.2.0-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1475009790.0
time file was last modified, in human readable format	2016-09-27 15:56:30
exact file size, in bytes	349560232
file size, in human friendly format	333.4 MiB
md5	96e5fe052b22d667da9360fb4edce363
sha256	e7b79a9886da3f840b52882c47ecab3eda0c97505019c1f8f0c8b7eb15c2d

### Hashes for Anaconda3-4.1.1-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1467994878.0
time file was last modified, in human readable format	2016-07-08 11:21:18
exact file size, in bytes	308116424
file size, in human friendly format	293.8 MiB
md5	39bd047c2169a9d072e98403f487c9e8
sha256	224e3dd90850651ae0d1c9216b4c317d1d553d8c118a83c9b7e315daf85f

### Hashes for Anaconda3-4.1.0-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1467131314.0
time file was last modified, in human readable format	2016-06-28 11:28:34
exact file size, in bytes	306794104
file size, in human friendly format	292.6 MiB
md5	2f96e23dd2e5f04f9a5059b8ef5d7fd2
sha256	4f444ed9400505e822bb475e986800fac058ef6f23298c2b00d285d05df0a

### Hashes for Anaconda3-4.0.0-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1459268182.0
time file was last modified, in human readable format	2016-03-29 11:16:22
exact file size, in bytes	296840248
file size, in human friendly format	283.1 MiB
md5	ae5c9ba0c6f4639fbf94848f81c3d4b4
sha256	b5a31a9d130a40c3110c0592a6c8fbd43a51522e32fdddf20afe15595db80

### Hashes for Anaconda3-2.5.0-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1454536013.0
time file was last modified, in human readable format	2016-02-03 15:46:53
exact file size, in bytes	310656088
file size, in human friendly format	296.3 MiB
md5	f7ce22122319026697cc8e7dda80300b
sha256	4a3441aaaa269d06f39e1430155f9f25a8a24122cf48b9fc6bbdccb0e96a82

### Hashes for Anaconda3-2.4.1-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1449608456.0
time file was last modified, in human readable format	2015-12-08 15:00:56
exact file size, in bytes	313632120
file size, in human friendly format	299.1 MiB
md5	78eef53e753cf9a72babe06c374db8ed
sha256	dfe50d13473547b5230f6194dfe6bdf961a8b7f5e3c22edef8c7788194b7

### Hashes for Anaconda3-2.4.0-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1446502945.0
time file was last modified, in human readable format	2015-11-02 16:22:25
exact file size, in bytes	331748568
file size, in human friendly format	316.4 MiB
md5	0d3b78e2a4747d5975097c47129c0e70
sha256	a69a9fe00ce337b0cfd7d024b79ba5141cd04b1d51982196658df26c0d370

### Hashes for Anaconda3-2.3.0-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1435775715.0
time file was last modified, in human readable format	2015-07-01 13:35:15
exact file size, in bytes	294752872
file size, in human friendly format	281.1 MiB
md5	8edec318e2957a934bd99a6062ddebd9
sha256	02d5f84da308f96d1a252a6669f3ca91e125c011d1b89ae33f05f6ebe4903

### Hashes for Anaconda3-2.2.0-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1427315479.0
time file was last modified, in human readable format	2015-03-25 15:31:19
exact file size, in bytes	291166920
file size, in human friendly format	277.7 MiB
md5	7c49a4e76e1c383038c4a1e8c4ac506f
sha256	20c46fff048fb313aaf1a49171c1a7b96a42f5be09e1e1e7052800dcec7ac

### Hashes for Anaconda3-2.1.0-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1411661341.0
time file was last modified, in human readable format	2014-09-25 11:09:01
exact file size, in bytes	323724400
file size, in human friendly format	308.7 MiB
md5	a2392f068d550bee23673529734ef5d4
sha256	8ffa252aa2b4f63889888ae85a81626ce952a1f9ac20d4c065070514acfac

### Hashes for Anaconda3-2.0.1-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1402603227.0
time file was last modified, in human readable format	2014-06-12 15:00:27
exact file size, in bytes	278631456
file size, in human friendly format	265.7 MiB
md5	cbf8ff3b86731df7225bd2f7fb2af7f6
sha256	b08803296d7439413d590fd1f967b20127916c8d766802a27badc15a3a81b



## Hashes for Anaconda3-2.0.0-Windows-x86.exe

All installer files are available at <https://repo.anaconda.com/archive/> .

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1401227953.0
time file was last modified, in human readable format	2014-05-27 16:59:13
exact file size, in bytes	269399872
file size, in human friendly format	256.9 MiB
md5	1fd12fc8c5c3defcfd3a0bee6f5129fa
sha256	37986ce4c104ed3c82838de74b3a4de17918cc2f408235b9de9d4283d3a55

## Graphical installers for Anaconda with Python 2 on macOS

To verify the file integrity using MD5 or SHA-256, see [cryptographic hash verification](#).

## Hashes for Anaconda2-2019.10-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/> .

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1571149650.1876655
time file was last modified, in human readable format	2019-10-15 09:27:30
exact file size, in bytes	666625158
file size, in human friendly format	635.7 MiB
md5	67dba3993ee14938fc4acd57cef60e87
sha256	d82b6aa37b41782b7823ff712b0899374cf2ac4f87e0ccf85d0a79089ecb6

## Hashes for Anaconda2-2019.07-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/> .

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.



If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1564065424.138896
time file was last modified, in human readable format	2019-07-25 09:37:04
exact file size, in bytes	664854967
file size, in human friendly format	634.1 MiB
md5	10a47bc056e166569ed805455d04aaed
sha256	7f8a0defa2905bd5e3ca679d6772c896befe2fcf27cb3d6dfc211e596796a

### Hashes for Anaconda2-2019.03-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1554411668.611738
time file was last modified, in human readable format	2019-04-04 16:01:08
exact file size, in bytes	654629979
file size, in human friendly format	624.3 MiB
md5	f45d327c921ec856da31494fb907b75b
sha256	4e335d60fc9dcfb31caee809143352e28d49e4b2df93a6eed97ee5a97045

### Hashes for Anaconda2-2018.12-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1545419670.279894
time file was last modified, in human readable format	2018-12-21 13:14:30
exact file size, in bytes	671854049
file size, in human friendly format	640.7 MiB
md5	c2bfeef310714501a59fd58166e6393d
sha256	f07fb39c41f9cc7839adababdece209d9da209a935418082f9a6270e9e56e

### Hashes for Anaconda2-5.3.1-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1542656258.683553
time file was last modified, in human readable format	2018-11-19 13:37:38
exact file size, in bytes	658971672
file size, in human friendly format	628.4 MiB
md5	d6139f371aa6cf81c3f002ecdd09b748
sha256	7dc614e281df33f09fa006b245a955b94883d37fdecea6bbdaee18ee42147

### Hashes for Anaconda2-5.3.0-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1538081952.1701682
time file was last modified, in human readable format	2018-09-27 15:59:12
exact file size, in bytes	658824275
file size, in human friendly format	628.3 MiB
md5	8e02050e148d48a31b99994d906900fb
sha256	834c221b413bdcbce434f0a3008511f5bd5532d6b3e7f482d03c11bd0dc8

### Hashes for Anaconda2-5.2.0-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1527703532.6788743
time file was last modified, in human readable format	2018-05-30 13:05:32
exact file size, in bytes	646731039
file size, in human friendly format	616.8 MiB
md5	2836c839d29be8d9569a715f4c631a3b
sha256	f7695a3571eb8e8ae71fe9f413c36f57c92bc8882174c0dbf778e17550ff3

### Hashes for Anaconda2-5.1.0-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1518707332.6606853
time file was last modified, in human readable format	2018-02-15 09:08:52
exact file size, in bytes	616553453
file size, in human friendly format	588.0 MiB
md5	4f9c197dfe6d3dc7e50a8611b4d3cfa2
sha256	edbe9ef1ee5cfe62e131d7650e07c031ab14fd0e8bd12c15a095b73039eb8

### Hashes for Anaconda2-5.0.1-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1508806872.3056438
time file was last modified, in human readable format	2017-10-23 20:01:12
exact file size, in bytes	590135749
file size, in human friendly format	562.8 MiB
md5	46fc99d1cf1e27f3b2a3eb63fee1a532
sha256	22350fe830e6786a263d7727e537f066b13fd9f4646982796bd20248da3f3

### Hashes for Anaconda2-5.0.0-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1506461108.192577
time file was last modified, in human readable format	2017-09-26 16:25:08
exact file size, in bytes	588579426
file size, in human friendly format	561.3 MiB
md5	8a2bbf7eb66290eb0bc82963056fb96c
sha256	3ee5cfe80d51685d6f374f83a9b76fa7ecbf7dc1a20f49a506e963641f2e1

### Hashes for Anaconda2-4.4.0-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1495841768.0
time file was last modified, in human readable format	2017-05-26 18:36:08
exact file size, in bytes	459233116
file size, in human friendly format	438.0 MiB
md5	d2d5d213764a0c849eb1d53acba0d418
sha256	e5acf026892eaebb055e6317af96f295d39cf1d1a06ce6a1c6ca154ae3cab

### Hashes for Anaconda2-4.3.1-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1488839178.0
time file was last modified, in human readable format	2017-03-06 16:26:18
exact file size, in bytes	439742086
file size, in human friendly format	419.4 MiB
md5	1961c7158bf89f4daf5b7a7d4f265075
sha256	f5d950451c038f9a7ca80d4036b6a8152c35d48fee685df3de486729dbae0

### Hashes for Anaconda2-4.3.0-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1485548783.0
time file was last modified, in human readable format	2017-01-27 14:26:23
exact file size, in bytes	438746148
file size, in human friendly format	418.4 MiB
md5	899e90455db3120d584b2d4961c4eede
sha256	3e1d1026d2c0b87213a8b4a5f28431060b0cfe5cdc8a368b39248dbb66b53

### Hashes for Anaconda2-4.2.0-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1476750791.0
time file was last modified, in human readable format	2016-10-17 19:33:11
exact file size, in bytes	423495522
file size, in human friendly format	403.9 MiB
md5	cd2ccc991b7f1503335367d80d0317b0
sha256	4a74d34c3a3a82df31673ab49497816b03547bab7054525fcd92eef63c8bc

### Hashes for Anaconda2-4.1.1-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1467994799.0
time file was last modified, in human readable format	2016-07-08 11:19:59
exact file size, in bytes	361721748
file size, in human friendly format	345.0 MiB
md5	e88beae19868dc01fae908dd1e067bda
sha256	879385461cc65bd9dbf9639bbf4471ecf1713611617eda8d3a05f33a45682

### Hashes for Anaconda2-4.1.0-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1467131309.0
time file was last modified, in human readable format	2016-06-28 11:28:29
exact file size, in bytes	360909420
file size, in human friendly format	344.2 MiB
md5	b2e2a6ee2fc2436a099ed0a3cc5e8fda
sha256	a97840be50d8c86b28caf8be1786bbe7485770b14501911e3e7331d33f2a3

### Hashes for Anaconda2-4.0.0-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1459268097.0
time file was last modified, in human readable format	2016-03-29 11:14:57
exact file size, in bytes	355703551
file size, in human friendly format	339.2 MiB
md5	7c4e4a25a38106d50dc3bc25a7a3009e
sha256	242691c7dc9e20143d7620fd9e0cc344fec7a2a534d1dba5f3b6522f04648

### Hashes for Anaconda2-2.5.0-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1454536531.0
time file was last modified, in human readable format	2016-02-03 15:55:31
exact file size, in bytes	385762781
file size, in human friendly format	367.9 MiB
md5	3256a5000b44e4fec1466e509aa641e6
sha256	0f546ed4f388299824e98a31ca9e3fe9823a49a2143d1cbd982caeb536e3c

### Hashes for Anaconda2-2.4.1-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.



exact time file was last modified, as Unix time stamp	1449608450.0
time file was last modified, in human readable format	2015-12-08 15:00:50
exact file size, in bytes	257787337
file size, in human friendly format	245.8 MiB
md5	0407becd94e2c67d500700863cccaf82
sha256	1e2445aaf9faf84e801404bf89091fbf4a018709712a3901490fb3f45d44c

### Hashes for Anaconda2-2.4.0-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1446502940.0
time file was last modified, in human readable format	2015-11-02 16:22:20
exact file size, in bytes	287613909
file size, in human friendly format	274.3 MiB
md5	1da04d414117e3d5ffdae13a686f300f
sha256	d6842135062f3c3d2f8bd33318133376d4f2c789c32818b24f9010ca2240b

### Hashes for Anaconda-2.3.0-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1435775709.0
time file was last modified, in human readable format	2015-07-01 13:35:09
exact file size, in bytes	297482814
file size, in human friendly format	283.7 MiB
md5	1fdb7eb4db925edb48f678c72f70f795
sha256	f920ae6211d9da3288b5e160100543667cf1ceb21fa09b16d6cda82f113e8



## Hashes for Anaconda-2.2.0-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1427315247.0
time file was last modified, in human readable format	2015-03-25 15:27:27
exact file size, in bytes	293316812
file size, in human friendly format	279.7 MiB
md5	53777c4bbba5b6e6f9124e041f024bc9
sha256	65784323db94b0c297e998bc81db5978e8951801c44808589e2b9665ad199

## Hashes for Anaconda-2.1.0-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1411662793.0
time file was last modified, in human readable format	2014-09-25 11:33:13
exact file size, in bytes	288368463
file size, in human friendly format	275.0 MiB
md5	0632392578c6b4796c9c2a3964f9f2f9
sha256	d8001bae990e7024b81e74c6b06d0f488dd8717a9e0779db20d3e8831435b

## Hashes for Anaconda-2.0.1-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1402603370.0
time file was last modified, in human readable format	2014-06-12 15:02:50
exact file size, in bytes	256197898
file size, in human friendly format	244.3 MiB
md5	8c3fa107375b1c4782531b7f6e7eddae
sha256	d6a0ce0422daa004929a4aef6b485d94f5e60b67f6d727047719815949fd5

### Hashes for Anaconda-2.0.0-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1401313841.0
time file was last modified, in human readable format	2014-05-28 16:50:41
exact file size, in bytes	247641929
file size, in human friendly format	236.2 MiB
md5	39d1624555ddc087785bc9557ecaa7b7
sha256	e2eb3805451a26235b2ed7f3e63535fc39bf32b46bfa8407f8b6240924cf8

### Hashes for Anaconda-1.9.2-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1397142332.0
time file was last modified, in human readable format	2014-04-10 10:05:32
exact file size, in bytes	294660294
file size, in human friendly format	281.0 MiB
md5	432ac816e681c51f0238f30e4207e789
sha256	2fff6dca12507f675b04ed1f303d0ee99d755402c3b2b64c131d93c3b4f14

### Hashes for Anaconda-1.9.1-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1392932644.0
time file was last modified, in human readable format	2014-02-20 15:44:04
exact file size, in bytes	294577771
file size, in human friendly format	280.9 MiB
md5	772b8e5dc385bf5ea3f78cdd21a8ec71
sha256	2aa707b162e71d488495085fd13232f8c30ac0f5003e6dd983c99897813d2

### Hashes for Anaconda-1.9.0-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1392049426.0
time file was last modified, in human readable format	2014-02-10 10:23:46
exact file size, in bytes	293412173
file size, in human friendly format	279.8 MiB
md5	e702b99930507a43b59fd258744bd456
sha256	b74134e7626f10fc4d86209a3ebbb19de3c4404d0aecf071bedfa184bab22

### Hashes for Anaconda-1.8.0-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1383595040.0
time file was last modified, in human readable format	2013-11-04 13:57:20
exact file size, in bytes	275773973
file size, in human friendly format	263.0 MiB
md5	2b909458ddc208807efa3516c9ecab2f
sha256	fb92afc7750bc58ac12f3cbd65c18ee0f80ec22b80f07e236e739bf5ec5e7

### Hashes for Anaconda-1.7.0-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1378746934.0
time file was last modified, in human readable format	2013-09-09 12:15:34
exact file size, in bytes	269206281
file size, in human friendly format	256.7 MiB
md5	6e9e2fe69d3c1d847ca162b2f723f7b2
sha256	d277f7e162c77043e416d03a754389a0d9fb83636dc78bbb67e7433e29097

### Hashes for Anaconda-1.6.1-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1372804212.0
time file was last modified, in human readable format	2013-07-02 17:30:12
exact file size, in bytes	206839424
file size, in human friendly format	197.3 MiB
md5	01fe24a1c6605bec8d482dcda9de314a
sha256	7c79819dd40a14e52439664c3e88e89ecba29c5f4d2fd72726124d7a138f5

## Graphical installers for Anaconda with Python 3 on macOS

To verify the file integrity using MD5 or SHA-256, see [cryptographic hash verification](#).

### Hashes for Anaconda3-2020.07-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1595524602.8617642
time file was last modified, in human readable format	2020-07-23 12:16:42
exact file size, in bytes	484710586
file size, in human friendly format	462.3 MiB
md5	2941ddbaf0cdb49b342c18cde51fee43
sha256	e095c487d2837e4c984d0fcd2217be42c615504a2d7d6651095d34c2fa980

### Hashes for Anaconda3-2020.02-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1583940777.1370583
time file was last modified, in human readable format	2020-03-11 10:32:57
exact file size, in bytes	463718746
file size, in human friendly format	442.2 MiB
md5	d1e7fe5d52e5b3ccb38d9af262688e89
sha256	4f7cc14b5b1d7aec3d9a5e781dede065e21cfe61915de4d3de192b9329195

### Hashes for Anaconda3-2019.10-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1571149653.2468076
time file was last modified, in human readable format	2019-10-15 09:27:33
exact file size, in bytes	685285794
file size, in human friendly format	653.5 MiB
md5	5b051bf25188cd4bdcb7794f5bea6886
sha256	8b2192cbd586939d68bac00b0f9cbd2bfe555798c52b4cf4a6ecf6f9442123

### Hashes for Anaconda3-2019.07-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1564065483.724647
time file was last modified, in human readable format	2019-07-25 09:38:03
exact file size, in bytes	684809889
file size, in human friendly format	653.1 MiB
md5	1c50485dde8e6a2c28e33c09b619ea78
sha256	bc1a4cb642b775159125521d1dbcf8bd1dd811b0880fd0c2a6612070d7b78

### Hashes for Anaconda3-2019.03-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1554411633.2091389
time file was last modified, in human readable format	2019-04-04 16:00:33
exact file size, in bytes	668331738
file size, in human friendly format	637.4 MiB
md5	c0c6fbeb5c781c510ba7ee44a8d8efcb
sha256	1d89450ec2b8236404bab5a47aaa9c69fd85b63c6a9b8c35960dfa11f7550

### Hashes for Anaconda3-2018.12-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1545419672.5039964
time file was last modified, in human readable format	2018-12-21 13:14:32
exact file size, in bytes	684396431
file size, in human friendly format	652.7 MiB
md5	34741dbb84e8b0f25c53acd056e7b95d
sha256	e40e076194df57f3fce8734acd5b2e3f60901ceea8ddbf5bd42284a2bce

### Hashes for Anaconda3-5.3.1-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1542656334.2480006
time file was last modified, in human readable format	2018-11-19 13:38:54
exact file size, in bytes	664821768
file size, in human friendly format	634.0 MiB
md5	6a5cbe559a5b83e2508b39a3b72e90c8
sha256	ee9fb23d4beb30e5ed9d27d5703b46a02e23a93601373bc0de18bf6282116



### Hashes for Anaconda3-5.3.0-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1538081958.0784323
time file was last modified, in human readable format	2018-09-27 15:59:18
exact file size, in bytes	664674040
file size, in human friendly format	633.9 MiB
md5	d3075bb9e63d560af3908d5f092e1c07
sha256	013e9968f437f91f7a1dfdfc4c7d6f9d3b7f7aeab5c6766a867ecb01c13ee

### Hashes for Anaconda3-5.2.0-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1527703620.9068272
time file was last modified, in human readable format	2018-05-30 13:07:00
exact file size, in bytes	642866657
file size, in human friendly format	613.1 MiB
md5	9c35bf27e9986701f7d80241616c665f
sha256	dae8befc73d32b480faef31fa6fb73332579442a524bc68f6d475743f5bb8

### Hashes for Anaconda3-5.1.0-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.



exact time file was last modified, as Unix time stamp	1518707346.8513427
time file was last modified, in human readable format	2018-02-15 09:09:06
exact file size, in bytes	623585451
file size, in human friendly format	594.7 MiB
md5	6ed496221b843d1b5fe8463d3136b649
sha256	d6bf6309cca84314d85ca7421fddc16057ac2d824d698a213ccd597e896

### Hashes for Anaconda3-5.0.1-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1508806879.6149647
time file was last modified, in human readable format	2017-10-23 20:01:19
exact file size, in bytes	596524910
file size, in human friendly format	568.9 MiB
md5	eef112a1b8cbe8854e189eea1969f699
sha256	50c28594c785f5828990c95053468488563c775038b6744951847f9853ed0

### Hashes for Anaconda3-5.0.0-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1506461110.7116904
time file was last modified, in human readable format	2017-09-26 16:25:10
exact file size, in bytes	594734978
file size, in human friendly format	567.2 MiB
md5	de004893c4d5714e06d4903e0780aabd
sha256	06d959384869290845bc61346bb33a18dd02573836f50ba263b72028d2a6a

### Hashes for Anaconda3-4.4.0-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1495841777.0
time file was last modified, in human readable format	2017-05-26 18:36:17
exact file size, in bytes	464033256
file size, in human friendly format	442.5 MiB
md5	c6cd9c30b94c2ba2a5449e6f234d15f5
sha256	c5fc645f11505ac3ef710023b4072b7fb24ad31634b48e793e50b067dc301

### Hashes for Anaconda3-4.3.1-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1488839187.0
time file was last modified, in human readable format	2017-03-06 16:26:27
exact file size, in bytes	444660396
file size, in human friendly format	424.1 MiB
md5	390ba506140e4dfb7e0ab368f6ab18d6
sha256	ca608d58b1acf77b5c77d10e937b9084e5997b8706445bac3754459e54c43

### Hashes for Anaconda3-4.3.0-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1485548792.0
time file was last modified, in human readable format	2017-01-27 14:26:32
exact file size, in bytes	443649282
file size, in human friendly format	423.1 MiB
md5	30b108a9cbc5d215a60187c5de89c459
sha256	f4522ac099ba292940bb47429e8e53eb9a0fe2ad3421513b2d618d0766337

### Hashes for Anaconda3-4.2.0-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1476750827.0
time file was last modified, in human readable format	2016-10-17 19:33:47
exact file size, in bytes	426843208
file size, in human friendly format	407.1 MiB
md5	51ed7f9af7436a1a23068eb00509d6ad
sha256	44fe57910aa10967c4afe41ab5663cb49235bc718a9b7c8912d3ec7f95485

### Hashes for Anaconda3-4.1.1-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1467994875.0
time file was last modified, in human readable format	2016-07-08 11:21:15
exact file size, in bytes	364773025
file size, in human friendly format	347.9 MiB
md5	9d396421683249ae850bd19637577f6e
sha256	b5e8cf44958d0aa03a7cc2da15fa835b1e14612b43b9772aef3270079d9b5

### Hashes for Anaconda3-4.1.0-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/> .

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1467131312.0
time file was last modified, in human readable format	2016-06-28 11:28:32
exact file size, in bytes	363587059
file size, in human friendly format	346.7 MiB
md5	665bf91beb7df29cfe36e6c135651ff5
sha256	83772b5fcd3d6deb945316ec96ecc7b0cdcd58c2c7a23f8f616771704e75a

### Hashes for Anaconda3-4.0.0-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/> .

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1459268168.0
time file was last modified, in human readable format	2016-03-29 11:16:08
exact file size, in bytes	358139390
file size, in human friendly format	341.5 MiB
md5	b25796c49f9d3b47561c6eac9bbc77f0
sha256	32a089b1be465a8b03c837041bbfbc761d644893719329ee59b253221456

### Hashes for Anaconda3-2.5.0-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/> .

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1454536564.0
time file was last modified, in human readable format	2016-02-03 15:56:04
exact file size, in bytes	387740293
file size, in human friendly format	369.8 MiB
md5	a3c5835e965b3afb05e4a0472fe36267
sha256	b1a6945f0f025086806624c59de5d92e5234bb39a18b5517d8b1e0dc30b3b

### Hashes for Anaconda3-2.4.1-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1449608454.0
time file was last modified, in human readable format	2015-12-08 15:00:54
exact file size, in bytes	259674929
file size, in human friendly format	247.6 MiB
md5	feb6c8b1553b4de35cfa8c8c18c50d34
sha256	95e9f2d370f7816ed72b862c9413c973efb2ca17edd4d84550ce33e0d16d8

### Hashes for Anaconda3-2.4.0-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1446502943.0
time file was last modified, in human readable format	2015-11-02 16:22:23
exact file size, in bytes	280419790
file size, in human friendly format	267.4 MiB
md5	64db05cc4c185354453c450ba7551331
sha256	791f045258bd39bbcd4c5425dce082ecd194074edd99fb401d746ad58da

### Hashes for Anaconda3-2.3.0-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1435775713.0
time file was last modified, in human readable format	2015-07-01 13:35:13
exact file size, in bytes	307072618
file size, in human friendly format	292.8 MiB
md5	51e3b628d2f7580d0753a4dabd46f1d3
sha256	0b936ab3067bbf32b5a52768f31ff437f0e01fbcee028698444d1a964209c

### Hashes for Anaconda3-2.2.0-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1427315292.0
time file was last modified, in human readable format	2015-03-25 15:28:12
exact file size, in bytes	302853736
file size, in human friendly format	288.8 MiB
md5	f6963a1d098dc1aa70b198490cde34cf
sha256	16a5154267d7d52d3e7e0d12ec3405077df799c77ce382a3358238352656a

### Hashes for Anaconda3-2.1.0-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1411663254.0
time file was last modified, in human readable format	2014-09-25 11:40:54
exact file size, in bytes	290765346
file size, in human friendly format	277.3 MiB
md5	c863fb1f7f714917e4cb4dfaafd9d03f
sha256	2780df02f400e44c0adcd209825fdcf955559fe42f5b3689d5c46a01bdec2

### Hashes for Anaconda3-2.0.1-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1402603205.0
time file was last modified, in human readable format	2014-06-12 15:00:05
exact file size, in bytes	241942876
file size, in human friendly format	230.7 MiB
md5	1c22595eedfc62ff18a8786934e19c9c
sha256	0d53815a83a50bdcfcb5ada686f582730bcc93b95295dd04572ee5162724e

### Hashes for Anaconda3-2.0.0-MacOSX-x86\_64.pkg

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1401226216.0
time file was last modified, in human readable format	2014-05-27 16:30:16
exact file size, in bytes	233699227
file size, in human friendly format	222.9 MiB
md5	e59bdfb282ec34a1a54db3eb3bb4eea0
sha256	4d4189ec0c514d344389e216b3ad4eeacd667426d902c5da416ebd7caa54d



## Command line installers for Anaconda with Python 2 on macOS

To verify the file integrity using MD5 or SHA-256, see [cryptographic hash verification](#).

### Hashes for Anaconda2-2019.10-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1571149651.059706
time file was last modified, in human readable format	2019-10-15 09:27:31
exact file size, in bytes	428689022
file size, in human friendly format	408.8 MiB
md5	311aeb49cbe6d296f499efcd01a73f5e
sha256	463cbd0b90c47d02ec341377110653870c7cc9d65572c655c5e44aaf2ccb2

### Hashes for Anaconda2-2019.07-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1564065465.266795
time file was last modified, in human readable format	2019-07-25 09:37:45
exact file size, in bytes	427641100
file size, in human friendly format	407.8 MiB
md5	14efcfe8646ad0a00f2e3ca2959dec94
sha256	3e63919eed116826e683ed7d480d06517de79564788fbc27cb8d8879697eb

### Hashes for Anaconda2-2019.03-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.



If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1554411634.2571862
time file was last modified, in human readable format	2019-04-04 16:00:34
exact file size, in bytes	555971416
file size, in human friendly format	530.2 MiB
md5	fc7f811d92e39c17c20fac1f43200043
sha256	414917d00deaeefa38719992e6437470f54793718ef4bedcd66b0e5a30dbe

### Hashes for Anaconda2-2018.12-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1545419671.3559437
time file was last modified, in human readable format	2018-12-21 13:14:31
exact file size, in bytes	573645950
file size, in human friendly format	547.1 MiB
md5	f4d8b10e9a754884fb96e68e0e0b276a
sha256	5c590b1b3cdc2eedd52edce0caabbce6665d84084d31b913e789e8c46a948

### Hashes for Anaconda2-5.3.1-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1542656263.4707713
time file was last modified, in human readable format	2018-11-19 13:37:43
exact file size, in bytes	565177387
file size, in human friendly format	539.0 MiB
md5	559606f0dda021daa1afd612b2e3e37c
sha256	df81e9d5d7d4c6595609a8d353eab80102a83b49cf8c19e5c1e5ad4ac0f39

### Hashes for Anaconda2-5.3.0-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1538082031.4787154
time file was last modified, in human readable format	2018-09-27 16:00:31
exact file size, in bytes	565054507
file size, in human friendly format	538.9 MiB
md5	de3314d20376ff56a7c0a62087962c86
sha256	bea3eb7667d265c8fe678ddde8432ac1f8286224baae498d092bb068b8185

### Hashes for Anaconda2-5.2.0-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1527703534.8069696
time file was last modified, in human readable format	2018-05-30 13:05:34
exact file size, in bytes	552703968
file size, in human friendly format	527.1 MiB
md5	b1f3fcf58955830b65613a4a8d75c3cf
sha256	d7d46e566306da5979cd5632079497fe6103b980e3a089ccf27a9f30cbee8

## Hashes for Anaconda2-5.1.0-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1518707333.7077339
time file was last modified, in human readable format	2018-02-15 09:08:53
exact file size, in bytes	530462553
file size, in human friendly format	505.9 MiB
md5	e9845ccf67542523c5be09552311666e
sha256	b686e01aeadb33526d9c154a0ac6f691dfad135080df96fb4d3ae1e4b128

## Hashes for Anaconda2-5.0.1-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1508806264.3489628
time file was last modified, in human readable format	2017-10-23 19:51:04
exact file size, in bytes	510164626
file size, in human friendly format	486.5 MiB
md5	17314016dced36614a3bef8ff3db7066
sha256	e3a9a5c84cb89ff079b0781ba773a3433d490fe0cfc24042c613a5674748c

## Hashes for Anaconda2-5.0.0-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1506461109.035615
time file was last modified, in human readable format	2017-09-26 16:25:09
exact file size, in bytes	508843477
file size, in human friendly format	485.3 MiB
md5	b8d555fae2b4994f1094c2da85c7e9a4
sha256	d85198c63657924fae11b6ea5961f50d81d09a1185d6f0a9a9d5bc69eb788

### Hashes for Anaconda2-4.4.0-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1495841752.0
time file was last modified, in human readable format	2017-05-26 18:35:52
exact file size, in bytes	393583324
file size, in human friendly format	375.4 MiB
md5	a57e5c631a7d0c63552519f05ab243a4
sha256	ab95aef1110c2a385fd39a17e5f11dfbaabce25c1a5944598de164d7a2772

### Hashes for Anaconda2-4.3.1-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1488839162.0
time file was last modified, in human readable format	2017-03-06 16:26:02
exact file size, in bytes	375651870
file size, in human friendly format	358.2 MiB
md5	eb1e7f853f64ad8babe1330a068e94e9
sha256	35261360f2b01793f441b29715a94052dceaf1137866b7323c76be83c5bc

## Hashes for Anaconda2-4.3.0-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1485548768.0
time file was last modified, in human readable format	2017-01-27 14:26:08
exact file size, in bytes	374699540
file size, in human friendly format	357.3 MiB
md5	80b7958fc805d371d60e133af826752c
sha256	834ac0287062929ab5930661735ee617fd379bdfe79f3e0a20aebd614835b

## Hashes for Anaconda2-4.2.0-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1475009402.0
time file was last modified, in human readable format	2016-09-27 15:50:02
exact file size, in bytes	363251366
file size, in human friendly format	346.4 MiB
md5	52f8b74e0c462575efc297c8f4e6cf14
sha256	a8b3ef86233635d9dcc3499dc384980762a0b42d354a318f8307029c399db

## Hashes for Anaconda2-4.1.1-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1467994800.0
time file was last modified, in human readable format	2016-07-08 11:20:00
exact file size, in bytes	310125837
file size, in human friendly format	295.8 MiB
md5	f62a0a47a42504e139a5122ad641b40c
sha256	3b2fb323eb26c1c58788f63c41e164c20c417f7f24e30b8057e92ab4d6102

### Hashes for Anaconda2-4.1.0-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1467131310.0
time file was last modified, in human readable format	2016-06-28 11:28:30
exact file size, in bytes	309460309
file size, in human friendly format	295.1 MiB
md5	c18a0f560668e9d1215ed600fb64b0cf
sha256	8b2c2a32f5e0da75cf8c81c568124cc1ea701a58cd46b7816133573a7f5b7

### Hashes for Anaconda2-4.0.0-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1459268099.0
time file was last modified, in human readable format	2016-03-29 11:14:59
exact file size, in bytes	304288480
file size, in human friendly format	290.2 MiB
md5	a3443b46f99bc6680c77c688af1b1f5a
sha256	aa7ba6e1a40e08e672660c00c3151f0124faa61b598d75bdd07ebe1d24873

### Hashes for Anaconda2-2.5.0-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1454535682.0
time file was last modified, in human readable format	2016-02-03 15:41:22
exact file size, in bytes	331485310
file size, in human friendly format	316.1 MiB
md5	57c024647fd3a149aa6d787feb35daa2
sha256	e7aa3b41210ee7ccf3c12e5b5ea43190d1811b58eaeca8584ccffa468ac8a

### Hashes for Anaconda2-2.4.1-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1449608451.0
time file was last modified, in human readable format	2015-12-08 15:00:51
exact file size, in bytes	222326344
file size, in human friendly format	212.0 MiB
md5	1aecf1e5808dbfb9fa81d139abdbeb34
sha256	f4bd45a21e0dff106e36d11cfd532f2b5050d3b792cc0627ab231089341d2

### Hashes for Anaconda2-2.4.0-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.



exact time file was last modified, as Unix time stamp	1446502940.0
time file was last modified, in human readable format	2015-11-02 16:22:20
exact file size, in bytes	251172115
file size, in human friendly format	239.5 MiB
md5	6e39a0b4470f6517c98f6edd21becd35
sha256	53c9123c9d508555100805fdb44d9845511c937e7a34f237beeb19168d655e

### Hashes for Anaconda-2.3.0-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1435775710.0
time file was last modified, in human readable format	2015-07-01 13:35:10
exact file size, in bytes	262015432
file size, in human friendly format	249.9 MiB
md5	a9c057a22f106748956b708c50f52239
sha256	c4bb59a57bf44dde80612041bbbcfd2e5cab8534842209ef456da7a46f919

### Hashes for Anaconda-2.2.0-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1427314653.0
time file was last modified, in human readable format	2015-03-25 15:17:33
exact file size, in bytes	259147994
file size, in human friendly format	247.1 MiB
md5	453ab3de72ee95b7cb7ee5ee7298fbdf
sha256	20570e2f3911e38a78d8f888f3ff445d6c0cf97a2fca40d6956b48d12aaef



### Hashes for Anaconda-2.1.0-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1411660393.0
time file was last modified, in human readable format	2014-09-25 10:53:13
exact file size, in bytes	252758049
file size, in human friendly format	241.0 MiB
md5	4d323aea34408b16a316ee5596817d47
sha256	128fd4f53e0895e0d23f33e924ae32e01171c2914b044d2b157a949710810

### Hashes for Anaconda-2.0.1-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1402603376.0
time file was last modified, in human readable format	2014-06-12 15:02:56
exact file size, in bytes	224812734
file size, in human friendly format	214.4 MiB
md5	85d261fd4e651f891ca5d0df69441e00
sha256	4ecda163c6f46e70cc6a1fe62dece4c6ecd6474845129cc95a1d4e18c42f8

### Hashes for Anaconda-2.0.0-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1401313845.0
time file was last modified, in human readable format	2014-05-28 16:50:45
exact file size, in bytes	216067773
file size, in human friendly format	206.1 MiB
md5	ec288bc9901facac5a1e098ded8c9936
sha256	ad6271ad21403166bf54d0734ba8c7f7eb65bb78a70d67c58c15b6874cddc

### Hashes for Anaconda-1.9.2-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1396996443.0
time file was last modified, in human readable format	2014-04-08 17:34:03
exact file size, in bytes	257273472
file size, in human friendly format	245.4 MiB
md5	9d4bfe3f859718c4ab9c06209c5b8175
sha256	be4611ca671f80b984fa330d4ecf82244c388abdbb5c7679a4e6e806b4dca

### Hashes for Anaconda-1.9.1-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1392922925.0
time file was last modified, in human readable format	2014-02-20 13:02:05
exact file size, in bytes	257212033
file size, in human friendly format	245.3 MiB
md5	6ef81bc54a6ab506f352b5589ea80f81
sha256	7e4358adbbae2db9e17d1e0e4263b9a0174394c8f115c89d285c3f0f9206f

## Hashes for Anaconda-1.9.0-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1392049427.0
time file was last modified, in human readable format	2014-02-10 10:23:47
exact file size, in bytes	256300639
file size, in human friendly format	244.4 MiB
md5	ddd474c01696cc02dcaea91da1d72389
sha256	722fe4d4406e88c5023e7ee21dc1401bb2a540d6c031d303f0330a95e6013

## Hashes for Anaconda-1.8.0-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1383592216.0
time file was last modified, in human readable format	2013-11-04 13:10:16
exact file size, in bytes	239935643
file size, in human friendly format	228.8 MiB
md5	9fd7dd485c5f04fb65699a290e69671c
sha256	5844ca595b5930399a1213db64ab53e9b7e2fc1c26d8f11769c161fe4f566

## Hashes for Anaconda-1.7.0-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1378745565.0
time file was last modified, in human readable format	2013-09-09 11:52:45
exact file size, in bytes	234119145
file size, in human friendly format	223.3 MiB
md5	16194eb9be2301eeb135f9f01695a566
sha256	046b592245bc2c11e733acb9700dc50947f2eff0f30fec4a4a5bf79368dfa

### Hashes for Anaconda-1.6.1-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1372784365.0
time file was last modified, in human readable format	2013-07-02 11:59:25
exact file size, in bytes	178279644
file size, in human friendly format	170.0 MiB
md5	4b60123e71864c447a0adc16398d5386
sha256	bbc15de34208ce8af5aceedeeal334636fe94c578b9890896729f1a61ace5

### Hashes for Anaconda-1.6.0-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1371842774.0
time file was last modified, in human readable format	2013-06-21 14:26:14
exact file size, in bytes	177173725
file size, in human friendly format	169.0 MiB
md5	cccd0353bfd46d3a93143fc6e47d728
sha256	e03317888c36c07451a349577b426f435a75075d1ee71e204eb9d5dd23936

### Hashes for Anaconda-1.5.1-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1368127580.0
time file was last modified, in human readable format	2013-05-09 14:26:20
exact file size, in bytes	174295689
file size, in human friendly format	166.2 MiB
md5	03942512daf1b39eb3ff9016fc7efa0c
sha256	6d3c86a2fdbaeec2a6c251d5c9034a32b7c68a0437f2fac0b8f25125fe68

### Hashes for Anaconda-1.5.0-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1368022724.0
time file was last modified, in human readable format	2013-05-08 09:18:44
exact file size, in bytes	174295630
file size, in human friendly format	166.2 MiB
md5	6fe90601dbcecb29a2afcaf44aeb37f6
sha256	c69609f0f48f33ca5a12d425a9e4d0fc91b2c09d0345a590e1d7772644672

### Hashes for Anaconda-1.4.0-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1362869217.0
time file was last modified, in human readable format	2013-03-09 16:46:57
exact file size, in bytes	163952262
file size, in human friendly format	156.4 MiB
md5	db8779f0a663e025da1b19755f372a57
sha256	e5d5dae6e93bb7df528abc19f5ed3a69cc4bc867836bdc56886c5a3768fcc

## Command line installers for Anaconda with Python 3 on macOS

To verify the file integrity using MD5 or SHA-256, see [cryptographic hash verification](#).

### Hashes for Anaconda3-2020.07-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/> .

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1595524604.7698503
time file was last modified, in human readable format	2020-07-23 12:16:44
exact file size, in bytes	476160269
file size, in human friendly format	454.1 MiB
md5	50f20c90b8b5bfdc09759c09e32dce68
sha256	3980c2a57fde5de2ccfd0d7973f95ac1a3fa63351642e6735c50fc3791ef

### Hashes for Anaconda3-2020.02-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/> .

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1583940754.2270095
time file was last modified, in human readable format	2020-03-11 10:32:34
exact file size, in bytes	450989230
file size, in human friendly format	430.1 MiB
md5	f0229959e0bd45dee0c14b20e58ad916
sha256	d237e6c976eb9c58368ca156a51bd913d63a3b5fea32689342733c99d14b6

### Hashes for Anaconda3-2019.10-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1571149651.9097455
time file was last modified, in human readable format	2019-10-15 09:27:31
exact file size, in bytes	444796542
file size, in human friendly format	424.2 MiB
md5	1a56194e89795b7ebbf405b09d9c42d
sha256	4f77299ff4170cda64fdfcc27ac609a37d654c158f36c9ff25048793fe8a3

### Hashes for Anaconda3-2019.07-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1564065426.3799994
time file was last modified, in human readable format	2019-07-25 09:37:06
exact file size, in bytes	456538380
file size, in human friendly format	435.4 MiB
md5	0596eb617cfa30e4666ae3498a958bba
sha256	dcbddbabb37c5b5f3873fe24d2617a4325bc7da28c0cd1d23a2edc7f0ebe08



### Hashes for Anaconda3-2019.03-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1554411627.8518968
time file was last modified, in human readable format	2019-04-04 16:00:27
exact file size, in bytes	567859422
file size, in human friendly format	541.6 MiB
md5	46709a416be6934a7fd5d02b021d2687
sha256	b232f0b16181f48667d2ca89c04a4ee4b3932475282b41c52acac87b4cdafe

### Hashes for Anaconda3-2018.12-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1545419593.1093435
time file was last modified, in human readable format	2018-12-21 13:13:13
exact file size, in bytes	584008163
file size, in human friendly format	557.0 MiB
md5	910c8f411f16b02813b3a2cd95462a81
sha256	4ccd3944d994fd47e5701c341725a63e984f8c042bf4dc19cd9dfc7c135e7c

### Hashes for Anaconda3-5.3.1-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.



exact time file was last modified, as Unix time stamp	1542656337.3351417
time file was last modified, in human readable format	2018-11-19 13:38:57
exact file size, in bytes	570132815
file size, in human friendly format	543.7 MiB
md5	3c9d849a305653f67edfefdbacddce4d
sha256	23c373abce2463d4df495f5a1c7e8b0faec6eda09542d98f41ed65a0fa0db

### Hashes for Anaconda3-5.3.0-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1538082101.527849
time file was last modified, in human readable format	2018-09-27 16:01:41
exact file size, in bytes	570009935
file size, in human friendly format	543.6 MiB
md5	e03e91c0aec76d4188b7656e1cec1b74
sha256	bc073b6e6d3b2ef29d01a2caf1de7c206c95968231ef0492d958eae1a314b

### Hashes for Anaconda3-5.2.0-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1527703623.1079257
time file was last modified, in human readable format	2018-05-30 13:07:03
exact file size, in bytes	548669102
file size, in human friendly format	523.3 MiB
md5	b5b789c01e1992de55ee911754c310d4
sha256	c8089121dc89ffe8f9a0c01205bab75a112821a13d413152d6690f5eef094

## Hashes for Anaconda3-5.1.0-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1518707424.3679326
time file was last modified, in human readable format	2018-02-15 09:10:24
exact file size, in bytes	536124653
file size, in human friendly format	511.3 MiB
md5	047e12523fd287149ecd80c803598429
sha256	be705b3c3a0ca29ee32ce7658890bb5edb32a9eadedc09dec3d7e3cfbfd23

## Hashes for Anaconda3-5.0.1-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1508806270.7502434
time file was last modified, in human readable format	2017-10-23 19:51:10
exact file size, in bytes	514894862
file size, in human friendly format	491.0 MiB
md5	3c0f4bf6d9a68d91f6da65051046e106
sha256	f438a0af923bc1edc7bca53f496c59a668d1a08b48c768f443ad7f5ea2b8b

## Hashes for Anaconda3-5.0.0-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1506461111.7357368
time file was last modified, in human readable format	2017-09-26 16:25:11
exact file size, in bytes	513706836
file size, in human friendly format	489.9 MiB
md5	a72e7b22c29f0b4e05579cb8453f89fa
sha256	23df1e3a38a6b4aaa0ab559d0c1e51be76eca5d75cb595d473d223c8d17e7

### Hashes for Anaconda3-4.4.0-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1495841759.0
time file was last modified, in human readable format	2017-05-26 18:35:59
exact file size, in bytes	398907650
file size, in human friendly format	380.4 MiB
md5	3958ac6cb84731e560dd833256aa5b15
sha256	10fe58f09ae524df2548d17b8bb1e75db17da597a6ec10d695ce01387a2d7

### Hashes for Anaconda3-4.3.1-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1488839169.0
time file was last modified, in human readable format	2017-03-06 16:26:09
exact file size, in bytes	381078558
file size, in human friendly format	363.4 MiB
md5	fdf4ad01fadb58415bb4c6119153e04a
sha256	a42267203e207cb5e0f539e0d879ead12e436311825c7114cd0edd880d001b

### Hashes for Anaconda3-4.3.0-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1485548775.0
time file was last modified, in human readable format	2017-01-27 14:26:15
exact file size, in bytes	380197908
file size, in human friendly format	362.6 MiB
md5	e080c503c27d5c072d3e324ee1822641
sha256	c53059b810c5e7a9a5ef9c46a7ed76675dfc7183f4ea867bd81449cbd5a0

### Hashes for Anaconda3-4.2.0-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1475009407.0
time file was last modified, in human readable format	2016-09-27 15:50:07
exact file size, in bytes	366497043
file size, in human friendly format	349.5 MiB
md5	7cb61e355eb860e342a5e27236e3f375
sha256	95448921601e1952e01a17ba9767cd3621c154af7fc52dd6b7f57d462155a

### Hashes for Anaconda3-4.1.1-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1467994877.0
time file was last modified, in human readable format	2016-07-08 11:21:17
exact file size, in bytes	313217912
file size, in human friendly format	298.7 MiB
md5	185aa68d5841869cb7cb3a031bd63936
sha256	7c3c06e9281c41f1213d357cb5f233fd99d6d0db6bdba8d9fd7cfad1f1a85

### Hashes for Anaconda3-4.1.0-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1467131313.0
time file was last modified, in human readable format	2016-06-28 11:28:33
exact file size, in bytes	312081344
file size, in human friendly format	297.6 MiB
md5	262c5c9a12d94a956ceb301d9f258c77
sha256	4c45c8d75665fa5194ebe4e355d3427f5aa385f77eb2b5002c0c78d8ae7f2

### Hashes for Anaconda3-4.0.0-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1459268181.0
time file was last modified, in human readable format	2016-03-29 11:16:21
exact file size, in bytes	306950558
file size, in human friendly format	292.7 MiB
md5	efd870aa3fab8f4865a1b9567e69b69
sha256	704a776c0cf3fcca6e0c5a1e6b6043728229cfac813bff28f003157771824

### Hashes for Anaconda3-2.5.0-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1454535687.0
time file was last modified, in human readable format	2016-02-03 15:41:27
exact file size, in bytes	333727463
file size, in human friendly format	318.3 MiB
md5	7223be67e908fe3db8199129e7253da1
sha256	9bb0f926927db210f8c2a8de881213d1a44c7b3d6dbcb93dfa6b99ed4bbd3

### Hashes for Anaconda3-2.4.1-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1449608454.0
time file was last modified, in human readable format	2015-12-08 15:00:54
exact file size, in bytes	224240817
file size, in human friendly format	213.9 MiB
md5	a5831d2a9b7baa9cdd42d7979b32f02c
sha256	22a3267638da9b7d64210d7da90d8762da7948234c21c0010a74f2621ee0e

### Hashes for Anaconda3-2.4.0-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1446502943.0
time file was last modified, in human readable format	2015-11-02 16:22:23
exact file size, in bytes	245160775
file size, in human friendly format	233.8 MiB
md5	9deaaec2262bbac751a75f8bed4c5ab6
sha256	f0cd785dbed0bab28dfc08a391c9de1b01633422fa317cb8365513a1ae5ae

### Hashes for Anaconda3-2.3.0-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1435775714.0
time file was last modified, in human readable format	2015-07-01 13:35:14
exact file size, in bytes	269910147
file size, in human friendly format	257.4 MiB
md5	96fb1d4ba62529e5534f23e143ce3967
sha256	6a0c94a49f41f9fda0138c8e966bd7b0a8965d6648fd21fffb645d1453848

### Hashes for Anaconda3-2.2.0-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1427314664.0
time file was last modified, in human readable format	2015-03-25 15:17:44
exact file size, in bytes	266868602
file size, in human friendly format	254.5 MiB
md5	793f030f8694659f125399b66123bb78
sha256	81a2089ea6127717f146454e99ea0be2bd595193e4151bb05b4c15749b1d8



### Hashes for Anaconda3-2.1.0-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1411660403.0
time file was last modified, in human readable format	2014-09-25 10:53:23
exact file size, in bytes	255307129
file size, in human friendly format	243.5 MiB
md5	59e2ffc9366dd32975c2da9e6eb8854a
sha256	efdb7e9d1e539cbcd62dc3874b0de6a141f36684e6fbc05018e072b217e24

### Hashes for Anaconda3-2.0.1-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1402603209.0
time file was last modified, in human readable format	2014-06-12 15:00:09
exact file size, in bytes	213128084
file size, in human friendly format	203.3 MiB
md5	65dfe2f379cc14d5c8f7e05a57ce32aa
sha256	7a08509d4e45efcc7055a6d06d8406a773716500bd869a4e85312ff131155

### Hashes for Anaconda3-2.0.0-MacOSX-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.



exact time file was last modified, as Unix time stamp	1401228173.0
time file was last modified, in human readable format	2014-05-27 17:02:53
exact file size, in bytes	204782483
file size, in human friendly format	195.3 MiB
md5	ba8d37fdafb2381585ddb24bde34b9ff
sha256	776a1cf8a8e898b41bb6558c093632cc922698dc48486fee35d1e8eae3f60

## Anaconda with Python 2 on 64-bit Linux

To verify the file integrity using MD5 or SHA-256, see [cryptographic hash verification](#).

### Hashes for Anaconda2-2019.10-Linux-ppc64le.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1571149573.5411055
time file was last modified, in human readable format	2019-10-15 09:26:13
exact file size, in bytes	309606026
file size, in human friendly format	295.3 MiB
md5	6b9809bf5d36782bfa1e35b791d983a0
sha256	0521743829c1b3c301542a20fa0daecda20ee85a69e57b5751a07c6290015

### Hashes for Anaconda2-2019.10-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1571149563.4156353
time file was last modified, in human readable format	2019-10-15 09:26:03
exact file size, in bytes	500592001
file size, in human friendly format	477.4 MiB
md5	69c64167b8cf3a8fc6b50d12d8476337
sha256	8b2e7dea2da7d8cc18e822e8ec1804052102f4eefb94c1b3d0e586e126e8c

### Hashes for Anaconda2-2019.07-Linux-ppc64le.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1564065389.6823053
time file was last modified, in human readable format	2019-07-25 09:36:29
exact file size, in bytes	312635356
file size, in human friendly format	298.2 MiB
md5	3b13ff785a73da85540d37d5aeac13af
sha256	ee7f61dab233cdd0acb376ad55e977b16fdc03602f87a98dafb10d5fe9f5a

### Hashes for Anaconda2-2019.07-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1564065361.519005
time file was last modified, in human readable format	2019-07-25 09:36:01
exact file size, in bytes	499266771
file size, in human friendly format	476.1 MiB
md5	63f63df5ffedf3dbbe8bbf3f56897e07
sha256	189e16e7adf9ba4b7b7d06ecdc10ce4ad4153e5e3505b9331f3d142243e18

## Hashes for Anaconda2-2019.03-Linux-ppc64le.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1554411636.0422668
time file was last modified, in human readable format	2019-04-04 16:00:36
exact file size, in bytes	305498479
file size, in human friendly format	291.3 MiB
md5	c65edf84f63c64a876aabc704a090b97
sha256	3ab35c11b50ff26965266655d7dc76cf229336ee11b8b0c364ec1ba596ba9

## Hashes for Anaconda2-2019.03-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1554411635.469241
time file was last modified, in human readable format	2019-04-04 16:00:35
exact file size, in bytes	660030560
file size, in human friendly format	629.5 MiB
md5	dd87c316e211891df8889c52d9167a5d
sha256	cedfee5b5a3f62fcdac0a1d2d12396d0f232d2213d24d6dc893df5d8e64b8

## Hashes for Anaconda2-2018.12-Linux-ppc64le.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1545419673.7410533
time file was last modified, in human readable format	2018-12-21 13:14:33
exact file size, in bytes	303768125
file size, in human friendly format	289.7 MiB
md5	d50ce6eb037f72edfe8f94f90d61aca6
sha256	4ff037544f9191e24887176b44b04100c27b846220d978ae35daa85507f5c

### Hashes for Anaconda2-2018.12-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1545419590.9742453
time file was last modified, in human readable format	2018-12-21 13:13:10
exact file size, in bytes	658699654
file size, in human friendly format	628.2 MiB
md5	84f39388da2c747477cf14cb02721b93
sha256	1821d4b623ed449e0acb6df3ecbabd3944cffa98f96a5234b7a102a7c0853

### Hashes for Anaconda2-5.3.1-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1542656251.7872381
time file was last modified, in human readable format	2018-11-19 13:37:31
exact file size, in bytes	647814227
file size, in human friendly format	617.8 MiB
md5	4da47b83b1eeac1ca8df0a43f6f580c8
sha256	f0650ad2f9ca4ae3f3162d7204a32950bc794f37f322eb47b5ad9412454f9

## Hashes for Anaconda2-5.3.0-Linux-ppc64le.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1538082022.933332
time file was last modified, in human readable format	2018-09-27 16:00:22
exact file size, in bytes	299539043
file size, in human friendly format	285.7 MiB
md5	20a0fad5ef7c3f3df10d350b8ec41bd2
sha256	b71cdf75ca10875d49170eb64a02920f47a69167d168fad694bb95ab91dbb

## Hashes for Anaconda2-5.3.0-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1538082025.1844337
time file was last modified, in human readable format	2018-09-27 16:00:25
exact file size, in bytes	647650387
file size, in human friendly format	617.6 MiB
md5	ae1da610739f953ea12e3c7d24bdef63
sha256	50eeaab24bfa2472bc6485fe8f0e612ed67e561eda1ff9fbf07b62c96443c

## Hashes for Anaconda2-5.2.0-Linux-ppc64le.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1527703471.0561135
time file was last modified, in human readable format	2018-05-30 13:04:31
exact file size, in bytes	282733770
file size, in human friendly format	269.6 MiB
md5	479633a95906ea6d41056ebe84a4c47b
sha256	a8fcac3f0884520c35103e76549fcc45d64d8806517ba02d8ade4028e1f77

### Hashes for Anaconda2-5.2.0-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1527703473.7962363
time file was last modified, in human readable format	2018-05-30 13:04:33
exact file size, in bytes	632688935
file size, in human friendly format	603.4 MiB
md5	5c034a4ab36ec9b6ae01fa13d8a04462
sha256	cb0d7a08b0e2cec4372033d3269979b4e72e2353ffd1444f57cb38bc96212

### Hashes for Anaconda2-5.1.0-Linux-ppc64le.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1518707329.6225448
time file was last modified, in human readable format	2018-02-15 09:08:49
exact file size, in bytes	280296529
file size, in human friendly format	267.3 MiB
md5	e894dcc547a1c7d67deb04f6bba7223a
sha256	ff9baa4d3710bb24bc3a6a40c0f4ef69150f7608af5be6ada1ff99d01d1be

### Hashes for Anaconda2-5.1.0-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1518707330.5935898
time file was last modified, in human readable format	2018-02-15 09:08:50
exact file size, in bytes	558878810
file size, in human friendly format	533.0 MiB
md5	5b1b5784cae93cf696e11e66983d8756
sha256	5f26ee92860d1dfdfcd20910ff2cf75572c39d2892d365f4e867a611cca2a

### Hashes for Anaconda2-5.0.1-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1508865232.4529853
time file was last modified, in human readable format	2017-10-24 12:13:52
exact file size, in bytes	532375438
file size, in human friendly format	507.7 MiB
md5	dc13fe5502cd78dd03e8a727bb9be63f
sha256	23c676510bc87c95184ecaeb327c0b2c88007278e0d698622e2dd8fb14d9f

### Hashes for Anaconda2-5.0.0.1-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.



exact time file was last modified, as Unix time stamp	1506959412.7513092
time file was last modified, in human readable format	2017-10-02 10:50:12
exact file size, in bytes	530931450
file size, in human friendly format	506.3 MiB
md5	35bea553072ea1f28090e851105c1b00
sha256	18730808d863a5c194ab3f59dd395c1a63cbd769c9bfb1df65efe61ee62fc

### Hashes for Anaconda2-5.0.0-Linux-ppc64le.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1506461107.2145326
time file was last modified, in human readable format	2017-09-26 16:25:07
exact file size, in bytes	296001230
file size, in human friendly format	282.3 MiB
md5	157890d591c61a9b511f8452476d6d19
sha256	e0512f3c81251e5dcd48fcf02fe2044a66071dc8681269b1375ac5443f971

### Hashes for Anaconda2-5.0.0-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1506454641.7079751
time file was last modified, in human readable format	2017-09-26 14:37:21
exact file size, in bytes	530296562
file size, in human friendly format	505.7 MiB
md5	2272857fcf773fc75a1bc49f6d507a48
sha256	58a7117f89c40275114bf7e824a613a963da2b0fe63f2ec3c1175fea785b4



## Hashes for Anaconda2-4.4.0.1-Linux-ppc64le.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1501103402.0
time file was last modified, in human readable format	2017-07-26 16:10:02
exact file size, in bytes	284629257
file size, in human friendly format	271.4 MiB
md5	ce166de6f116acd08cd313f9c55c04d6
sha256	e14acab146181699e47ca108fc624ecebbaaac52851312962c649899459d9

## Hashes for Anaconda2-4.4.0-Linux-ppc64le.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1495053920.0
time file was last modified, in human readable format	2017-05-17 15:45:20
exact file size, in bytes	290045511
file size, in human friendly format	276.6 MiB
md5	511fdc6f6c29b1c3a702f3792182faf0
sha256	c19edfd9a3bd2fcb37ddb0c3aa09339c9e23145269957fac75e9b2abca408

## Hashes for Anaconda2-4.4.0-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1495840968.0
time file was last modified, in human readable format	2017-05-26 18:22:48
exact file size, in bytes	508722275
file size, in human friendly format	485.2 MiB
md5	d72add23bc937ccdfc7de4f47deff843
sha256	2d30b91ed4d215b6b4a15162a3389e9057b15445a0c02da71bd7bd272e7b8

### Hashes for Anaconda2-4.3.1-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1488838334.0
time file was last modified, in human readable format	2017-03-06 16:12:14
exact file size, in bytes	484472684
file size, in human friendly format	462.0 MiB
md5	51336ab38e15ce607b55539c60be2c29
sha256	e9b8f2645df6b1527ba56d61343162e0794acc3ee8dde2a6bba353719e2d8

### Hashes for Anaconda2-4.3.0-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1485548108.0
time file was last modified, in human readable format	2017-01-27 14:15:08
exact file size, in bytes	483530594
file size, in human friendly format	461.1 MiB
md5	5f2c3bd60ddbd0e213f7a1fc25bb88b4
sha256	7c52e6e99aabb24a49880130615a48e685da444c3c14eb48d6a65f3313bf7

## Hashes for Anaconda2-4.2.0-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1475009394.0
time file was last modified, in human readable format	2016-09-27 15:49:54
exact file size, in bytes	467689464
file size, in human friendly format	446.0 MiB
md5	a0d1fbe47014b71c6764d76fb403f217
sha256	beee286d24fb37dd6555281bba39b3deb5804baec509a9dc5c69185098cf6

## Hashes for Anaconda2-4.1.1-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1467994796.0
time file was last modified, in human readable format	2016-07-08 11:19:56
exact file size, in bytes	419038579
file size, in human friendly format	399.6 MiB
md5	f7bb3c0ccf23c9789bb895335aa68bf3
sha256	9413b1d3ca9498ba6f53913df9c43d685dd973440ff10b7fe0c45b1cbdc5

## Hashes for Anaconda2-4.1.0-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1467131308.0
time file was last modified, in human readable format	2016-06-28 11:28:28
exact file size, in bytes	418188731
file size, in human friendly format	398.8 MiB
md5	e24d4264205d8d0c8533617db99ff1d3
sha256	3b7e504ca0132fb555d1f10e174cae07007f1bc6898cad0f7d416a68aca01

### Hashes for Anaconda2-4.0.0-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1459268095.0
time file was last modified, in human readable format	2016-03-29 11:14:55
exact file size, in bytes	411562823
file size, in human friendly format	392.5 MiB
md5	31ed3ef07435d7068e1e03be49381b13
sha256	ae312143952ca00e061a656c2080e0e4fd3532721282ba8e2978177cad71a

### Hashes for Anaconda2-2.5.0-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1454535678.0
time file was last modified, in human readable format	2016-02-03 15:41:18
exact file size, in bytes	409842279
file size, in human friendly format	390.9 MiB
md5	f8eb687af8c9b4e81968de8c63b0d991
sha256	e10abf459cde4a838bd6fc5ca03023c3401b81ad470627acde5a298d56715

### Hashes for Anaconda2-2.4.1-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1449608449.0
time file was last modified, in human readable format	2015-12-08 15:00:49
exact file size, in bytes	277827702
file size, in human friendly format	265.0 MiB
md5	c9317dcb28a2e0c98c34ebc341e0d145
sha256	2de682c96edf8cca2852071a84ff860025fbe8c502218e1995acd5ab47e8c

### Hashes for Anaconda2-2.4.0-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1446502939.0
time file was last modified, in human readable format	2015-11-02 16:22:19
exact file size, in bytes	302444354
file size, in human friendly format	288.4 MiB
md5	1ab870a0184b84594fccf2027c9be887
sha256	49d19834da06b1b82b6fa85bc647d2e78fa5957d0cbae3cccd6c695a541bef

### Hashes for Anaconda2-2.3.0-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1435775708.0
time file was last modified, in human readable format	2015-07-01 13:35:08
exact file size, in bytes	339594168
file size, in human friendly format	323.9 MiB
md5	c3100392685b5a62c8509c0588ce9376
sha256	7c02499e9511c127d225992cfe1cd815e88fd46cd8a5b3cdf764f3fb4d8d4

### Hashes for Anaconda-2.2.0-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1427314808.0
time file was last modified, in human readable format	2015-03-25 15:20:08
exact file size, in bytes	332753610
file size, in human friendly format	317.3 MiB
md5	3234b2b2d7f7031432c1fd9870d15f58
sha256	ca2582cb2188073b0f348ad42207211a2b85c10b244265b5b27bab04481b8

### Hashes for Anaconda-2.1.0-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1411660215.0
time file was last modified, in human readable format	2014-09-25 10:50:15
exact file size, in bytes	353806962
file size, in human friendly format	337.4 MiB
md5	74a888f8683f67053a030e37d0eae1cf
sha256	191fbf290747614929d0bdd576e330c944b22a67585d1c185e0d2b3a3e65e

### Hashes for Anaconda-2.0.1-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1402603353.0
time file was last modified, in human readable format	2014-06-12 15:02:33
exact file size, in bytes	343791922
file size, in human friendly format	327.9 MiB
md5	ae96da7de52ab1a64d4ed3fa4b43da25
sha256	074204fa26872b4a946123071d15b8390c0e5441352c6b65b2abd32511bfff

### Hashes for Anaconda-2.0.0-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1401313830.0
time file was last modified, in human readable format	2014-05-28 16:50:30
exact file size, in bytes	332323121
file size, in human friendly format	316.9 MiB
md5	480ba8864579a457db91cd774bd373c1
sha256	3aa27ddf4a0ba5046ba52b97da99e20eb0614273d905bd73e016852451908

### Hashes for Anaconda-1.9.2-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.



exact time file was last modified, as Unix time stamp	1396996358.0
time file was last modified, in human readable format	2014-04-08 17:32:38
exact file size, in bytes	507498869
file size, in human friendly format	484.0 MiB
md5	863ee49f52bda17810ab1b94a52f8c95
sha256	7181d399833a2549a9584255bb477487f2fde1fda4c7f7215d6034ea2fcfa

### Hashes for Anaconda-1.9.1-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1392924916.0
time file was last modified, in human readable format	2014-02-20 13:35:16
exact file size, in bytes	507437430
file size, in human friendly format	483.9 MiB
md5	9d973e9ac715ce3241c3785704565971
sha256	f6455e06a72b8cc11c8a96fb88a85518a2f7b2a1d6f1065f777d7ab4386f0

### Hashes for Anaconda-1.9.0-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1392049385.0
time file was last modified, in human readable format	2014-02-10 10:23:05
exact file size, in bytes	648831310
file size, in human friendly format	618.8 MiB
md5	52ed5f32f7e36b75b5f951ab58a4bc08
sha256	855f1265e4c0b40d50f5a3a0fe7bae05b1cccb0a5301b378a19e0a8f72629



## Hashes for Anaconda-1.8.0-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1383601032.0
time file was last modified, in human readable format	2013-11-04 15:37:12
exact file size, in bytes	488287119
file size, in human friendly format	465.7 MiB
md5	398d4b7ddc5c0a16c556c415b2444266
sha256	69f42966d918f4197040e4dd126d2e3cc3c267bb49869dbf2d6ef277ed5de

## Hashes for Anaconda-1.7.0-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1378677719.0
time file was last modified, in human readable format	2013-09-08 17:01:59
exact file size, in bytes	474606301
file size, in human friendly format	452.6 MiB
md5	01dc7d6df2ed592e5401ab4fbe3aed4a
sha256	6115cfae55a0746b4ae4128be839c99db39d02124160d9c531ca086c4d606

## Hashes for Anaconda-1.6.1-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1372784262.0
time file was last modified, in human readable format	2013-07-02 11:57:42
exact file size, in bytes	333017000
file size, in human friendly format	317.6 MiB
md5	70a1294c01e3ab5925fc52f2603de159
sha256	81d1819ba08069343f228b9c819cdba0e4d15f2142c0c033657599808c396

### Hashes for Anaconda-1.6.0-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1371842631.0
time file was last modified, in human readable format	2013-06-21 14:23:51
exact file size, in bytes	324528041
file size, in human friendly format	309.5 MiB
md5	207a0b4ebde49bcde67925ac8c72fe37
sha256	20f5b70193af4b0b8f10aa0e66aabca552846ec8f4958757ff3f4b79ef7b3

### Hashes for Anaconda-1.5.0-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1368022716.0
time file was last modified, in human readable format	2013-05-08 09:18:36
exact file size, in bytes	321578266
file size, in human friendly format	306.7 MiB
md5	8319288082262fefbe322451aeae06ce
sha256	f4cdc194f076e1b438c8a34e7e5f53e70c2200b411b2d0af719e23fe35c64

## Hashes for Anaconda-1.4.0-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1362869198.0
time file was last modified, in human readable format	2013-03-09 16:46:38
exact file size, in bytes	300831068
file size, in human friendly format	286.9 MiB
md5	9be0e7340f0cd2d2cbd5acbe8e988f45
sha256	85ae8a0a6e3a41cf7845be3def36ed40582d3dc6e6a50e99063eaf6f1abee

## Anaconda with Python 3 on 64-bit Linux

To verify the file integrity using MD5 or SHA-256, see [cryptographic hash verification](#).

## Hashes for Anaconda3-2020.07-Linux-ppc64le.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1595524607.8539894
time file was last modified, in human readable format	2020-07-23 12:16:47
exact file size, in bytes	304505170
file size, in human friendly format	290.4 MiB
md5	daf3de1185a390f435ab80b3c2212205
sha256	0df7c3784973ab46a9ef9848aced01311d08a71d79a18d5ed79dcccdae8c8d

## Hashes for Anaconda3-2020.07-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1595524610.0520885
time file was last modified, in human readable format	2020-07-23 12:16:50
exact file size, in bytes	576830621
file size, in human friendly format	550.1 MiB
md5	1046c40a314ab2531e4c099741530ada
sha256	38ce717758b95b3bd0b1797cc6ccfb76f29a90c25bdfa50ee45f11e583edf

### Hashes for Anaconda3-2020.02-Linux-ppc64le.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1583940752.6769385
time file was last modified, in human readable format	2020-03-11 10:32:32
exact file size, in bytes	289452147
file size, in human friendly format	276.0 MiB
md5	fef889d3939132d9caf7f56ac9174ff6
sha256	d6d1827a38b988cbb714d6e0357c9e251c84641a0c70cda51861ed9abb38

### Hashes for Anaconda3-2020.02-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1583940757.9001777
time file was last modified, in human readable format	2020-03-11 10:32:37
exact file size, in bytes	546910666
file size, in human friendly format	521.6 MiB
md5	17600d1f12b2b047b62763221f29f2bc
sha256	2b9f088b2022edb474915d9f69a803d6449d5fdb4c303041f60ac4aefcc20

### Hashes for Anaconda3-2019.10-Linux-ppc64le.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1571149571.932031
time file was last modified, in human readable format	2019-10-15 09:26:11
exact file size, in bytes	335851146
file size, in human friendly format	320.3 MiB
md5	9dd413b0f2d0c68f387541428fe8d565
sha256	118c579f625555e1b116f0c3fd3842772e8fa0254cb2262c1c94e9eb40ba5

### Hashes for Anaconda3-2019.10-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1571149565.9347522
time file was last modified, in human readable format	2019-10-15 09:26:05
exact file size, in bytes	530308481
file size, in human friendly format	505.7 MiB
md5	b77a71c3712b45c8f33c7b2ecade366c
sha256	46d762284d252e51cd58a8ca6c8adc9da2eadc82c342927b2f66ed011d1d8

### Hashes for Anaconda3-2019.07-Linux-ppc64le.sh

All installer files are available at <https://repo.anaconda.com/archive/> .

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1564065416.491543
time file was last modified, in human readable format	2019-07-25 09:36:56
exact file size, in bytes	341809116
file size, in human friendly format	326.0 MiB
md5	d085409443c102cc5b75f80ebcca8c89
sha256	e788094f7a18bfe14038accb26c8809a81291ed97f1fce29425f366aa8105

### Hashes for Anaconda3-2019.07-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/> .

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1564065380.5078816
time file was last modified, in human readable format	2019-07-25 09:36:20
exact file size, in bytes	541906131
file size, in human friendly format	516.8 MiB
md5	ec6a6bf96d75274c2176223e8584d2da
sha256	69581cf739365ec7fb95608eef694ba959d7d33b36eb961953f2b82cb25b0

### Hashes for Anaconda3-2019.03-Linux-ppc64le.sh

All installer files are available at <https://repo.anaconda.com/archive/> .

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1554411658.5022814
time file was last modified, in human readable format	2019-04-04 16:00:58
exact file size, in bytes	329736128
file size, in human friendly format	314.5 MiB
md5	510c8d6f10f2ffad0b185adbbdddf7f9
sha256	b4ecfca3b6d6c284a3f9370f6a5ccfac1b6be7fa75af9f6750a98fb315601

### Hashes for Anaconda3-2019.03-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1554411631.8810787
time file was last modified, in human readable format	2019-04-04 16:00:31
exact file size, in bytes	685906562
file size, in human friendly format	654.1 MiB
md5	43caea3d726779843f130a7fb2d380a2
sha256	45c851b7497cc14d5ca060064394569f724b67d9b5f98a926ed49b834a6bb

### Hashes for Anaconda3-2018.12-Linux-ppc64le.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1545419583.4789004
time file was last modified, in human readable format	2018-12-21 13:13:03
exact file size, in bytes	328855685
file size, in human friendly format	313.6 MiB
md5	a775fb6d6c441b899ff2327bd9dad6d
sha256	f636f747d5b581ea05e5f20edb1c9ae5db7d9a7923f404761495dfc75966a



### Hashes for Anaconda3-2018.12-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1545419586.1690242
time file was last modified, in human readable format	2018-12-21 13:13:06
exact file size, in bytes	684237703
file size, in human friendly format	652.5 MiB
md5	c9af603d89656bc89680889ef1f92623
sha256	1019d0857e5865f8a6861eaf15bfe535b87e92b72ce4f531000dc672be7fc

### Hashes for Anaconda3-5.3.1-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1542656326.2786372
time file was last modified, in human readable format	2018-11-19 13:38:46
exact file size, in bytes	667976437
file size, in human friendly format	637.0 MiB
md5	334b43d5e8468507f123dbfe7437078f
sha256	d4c4256a8f46173b675dd6a62d12f566ed3487f932bab6bb7058f06c124bc

### Hashes for Anaconda3-5.3.0-Linux-ppc64le.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.



exact time file was last modified, as Unix time stamp	1538082093.2364779
time file was last modified, in human readable format	2018-09-27 16:01:33
exact file size, in bytes	319895712
file size, in human friendly format	305.1 MiB
md5	ee13966b6528f0398a8216f394539255
sha256	550dd67626172a42eb0dd02a08bc78a67e8c8e97a08a5914e402f31e14f48

### Hashes for Anaconda3-5.3.0-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/> .

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1538082095.448577
time file was last modified, in human readable format	2018-09-27 16:01:35
exact file size, in bytes	667822837
file size, in human friendly format	636.9 MiB
md5	4321e9389b648b5a02824d4473cfdb5f
sha256	cfbf5fe70dd1b797ec677e63c61f8efc92dad930fd1c94d60390bb07fdc09

### Hashes for Anaconda3-5.2.0-Linux-ppc64le.sh

All installer files are available at <https://repo.anaconda.com/archive/> .

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1527703540.2002113
time file was last modified, in human readable format	2018-05-30 13:05:40
exact file size, in bytes	302261137
file size, in human friendly format	288.3 MiB
md5	cbd1d5435ead2b0b97dba5b3cf45d694
sha256	024c811526ffc40ed6fa243a25795fbab5b41413372cd5a276aca69a930ef

### Hashes for Anaconda3-5.2.0-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1527703543.880376
time file was last modified, in human readable format	2018-05-30 13:05:43
exact file size, in bytes	651745206
file size, in human friendly format	621.6 MiB
md5	3e58f494ab9fbe12db4460dc152377b5
sha256	09f53738b0cd3bb96f5b1bac488e5528df9906be2480fe61df40e0e0d19e3

### Hashes for Anaconda3-5.1.0-Linux-ppc64le.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1518707336.279853
time file was last modified, in human readable format	2018-02-15 09:08:56
exact file size, in bytes	299557404
file size, in human friendly format	285.7 MiB
md5	47b5b2b17b7dbac0d4d0f0a4653f5b1c
sha256	58d1d093450dabe9ef9279694c9345afed78acf1c334d64a9241bc725f45a

### Hashes for Anaconda3-5.1.0-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1518707337.4719083
time file was last modified, in human readable format	2018-02-15 09:08:57
exact file size, in bytes	577996269
file size, in human friendly format	551.2 MiB
md5	966406059cf7ed89cc82eb475ba506e5
sha256	7e6785caad25e33930bc03fac4994a434a21bc8401817b7efaf28f53619fa9

### Hashes for Anaconda3-5.0.1-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1508799175.9727552
time file was last modified, in human readable format	2017-10-23 17:52:55
exact file size, in bytes	550796553
file size, in human friendly format	525.3 MiB
md5	c989ecc8b648ab8a64731aaee9ed2e7e
sha256	55e4db1919f49c92d5abbf27a4be5986ae157f074bf9f8238963cd4582a40

### Hashes for Anaconda3-5.0.0.1-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1506959414.4703865
time file was last modified, in human readable format	2017-10-02 10:50:14
exact file size, in bytes	549434488
file size, in human friendly format	524.0 MiB
md5	614cc8f244e956b41c75417dd1ec96fd
sha256	092c92427f44687d789a41922ce8426fbdc3c529cc9d6d4ee6de5b62954b9

## Hashes for Anaconda3-5.0.0-Linux-ppc64le.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1506368371.0870926
time file was last modified, in human readable format	2017-09-25 14:39:31
exact file size, in bytes	310695077
file size, in human friendly format	296.3 MiB
md5	8fe5b29ca5be3ff11411621f79babfc2
sha256	3574d423084e604a9d85a9f38ea481e0fc9e678923e2d3b9c4ec7340e1644

## Hashes for Anaconda3-5.0.0-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1506454642.7570226
time file was last modified, in human readable format	2017-09-26 14:37:22
exact file size, in bytes	548789360
file size, in human friendly format	523.4 MiB
md5	bb2656314d22aeca6af243ddbbfb32c
sha256	67f5c20232a3e493ea3f19a8e273e0618ab678fa14b03b59b178361306214

## Hashes for Anaconda3-4.4.0.1-Linux-ppc64le.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1501103322.0
time file was last modified, in human readable format	2017-07-26 16:08:42
exact file size, in bytes	299425582
file size, in human friendly format	285.6 MiB
md5	fe7c87abd9fd70dc0cb4f83cc22d336f
sha256	d7c367c9c4fffec37c31c6570218c9944867c96fde5e9b0249673beda24ba

### Hashes for Anaconda3-4.4.0-Linux-ppc64le.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1495053950.0
time file was last modified, in human readable format	2017-05-17 15:45:50
exact file size, in bytes	304862316
file size, in human friendly format	290.7 MiB
md5	8c663e2056c7c57ac0075774b1f790be
sha256	605251829edecd0c39df8db856d4f09e406454468c3f128c14a7446a4efdf

### Hashes for Anaconda3-4.4.0-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1495840984.0
time file was last modified, in human readable format	2017-05-26 18:23:04
exact file size, in bytes	523283080
file size, in human friendly format	499.0 MiB
md5	50f19b935dae7361978a04d9c7c355cd
sha256	3301b37e402f3ff3df216fe0458f1e6a4ccbb7e67b4d626eae9651de5ea3a

### Hashes for Anaconda3-4.3.1-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1488838344.0
time file was last modified, in human readable format	2017-03-06 16:12:24
exact file size, in bytes	497343851
file size, in human friendly format	474.3 MiB
md5	9209864784250d6855886683ed702846
sha256	4447b93d2c779201e5fb50cfc45de0ec96c3804e7ad0fe201ab6b99f73e90

### Hashes for Anaconda3-4.3.0-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1485548121.0
time file was last modified, in human readable format	2017-01-27 14:15:21
exact file size, in bytes	496412001
file size, in human friendly format	473.4 MiB
md5	dbe2e78adeca1923643be2ecaacd6227
sha256	e9169c3a5029aa820393ac92704eb9ee0701778a085ca7bdc3c57b388ac1b

### Hashes for Anaconda3-4.2.0-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1475009404.0
time file was last modified, in human readable format	2016-09-27 15:50:04
exact file size, in bytes	478051940
file size, in human friendly format	455.9 MiB
md5	4692f716c82deb9fa6b59d78f9f6e85c
sha256	73b51715a12b6382dd4df3dd1905b531bd6792d4aa7273b2377a0436d45f0

### Hashes for Anaconda3-4.1.1-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1467994802.0
time file was last modified, in human readable format	2016-07-08 11:20:02
exact file size, in bytes	425991075
file size, in human friendly format	406.3 MiB
md5	d0dc08d241f83ffc763504db50008e5b
sha256	4f5c95feb0e7efeadd3d348dcef117d7787c799f24b0429e45017008f3534

### Hashes for Anaconda3-4.1.0-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1467131311.0
time file was last modified, in human readable format	2016-06-28 11:28:31
exact file size, in bytes	424649707
file size, in human friendly format	405.0 MiB
md5	487d9ba7ae4955e1481ec59de40e51c5
sha256	11d32cf4026603d3b327dc4299863be6b815905ff51a80329085e1bb9f96c



### Hashes for Anaconda3-4.0.0-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1459268102.0
time file was last modified, in human readable format	2016-03-29 11:15:02
exact file size, in bytes	417798602
file size, in human friendly format	398.4 MiB
md5	546d1f02597587c685fa890c1d713b51
sha256	36a558a1109868661a5735f5f32607643f6dc05cf581fefb1c10fb8abbe22

### Hashes for Anaconda3-2.5.0-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1454535687.0
time file was last modified, in human readable format	2016-02-03 15:41:27
exact file size, in bytes	414838933
file size, in human friendly format	395.6 MiB
md5	02bac549e486be7096070db8d50d0c7f
sha256	addadcb927f15cb0b5b6e36890563d3352a8ff6a901ea753d389047d274a2

### Hashes for Anaconda3-2.4.1-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.



exact time file was last modified, as Unix time stamp	1449608453.0
time file was last modified, in human readable format	2015-12-08 15:00:53
exact file size, in bytes	283797156
file size, in human friendly format	270.7 MiB
md5	45249376f914fdc9fd920ff419a62263
sha256	0735e69199fc37135930ea2fd4fb6ad0adef215a2a7ba9fd6b0a0a4daadb

### Hashes for Anaconda3-2.4.0-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1446502942.0
time file was last modified, in human readable format	2015-11-02 16:22:22
exact file size, in bytes	299023674
file size, in human friendly format	285.2 MiB
md5	48b6d696c73b5f3d573da3300946591d
sha256	fb4e480059e991f2fa632b5a9bcdd284c7f0677814cd719c11d524453f96a

### Hashes for Anaconda3-2.3.0-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1435775712.0
time file was last modified, in human readable format	2015-07-01 13:35:12
exact file size, in bytes	353018424
file size, in human friendly format	336.7 MiB
md5	7e10dbd2b620b4aaa360fe90cf5c6790
sha256	3be5410b2d9db45882c7de07c554cf4f1034becc274ec9074b23fd37a5c87

### Hashes for Anaconda3-2.2.0-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1427314814.0
time file was last modified, in human readable format	2015-03-25 15:20:14
exact file size, in bytes	342778122
file size, in human friendly format	326.9 MiB
md5	a271fee559b46cf15ba98f21b8549235
sha256	4aac68743e7706adb93f042f970373a6e7e087dbf4b02ac467c94ca4ce33d

### Hashes for Anaconda3-2.1.0-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1411660220.0
time file was last modified, in human readable format	2014-09-25 10:50:20
exact file size, in bytes	349003566
file size, in human friendly format	332.8 MiB
md5	934cccd6f6fa894820d2942ea567dca93
sha256	af3225ccbe8df0ffb918939e009aa57740e35058ebf9dfcf5fec794a77556

### Hashes for Anaconda3-2.0.1-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1402603193.0
time file was last modified, in human readable format	2014-06-12 14:59:53
exact file size, in bytes	319624556
file size, in human friendly format	304.8 MiB
md5	aa7c27b54f710f3004cc17f2db5ff761
sha256	3c3b834793e461f3316ad1d9a9178c67859a9d74aaf7bcade076f04134dd1

### Hashes for Anaconda3-2.0.0-Linux-x86\_64.sh

All installer files are available at <https://repo.anaconda.com/archive/> .

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1401226019.0
time file was last modified, in human readable format	2014-05-27 16:26:59
exact file size, in bytes	308739435
file size, in human friendly format	294.4 MiB
md5	c9af4bee8d2da4d74de0d02400ac1c10
sha256	57ce4f97e300cf94c5724f72d992e9eecef708fdaa13bc672ae9779773056

### Anaconda with Python 2 on 32-bit Linux

To verify the file integrity using MD5 or SHA-256, see [cryptographic hash verification](#).

### Hashes for Anaconda2-2018.12-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/> .

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1545419595.0644333
time file was last modified, in human readable format	2018-12-21 13:13:15
exact file size, in bytes	543837797
file size, in human friendly format	518.6 MiB
md5	7d26c7551af6802eb83ecd34282056d7
sha256	e086c041695c0e50642aee8f4e7adad3185c6ce1d11737665653497d2edd7

### Hashes for Anaconda2-5.3.1-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1542656255.5344093
time file was last modified, in human readable format	2018-11-19 13:37:35
exact file size, in bytes	532286994
file size, in human friendly format	507.6 MiB
md5	5685ac1d4a14c4c254cba6c612c77e77
sha256	a38017dfa59141c63ec9882a15bd35e7ce63810ae0d1bcf47c79b7fb9f83e

### Hashes for Anaconda2-5.3.0-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1538082027.2525263
time file was last modified, in human readable format	2018-09-27 16:00:27
exact file size, in bytes	532194834
file size, in human friendly format	507.5 MiB
md5	a476ae6c3fe66711ec9e99f1d46f68e0
sha256	58d4229ad7097e1f3387d7f6582dcf2bbcb684bffe284cd25096bd87530ba

## Hashes for Anaconda2-5.2.0-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1527703530.1317601
time file was last modified, in human readable format	2018-05-30 13:05:30
exact file size, in bytes	512451078
file size, in human friendly format	488.7 MiB
md5	758e172a824f467ea6b55d3d076c132f
sha256	402758c24767e9eb3b77312c388725a058f76e03316464797c3ca404e6eeb

## Hashes for Anaconda2-5.1.0-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1518707331.3896265
time file was last modified, in human readable format	2018-02-15 09:08:51
exact file size, in bytes	452219193
file size, in human friendly format	431.3 MiB
md5	e26fb9d3e53049f6e32212270af6b987
sha256	5af0c7a09a5f3aaf3666c0b362246d342d80e782128ef043998c9ead5ad41

## Hashes for Anaconda2-5.0.1-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1508865187.3479636
time file was last modified, in human readable format	2017-10-24 12:13:07
exact file size, in bytes	433272941
file size, in human friendly format	413.2 MiB
md5	ae155b192027e23189d723a897782fa3
sha256	88c8d698fff16af15862daca10e94a0a46380dcffda45f8d89f5fe03f6bd2

### Hashes for Anaconda2-5.0.0.1-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1506959413.5703459
time file was last modified, in human readable format	2017-10-02 10:50:13
exact file size, in bytes	431941593
file size, in human friendly format	411.9 MiB
md5	5d4b38769f4ee4c33b5cffaa8603356e
sha256	00fbd979c815ede0bbad48fb4ef62cda333c7ad6330184962862a30724792

### Hashes for Anaconda2-5.0.0-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1506455282.2088542
time file was last modified, in human readable format	2017-09-26 14:48:02
exact file size, in bytes	431409105
file size, in human friendly format	411.4 MiB
md5	a574e495c157d59bf4ec337fa4f72ddd
sha256	a3ed8769d20d55a41c04cf7c04e81c95974ea8eb614afab7bbbc0c06fa6a52

### Hashes for Anaconda2-4.4.0-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1495841010.0
time file was last modified, in human readable format	2017-05-26 18:23:30
exact file size, in bytes	435148039
file size, in human friendly format	415.0 MiB
md5	b0f8f5ade832b0238357c2f973338b17
sha256	452aa91ac83d3b6a68b79cea3042170ec591d468d6966307ff9af18fdbce9

### Hashes for Anaconda2-4.3.1-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1488838351.0
time file was last modified, in human readable format	2017-03-06 16:12:31
exact file size, in bytes	406525905
file size, in human friendly format	387.7 MiB
md5	aae1a3192abee1f0abba6c0e1b292cec
sha256	4519ac724d5120d21bb80289c5509c0d1fd9f99c6e9b9a4c6fb352d8bda4a

### Hashes for Anaconda2-4.3.0-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.



exact time file was last modified, as Unix time stamp	1485548055.0
time file was last modified, in human readable format	2017-01-27 14:14:15
exact file size, in bytes	405573575
file size, in human friendly format	386.8 MiB
md5	65546028c4a48f4bb582c4ee3e43b893
sha256	b80d471839e8cf7b100e59308720cc13c141deb1ba903a4776c9a05f613e5

### Hashes for Anaconda2-4.2.0-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1475009420.0
time file was last modified, in human readable format	2016-09-27 15:50:20
exact file size, in bytes	382758938
file size, in human friendly format	365.0 MiB
md5	e26582ebdf1d982e18efb2bdf52c5ee6
sha256	618b720f309fe8da4f235415f11b6ce3db0a16d702ca67fdceecf6bec78c

### Hashes for Anaconda2-4.1.1-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1467994797.0
time file was last modified, in human readable format	2016-07-08 11:19:57
exact file size, in bytes	340385173
file size, in human friendly format	324.6 MiB
md5	8813071788e08e236a323b5f7d337759
sha256	1ab001c7a469345a90d549ebf4afa3376f0f3a57a0df5f042cac7d773b0e0



## Hashes for Anaconda2-4.1.0-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1467131308.0
time file was last modified, in human readable format	2016-06-28 11:28:28
exact file size, in bytes	340190685
file size, in human friendly format	324.4 MiB
md5	96e842ef2d5789411c550b0f9bce2314
sha256	54c06cd1b11cb687db6ba3613df443c057f769cdb87693e11674d956d8e50

## Hashes for Anaconda2-4.0.0-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1459268097.0
time file was last modified, in human readable format	2016-03-29 11:14:57
exact file size, in bytes	348392297
file size, in human friendly format	332.3 MiB
md5	f87d5a014499bd9a579ada3939eb22b1
sha256	41341c840cea4185ef5bd82520c1de72b42e7dc43c703fb13b032f04dc0e3

## Hashes for Anaconda2-2.5.0-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1454535714.0
time file was last modified, in human readable format	2016-02-03 15:41:54
exact file size, in bytes	346405513
file size, in human friendly format	330.4 MiB
md5	aeefe284ae4b870ca252da9e46c5d46c9
sha256	4911047df51c46661f551d6022aee21a7e5d31df051d3433b8ff3ea3c2e77

### Hashes for Anaconda2-2.4.1-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1449608450.0
time file was last modified, in human readable format	2015-12-08 15:00:50
exact file size, in bytes	260583576
file size, in human friendly format	248.5 MiB
md5	2e6983f8fdd5f07025f3a81587c82549
sha256	2388cc714567afe7697bf43b4063ff0ea2150a71b9beb17f75bc7e4879d9b

### Hashes for Anaconda2-2.4.0-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1446502939.0
time file was last modified, in human readable format	2015-11-02 16:22:19
exact file size, in bytes	293453735
file size, in human friendly format	279.9 MiB
md5	3fc53407f4a14fe18974d6fb59fc4d3e
sha256	478a8fdde3a6e4040a68c57d7bdd6fab1a4f7f6e813948d46dad54867014c

## Hashes for Anaconda-2.3.0-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1435775709.0
time file was last modified, in human readable format	2015-07-01 13:35:09
exact file size, in bytes	324643869
file size, in human friendly format	309.6 MiB
md5	f2459d60a668eb82ff590f97755d93e0
sha256	73fdbbb3e38207ed18e5059f71676d18d48fdccbc455a1272eb45a60376cc

## Hashes for Anaconda-2.2.0-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1427314794.0
time file was last modified, in human readable format	2015-03-25 15:19:54
exact file size, in bytes	317885231
file size, in human friendly format	303.2 MiB
md5	e3c3a2dae51a41c5a1cbb959ef68ef2c
sha256	6437d5b08a19c3501f2f5dc3ae1ae16f91adf6bed0f067ef0806a9911b1be

## Hashes for Anaconda-2.1.0-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1411660230.0
time file was last modified, in human readable format	2014-09-25 10:50:30
exact file size, in bytes	336767704
file size, in human friendly format	321.2 MiB
md5	3289883a21fdd9fe4fb84748bfff677bf
sha256	fd70c08719e6b5caae45b7c8402c6975a8cbc0e3e2a9c4c977554d1784f28

### Hashes for Anaconda-2.0.1-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1402603361.0
time file was last modified, in human readable format	2014-06-12 15:02:41
exact file size, in bytes	324151704
file size, in human friendly format	309.1 MiB
md5	0f680aa6dc7150d15123e5490e46eaaad
sha256	e8fffc63f31673b5ce41a95796a1f729ddcf4c7db19d6dbe29bedaeaaaf8478

### Hashes for Anaconda-2.0.0-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1401313836.0
time file was last modified, in human readable format	2014-05-28 16:50:36
exact file size, in bytes	312856983
file size, in human friendly format	298.4 MiB
md5	48b6773dacf45e4df0da91cfc149bb23
sha256	efb9d3987134d484d88a9d915437b1bd568d065b4fefbd538e0281694bd90

## Hashes for Anaconda-1.9.2-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1396996389.0
time file was last modified, in human readable format	2014-04-08 17:33:09
exact file size, in bytes	431825310
file size, in human friendly format	411.8 MiB
md5	c8f72746dd5dc68f014d5fccd1f060e8
sha256	1f7c850d0b98c011a717b3b757d82077accf0704dd7627f6962267bfb4476

## Hashes for Anaconda-1.9.1-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1392924896.0
time file was last modified, in human readable format	2014-02-20 13:34:56
exact file size, in bytes	431763871
file size, in human friendly format	411.8 MiB
md5	f1505963a1c7d2bfe7a73c079b22762d
sha256	9aa39c05f723fee18c54a9cc1729986193216affedbae125ca5faa0674030

## Hashes for Anaconda-1.9.0-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1392049410.0
time file was last modified, in human readable format	2014-02-10 10:23:30
exact file size, in bytes	571806071
file size, in human friendly format	545.3 MiB
md5	11af2251aece5fc4333822dc25f78938
sha256	16471e90b3deb7be1b3d449d8883983d81f035dfaa1a3391497de20577de6

### Hashes for Anaconda-1.8.0-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1383601049.0
time file was last modified, in human readable format	2013-11-04 15:37:29
exact file size, in bytes	412040120
file size, in human friendly format	393.0 MiB
md5	5028bf0aa7ff8a071d5532b8f8ec924c
sha256	2c08a5cd6ccaa9dc84063b0ee9b007aa82e35a75c340fb272b394896de853

### Hashes for Anaconda-1.7.0-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1378677746.0
time file was last modified, in human readable format	2013-09-08 17:02:26
exact file size, in bytes	399536902
file size, in human friendly format	381.0 MiB
md5	bbde22bd0346ad9c8932b4d98c0f4000
sha256	af372a27a1887e11061485e2a854c535775fd519713e028c38901f90c869c

## Hashes for Anaconda-1.6.1-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1372784347.0
time file was last modified, in human readable format	2013-07-02 11:59:07
exact file size, in bytes	259053521
file size, in human friendly format	247.1 MiB
md5	06412ae8de02c87b8de7d7e6d35ed092
sha256	745b9452fd18720deefb465a6687c0d66df8f11edceadcee758082dea1b8e

## Hashes for Anaconda-1.6.0-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1371842619.0
time file was last modified, in human readable format	2013-06-21 14:23:39
exact file size, in bytes	253329362
file size, in human friendly format	241.6 MiB
md5	7a7f1f53684d38a7aa36935e34af30a3
sha256	d6aeedfcb39d648fdb5bd72c4d0b3063a9d4f4866baf5052aa0645bf5d2c

## Hashes for Anaconda-1.5.0-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.



exact time file was last modified, as Unix time stamp	1368022723.0
time file was last modified, in human readable format	2013-05-08 09:18:43
exact file size, in bytes	250369347
file size, in human friendly format	238.8 MiB
md5	2a75cab6536838635fd38ee7fd3e2411
sha256	ca7e356dc1b8c8ef27dfb74b32c77563df704c6ddb39e69cac65ec416ebfe

### Hashes for Anaconda-1.4.0-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/> .

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1362869213.0
time file was last modified, in human readable format	2013-03-09 16:46:53
exact file size, in bytes	231260549
file size, in human friendly format	220.5 MiB
md5	d5826bb10bb25d2f03639f841ef2f65f
sha256	065284c5de369c9b89dcae79e7169ce9b734dc3bbe6c409a67a5ec6480cc0

### Anaconda with Python 3 on 32-bit Linux

To verify the file integrity using MD5 or SHA-256, see [cryptographic hash verification](#).

### Hashes for Anaconda3-2018.12-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/> .

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.



exact time file was last modified, as Unix time stamp	1545419594.11939
time file was last modified, in human readable format	2018-12-21 13:13:14
exact file size, in bytes	569068646
file size, in human friendly format	542.7 MiB
md5	4c9922d1547128b866c6b9cf750c03c7
sha256	7895052814921d45ed0585d1fb19f8edd6fbd02b61639310f770e2ebe85cc

### Hashes for Anaconda3-5.3.1-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1542656329.3057752
time file was last modified, in human readable format	2018-11-19 13:38:49
exact file size, in bytes	552879060
file size, in human friendly format	527.3 MiB
md5	6878b6393add83e5fe77d7a1a27ee789
sha256	5dab8b2c95595df7fa55b88643f8372135c14faabd9ec05a34021551bb099

### Hashes for Anaconda3-5.3.0-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1538082097.2866592
time file was last modified, in human readable format	2018-09-27 16:01:37
exact file size, in bytes	552786900
file size, in human friendly format	527.2 MiB
md5	34fe38d086f069656c2f3cbf13b87460
sha256	c15ffac2ae35179a15dc5872e5bb405b4027a0fd76c6817e9cee39545bc5c

### Hashes for Anaconda3-5.2.0-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/> .

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1527703546.172479
time file was last modified, in human readable format	2018-05-30 13:05:46
exact file size, in bytes	531957909
file size, in human friendly format	507.3 MiB
md5	81d5a1648e3aca4843f88ca3769c0830
sha256	f3527d085d06f35b6aeb96be2a9253ff9ec9ced3dc913c8e27e086329f3db

### Hashes for Anaconda3-5.1.0-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/> .

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1518707338.3619494
time file was last modified, in human readable format	2018-02-15 09:08:58
exact file size, in bytes	471561932
file size, in human friendly format	449.7 MiB
md5	793a94ee85baf64d0ebb67a0c49af4d7
sha256	0e940272517d8f8a6f26316a19e4be2bdaea8477a3a32cc2ecee7b48fd0fa

### Hashes for Anaconda3-5.0.1-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/> .

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1508800071.267042
time file was last modified, in human readable format	2017-10-23 18:07:51
exact file size, in bytes	451929576
file size, in human friendly format	431.0 MiB
md5	d967f023a23698109fe213103a2c07bf
sha256	991a4b656fcb0236864fbb27ff03bb7f3d98579205829b76b66f65cfa6734

### Hashes for Anaconda3-5.0.0.1-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1506959415.21842
time file was last modified, in human readable format	2017-10-02 10:50:15
exact file size, in bytes	450639191
file size, in human friendly format	429.8 MiB
md5	8b6902d20063e6c3b98ebe70060f3131
sha256	407576899d3aa546bc3c2c4a13cbc18ab5bab372c3388ea80087f29b32184

### Hashes for Anaconda3-5.0.0-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1506455282.980888
time file was last modified, in human readable format	2017-09-26 14:48:02
exact file size, in bytes	450106703
file size, in human friendly format	429.3 MiB
md5	8120fcd072916e4a28d0179be8d29053
sha256	634d2dfa97d19f2cc15e941cb4d059bc83a31facedfb9d02a980c4fa74f27

### Hashes for Anaconda3-4.4.0-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1495841025.0
time file was last modified, in human readable format	2017-05-26 18:23:45
exact file size, in bytes	449473324
file size, in human friendly format	428.7 MiB
md5	8556e85f81206c08ee2a30b67d1bb707
sha256	b0e492206d43067314b25963bc7d1f012096ca0323b7629f4ebcd071b0390

### Hashes for Anaconda3-4.3.1-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1488838367.0
time file was last modified, in human readable format	2017-03-06 16:12:47
exact file size, in bytes	418659792
file size, in human friendly format	399.3 MiB
md5	d8986b1503f3b42220be9bfb8a92100e
sha256	7b70bdba282a18ddbdc167afe8131f7532076cb1df8d3fbbd13e79ca3afaa

### Hashes for Anaconda3-4.3.0-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1485548069.0
time file was last modified, in human readable format	2017-01-27 14:14:29
exact file size, in bytes	417717702
file size, in human friendly format	398.4 MiB
md5	3f173aa1ab2c2b6ab3f8a6bd22827fd7
sha256	f7ce2eeec3e42c2ba1ee3b9fcd670478fd30f4be547c6e0a675d183c4ca9d

### Hashes for Anaconda3-4.2.0-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1475009434.0
time file was last modified, in human readable format	2016-09-27 15:50:34
exact file size, in bytes	392066694
file size, in human friendly format	373.9 MiB
md5	7aca10e1ea5b9db0a318b4eed5253747
sha256	1a8320635f2f06ec9d8610e77d6d0f9cb2c5d11d20a4ff7fcdad113e04b0a8

### Hashes for Anaconda3-4.1.1-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1467994802.0
time file was last modified, in human readable format	2016-07-08 11:20:02
exact file size, in bytes	345064389
file size, in human friendly format	329.1 MiB
md5	0576a0df8987ca62d5c13491102547d9
sha256	931626363f4030c7a1e8897549b1d3589dc3f429874dc3dd8a79869ecf5c8

### Hashes for Anaconda3-4.1.0-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1467131312.0
time file was last modified, in human readable format	2016-06-28 11:28:32
exact file size, in bytes	344388621
file size, in human friendly format	328.4 MiB
md5	302fddc310233f5e6f120753ec3e392d
sha256	7764093f337a43e4962b12d01508c1a385f0f62c1ddc006b69af95ae763fc

### Hashes for Anaconda3-4.0.0-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1459268103.0
time file was last modified, in human readable format	2016-03-29 11:15:03
exact file size, in bytes	353266156
file size, in human friendly format	336.9 MiB
md5	c88cbe27cc8fb4976e6bd38068cc57d6
sha256	e1469fa0d24de12f33661ce3d7a06d77968be8822f366a61a0018a3850ab5

### Hashes for Anaconda3-2.5.0-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1454535727.0
time file was last modified, in human readable format	2016-02-03 15:42:07
exact file size, in bytes	350634167
file size, in human friendly format	334.4 MiB
md5	e1d4e9480b44ea0905cbf39846778f8b
sha256	22ac26c8bde7c4153ea859f6f6d8aca93bbf1e213d800167ad5ea530c6295

### Hashes for Anaconda3-2.4.1-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1449608453.0
time file was last modified, in human readable format	2015-12-08 15:00:53
exact file size, in bytes	265518790
file size, in human friendly format	253.2 MiB
md5	82f1f438ac83ed8b7d36284995f6939b
sha256	00d13413f5b8129e863dabcc2296a181c697056c5ed210739a0aa06454ab7

### Hashes for Anaconda3-2.4.0-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1446502942.0
time file was last modified, in human readable format	2015-11-02 16:22:22
exact file size, in bytes	290842015
file size, in human friendly format	277.4 MiB
md5	423f0300cbec30c206a6c61f7e5dc9bd
sha256	f6080c6493cefc603cfeb67aaf6c3c4c6b80a66788f03db48ffd3cfa52017



### Hashes for Anaconda3-2.3.0-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/> .

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1435775713.0
time file was last modified, in human readable format	2015-07-01 13:35:13
exact file size, in bytes	338272927
file size, in human friendly format	322.6 MiB
md5	72b14bfd85f2597089c4372225a96d42
sha256	4cc10d65c303191004ada2b6d75562c8ed84e42bf9871af06440dd956077b

### Hashes for Anaconda3-2.2.0-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/> .

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1427314807.0
time file was last modified, in human readable format	2015-03-25 15:20:07
exact file size, in bytes	328483185
file size, in human friendly format	313.3 MiB
md5	fe3681d49ff5b0d755181f553689ed9e
sha256	223655cd256aa912dfc83ab24570e47bb3808bc3b0c6bd21b5db0fcf27508

### Hashes for Anaconda3-2.1.0-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/> .

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.



exact time file was last modified, as Unix time stamp	1411660235.0
time file was last modified, in human readable format	2014-09-25 10:50:35
exact file size, in bytes	333141910
file size, in human friendly format	317.7 MiB
md5	462665c149b14f7c3993bc51e4d10f88
sha256	657cb599004c21e37ce693515ea33922e0084fd7c159ef1b96b57c86eed83

### Hashes for Anaconda3-2.0.1-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1402603200.0
time file was last modified, in human readable format	2014-06-12 15:00:00
exact file size, in bytes	301673940
file size, in human friendly format	287.7 MiB
md5	86213516c4c2e479d8d9834b89c95bed
sha256	21293fabbd3d5cfbb1afe0c9a8b39e0bc4d283cd7dbe3c84a60b335481a41

### Hashes for Anaconda3-2.0.0-Linux-x86.sh

All installer files are available at <https://repo.anaconda.com/archive/>.

You can verify the data integrity of the Anaconda installer files by [running a local program to generate their MD5 or SHA-256 cryptographic hashes](#) and checking the output to be sure it matches the hashes (or “checksums”) below.

If the MD5 or SHA-256 hash that you generate does not match the one here, the file may not have downloaded completely. Please download it again and re-check. If repeated downloads produce the same result, please [contact us](#) to report the problem, including the file name, whether you used MD5 or SHA-256, the hash you generated, and the hash on the site.

exact time file was last modified, as Unix time stamp	1401226555.0
time file was last modified, in human readable format	2014-05-27 16:35:55
exact file size, in bytes	290973139
file size, in human friendly format	277.5 MiB
md5	860a11c39e58bb574bad5be9d44e2063
sha256	439761159d5604e182951650a478dd53caff52e9dccc17c20ae66689b7b28

### Updating from older versions

You can easily update Anaconda to the latest version.

- Windows: Open the Start Menu and choose Anaconda Prompt.
- macOS or Linux: Open a terminal window.

Enter these commands:

```
conda update conda
conda update anaconda=VersionNumber
```

### More information

The below content provides more details about what is happening when you update Anaconda.

`conda update anaconda=VersionNumber` grabs the specific release of the Anaconda metapackage, for example `conda update anaconda=2019.10`. That metapackage represents a pinned state that has undergone testing as a collection. Read more about [metapackages](#).

There is a special “custom” version of the Anaconda metapackage that has all the package dependencies, but none of them are constrained. The “custom” version is lower in version ordering than any actual release number. `conda update anaconda=VersionNumber` may remove packages if the new metapackage that is replacing your old one has removed packages. As of conda 4.7, when a package loses its connection to the set of specs that have been requested in the past, it gets removed.

See all of the [available Anaconda versions](#).

`conda update --all` will unpin everything. This updates all packages in the current environment to the latest version. In doing so, it drops all the version constraints from the history and tries to make everything as new as it can.

This has the same behavior with removing packages. If any packages are orphaned by an update, they are removed. `conda update --all` may not be able to make everything the latest versions because you may have conflicting constraints in your environment.

With Anaconda 2019.07’s newer Anaconda metapackage, `conda update --all` will make the metapackage go to the custom version in order to update other specs.

`conda update --all` will only update the selected environment. If you have other environments you’d like to update, you can update them in the command line:

```
conda update -n myenv --all
```

When you use `conda update pkgName` or `conda install pkgName`, conda may not be able to update or install that package without changing something else you specified in the past.

In the case of the Anaconda metapackage, when you say `conda update ipython` but you have Anaconda 2019.03, conda can and should “downgrade” Anaconda to the “custom” version so that iPython can be updated.

When conda cannot fulfill the request for the latest package available, it usually means that newer packages exist for your spec but are in conflict. To force the change, you can try `conda install pkg=newversion`.

### Uninstalling Anaconda

To uninstall Anaconda, you can do a simple remove of the program. This will leave a few files behind, which for most users is just fine. See Option A.

If you also want to remove all traces of the configuration files and directories from Anaconda and its programs, you can download and use the Anaconda-Clean program first, then do a simple remove. See Option B.

1. Option A. Use simple remove to uninstall Anaconda:

- **Windows**

- Use Windows Explorer to delete the envs and pkgs folders prior to running the uninstall in the root of your installation.
- In the Control Panel, choose Add or Remove Programs or Uninstall a program, and then select Python 3.6 (Anaconda) or your version of Python.

- **macOS**

- Open the Terminal.app or iTerm2 terminal application, and then remove your entire Anaconda directory, which has a name such as `anaconda2`, `anaconda3`, or `~/opt`. Enter `rm -rf ~/anaconda3` to remove the directory.

- **Linux**

- Open a terminal window, and then remove your entire Anaconda directory, which has a name such as `anaconda2` or `anaconda3`, by entering `rm -rf ~/anaconda3`.

2. Option B. Full uninstall using Anaconda-Clean and simple remove.

---

**Note:** Anaconda-Clean must be run before simple remove.

---

- Install the Anaconda-Clean package from Anaconda Prompt (terminal on Linux or macOS):

```
conda install anaconda-clean
```

- In the same window, run one of these commands:

- Remove all Anaconda-related files and directories with a confirmation prompt before deleting each one:

```
anaconda-clean
```

- Or, remove all Anaconda-related files and directories without being prompted to delete each one:

```
anaconda-clean --yes
```

Anaconda-Clean creates a backup of all files and directories that might be removed in a folder named `.anaconda_backup` in your home directory. Also note that Anaconda-Clean leaves your data files in the `AnacondaProjects` directory untouched.

- After using Anaconda-Clean, follow the instructions above in Option A to uninstall Anaconda.

## Removing Anaconda path from `.bash_profile`

If you use Linux or macOS, you may also wish to check the `.bash_profile` file in your home directory for a line such as:

```
export PATH="/Users/jsmith/anaconda3/bin:$PATH"
```

---

**Note:** Replace `/Users/jsmith/anaconda3/` with your actual path.

---

This line adds the Anaconda path to the PATH environment variable. It may refer to either Anaconda or Miniconda. After uninstalling Anaconda, you may delete this line and save the file.

### Silent mode install

You can use *silent mode* to automatically accept default settings and have no screen prompts appear during installation.

### Using Anaconda on older operating systems

We recommend upgrading your operating system. Most OS that are no longer supported in the latest Anaconda are no longer getting security updates. Upgrading your OS allows you to get the latest packages, performance improvements, bug fixes, etc.

To use Anaconda on older operating systems, download from our [archive](#). You will not be able to use conda to update or install packages beyond the Anaconda version noted in the table below, unless you limit it to versions available at the time that particular version of Anaconda was released. You can see what was available by checking the [package table archives](#).

Table 32: Outdated operating system support

Operating system	How to install Anaconda
macOS 10.10-10.12; Windows 7	Use the command line or graphical installers for Anaconda versions 2019.10 and earlier. Download from our <a href="#">archive</a> .
macOS 10.9	Use the command line or graphical installers for Anaconda versions 5.1 and earlier.  <b>Note:</b> Qt and other packages released after Anaconda Distribution 5.1 (February 15th, 2018) may not work on macOS 10.9, so it may be necessary to not update certain packages beyond this point.
macOS 10.7 and 10.8	Use the command line installers for Anaconda versions 4.2 and earlier.
macOS 10.5 and 10.6	Use the command line installers for Anaconda versions 1.8 and earlier.  <b>Note:</b> These installer files end in <code>.sh</code> , not <code>.pkg</code> .
Windows XP	Use Anaconda versions 2.2 and earlier.
Centos5 (or equivalent)	Use Anaconda versions 4.3 and earlier.

### Installing Anaconda on a non-networked machine (air gap)

1. Obtain a local copy of the appropriate Anaconda installer for the non-networked machine. You can copy the Anaconda installer to the target machine using many different methods including a portable hard drive, USB drive, or CD.

2. After copying the installer to the non-networked machine, follow the detailed installation instructions for your operating system.

---

**Note:** You can install offline copies of both [docs.anaconda.com](https://docs.anaconda.com) and [enterprise-docs.anaconda.com](https://enterprise-docs.anaconda.com) by installing the conda package `anaconda-docs`: `conda install anaconda-docs`

You can install offline copies of documentation for many of Anaconda's open-source packages by installing the conda package `anaconda-oss-docs`: `conda install anaconda-oss-docs`

---

### Other ways to get Anaconda or Miniconda

You can find the official [Anaconda or Miniconda AMIs](#) on the AWS Marketplace.

You can find the official [Anaconda and Miniconda Docker images](#) on Docker Hub.

If you have a CDH cluster, you can [install the Anaconda parcel](#) using Cloudera Manager. The Anaconda parcel provides a static installation of Anaconda, based on Python 2.7, that can be used with Python and PySpark jobs on the cluster.

### Troubleshooting

If you experience errors during the installation process, review our [Troubleshooting topics](#).

## 4.2.2 User guide

Use the following resources to learn how to use Anaconda Individual Edition, including Anaconda Navigator and conda.

### Just starting out?

If you're new to Anaconda, follow the directions at [Getting started with Anaconda](#) to write your first Python project using Anaconda. Use the navigation tabs at the bottom of the page to go through the user guide in order.

### New to Navigator?

Read the [Navigator user guide](#) to learn how to use Anaconda's graphical user interface. Get an [overview of the interface](#) and take your first steps using Navigator at [Getting started with Navigator](#).

### Interested in conda?

Conda is an open source package management system and environment management system included in Anaconda and Miniconda. Learn [how to get started with conda](#).

### Ready to dive deeper?

Explore what you can do with Anaconda. The [tasks page](#) shows you how to [install conda packages](#), [switch between environments](#), [use IDEs](#), and more.

### Ready to contribute to Anaconda?

See [How to contribute to Anaconda](#) by helping resolve issues, improve documentation, add to feedstocks, and contribute code.

### Additional resources

- [Anaconda cheatsheet](#)
- [Frequently asked questions](#)

## Getting started with Anaconda

Anaconda Individual Edition contains [conda](#) and [Anaconda Navigator](#), as well as Python and hundreds of scientific [packages](#). When you installed Anaconda, you installed all these too.

Conda works on your command line interface such as Anaconda Prompt on Windows and terminal on macOS and Linux.

Navigator is a desktop graphical user interface that allows you to launch applications and easily manage conda packages, environments, and channels without using command-line commands.

You can try both conda and Navigator to see which is right for you to manage your packages and environments. You can even switch between them, and the work you do with one can be viewed in the other.

Try this simple programming exercise, with [Navigator](#) and the [command line](#), to help you decide which approach is right for you.

When you're done, see [What's next?](#).

## Your first Python program: Hello, Anaconda!

Use Anaconda Navigator to launch an application. Then, create and run a simple Python program with Spyder and Jupyter Notebook.

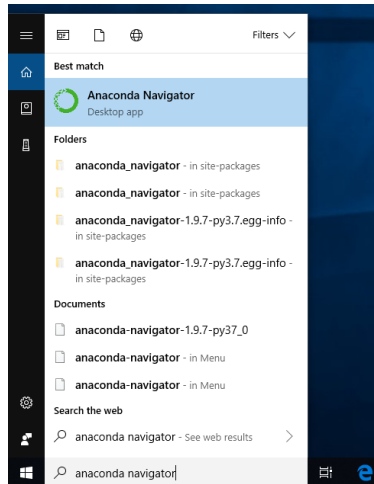
## Open Navigator

Choose the instructions for your operating system.

- *Windows.*
- *macOS.*
- *Linux.*

### Windows

From the Start menu, click the Anaconda Navigator desktop app.



### macOS

Open Launchpad, then click the Anaconda Navigator icon.



### Linux

Open a terminal window and type `anaconda-navigator`.

## Run Python in Spyder IDE (integrated development environment)

---

**Tip:** Navigator's Home screen displays several applications for you to choose from. For more information, see links at the bottom of this page.

---

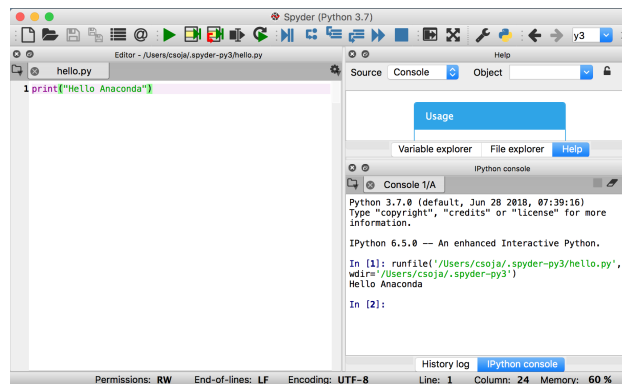
1. On Navigator's Home tab, in the Applications pane on the right, scroll to the Spyder tile and click the Install button to install Spyder.

---

**Note:** If you already have Spyder installed, you can jump right to the Launch step.

---

2. Launch Spyder by clicking Spyder's Launch button.
3. In the new file on the left, delete any placeholder text, then type or copy/paste `print ("Hello Anaconda")`.
4. In the top menu, click File - Save As and name your new program `hello.py`.
5. Run your new program by clicking the triangle Run button.
6. You can see your program's output in the bottom right Console pane.



## Close Spyder

From Spyder's top menu bar, select Spyder - Quit Spyder (In macOS, select Python - Quit Spyder).

## Run Python in a Jupyter Notebook

1. On Navigator's Home tab, in the Applications pane on the right, scroll to the Jupyter Notebook tile and click the Install button to install Jupyter Notebook.

---

**Note:** If you already have Jupyter Notebook installed, you can jump right to the Launch step.

---

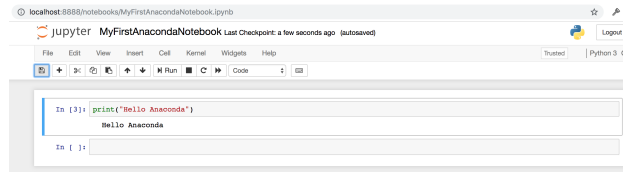
2. Launch Jupyter Notebook by clicking Jupyter Notebook's Launch button.

This will launch a new browser window (or a new tab) showing the [Notebook Dashboard](#).





3. On the top of the right hand side, there is a dropdown menu labeled “New”. Create a new Notebook with the Python version you installed.
4. Rename your Notebook. Either click on the current name and edit it or find rename under File in the top menu bar. You can name it to whatever you’d like, but for this example we’ll use MyFirstAnacondaNotebook.
5. In the first line of the Notebook, type or copy/paste `print ("Hello Anaconda")`.
6. Save your Notebook by either clicking the save and checkpoint icon or select File - Save and Checkpoint in the top menu.
7. Run your new program by clicking the Run button or selecting Cell - Run All from the top menu.



## Close Jupyter Notebook

1. From Jupyter Notebooks top menu bar, select File - Close and Halt.
2. Click the Quit button at the upper right of the Notebook Dashboard and close the window or tab.

## Close Navigator

From Navigator’s top menu bar, select Anaconda Navigator - Quit Anaconda-Navigator.

## Write a Python program using Anaconda Prompt or terminal

### Open Anaconda Prompt

Choose the instructions for your operating system.

- *Windows.*
- *macOS.*
- *Linux.*

#### Windows

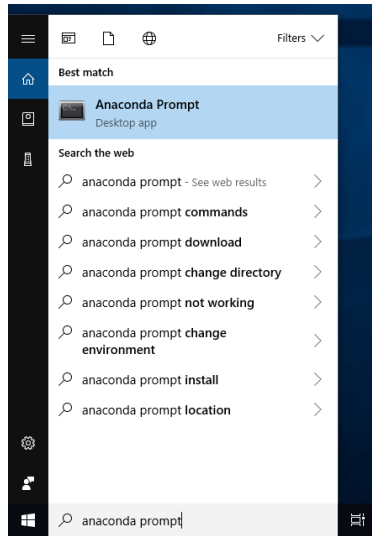
From the Start menu, search for and open “Anaconda Prompt”:

#### macOS

Open Launchpad, then click the terminal icon.

#### Linux

Open a terminal window.



### Start Python

At Anaconda Prompt (terminal on Linux or macOS), type `python` and press Enter.

The `>>>` means you are in Python.

### Write a Python program

At the `>>>`, type `print ("Hello Anaconda!")` and press Enter.

When you press enter, your program runs. The words “Hello Anaconda!” print to the screen. You’re programming in Python!

### Exit Python

On Windows, press CTRL-Z and press Enter. On macOS or Linux type `exit()` and press Enter.

### Optional: Launch Spyder or Jupyter Notebook from the command line

1. At the Anaconda Prompt (terminal on Linux or macOS), type `spyder` and press Enter. Spyder should start up just like it did when you launched it from Anaconda Navigator.
2. Close Spyder the same way you did in the previous exercise.
3. At the Anaconda Prompt (terminal on Linux or macOS), type `jupyter-notebook` and press Enter.

Jupyter Notebook should start up just like it did when you launched it from Anaconda Navigator. Close it the same way you did in the previous exercise.

### What’s next?

#### Using Navigator

- [Getting started with Navigator \(10 minutes\)](#)

- [Navigator user guide](#)

## Using conda

- [Getting started with conda \(20 minutes\)](#)
- [Conda cheat sheet](#)
- [Conda user guide](#)

## Using Spyder

- [Spyder Project Homepage](#)
- [Spyder Documentation](#)

## Using Jupyter Notebook

- [Jupyter Notebook Beginner's Guide](#)
- [Jupyter Project Homepage](#)
- [Jupyter Notebook Documentation](#)

## Links to IDE documentation

- [\*Eclipse and PyDev\*](#)
- [\*IDLE\*](#)
- [\*Sublime Text\*](#)
- [\*Ninja IDE\*](#)
- [\*Python Tools for Visual Studio \(PTVS\)\*](#)
- [\*Python for Visual Studio Code\*](#)
- [\*Spyder\*](#)
- [\*Wing IDE\*](#)
- [\*IntelliJ\*](#)

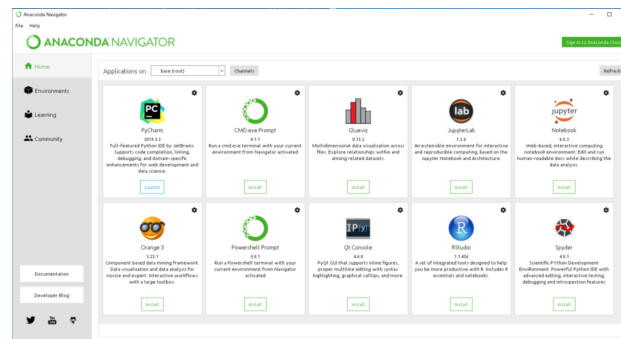
## Anaconda Navigator

*Desktop Portal to Data Science*

## Overview

This page describes the tabs, menus, and buttons in the Anaconda Navigator window.

- *Online and offline modes*
- *Home tab*
- *Environments tab*
- *Learning tab*
- *Community tab*
- *File menu*
- *Help menu*
- *Navigator window buttons*



The tabs in the left column represent the main components in Navigator. Click a tab to open it.

**Tip:** To learn more about terms used in Anaconda, see the *Glossary*.

## Online and offline modes

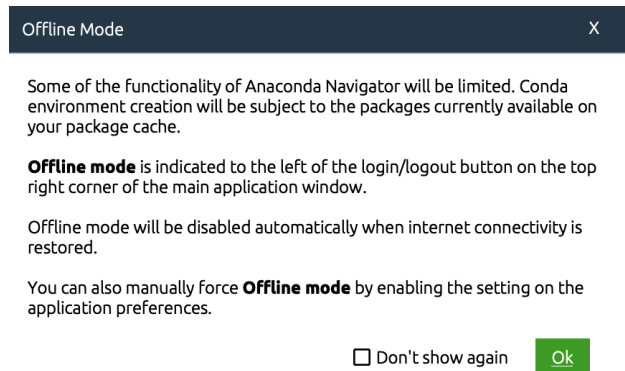
Normally Navigator is used online so that it can download and install packages.

In online mode, Navigator must be able to reach these sites, so they may need to be whitelisted in your network's firewall settings.

- <https://repo.anaconda.com>
- <https://conda.anaconda.org> for conda-forge and other channels on Anaconda Cloud (anaconda.org)
- google-public-dns-a.google.com (8.8.8.8:53) to check internet connectivity with [Google Public DNS](#)

## Offline mode

If Navigator detects that internet access is not available, it automatically enables offline mode and displays this message:



In the Preferences dialog, select “Enable offline mode” to enter offline mode even if internet access is available.

Using Navigator in offline mode is equivalent to using the command line conda commands `create`, `install`, `remove`, and `update` with the flag `--offline` so that conda does not connect to the internet.

## Home tab

The **Home** tab, shown in the image above, displays all of the available applications that you can manage with Navigator.

The first time you open Navigator, the following popular graphical Python applications are already installed or are available to install:

- JupyterLab
- Jupyter notebook
- Orange data visualization
- Spyder IDE
- Glueviz multidimensional data visualization
- R Studio IDE
- PyCharm
- VS Code
- Anaconda Prompt (Windows only)
- Anaconda PowerShell (Windows only)

You can also *build your own Navigator applications*.

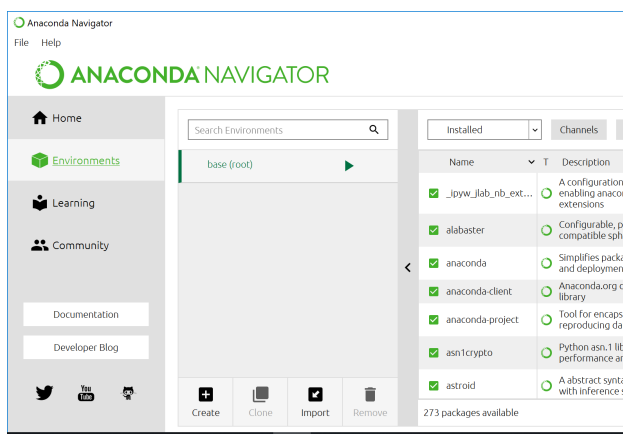
In each application box, you can:

- Launch the application—Click its Launch button.
- Install an application—Click its Install button.
- Update, remove, or install a specific version of an application—Click the gear icon in the top right corner of the application box.

Applications are installed in the active environment, which is displayed in the “Applications on” list. To install an application in a specific environment, first select the environment in the list, then click the application’s Install button. You can also create a new environment on the **Environments** tab, then return to the **Home** tab to install packages in the new environment.

### Environments tab

The **Environments** tab allows you to manage installed *environments*, *packages*, and *channels*.



The left column lists your environments. Click an environment to activate it.

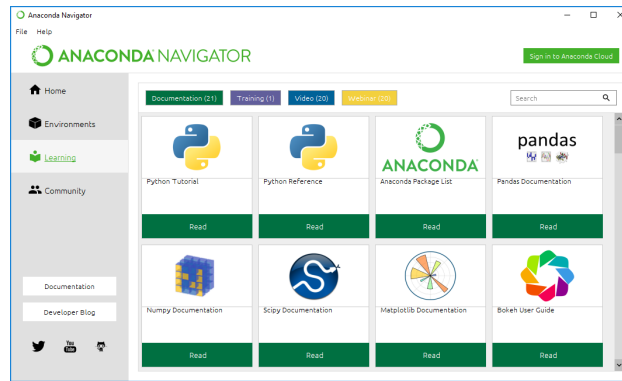
With Navigator, like with conda, you can create, export, list, remove, and update environments that have different versions of Python and/or packages installed. Switching or moving between environments is called activating the environment. Only one environment is active at any point in time. For more information, see [Managing environments](#).

The right column lists packages in the current environment. The default view is Installed packages. To change which packages are displayed, click the arrow next to the list, then select Not Installed, Upgradeable, or All packages. For more information, see [Managing packages](#).

Channels are locations where Navigator or conda looks for packages. Click the Channels button to open the Channels Manager. For more information, see [Managing channels](#).

### Learning tab

On the **Learning** tab you can learn more about Navigator, the Anaconda platform and open data science. Click the Documentation, Training, Webinars, or Video buttons, then click any item to open it in a browser window.



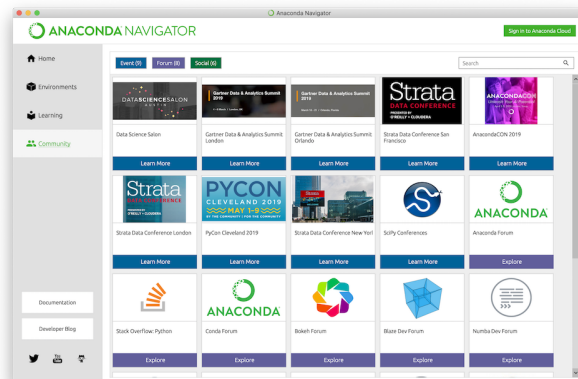
## Community tab

On the **Community** tab you can learn more about events, free support forums, and social networking relating to Navigator. Click the Events, Forum, or Social buttons, then click any item to open it in a browser window.

---

**Tip:** To get help with Anaconda and Navigator from the community, join the [Anaconda forum](#).

---



## File menu

The Navigator **File** menu (**Anaconda Navigator** on macOS) contains the following options:

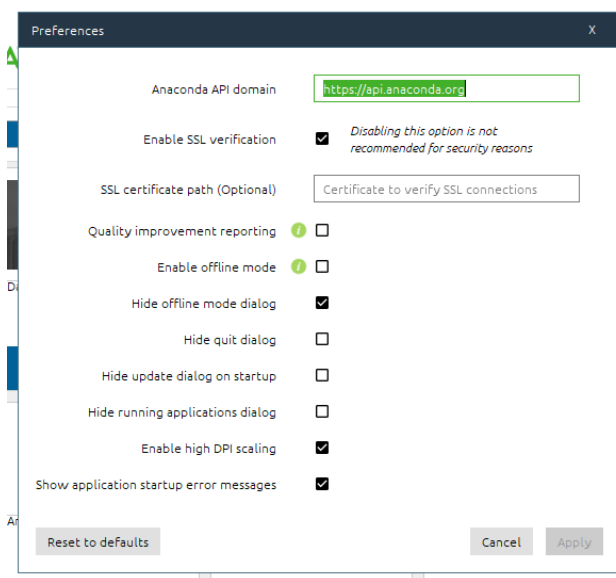
- About—displays information about Navigator, including a link for bug reports and feature requests. In Linux this is in the Help menu.
- Preferences—allows you to set your Navigator preferences. In the Preferences window you can:
  - Reset the Anaconda API domain to point to a local Anaconda repository instead of Anaconda Cloud.
  - Enable or disable SSL verification.
  - Optionally set a certificate to verify SSL connections.
  - Toggle the option to provide personally non-identifiable information to help improve the product.

- Enable or disable offline mode.
- Hide the offline mode dialog box.
- Hide the Quit dialog box when exiting the program.
- Hide the Update dialog box when starting the program.
- Hide the Close running applications dialog, which normally displays when exiting the program if there are still running applications that were launched from Navigator.
- Modify Navigator’s display with Enable High DPI scaling option. This option can be useful if Navigator isn’t displaying correctly on some high DPI screens.
- Show application startup error messages.

---

**Tip:** Click the Reset to defaults button to change preferences back to their default values.

---



- Services (macOS only)—links to your computer’s system preferences menu.
- Hide Anaconda-Navigator (macOS only)—hides the Navigator window.
- Hide Others (macOS only)—hides all windows except the Navigator window.
- Show All (macOS only)—shows all windows including the Navigator window.
- Quit Anaconda-Navigator—exits Navigator.

## Help menu

The **Help** menu contains the following options:

- Search—links to your computer’s Help (Windows and macOS only).



- Online Documentation—links to this documentation, which you can read in any web browser. You can also open the documentation by clicking the Documentation button at the bottom left of the Navigator window.
- Logs viewer—allows you to review the logs of all actions performed in Navigator in the current session. This option displays a list of log files, including `navigator.log`, which contains Navigator application logs, and `condamanager.log`, which contains logs written by the conda-manager component.

---

**Note:** A new log file is created every time you run Navigator, with a sequential number appended to the file name. More recent log files have higher numbers.

---

### Navigator window buttons

- Sign in to Anaconda Cloud—displayed at the top right. Click to sign into Anaconda Cloud (Anaconda.org) and enable searching for packages on it. After you have logged in, the button label changes to “Signed in as [username].”
- Documentation—displayed at the bottom left. Click to open Navigator documentation in a browser.
- Developer Blog—displayed at the bottom left. Click to read what our developers have to say about Navigator development.
- Social media—displayed at the bottom left. Click to see our Twitter, YouTube, and GitHub pages.

## Installation

### System requirements

Operating systems: Navigator supports the same operating systems that the Anaconda Distribution supports. These include:

- Windows 8 or newer, 32-bit or 64-bit.
- macOS 10.13+, 64-bit.
- Ubuntu 14+/Centos6+, 64-bit.

Python: Versions 2.7, 3.6, 3.7, and 3.8.

To use Navigator in *online mode*, you must be able to reach these sites, so you may need to add them to a whitelist in your network’s firewall settings.

- <https://repo.anaconda.com> for repositories and installers
- <https://conda.anaconda.org> for conda-forge and other channels on Anaconda Cloud (anaconda.org)
- google-public-dns-a.google.com (8.8.8.8:53) to check internet connectivity with [Google Public DNS](#)

### Installing Navigator

Navigator is automatically installed when you install *Anaconda* version 4.0.0 or higher.

If you have *Miniconda* or an older version of Anaconda installed, you can install Navigator from an Anaconda Prompt by running the command `conda install anaconda-navigator`.

To start Navigator, see *Getting Started*.

## Uninstalling Navigator

To uninstall Anaconda Navigator, open the Anaconda Prompt (terminal on macOS or Linux), and enter this command:

```
conda remove anaconda-navigator
```

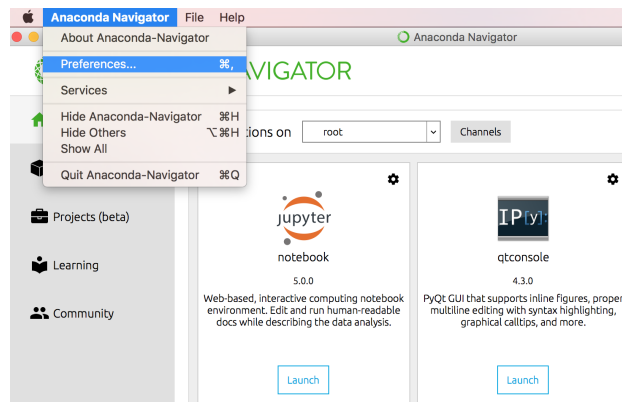
To uninstall all of Anaconda see [Uninstalling Anaconda](#).

## Configuring Navigator to work with a local Anaconda Repository

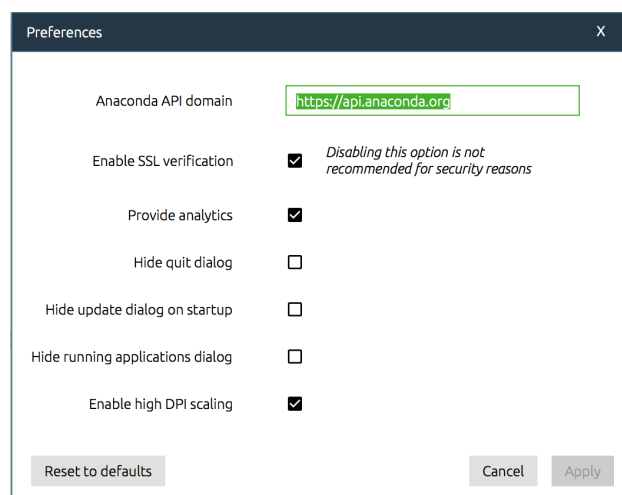
If you're an Anaconda Enterprise subscriber, you can configure Navigator to search for packages in your local Anaconda Repository instead of searching on [Anaconda.org](https://anaconda.org).

To configure Navigator to search in a local Anaconda Repository:

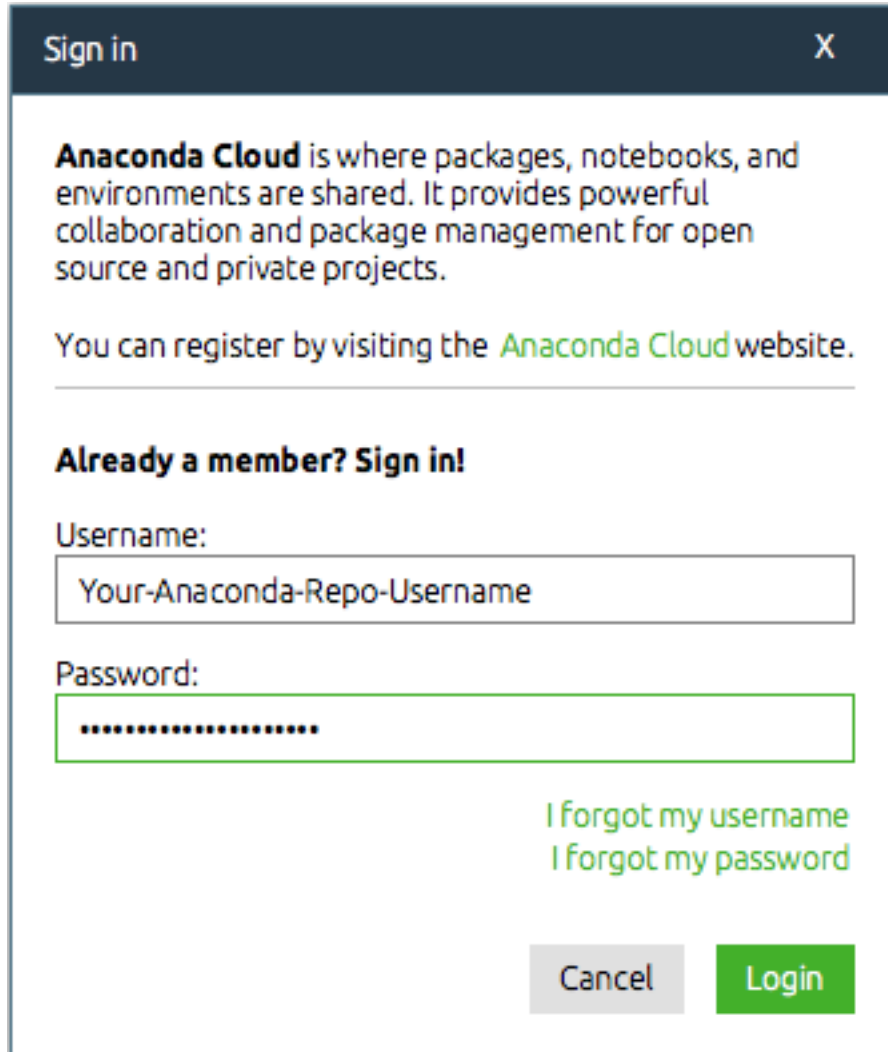
1. In the top menu bar's **Anaconda Navigator** menu (on macOS it's **File**), select Preferences.



2. In the Anaconda API domain field, type the address of your local Anaconda Repository.



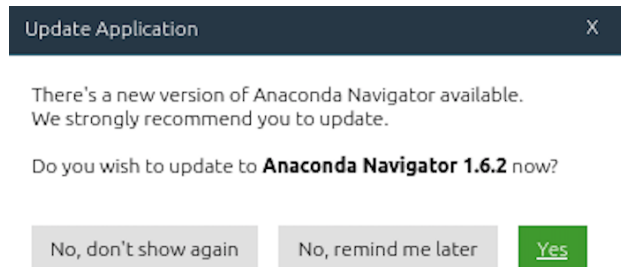
3. Click the Apply button.
4. At the top of the Navigator window, click the Sign in to Anaconda Cloud button.
5. In the Username and Password fields, type your Anaconda Repository username and password.

A screenshot of the 'Sign in' dialog box in Anaconda Cloud. The dialog has a dark blue header with the text 'Sign in' and a close button 'X'. The main content area is white and contains the following text: 'Anaconda Cloud is where packages, notebooks, and environments are shared. It provides powerful collaboration and package management for open source and private projects.' followed by 'You can register by visiting the Anaconda Cloud website.' Below this is a section titled 'Already a member? Sign in!' with two input fields: 'Username:' containing 'Your-Anaconda-Repo-Username' and 'Password:' containing a series of dots. To the right of the password field are two links: 'I forgot my username' and 'I forgot my password'. At the bottom right are two buttons: 'Cancel' (grey) and 'Login' (green).

6. Click the Login button.

## Updating Navigator

Every time Navigator starts, it checks whether a new version is available. If one is available, a dialog box is displayed that allows you to upgrade to a new Navigator version or keep your current version.



---

**Note:** We recommend that you keep Navigator updated to the latest version.

---

### Alternate method

If you prefer, you may update Navigator manually.

Open the Anaconda prompt (terminal on Linux or macOS):

Run this command to deactivate conda:

```
conda deactivate
```

Then run this command to update Navigator:

```
conda update anaconda-navigator
```

### Getting started with Navigator

Anaconda Navigator is a graphical user interface to the conda package and environment manager.

This 10-minute guide to Navigator will have you navigating the powerful conda program in a web-like interface without having to learn command line commands.

SEE ALSO: [Getting started with conda](#) to learn how to use conda. Compare the Getting started guides for each to see which program you prefer.

### Before you start

You should have already *installed Anaconda*.

### Contents

- *Starting Navigator* on Windows, macOS, or Linux. 1 MINUTE
- *Managing Navigator*. Verify that Anaconda is installed and check that Navigator is updated to the current version. 1 MINUTE

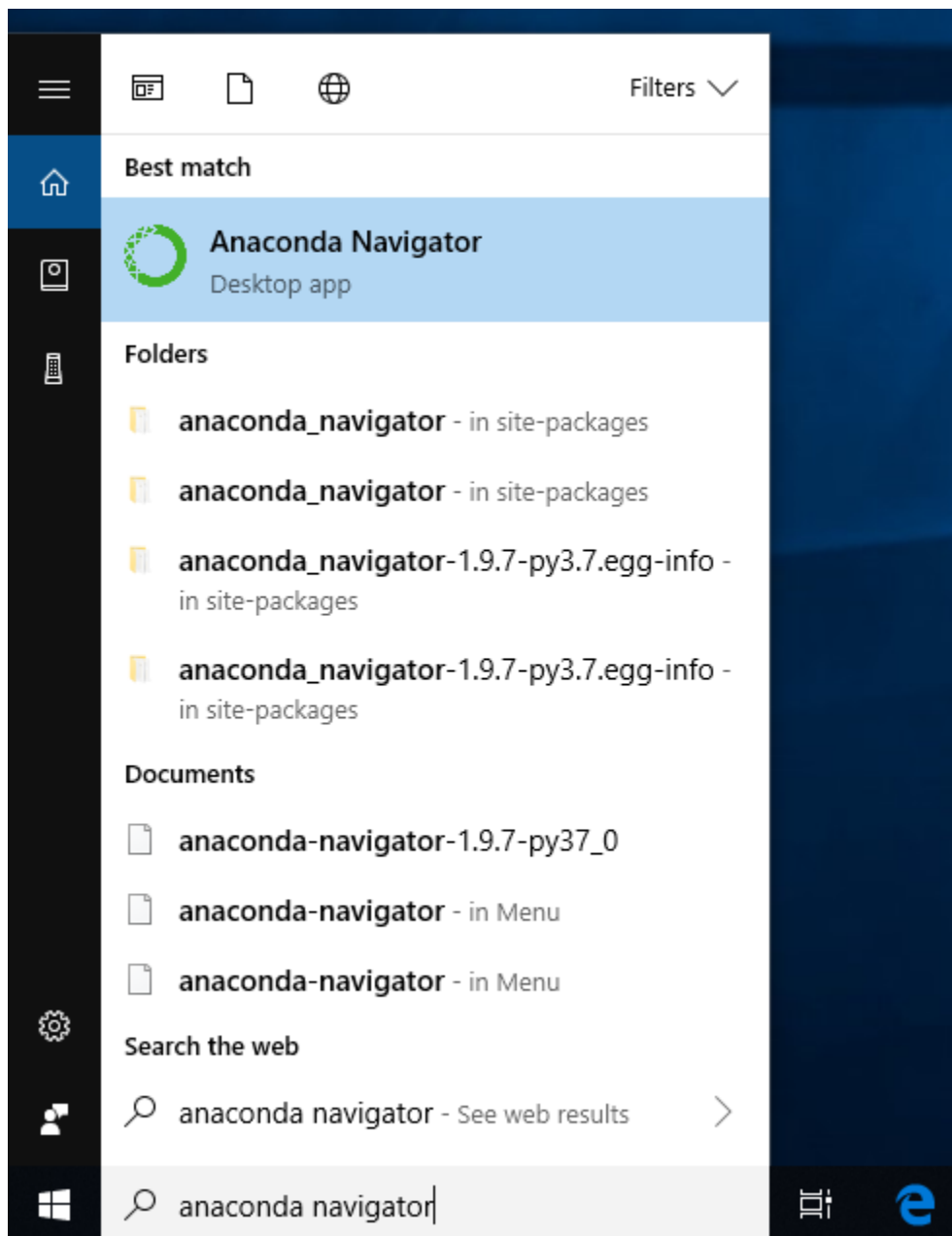
- *Managing environments*. Create environments and move easily between them. 3 MINUTES
- *Managing Python*. Create an environment that has a different version of Python. 2 MINUTES
- *Managing packages*. Find packages available for you to install. Install packages. 3 MINUTES

TOTAL TIME: 10 MINUTES

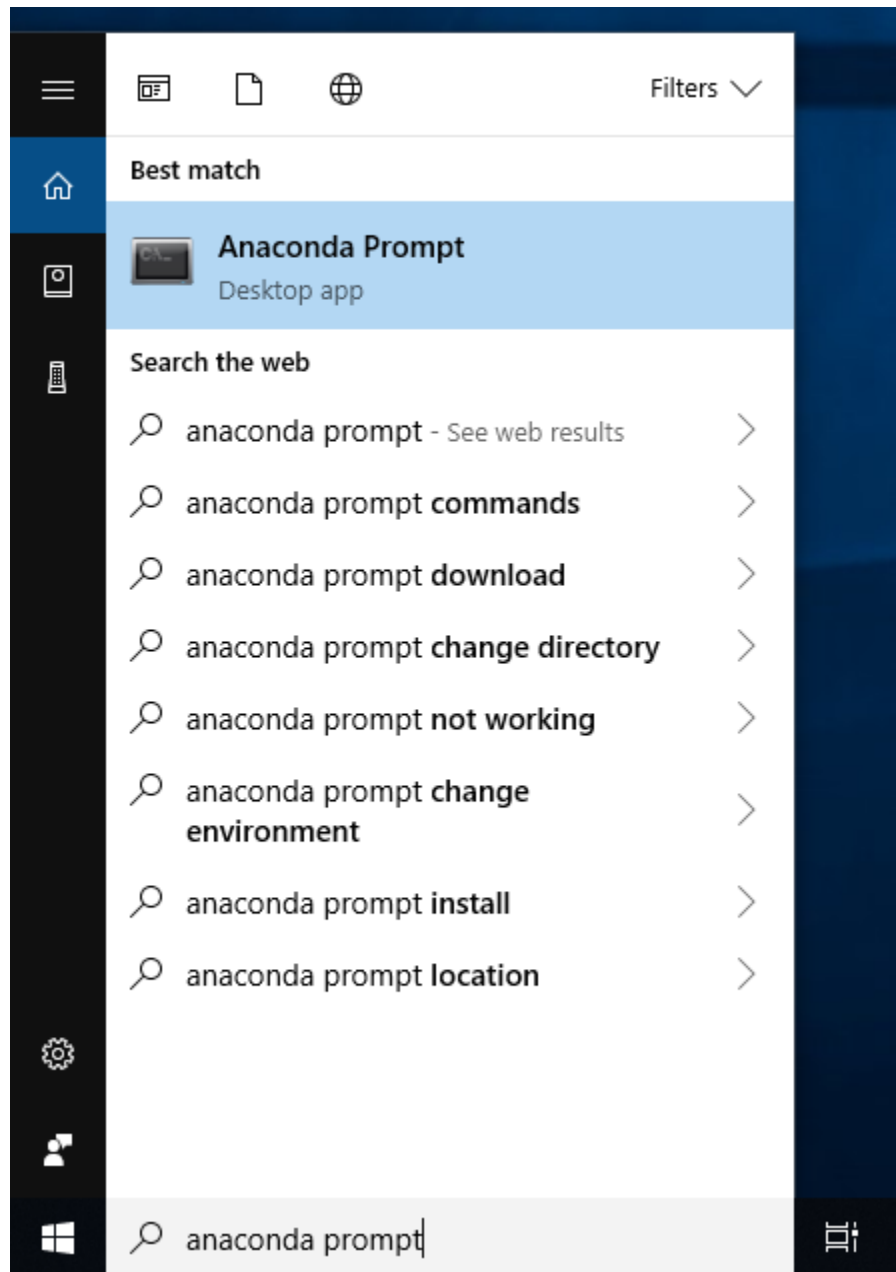
## Starting Navigator

### Windows

- From the Start menu, click the Anaconda Navigator desktop app.



- Or from the Start menu, search for and open “Anaconda Prompt” and type the command `anaconda-navigator`.



## MacOS

- Open Launchpad, then click the Anaconda-Navigator icon.

- Or open Launchpad and click the terminal icon. Then in terminal, type `anaconda-navigator`.

## Linux

- Open a terminal window and type `anaconda-navigator`.

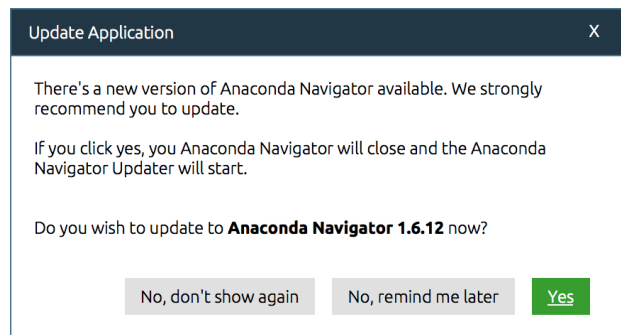
## Managing Navigator

Verify that Anaconda is installed and running on your system.

- When Navigator starts up, it verifies that Anaconda is installed.
- If Navigator does not start up, go back to Anaconda installation and make sure you followed all the steps.

Check that Navigator is updated to the current version.

- When you start Navigator, it automatically checks for a new version. If Navigator finds a new version, you will see a dialog box like this:



Click the “Yes” button to update Navigator to the current version.

---

**Tip:** We recommend that you always keep Navigator updated to the latest version.

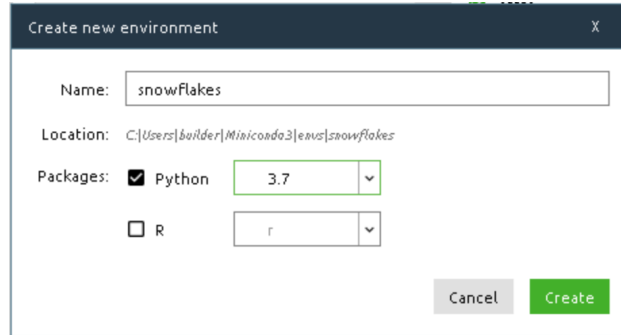
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## Managing Environments

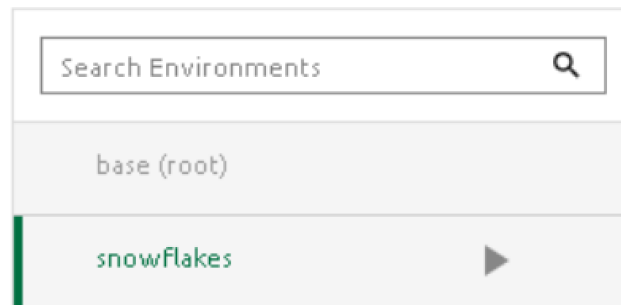
Navigator uses conda to create separate environments containing files, packages, and their dependencies that will not interact with other environments.

Create a new environment named `snowflakes` and install a package in it:

1. In Navigator, click the **Environments** tab, then click the Create button. The **Create new environment** dialog box appears.
2. In the **Environment** name field, type a descriptive name for your environment.



3. Click **Create**. Navigator creates the new environment and activates it.



Now you have two environments, the default environment `base (root)`, and `snowflakes`.

4. Switch between them (activate and deactivate environments) by clicking the name of the environment you want to use.

---

**Tip:** The active environment is the one with the arrow next to its name.

---

5. Return to the other environment by clicking its name.

## Managing Python

When you create a new environment, Navigator installs the same Python version you used when you downloaded and installed Anaconda. If you want to use a different version of Python, for example Python 3.5, simply create a new environment and specify the version of Python that you want in that environment.

Create a new environment named “snakes” that contains Python 3.5:

1. In Navigator, click the **Environments** tab, then click the Create button.

The Create new environment dialog box appears.

2. In the Environment name field, type the descriptive name “snakes” and select the version of Python you want to use from the Python Packages box (3.8, 3.7, 3.6, 3.5, or 2.7). Select a different version of Python than is in your other environments, `base` or `snowflakes`.
3. Click the Create button.

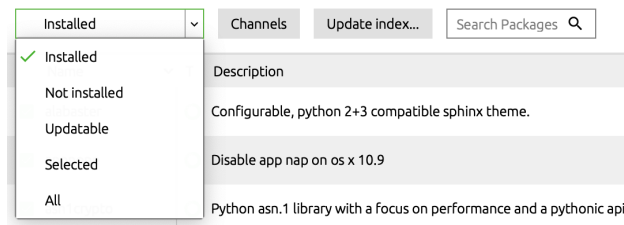


4. Activate the version of Python you want to use by clicking the name of that environment.

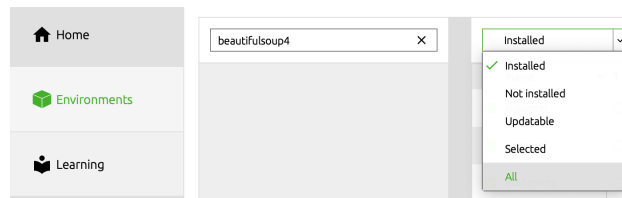
## Managing packages

In this section, you check which packages you have installed, check which are available, and look for a specific package and install it.

1. To find a package you have already installed, click the name of the environment you want to search. The installed packages are displayed in the right pane.
2. You can change the selection of packages displayed in the right pane at any time by clicking the drop-down box above it and selecting Installed, Not Installed, Updatable, Selected, or All.



3. Check to see if a package you have not installed named “beautifulsoup4” is available from the Anaconda repository (must be connected to the Internet). On the Environments tab, in the Search Packages box, type `beautifulsoup4`, and from the Search Subset box select All or Not Installed.



4. To install the package into the current environment, check the checkbox next to the package name, then click the bottom Apply button.

The newly installed program is displayed in your list of installed programs.

## More information

- [Full documentation](#)

Not installed ▼			Channels	Update index...	Search Packages 🔍
Name ▼	T	Description	Version		
<input type="checkbox"/> _ipyw_jlab_nb_ex...	○	A configuration metapackage for enabling anaconda-bundled jupyter extensions	0.1.0		
<input checked="" type="checkbox"/> _mutex_mxnet	○		0.0.40		
<input type="checkbox"/> _nb_ext_conf	○		0.4.0		
<input type="checkbox"/> _py-xgboost-mutex	○		2.0		
<input checked="" type="checkbox"/> _r-mutex	○		1.0.0		
<input type="checkbox"/> _r-xgboost-mutex	○		2.0		
<input type="checkbox"/> _tflow_1100_select	○		0.0.2		
1783 packages available			2 packages selected		<input type="button" value="Apply"/> <input type="button" value="Clear"/>

- Free community support
- Paid support options
- Training

## Troubleshooting

### Navigator error on start up

This is often the result of a corrupted `.condarc` file. To resolve, delete the `.condarc` file and restart Navigator.

1. Find the `.condarc` file.

In Anaconda Prompt or the terminal, enter the command `conda info`. The output will tell you the location of your `.condarc` file(s). You can also search for “`.condarc`” on your computer.

The `.condarc` file is frequently found in:

- macOS: `/Users/Username`
- Linux: `~/condarc`
- Windows: `C:\Users\Username`

2. Optional: Save custom configurations.

If you had custom configuration in your `.condarc` file before it was corrupted, save the information so you can add that configuration back to the new file.

3. Delete the `.condarc` file.
4. Restart Navigator.

### Issues launching or initializing

If you are having problems launching Anaconda Navigator, follow [these steps](#).

If you cannot launch the Anaconda Navigator desktop app, you can still launch it from the terminal or an Anaconda Prompt with `anaconda-navigator`.

If you have permissions issues, there may be a problem with the licenses directory, `.continuum`. Open a terminal or Anaconda Prompt and delete the `.continuum` directory. Run `rm -rf ~/.continuum` on macOS and Linux and `rd /s .continuum` on Windows.

Then relaunch Navigator from the desktop app, terminal, or Anaconda Prompt.

If removing the licenses directory does not resolve the issue, manually update Navigator from a terminal or an Anaconda Prompt:

```
conda update anaconda-navigator
```

If you have updated Navigator and still have problems, remove Anaconda Navigator, then reinstall from terminal or Anaconda Prompt:

```
conda remove anaconda-navigator
conda install anaconda-navigator
```

If none of the above work, please reset Anaconda Navigator configuration back to default values:

```
anaconda-navigator --reset
```

## PermissionError on macOS Catalina

MacOS Catalina users may experience permission errors where the system does not prompt you for permission to folders requiring access.

First, update Navigator.

```
conda update anaconda-navigator
```

Once updated, you can have Navigator generate the permissions prompt for the first time by launching Spyder and running something like this in the console (you can replace Desktop with Downloads/Documents folder depending on which you need access to):

```
import os
os.listdir('Desktop')
```

## Access denied error

This is caused by a lock file that sometimes gets stuck and isn't removed when it should be.

In Anaconda Prompt or a terminal, run:

```
conda update conda
conda update anaconda-navigator
conda update navigator-updater
anaconda-navigator --reset
```

The last command is the key to fixing the issue as it removes the lock file causing the problem.

## Navigator buttons are missing

If your Navigator buttons are missing, try the following:

- Run “Update Index” from the Environments tab of Navigator.
- Quit and restart Navigator.
- If still broken, confirm that your `.condarc` file is not *corrupt*. Specifically confirm that your channel settings contain “defaults”.
- If it’s still broken, try running `conda search python` from the command line. This will download a fresh copy of the repodata, which should resolve the problem.
- If none of the above options work, [open an issue](#) detailing the error.

### Navigator ignores the “Ok, and don’t show again” option on the help Anaconda improve pop up

After starting Navigator, a pop up appears asking if you’d like to provide anonymized usage information to Anaconda. If you select “Okay, and don’t show again” and the pop up appears again the next time you start Navigator, it may be due to a privilege conflict.

Specifically, this can occur when Navigator was installed by a user with Administrator privileges, but you are using it as a regular user without the Administrator privileges. The pop up continues to appear because you do not have permission to change the pop up box setting.

To resolve this, switch to using an account with Administrator privileges and select the “Ok, and don’t show again” option in the pop up box. This will apply to all user accounts.

Alternatively, you can edit the `.anaconda/navigator/anaconda-navigator.ini` configuration file such that `show_startup = False`. If `show_startup = True`, you will continue to see the pop up box.

### RStudio fails to install in Navigator 1.6.2 if special characters are in install path

This is a known issue in Navigator 1.6.2 on Windows 7 64-bit.

## Tutorials

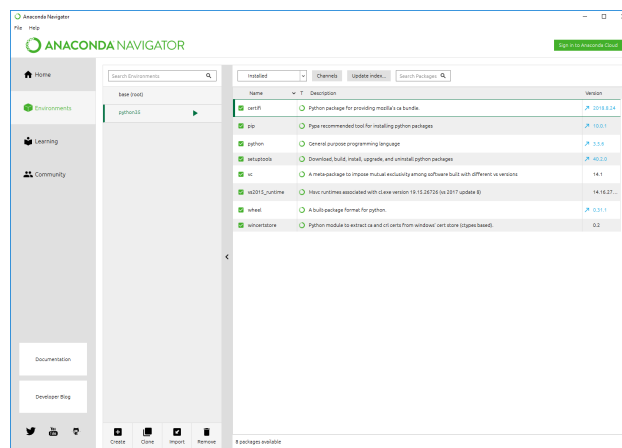
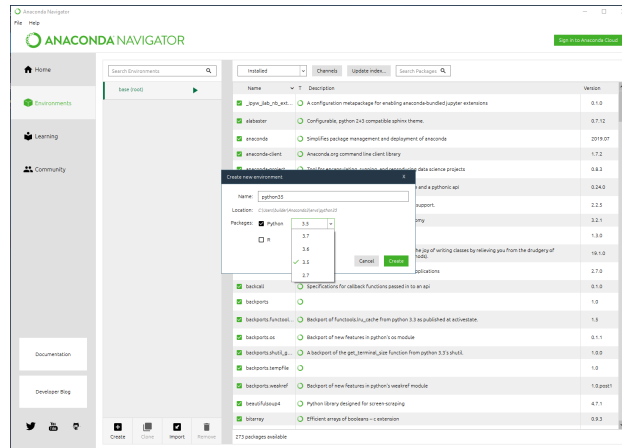
General tasks:

### Creating a Python 3.5 environment from Anaconda2 or Anaconda3

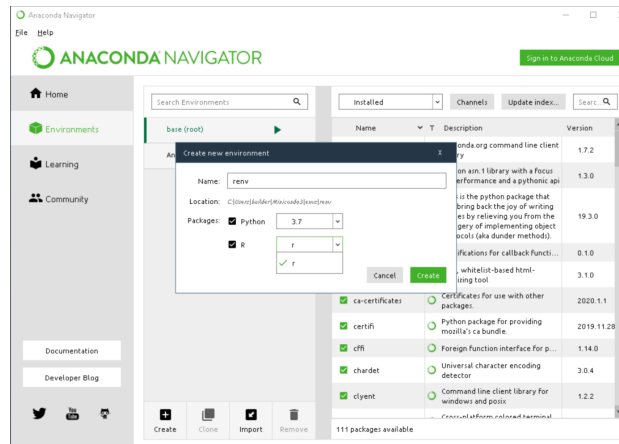
1. In Navigator, click the Environments tab, then click the Create button. The Create new environment dialog box appears.
2. In the Environment name field, type a descriptive name for your environment.
3. In the Packages list, select “Python” and in the Python version list select “3.5”.
4. Click the Create button.
5. Navigator creates the new environment and activates it, as shown by the highlighted green bar. All actions take place in the active environment.

### Creating an R environment and running RStudio

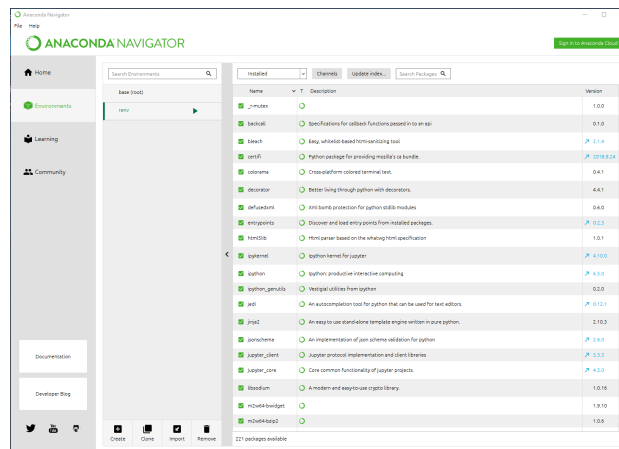
1. In Navigator, click the Environments tab, then click the Create button. The Create new environment dialog box appears.



- In the Environment name field, type a descriptive name for your environment.



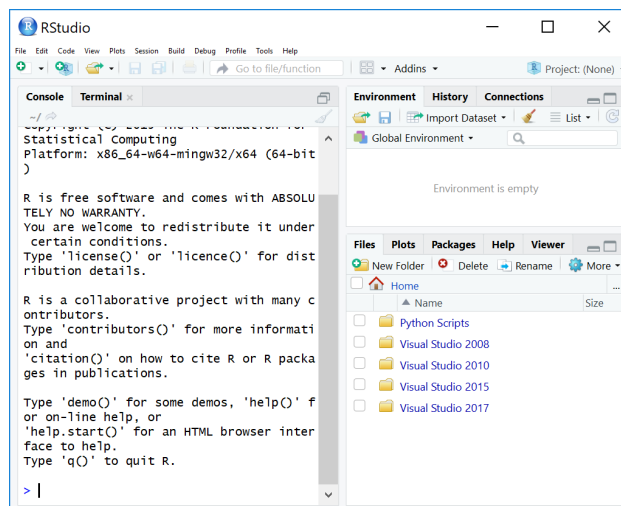
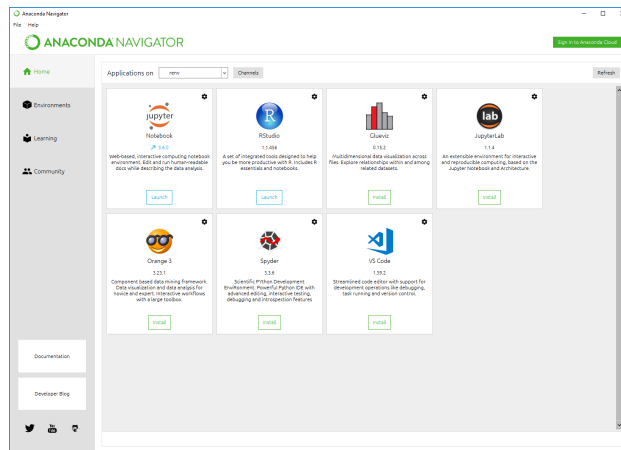
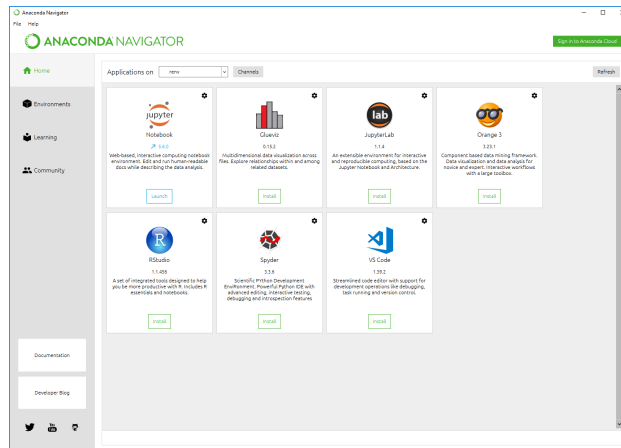
- In the Packages list, select “R”.
- On the drop-down menu, select `r` to install R with the packages `r-base` and `r-essentials`. For more information please see [Using R language with Anaconda](#).
- Click the Create button.
- Navigator creates the new environment and activates it, as shown by the highlighted green bar. All actions take place in the active environment.



- With the new environment active, click the Home button and then click the Install button on the RStudio application.
- Click Launch to run RStudio from Navigator.
- You will see RStudio running from Navigator.

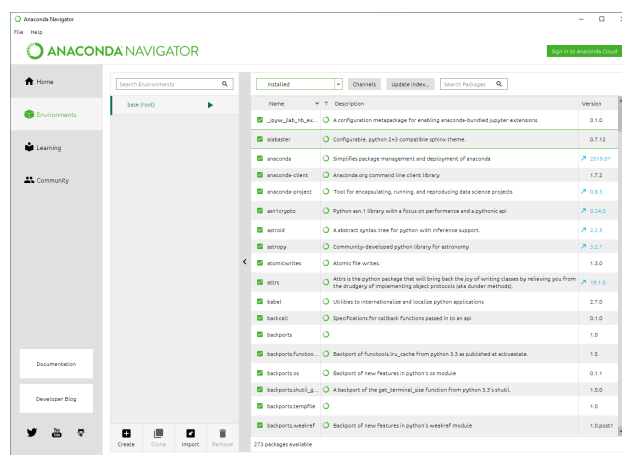
## Managing environments

- [Searching for an environment](#)
- [Creating a new environment](#)



- *Using an environment*
- *Cloning an environment*
- *Importing an environment*
- *Removing an environment*
- *Advanced environment management*

On the **Environments** tab, the left column displays your environments.



## Searching for an environment

In the Search Environments box, type all or part of the environment name.

## Creating a new environment

1. At the bottom of the environments list, click the Create button.
2. In the Create Environment dialog box, type a descriptive name for the new environment.
3. Select Python, R, or both for a mixed environment.
4. If applicable, choose a Python version for the new environment.
5. Click the Create button.

When you install an R language environment, the <https://anaconda.org/r> channel is automatically added and made active and a new channel automatically appears in `.condarc`.



## Using an environment

1. In the environments list, click the environment name.
2. Click the arrow button next to the name. The activation options dialog appears.
3. Select one of the following options for opening the environment: terminal, Python interpreter, IPython Console, or Jupyter Notebook.

---

**Note:** Some of these options may not be available if they were not installed in the environment.

---

## Cloning an environment

1. Click the name of the environment you want to clone.
2. At the bottom of the environments list, click the Clone button.
3. Type a descriptive name for the new environment.

## Importing an environment

Each environment has a YAML-formatted configuration file. If someone has given you an environment file that you want to use, for example my-environment-file.yml, and you have saved it to your computer, you can import it into Navigator.

1. At the bottom of the environments list, click the Import button.
2. In the Import dialog box, type a descriptive name for the new environment.
3. Click the file folder icon to browse to the YAML file, or type the file name, including its path.
4. Click the Import button.

## Removing an environment

1. In the environments list, click the environment you want to remove.
2. At the bottom of the list, click the Remove button.

## Advanced environment management

Navigator provides a convenient graphical interface for managing conda environments, channels, and packages. If you're comfortable working with Anaconda prompt (terminal on Linux or macOS), you can access additional, advanced management features. To learn more, see [Managing environments](#) with conda.

## Managing packages

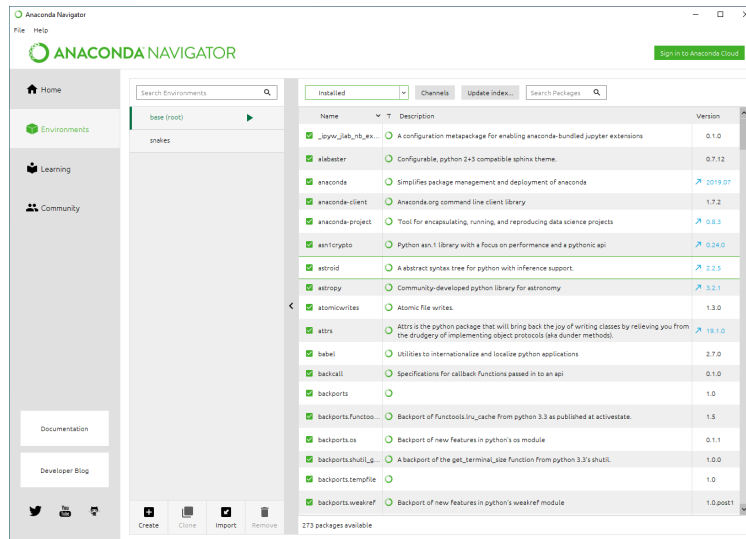
- *Filtering the packages table*
- *Finding a package*

- *Installing a package*
- *Updating a package*
- *Installing a different package version*
- *Removing a package*
- *Advanced package management*

On the Navigator **Environments** tab, the packages table in the right column lists the packages included in the environment selected in the left column.

**Note:** Packages are managed separately for each environment. Changes you make to packages only apply to the active environment.

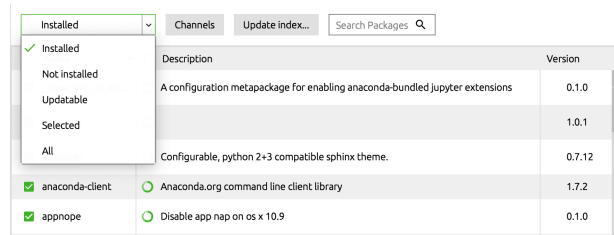
**Tip:** Click a column heading in the table to sort the table by package name, description, or version.



**Tip:** The Update Index button updates the packages table with all packages that are available in any of the enabled channels.

## Filtering the packages table

By default, only installed packages are shown in the packages table. To filter the table to show different packages, click the arrow next to Installed, then select which packages to display: Installed, Not installed, Updatable, Selected, or All.




---

**Note:** Selecting the Updatable filter lists packages that are installed and have updates available.

---

## Finding a package

In the Search Packages box, type the name of the package.

## Installing a package

1. Select the Not Installed filter to list all packages that are available in the environment's channels but are not installed.

---

**Note:** Only packages that are compatible with your current environment are listed.

---

2. Select the name of the package you want to install.
3. Click the Apply button.
4. Review the Install Packages information.

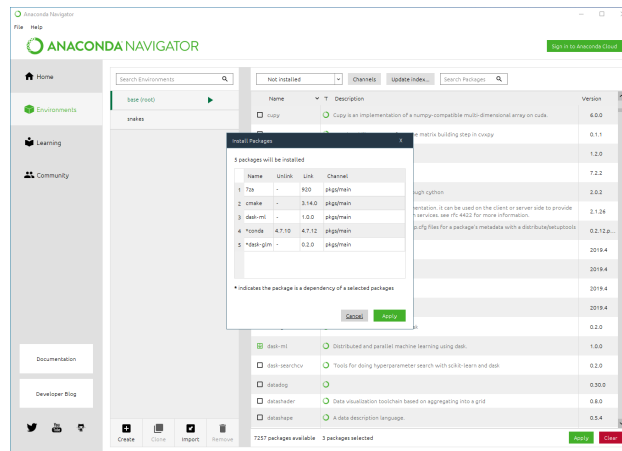
You can filter your packages to be installed by Name, Unlink, Link, and Channel. Unlink indicates what is being removed. Link is what is being installed in place of the package that is unlinked. Channel shows from where the package is being installed.

Packages are in a cache and they rely on other packages using hard links, which essentially point to a package instead of copying it to the environment. Unlink removes the hard link to that package. If the package you are trying to install is a dependency of other packages, the Link column will show the hard link to the package version that is being created in order to install your selected package.

---

**Tip:** If after installing a new package it doesn't appear in the packages table, select the **Home** tab, then click the Refresh button to reload the packages table.

---



## Updating a package

1. Select the Updatable filter to list all installed packages that have updates available.
2. Click the checkbox next to the package you want to update, then in the menu that appears select Mark for Update.

OR

In the Version column, click the blue up arrow that indicates there is a newer version available.

3. Click the Apply button.

## Installing a different package version

1. Click the checkbox next to the package whose version you want to change.
2. In the menu that appears, select Mark for specific version installation.

If other versions are available for this package, they are displayed in a list.

3. Click the package version you want to install.
4. Click the Apply button.

## Removing a package

1. Click the checkbox next to the package you want to remove.
2. In the menu that appears, select Mark for removal.
3. Click the Apply button.

## Advanced package management

Navigator provides a convenient graphical interface for managing conda environments, channels, and packages. But if you're comfortable working with Anaconda Prompt (terminal on Linux or macOS), you can access additional, advanced management features. To learn more, see [Managing packages with conda](#).

## Managing channels

- *Adding a channel*
- *Deleting a channel*

Channels are locations where Navigator and conda look for packages.

You can search and browse packages and channels on [Anaconda Cloud](#).

---

**Note:** Navigator and conda only search for packages in active channels. You can temporarily disable a channel by making it inactive.

---

EXAMPLE: Let's say you want to look for packages on the "Milagro" channel of Anaconda Cloud. All three of these channel variations will look for packages in the same place on Cloud:

- By URL—<https://anaconda.org/milagro>.
- By conda URL—<https://conda.anaconda.org/milagro>.
- By name—milagro.

On the **Environment** tab, click the Channels button to open the Channels Manager.

### Adding a channel

1. Click the Add button.
2. Type or paste the channel name, the URL, or the conda URL.

---

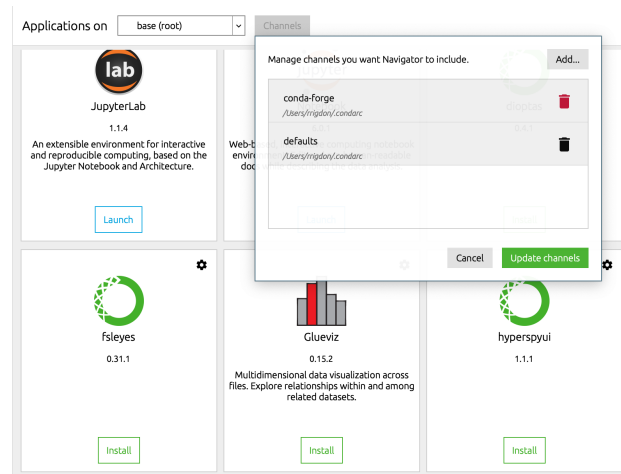
**Note:** A URL can also contain an access token parameter and value. A URL will automatically be transformed to a conda URL.

---

3. Click the Save button.

### Deleting a channel

1. Click the trash can icon next to the channel name.
2. Click the Update Channels button.



## Building Anaconda Navigator applications

- *Who is this for?*
- *Before you start*
- *Using a recipe*
- *Build architecture*
- *App entry in meta.yaml*
- *Build*
- *Upload to Anaconda Cloud*
- *Configure Anaconda Navigator*
- *Troubleshooting*
- *Additional Information*

This tutorial will build an Anaconda Navigator Application (app) of JupyterLab.

Three modifications to the files in the build recipe are required to declare the package as an app. Then, we'll build JupyterLab with these recipe modifications. After we build the package, we will upload it to an Anaconda Cloud channel. Finally, after adding the channel in Anaconda Navigator, the app will appear on the Home pane.

### Who is this for?

This tutorial is for Windows, macOS, and Linux users who wish to generate an Anaconda Navigator app conda package from a given recipe. Prior knowledge of conda-build or conda recipes is recommended.

## Before you start

**Note:** Applications to be built for Anaconda Navigator should have a graphical user interface. Not all conda packages have graphical interfaces.

You should already have installed Miniconda or Anaconda. Install conda-build:

```
conda install conda-build
```

It is recommended that you use the latest versions of conda and conda-build. To upgrade both packages run:

```
conda upgrade conda
conda upgrade conda-build
```

You will also need an account on Anaconda Cloud. Your username will be referred to as your Anaconda Cloud channel.

## Using a recipe

First, make a new directory called jupyterlab and then change to the new directory:

```
mkdir jupyterlab
cd jupyterlab
```

Create the recipe by opening a text file and name it meta.yaml. Copy the recipe from the [feedstock](#):

```
{% set version = "1.2.4" %}
{% set sha256 = "6adb88acd05b51512c37df477a18c36240823a591c2a51bf6556198414026d8f" %}

package:
  name: jupyterlab
  version: {{ version }}

source:
  fn: jupyterlab-{{ version }}.tar.gz
  url: https://pypi.io/packages/source/j/jupyterlab/jupyterlab-{{ version }}.tar.gz
  sha256: {{ sha256 }}
build:
  noarch: python
  number: 0
  script: {{ PYTHON }} -m pip install --install-option="--skip-npm" . -vv
  entry_points:
    - jupyter-lab = jupyterlab.labapp:main
    - jupyter-labextension = jupyterlab.labextensions:main
    - jupyter-labhub = jupyterlab.labhubapp:main
    - jlpm = jupyterlab.jlpmapp:main
app:
  entry: jupyter lab
  icon: icon.png
  summary: JupyterLab PRE-ALPHA
  type: desk

requirements:
```

(continues on next page)

(continued from previous page)

```
host:
  - python >=3.5
  - pip
  - nodejs >=8
run:
  - python >=3.5
  - jupyterlab_server >=1.0.0,<2.0.0
  - notebook >=4.3.1
  - tornado !=6.0.0,!6.0.1,!6.0.2
  - jinja2 >=2.10
test:
  requires:
    - nodejs
  imports:
    - jupyterlab
  commands:
    - jupyter lab --version
    - jlpm --version
    - jlpm versions
    - jupyter labextension list
    - jupyter lab path
    - jupyter lab build
    - jupyter lab clean

about:
  home: https://github.com/jupyterlab/jupyterlab
  license: BSD-3-Clause
  license_family: BSD
  license_file: LICENSE
  summary: >
    An extensible environment for interactive and reproducible computing, based
    on the Jupyter Notebook and Architecture.
  doc_url: https://jupyterlab.readthedocs.io
  dev_url: https://github.com/jupyterlab/jupyterlab
  description: >
    JupyterLab is the next-generation user interface for Project Jupyter. It
    offers all the familiar building blocks of the classic Jupyter Notebook
    (notebook, terminal, text editor, file browser, rich outputs, etc.) in a
    flexible and powerful user interface. Eventually, JupyterLab will replace
    the classic Jupyter Notebook.
    JupyterLab can be extended using extensions that are npm packages and use
    our public APIs. You can search for the GitHub topic or npm keyword
    `jupyterlab-extension` to find extensions. To learn more about extensions,
    see our user documentation.
    JupyterLab is suitable for general usage. For JupyterLab extension
    developers, the extension APIs will continue to evolve.

extra:
  recipe-maintainers:
    - jasongrout
    - blink1073
    - jochym
    - ian-r-rose
    - afshin
    - ellisonbg
```



## Build architecture

The recipe, as given, is a noarch recipe. This is not compatible with older versions of Navigator. Under the build section, remove `noarch: python`.

## App entry in meta.yaml

To declare a conda package as an app, the app parameter must be added to the meta.yaml file. The app section will contain three keys: entry, summary, and type. In the case of the JupyterLab recipe, replace the app section in the meta.yaml with the values below.

In the app section, the entry tag defines how the package is to be launched by Anaconda Navigator. For JupyterLab, separate entry tags are required for Windows, macOS, and Linux operating systems.

In your text editor, open the meta.yaml file and add the following lines. On Windows and Linux the entry tag is:

```
app:
  entry: jupyterlab . [win]

  entry: jupyterlab . [linux]
```

## Launch script

For macOS, a launch script must also be provided. In a text editor, create a new file in the conda-build recipe directory called `jupyterlab_mac.command`. The contents of this file are:

```
DIR=$(dirname $0)
$DIR/jupyterlab_mac.command ${HOME}
```

## Build.sh script

To make sure that the file gets installed, create a new file in the same directory as the meta.yaml. Title it `build.sh` and add these lines to the `build.sh` script:

```
$PYTHON -m pip install . --no-deps --ignore-installed -vv
if [ `uname` == Darwin ]
then
    cp $RECIPE_DIR/jupyterlab_mac.command $PREFIX/bin
fi
```

Remove the script key under the build section in the meta.yaml.

## Build.bat

Create a new file called `build.bat`. Include the following:

```
%PYTHON% -m pip install . --no-deps --ignore-installed -vv
```

### Entry key

Then in the meta.yaml, add this line to the app section:

The completed app section should look like this:

---

**Note:** The app icon defaults to the Anaconda logo.

---

### Build

Now that you have the conda-build recipe ready, you can use the conda-build tool to create the package. You will have to build and upload the JupyterLab package separately on Windows, macOS, and Linux machines in order for the package to be available on all platforms. If you're already in the JupyterLab directory, you can type `conda build .` in your terminal. Otherwise type `conda-build jupyterlab`.

When conda-build is finished, it displays the exact path and filename of the conda package. See the [Troubleshooting](#) section if the conda-build command fails.

Windows example file path: `C:\Users\username\miniconda\conda-bld\win-64\jupyterlab-1.2.4-py38_0.tar.bz2`

macOS example file path: `/Users/username/anaconda3/conda-bld/osx-64/jupyterlab-1.2.4-py38_0.tar.bz2`

Linux example file path: `/home/username/miniconda/conda-bld/linux-64/bjupyterlab-1.2.4-py38_0.tar.bz2`

---

**Note:** The path and filename will vary depending on your installation and operating system.

---

Save the path and filename information for the next step.

### Upload to Anaconda Cloud

Now you can upload the new local packages to Anaconda Cloud. First, log in to Anaconda Cloud from your terminal:

```
anaconda login
```

You will be asked for your Anaconda Cloud account name and password. If the login was successful you will see output like the following:

---

**Note:** This step must be done in the root conda environment.

---

Now that you are logged into your channel, you can upload the JupyterLab conda package as follows:

Windows users: `anaconda upload C:\Users\username\miniconda\conda-bld\win-64\jupyterlab-1.2.4-py38_0.tar.bz2`

Linux and macOS users: `anaconda upload /Users/username/miniconda/conda-bld/osx-64/jupyterlab-1.2.4-py38_0.tar.bz2`

---

**Note:** Change your username, path, and filename to the exact username, path, and filename you saved in Step 2. These will vary depending on your installation and operating system.

---

For more information about Anaconda Cloud, see the [Anaconda Cloud documentation](#) page.

## Configure Anaconda Navigator

Now that the JupyterLab package has been uploaded to your Anaconda Cloud channel, you need to add the channel to Anaconda Navigator.

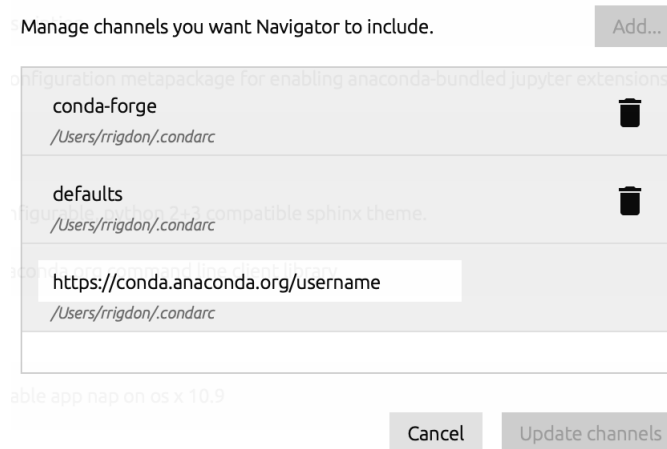
1. Launch the Anaconda Navigator app. In Windows and Linux it will be available from the Start Menu. On macOS, you can find it either on the Desktop or through Spotlight.
2. Open the Environments pane on the far left.
3. To add your channel, first click the Channel button. Second, click the Add button. Third, type in the URL to your Anaconda Cloud channel: <https://conda.anaconda.org/channel>

---

**Note:** Replace “channel” with your Anaconda Cloud username.

---

4. Press Enter and select Update Channels.



5. Close and restart Anaconda Navigator. The JupyterLab app will be displayed on the Home pane.

## Troubleshooting

### A. Conda-build fails

If the conda recipe fails to build consult the [Troubleshooting](#) guide.

### B. App does not appear on the home pane

Check that the conda package has been uploaded to your Anaconda Cloud channel. Check that your channel has been added to the Channels list.

You may have to remove your `.anaconda/navigator` directory and restart Navigator. This directory is in your Home directory.

## C. App does not launch

If after installing the application it does not launch, check that it works correctly on the command line with the following command: `conda run jupyterlab`

If JupyterLab starts correctly then you may have to remove your `.anaconda/navigator` directory and restart Navigator. This directory is in your Home directory.

## Additional Information

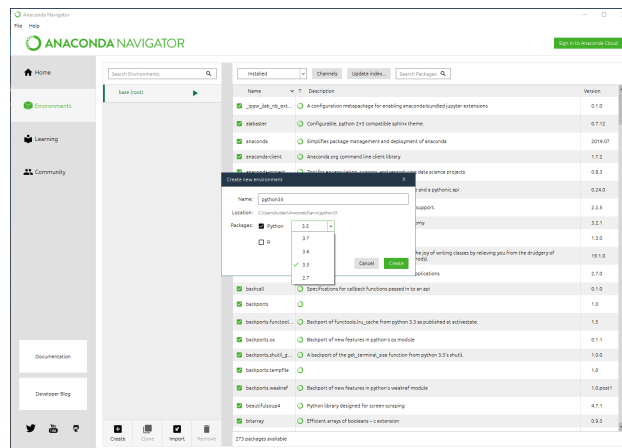
For more information about adding Start Menu entries in Windows, see the [menuinst](#) documentation.

## Using multiple versions of Python with Navigator

With Navigator you can have different versions of Python on your computer and easily switch between them by keeping them in different **environments**.

To use a different version of Python than the one you are currently using, set up a new environment:

1. In Navigator, click the Environments tab, then click the Create button. The Create new environment dialog box appears.
2. In the Environment name field, type a descriptive name for your environment.

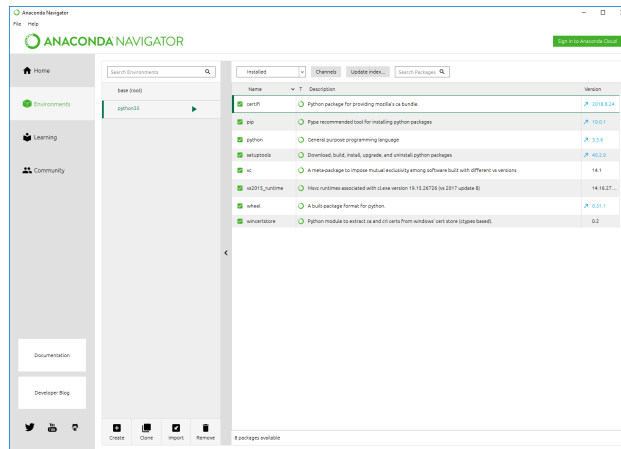


3. In the Packages list select “Python” and in the Python version list select the version you want to use.
4. Click the Create button.
5. Navigator creates the new environment and activates it, as shown by the highlighted green bar. All actions take place in the active environment.

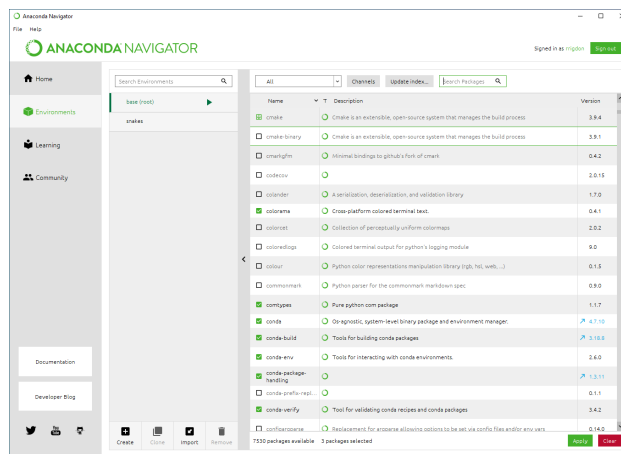
## Searching Anaconda Cloud

To search Anaconda Cloud using Anaconda Navigator:

1. If you haven’t already, sign into Anaconda Cloud by clicking the top right sign-in button. If you don’t yet have an account, you can create one.
2. In Navigator, click the left Environments tab.



3. In the list at the top left of the packages area, select All to search All packages on Anaconda Cloud.
4. In the Search Packages box, type the name of the package you want to search for on Anaconda Cloud.



All packages with that text string are displayed in the Search Results.

For more information on installing and using the packages you find on Anaconda Cloud, see *Package installation for Anaconda*.

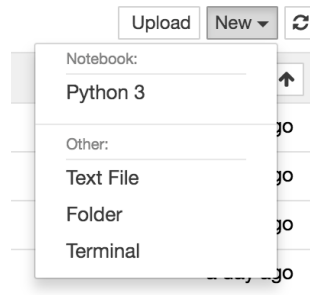
Specific examples:

## Displaying BioPython help text

After installing a package, you can confirm that the package was installed correctly by opening a Jupyter Notebook in that environment, importing the package and displaying its help text. In this example we will use the BioPython

package.

1. *Start Navigator*.
2. To install the BioPython package, follow the instructions in *Managing packages*.
3. Click the icon to open a Jupyter Notebook.
4. In the Jupyter Notebook, click the New button and select your installed Python version.



5. Copy and paste the following code into the first cell:

```
import Bio
help(Bio)
```

6. To run the code, in the menu bar, click Cell then select Run Cells, or use the keyboard shortcut Ctrl-Enter.  
The BioPython help text is displayed.

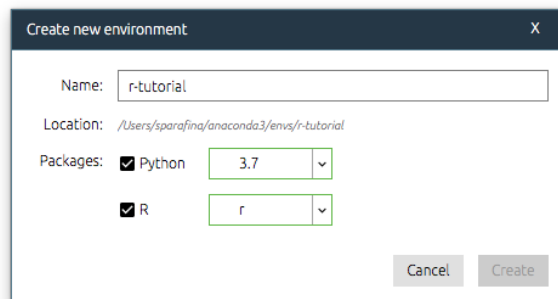
### Using the R programming language in Jupyter Notebook

R is a popular programming language for statistics.

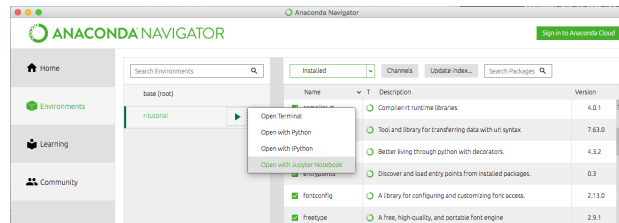
To install and run R in a Jupyter Notebook:

1. *Start Navigator*.
2. To install the R language and r-essentials packages, select **Environments** to create a new environment. Click **Create**.

Name the environment “r-tutorial”. Next to Packages, select Python 3.7 and R. Select **r** from the dropdown menu. Click **Create**.



3. *Open the environment with the R package* using the Open with Jupyter Notebook option.



4. To create a new notebook for the R language, in the Jupyter Notebook menu, select **New**, then select **R**.



5. We will use dplyr to read and manipulate Fisher's Iris multivariate data set in this tutorial. Copy and paste the following code into the first cell:

```
library(dplyr)
iris
```

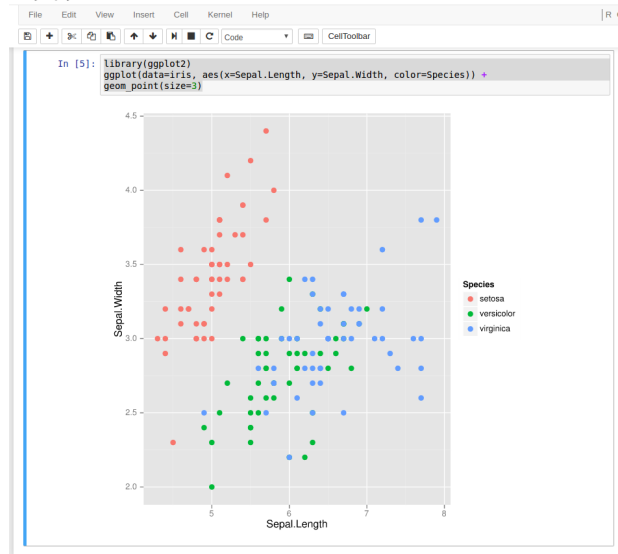
6. To run the code, in the menu bar, click **Cell** then select **Run Cells**, or use the keyboard shortcut Ctrl-Enter.
7. The iris data table is displayed.
8. Using ggplot, we can create a scatter plot comparing sepal length and width of three iris species. Click + to open a second cell, then copy and paste the following code into the second cell:

```
library(ggplot2)
ggplot(data=iris, aes(x=Sepal.Length, y=Sepal.Width, color=Species)) + geom_
  ↪ point(size=3)
```

9. To run the code, in the menu bar, click **Cell** then select **Run Cells**, or use the keyboard shortcut Ctrl-Enter.

For more resources on using R with Anaconda, see [Using R language with Anaconda](#).

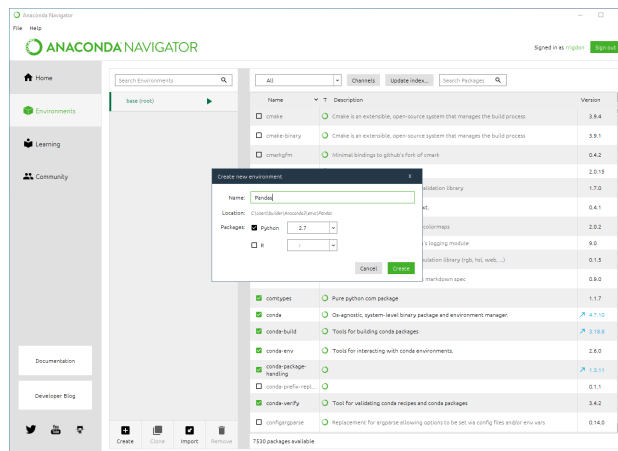




## Installing and running Pandas

Pandas is a common Python tool for data manipulation and analysis. This task explains how to use Navigator to set up and begin working with Pandas in your choice of terminal, Python, IPython, or Jupyter Notebook. The steps are similar for *installing and opening* nearly any package.

1. *Start Navigator.*
2. Click the **Environments** tab.
3. Click the Create button. When prompted, enter a descriptive name for the environment, such as “Pandas.”



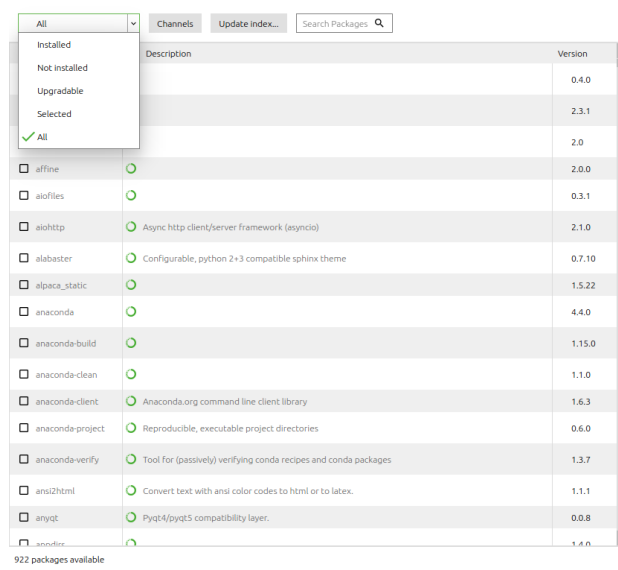
4. Select a Python version to run in the environment.
5. Click OK.

The new environment appears in the environments list.

6. Click the name of the new environment to activate it.

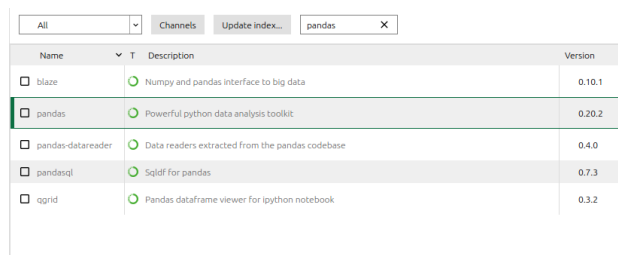
The environment is highlighted with a green background.

7. In the list above the packages table, select All to filter the table to show all packages in all channels.

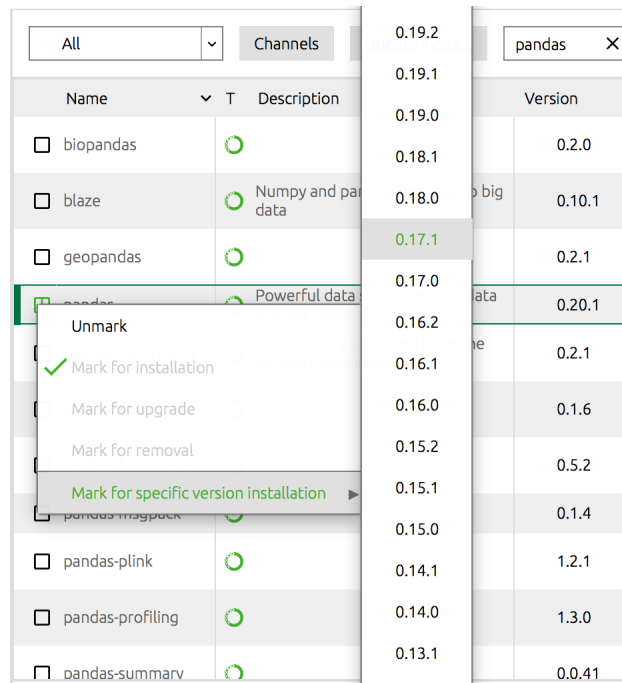


8. In the Search Packages box, type Pandas.

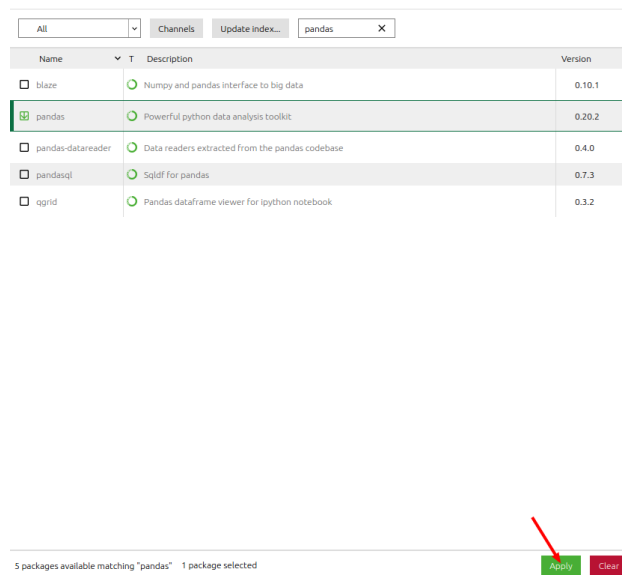
Pandas appears as a package available for installation.



9. Select the checkbox in front of the Pandas package name.
10. In the menu that appears, select Mark for specific version installation.
11. In the list that appears, select the Pandas version you want to install.



12. Click the Apply button.

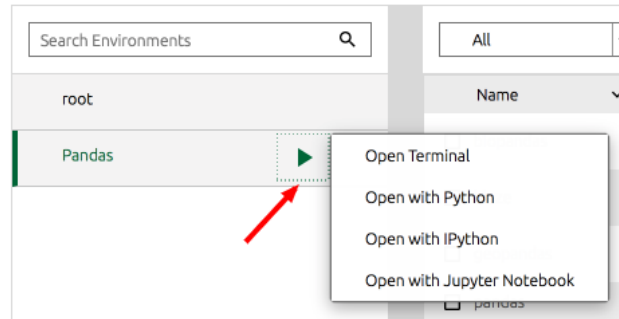


A progress bar appears below the Packages pane while Pandas and its dependencies are installed.

13. To begin using your new environment, click the **Environments** tab.

14. Click the arrow button next to the Pandas environment name.

15. In the list that appears, select the tool to use to open Pandas: Terminal, Python, IPython, or Jupyter Notebook.



### Learn more about Pandas

- [10 Minutes to Pandas](#)
- [Pandas Cookbook](#)

### Help and support

Anaconda Navigator is copyright 2016-2017 Anaconda®, Inc. It may be copied and distributed freely only as part of an Anaconda or Miniconda installation.

For free community support for Anaconda and Navigator, join the [Anaconda Mailing List](#).

For Anaconda installation or technical support options, visit our [support offerings page](#).

### Training and consulting

Training and consulting is available for all Anaconda products, including Navigator. For more information, please contact your account representative or email [sales@anaconda.com](mailto:sales@anaconda.com).

### Reporting bugs

Please report bugs on the [Anaconda GitHub issue tracker](#).

### Release notes

#### 1.9.12 – February 10, 2020

- Add PyCharm Tile to homepage when installed.
- Add Anaconda Prompt, Anaconda PowerShell Tiles on homepage (Windows only).
- Display pip installed packages in environments.
- Improved the macOS Catalina experience with Navigator,

around granting permissions to the various applications Navigator launches.

- Numerous bug fixes.

## 1.9 – October 2, 2018

- Add support for **Offline Mode** for all environment related actions.
- Add support for custom configuration of main windows links.
- Numerous bug fixes and performance enhancements.

## 1.8 – February 28, 2018

- **Remove “Projects” tab.**
- Support environment names with spaces on Windows.
- Improve switching between Anaconda API domains.
- Better integration with Visual Studio Code.
- Numerous bug fixes and performance enhancements.

## 1.7 – February 13, 2018

- Add R and MRO documentation tiles.
- Add custom spinner.
- Better handling of Access Denied errors.
- Better integration with Visual Studio Code.
- Numerous bug fixes and performance enhancements.

## 1.6 – May 19, 2017

- Better logging for application launches
- Package list can be filtered by “to be installed”
- Selecting an environment on the Home or Environments tab now selects it on both
- Numerous bug fixes and performance enhancements

## 1.5 – March 2, 2017

- New Projects tab for working with Anaconda Projects, still in beta status
- Added Navigator Updater and increased visibility of available updates
- Numerous bug fixes and performance enhancements

## 1.4 – January 31, 2017

- Navigator is out of beta status.  
The word “Beta” no longer appears in the title bar.

- R Studio available from the Navigator **Home** tab.

R Studio is an open-source integrated development environment (IDE) for the R programming language. R Studio has been added to the R channel and can now be installed and launched from the Navigator **Home** tab. To install and launch R Studio, in the R Studio pane, click the Install button, then click the Launch button.

- Orange app returns to the **Home** tab.

Orange app was removed from version 1.3 due to compatibility issues that have since been resolved. Orange app is pre-installed starting from version 1.4, so you can click the Launch button to launch it, with no need to install it first.

- Option to disable or enable SSL verification.

From the top menu bar, select Preferences, select or clear the Enable SSL verification checkbox, then click the Apply button.

- Support for Anaconda Fusion licenses.

Navigator now supports packages that require a license, including Anaconda Fusion. Installing Anaconda Fusion now automatically downloads a Fusion trial license from [Anaconda Cloud](#). This license is generated once per user, so if a user uninstalls Fusion and reinstalls it, the user receives the original license. Trial licenses require users to register for a free account on Anaconda Cloud.

- Correct display of “no arch” packages.

When Navigator installs “no arch” packages, they now appear correctly on the **Environments** tab.

- Friendly warning about updating channels for long-term users.

If users have created `.condarc` files that try to access `binstar.org`—the original name of `anaconda.org`—Navigator now warns that `binstar.org` channels are outdated.

### 1.3 – September 27, 2016

- License Manager dialog.

You can now easily upload licenses for applications that require them.

- Applications per environment.

You can install applications to any environment. To do this, on the **Home** tab, click the **Applications** menu, then select the environment in which you want to install an application. If an environment is not selected, applications are installed by default in the root environment.

- One-click updates and installs.

You can install a new package or update an installed package in the active environment. See [Managing packages](#).

- Clearer indication of option to delete a search filter.

On the **Environments** tab, when the packages are filtered by a user-defined search string, hovering over the X button now turns the cursor into an arrow and the X turns red, to emphasize that clicking the X will clear the search string.

- Channels now support tokens.

The Channel manager now supports security tokens. See [Adding a channel](#).

- Channel name copy and paste support.

- Navigator in a specific environment.

Installing Navigator in an environment other than root now makes that environment the default upon Navigator startup, both for the **Home** tab and the **Environments** tab.

- Table pre-filtering according to Python version.

To avoid unnecessary conflicts, the table that displays a filtered view of packages—according to the Installed, Not Installed, Upgradeable and Downgradable filter values—does not display packages that are incompatible with the installed version of Python.

- Dialog size restore.

Upon restart, the application window's last size and location are preserved, instead of the window's being maximized upon startup.

## 1.2 – August 1, 2016

- Improved conda rc support.

Navigator now reads from and writes to the conda configuration file (`.condarc`). In previous releases, updates made within Navigator to the conda configuration were not reflected in the `.condarc` file, and vice versa. Starting from version 1.2, when you add channels inside Navigator, the `.condarc` file is updated, and if `.condarc` is updated outside Navigator, Navigator correctly reads the available channels.

- Improved channels support.

You can now *manage the channels* on Anaconda Cloud that you want Navigator to consider active. Active channels are included when you search for packages and other assets.

- R environment creation support.

Navigator now allows you to *install a standalone R language environment or a mixed Python and R environment*.

- Conda environment file import.

Navigator now allows you to *import environment.yml files*.

- Updates for Enterprise users.

---

**Note:** You cannot use an Enterprise version of Anaconda Cloud with Navigator.

---

- Simplified preferences.

Preference options are simplified so that only one URL is needed to set up the API. Changing this value affects the URL setting of the anaconda-client configuration.

---

**Note:** Changing the *URL setting in the CLI* affects the value displayed in the preferences.

---

- Proxy.

When using Navigator behind a proxy, the settings must be manually set inside the conda configuration file. See the [conda proxy documentation](#).

## Glossary

### Anaconda

A downloadable, free, open-source, high-performance, optimized Python and R distribution with 250+ packages automatically included. Anaconda provides the option to easily install an additional 7,500+ open-source packages for data science, including advanced and scientific analytics.

Anaconda includes *Anaconda Navigator* and *conda* management utilities. Available for Windows, macOS and Linux. All versions are supported by the development community.

### Anaconda Cloud

A web-based repository hosting service in the cloud. *Packages* created locally can be published to your *channel* on Anaconda Cloud to be shared with the public. Paid subscriptions to Anaconda Cloud can designate packages as private, to be shared only with authorized users. Anaconda Cloud is Anaconda's repository product made available to the public. Anaconda repository is also available for purchase by companies that wish to maintain their own on-site version of Anaconda Cloud. See [Anaconda business subscriptions](#).

### Anaconda Enterprise

Anaconda version that includes enterprise technical support, indemnification for a select number of open source packages, collaborative notebooks, high performance scalability, Hadoop, interactive visualization, governance and security. See [Anaconda business subscriptions](#).

### Anaconda Navigator

A desktop graphical user interface (GUI) included in all versions of *Anaconda* that allows you to easily manage *conda packages*, *environments*, *channels* and notebooks without the need to use the *command line interface (CLI)*.

### Anaconda Repository

A private enterprise server on your network where open source and proprietary packages may be stored and retrieved for installation on a local computer. Anaconda Repository is different from [Anaconda Cloud](#) or the [default conda repository](#). The Anaconda Repository is used to govern access to data science assets including packages and notebooks.

### Channels

The locations of the repositories where conda looks for packages, often on Anaconda Cloud (Anaconda.org). Channels may also go to a private location on a remote or local repository that you or your organization manage.

### Command line interface (CLI)

A program in which commands are entered as text, one line at a time, for a computer to execute. This is done in the Anaconda Prompt in Windows, and in a terminal in macOS and Linux. Conda is executed in a CLI. Contrast with *Graphical User Interface (GUI)*.



## Conda

A package and environment manager program that is packaged with *Anaconda* and run in a CLI. Using conda, you can install and update *conda packages* and their dependencies, and switch between *conda environments* on your local computer. Contrast to *Anaconda Navigator*.

### Conda environment

A folder or directory that contains a specific collection of *conda packages* and their dependencies, so they can be maintained and run independently without interfering with each other. Environments in Anaconda Navigator are conda environments.

EXAMPLE: It can be useful to create one environment for packages that run on Python 2, and another for packages that run on Python 3.

Changes to one environment do not affect other environments.

EXAMPLE: If you upgrade a program in one environment, this will not upgrade the same program in another environment.

### Conda package

An archive file that contains everything that a software program needs in order to be installed and run, so you do not have to manually find and install each dependency separately. This can include system-level libraries, Python modules, executable programs and other components. Managed with *conda* or *Anaconda Navigator*. Packages in Anaconda Navigator are conda packages.

### Conda repository

A cloud-based repository that contains 720+ open source certified packages that are easily installed locally via the `conda install` command. Can be viewed directly at <https://repo.anaconda.com/pkgs/> and used within *Anaconda Navigator* when downloading and installing packages from their Environments tab, or by using *conda* commands in a *Command Line Interface*.

### Graphical user interface (GUI)

A program with graphic images, icons and menus in which commands are entered by clicking with a mouse and/or entering text in edit boxes. *Anaconda Navigator* is a graphical user interface that overlays the conda utility.

### Miniconda

A minimal installer for conda that is run from a command line interface (CLI). Like Anaconda, Miniconda is a free software package that includes the conda package and environment manager, but Miniconda does not include Anaconda, Anaconda Navigator, or any packages other than those dependencies needed to install it. After Miniconda is installed, additional conda packages may be installed directly from the command line interface with the command `conda install`. See also *Anaconda* and *conda*.

### Package manager

A collection of software tools that automates the process of installing, updating, configuring, and removing computer programs on a computer. Also known as a package management system. *Anaconda Navigator* includes the conda package manager with a GUI overlay for ease of use.

### Packages

Software program files and information about the software, such as its name, the specific version and a description, bundled into a file that can be installed and managed by a package manager.

### R packages

*Conda packages* that install and run the R computer language. Examples include R Essentials, a bundle of 210 popular open source software programs written in the R computer language. To learn more, see <http://conda.pydata.org/docs/r-with-conda.html>.

### Repository

Any storage location from which software or software assets may be retrieved and installed on a local computer. See also: *Anaconda Repository* and *conda repository*.

Review this page to learn what Anaconda Navigator is. When you're ready to start working in Navigator, check out the user guide topics:

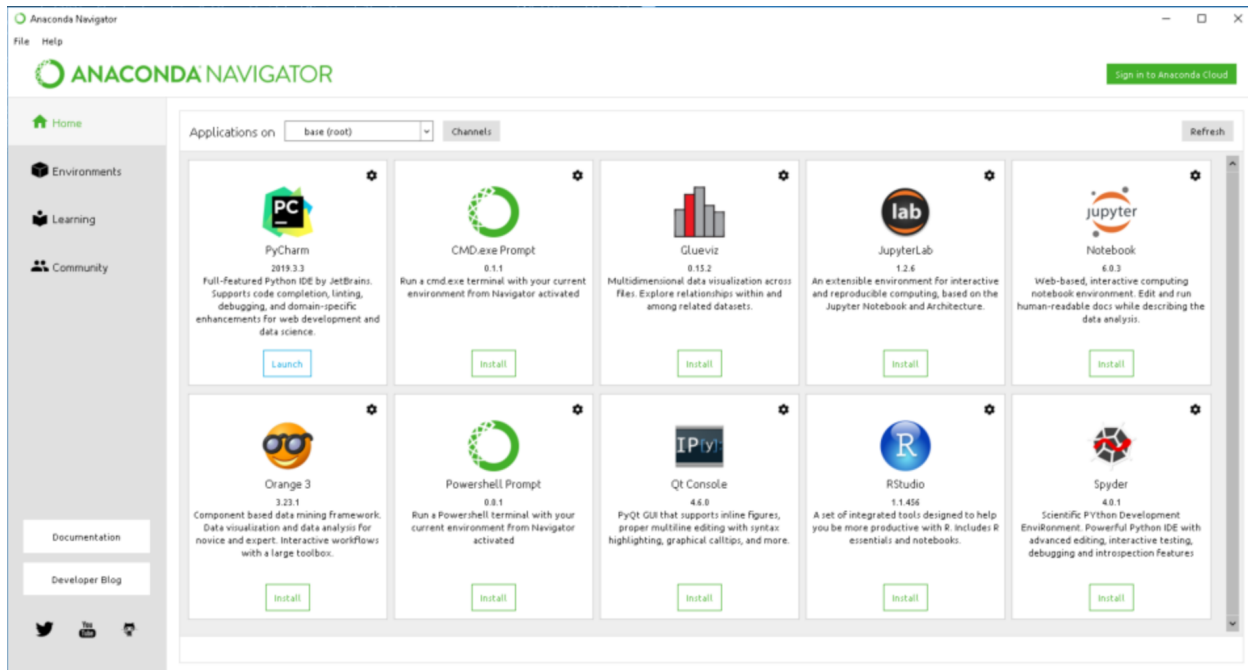
*Overview* | *Installation* | *Glossary* | *Getting started with Navigator* | *Tutorials* | *Troubleshooting* | *Release notes* | *Help and support*

### What is Anaconda Navigator?

Anaconda Navigator is a desktop graphical user interface (GUI) included in Anaconda® distribution that allows you to launch applications and easily manage conda packages, environments, and channels without using command-line commands. Navigator can search for packages on Anaconda Cloud or in a local Anaconda Repository. It is available for Windows, macOS, and Linux.

To get Navigator, get the Navigator Cheat Sheet and *install Anaconda*.

The *Getting started with Navigator* section shows how to start Navigator from the shortcuts or from a terminal window.



## Why use Navigator?

In order to run, many scientific packages depend on specific versions of other packages. Data scientists often use multiple versions of many packages and use multiple environments to separate these different versions.

The command-line program conda is both a package manager and an environment manager. This helps data scientists ensure that each version of each package has all the dependencies it requires and works correctly.

Navigator is an easy, point-and-click way to work with packages and environments without needing to type conda commands in a terminal window. You can use it to find the packages you want, install them in an environment, run the packages, and update them – all inside Navigator.

## What applications can I access using Navigator?

The following applications are available by default in Navigator:

- JupyterLab
- Jupyter Notebook
- Spyder
- PyCharm
- VSCode
- Glueviz
- Orange 3 App
- RStudio
- Anaconda Prompt (Windows only)
- Anaconda PowerShell (Windows only)

Advanced conda users can also *build their own Navigator applications*.

### How can I run code with Navigator?

The simplest way is with Spyder. From the Navigator Home tab, click Spyder, and write and execute your code.

You can also use Jupyter Notebooks the same way. Jupyter Notebooks are an increasingly popular system that combine your code, descriptive text, output, images, and interactive interfaces into a single notebook file that is edited, viewed, and used in a web browser.

### Navigator user guide

- [Overview](#)
- [Getting started with Navigator](#)
- [Tutorials](#)
- [Troubleshooting](#)
- [Release notes](#)

---

**Note:** We do not support macOS<10.12 for Anaconda Navigator.

---

### Tasks

#### Installing conda packages

For more information about using the conda package manager in Anaconda Prompt (terminal on Linux or macOS), see the [conda documentation](#).

You can also use the graphical interface *Anaconda Navigator* to install conda packages with just a few clicks.

Open an Anaconda Prompt (terminal on Linux or macOS) and follow these instructions.

#### Installing a conda package

Enter the command:

```
conda install package-name
```

#### Installing specific versions of conda packages

Include the desired version number or its prefix after the package name:

```
conda install package-name=2.3.4
```

To specify only a major version, run:

```
conda install package-name=2
```

These commands install into the environment that is currently active. To install into a named environment, run:

```
conda install package-name=2.3.4 -n some-environment
```

If the package is specific to a Python version, conda uses the version installed in the current or named environment. For details on versions, dependencies and channels, see [Conda FAQ](#) and [Conda Troubleshooting](#).

## Installing packages on a non-networked (air-gapped) computer

To directly install a conda package from your local computer, run:

```
conda install /package-path/package-filename.tar.bz2
```

Conda installs packages into the `anaconda/pkgs` directory.

To install a `.tar` file containing many conda packages, run the following command:

```
conda install /packages-path/packages-filename.tar
```

If conda cannot find the file, try using an absolute path name instead of a relative path name.

---

**Note:** Installing packages directly from the file does not resolve dependencies. If your installed package does not work, it may have missing dependencies that need to be resolved manually.

---

## Switching between Python 2 and Python 3 environments

You can easily maintain separate environments for Python 2 programs and Python 3 programs on the same computer, without worrying about the programs interacting with each other. Switching to an environment is called activating it.

1. Create a Python 2 environment named `py2`, install Python 2.7:

```
conda create --name py2 python=2.7
```

2. Create a new environment named `py3`, install Python 3.5:

```
conda create --name py3 python=3.5
```

Now you have two environments with which to work. You can install packages and run programs as desired in either one.

3. Activate and use the Python 2 environment.

Windows:

```
activate py2
```

macOS, Linux:

```
conda activate py2
```

4. Deactivate the Python 2 environment. Use your py2 environment to install packages and run programs as desired. When finished, deactivate the environment.

Windows:

```
deactivate
```

macOS, Linux:

```
conda deactivate
```

5. Activate and use the Python 3 environment.

Windows:

```
activate py3
```

macOS, Linux:

```
conda activate py3
```

Use the py3 environment to install and run programs as desired. When finished, deactivate the environment

6. Deactivate the Python 3 environment.

Windows:

```
deactivate
```

macOS, Linux:

```
conda deactivate
```

## Configuring a shared package cache

If you have your own installation of Anaconda or Miniconda on your system, you can improve the speed at which packages are installed or new environments are created and save disk space by setting up the configuration to use a shared package cache.

Normal installation sets a package cache relative to the install directory. This can be found with the following command listed under package cache:

```
conda info
```

The normal path to the package cache is:

**Windows** - C:\Users\username\Anaconda{2,3}\pkgs

**macOS** - ~/opt/anaconda{2,3}

**Linux** - /home/username/anaconda{2,3}/pkgs

Each user has their own package cache so when a package is installed, the package is put into their own cache and not shared with anyone else.

The benefit of a shared package cache is that once a particular version of a package has already been downloaded by a user it will not be downloaded again and stored in a separate cache. This saves disk usage and speeds up the install as it does not need to download the package again.

## Shared package cache setup

Create a directory on your system where the shared users have read and write access.

Then, for each user who will have access, edit the `.condarc` file found in their home directory.

**Windows** - `C:\Users\username\.condarc`

**macOS and Linux** - `/home/username/.condarc`

Edit the `.condarc` with the following entry, specifying the full path to the shared directory:

```
pkgs_dirs:
- /path/to/shared_directory
```

Verify the package cache by running `conda info` again.

## Using R language with Anaconda

With Anaconda, you can easily install the R programming language and over 6,000 commonly used R packages for data science. You can also create and share your own custom R packages.

**Note:** When using `conda` to install R packages, you will need to add `r-` before the regular package name. For instance, if you want to install `rbokeh`, you will need to use `conda install r-rbokeh` or for `rJava`, type `conda install r-rjava`.

The R Essentials bundle contains approximately 200 of the most popular R packages for data science, including the `IRKernel`, `dplyr`, `shiny`, `ggplot2`, `tidyr`, `caret`, and `nnet`. It is used as an example in the following guides.

R is the default interpreter installed into new environments. You can specify the R interpreter with the `r-base` package. Unless you change the R interpreter, `conda` will continue to use the default interpreter in each environment.

To run the commands below on Windows, use Start - Anaconda Prompt. On macOS or Linux, open a terminal.

## Updating R packages

- Update all of the packages and their dependencies with one command:

```
conda update r-caret
```

- If a new version of a package is available in the R channel, you can use `conda update` to update specific packages.

## Creating and sharing custom R bundles

Creating and sharing custom R bundles is similar to creating and sharing `conda` packages.

EXAMPLE: Create a simple custom R bundle metapackage named “Custom-R-Bundle” that contains several popular programs and their dependencies:

```
conda metapackage custom-r-bundle 0.1.0 --dependencies r-irkernel jupyter r-ggplot2 r-
↳ dplyr --summary "My custom R bundle"
```

Share the new metapackage by uploading it to your channel on [Anaconda Cloud](#):

```
conda install anaconda-client
anaconda login
anaconda upload custom-r-bundle-0.1.0-0.tar.bz2
```

Anyone can now access your custom R bundle from any computer:

```
conda install -c <your anaconda.org username> custom-r-bundle
```

### Creating an environment with R

1. [Download and install Anaconda.](#)
2. Create a new conda environment with all the r-essentials conda packages built from CRAN:

```
conda create -n r_env r-essentials r-base
```

3. Activate the environment:

```
conda activate r_env
```

4. List the packages in the environment:

```
conda list
```

The list shows that the package r-base is installed and r is listed in the build string of the other R packages in the environment.

Anaconda Navigator, the Anaconda graphical package manager and application launcher, creates R environments by default.

### Creating a new environment with R

When creating a new environment, you can use R by explicitly including r-base in your list of packages.

With conda 4.6:

```
conda create -n r-environment r-essentials r-base
conda activate r-environment
```

### Mirroring the R channel

Many Anaconda Enterprise customers maintain a local mirror of the R channel.

When mirroring the R channel for the first time, clean the existing packages by running the command `anaconda-server-sync-conda` with the option `--clean`.

### Uninstalling R Essentials

To uninstall the R Essentials package, run: `conda remove r-essentials`

---

**Note:** This removes only R Essentials and disables R language support. Other R language packages are not removed.

---



## Using MRO with Anaconda

If you prefer to use the Microsoft R Open (MRO) platform with Anaconda, as opposed to R, you can switch the default R interpreter from R to MRO. To get MRO, you need to explicitly include `mro-base`. Anaconda will maintain an archive of MRO packages but will not update MRO packages. Support for MRO packages will be on a case-by-case basis.

If you are using MRO, it is recommended to migrate to R. Follow the [migration directions](#).

### Switch the default R interpreter from R to MRO

Run `conda info` and check your version of conda. If your version of conda is below 4.6, run `conda update conda` to update conda to the latest version.

Run:

```
conda config --system --set pinned_packages _r-mutex==anacondar*
```

The default R interpreter will switch from R to MRO.

To learn more about how to use MRO with Anaconda, see [Using MRO language with Anaconda](#).

## Resources

Here are some additional resources on using Anaconda with the R programming language:

- [R Language packages available for use with Anaconda](#)—There are hundreds of R language packages now available and several ways to get them.
- [Navigator tutorial](#)—Use the R programming language with Anaconda Navigator. The Anaconda Navigator graphical interface (GUI) makes it easy for even new users to use and run the R language in a Jupyter Notebook.
- [Using R packages with Anaconda and Cloudera CDH](#)—Anaconda Scale provides resource management tools to easily deploy Anaconda across a cluster. It helps you manage multiple conda environments and packages, including Python and R language, on bare-metal or cloud-based clusters.
- [Webinar: Anaconda for R Users](#)—Download the slides from the webinar to see how Anaconda makes package, dependency and environment management easy with R language and other Open Data Science languages.

### Using MRO language with Anaconda

Microsoft R Open (MRO) is the enhanced distribution of R from Microsoft, a complete and free open source platform for statistical analysis and data science.

MRO was previously the default R interpreter in Anaconda. As of 2019 releases, Anaconda defaults to internal builds of R, henceforth the “Anaconda R ecosystem.” [Learn more about how to use R with Anaconda](#).

Anaconda maintains an archive of MRO packages but will not update MRO packages. Support for MRO packages will be on a case-by-case basis.

If you are using MRO, it is recommended to migrate to R. Follow the migration directions below.

## Migrate MRO conda environments to use Anaconda R

If you have an MRO-based conda environment and you want to shift over to Anaconda R to fix library errors or for updates, using conda will fail:

```
conda install r-base
```

Using conda will result in unsatisfiable errors because the MRO packages in your environment will conflict with Anaconda R counterparts. They're not compatible and the metadata is designed to prevent this coexistence. You can create a new environment but that could require more effort depending on how many dependencies you have.

To resolve this, use the [MRO-migrator tool](#). This tool removes all MRO-specific packages then updates the remaining packages to use Anaconda R instead of MRO. The remove-update cycle takes care of the unsatisfiability.

**Warning:** There's minimal error handling in this tool. If your environment is not readily reproducible, back it up before running this tool.

To use the MRO-migrator tool, run its command line:

```
mro-migrator ~/miniconda3/envs/your-r-env
```

The default behavior lists which MRO-only packages will be removed. The tool does not change anything by default. To perform a migration, pass the `--execute` flag:

```
mro-migrator --execute ~/miniconda3/envs/your-r-env
```

## MRO-supported operating systems

64-bit systems only for all operating systems - Windows, macOS, and Linux.

Windows 7.0 SP1, Windows 8.1, Windows 10, Windows Server 2008 R2 SP1, and Windows Server 2012.

Linux - CentOS, Red Hat Enterprise Linux, Debian, and Ubuntu.

When using MRO conda packages, starting the R interactive interpreter shows Microsoft R Open in the startup message. Anaconda Navigator, the Anaconda graphical package manager and application launcher, also creates R environments by default. You may instead select MRO when creating a new conda environment from within Navigator.

## Microsoft R Client

Microsoft R Client is a free, community-supported data science tool for high-performance analytics built on top of MRO. Additionally, R Client introduces the powerful ScaleR technology and its proprietary functions to benefit from parallelization and remote computing.

Microsoft R Client is available as a conda package (`r-mrclient`). Users of Windows or RHEL-7/CentOS7/Ubuntu 14.04 and above also have the option to conda install the MicrosoftML R package for machine learning (`r-mrclient-mml`) and the pre-trained models for sentiment analysis and image detection (`r-mrclient-mlm`).

## Creating a new environment with MRO instead of R

When creating a new environment, you can use MRO and not R by explicitly including `mro-base` in your list of packages.

With conda 4.6.4:

```
conda create -n mro-environment r-essentials mro-base
conda activate mro-environment
```

## Switch an environment from R to MRO

We recommend using R as your default interpreter in Anaconda, however the directions below show you how to switch an environment from R to MRO.

## Activate the environment containing R

If you use conda 4.4 or later, run:

```
conda install mro-base
```

If you use conda 4.3, run:

```
conda remove --force r-base _r-mutex
conda install mro-base
```

The environment's R interpreter will switch from R to MRO.

**mro-basics:** The MRO Basics metapackage contains everything in the Microsoft MRO installers. It does not include `r-mrclient`, `r-mrclient-mml`, or `r-mrclient-mlm`.

**r-mrclient:** Microsoft R Client is a free, community-supported, data science tool for high performance analytics.

**r-mrclient-mml:** MicrosoftML provides state-of-the-art fast, scalable machine learning algorithms and transforms for R. Depends on `r-mrclient`.

**r-mrclient-mlm:** MicrosoftML Machine Learning Models are pre-trained machine learning models for sentiment analysis and image detection. Depends on `r-mrclient-mml`.

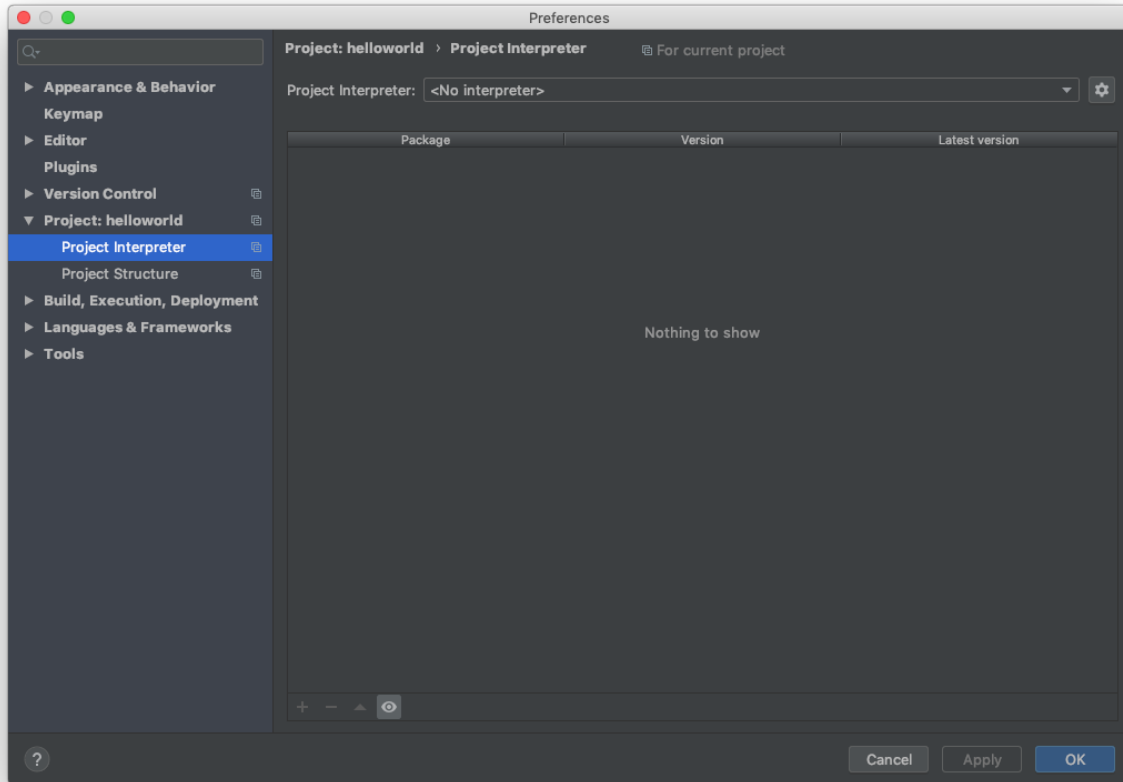
## Using PyCharm

PyCharm is an IDE that integrates with IPython Notebook, has an interactive Python console, and supports [Anaconda](#) as well as multiple scientific packages. PyCharm supports creating virtual environments for Python with conda.

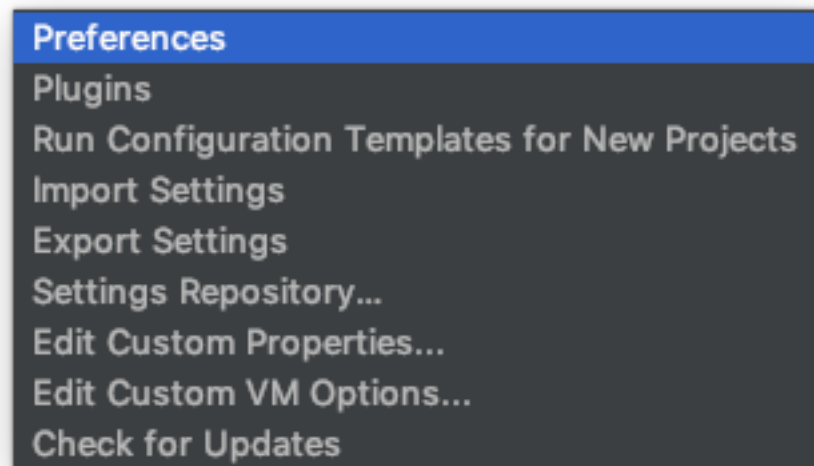
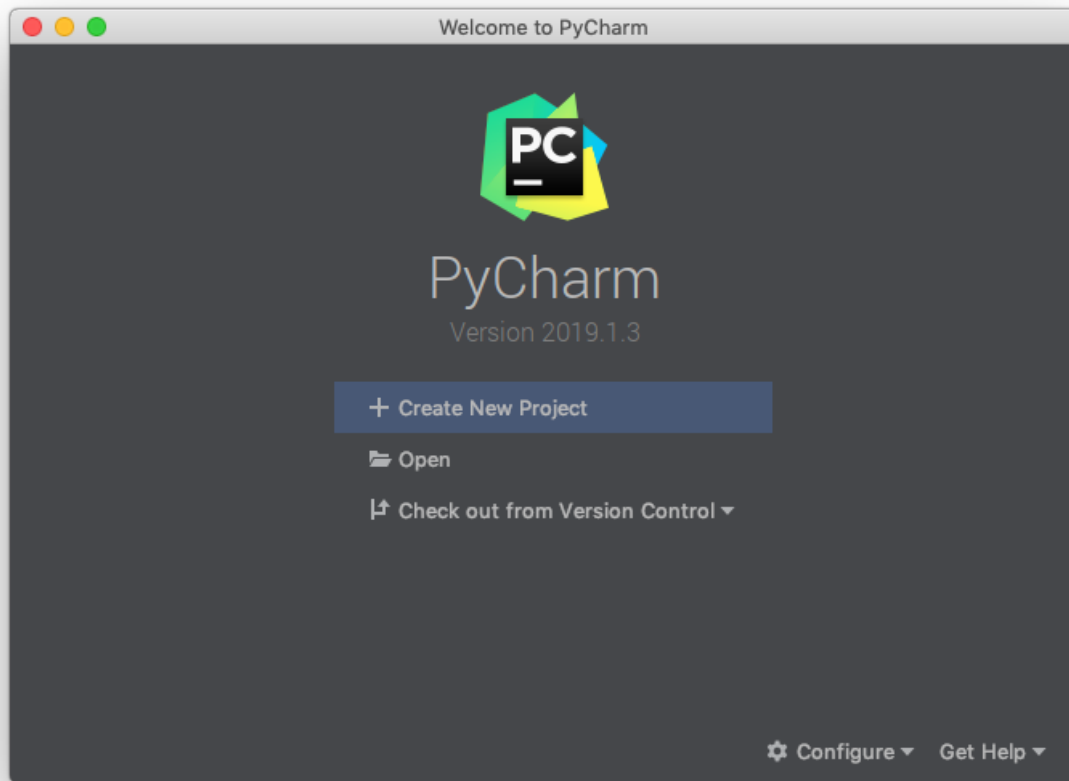
- *Configuring a conda environment in PyCharm*
- *Adding a package to a project*
- *Adding a repository to a project*

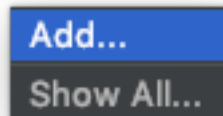
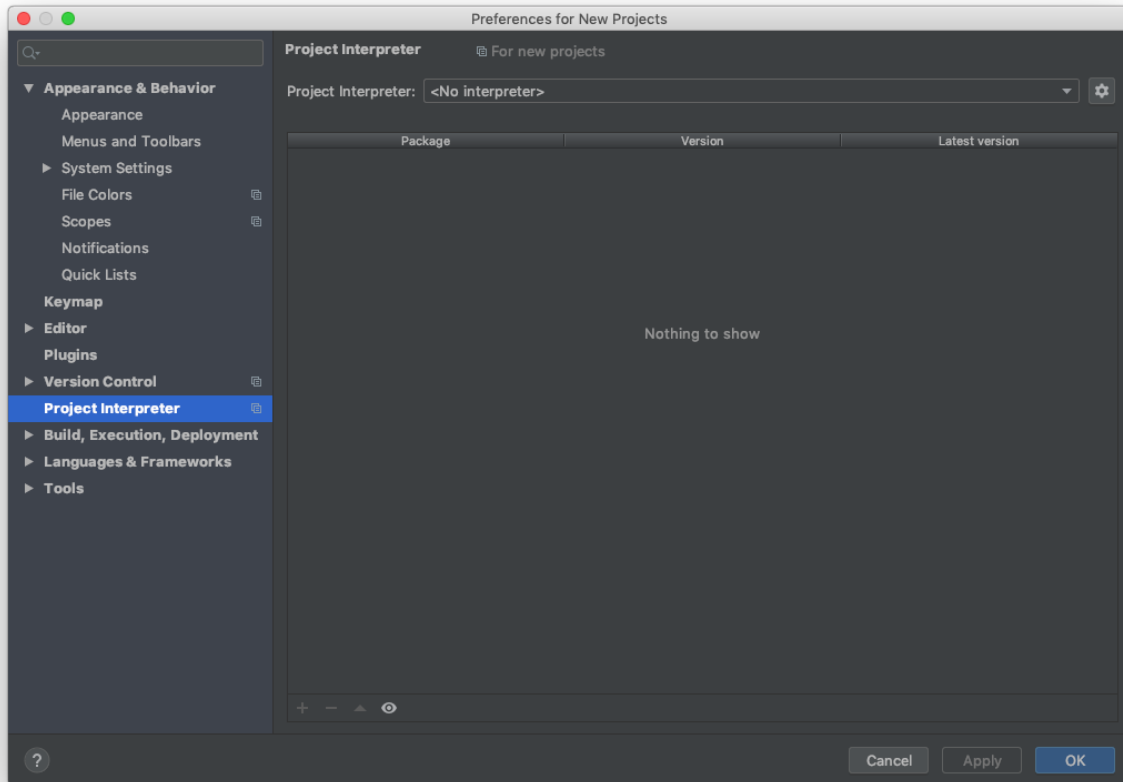
## Configuring a conda environment in PyCharm

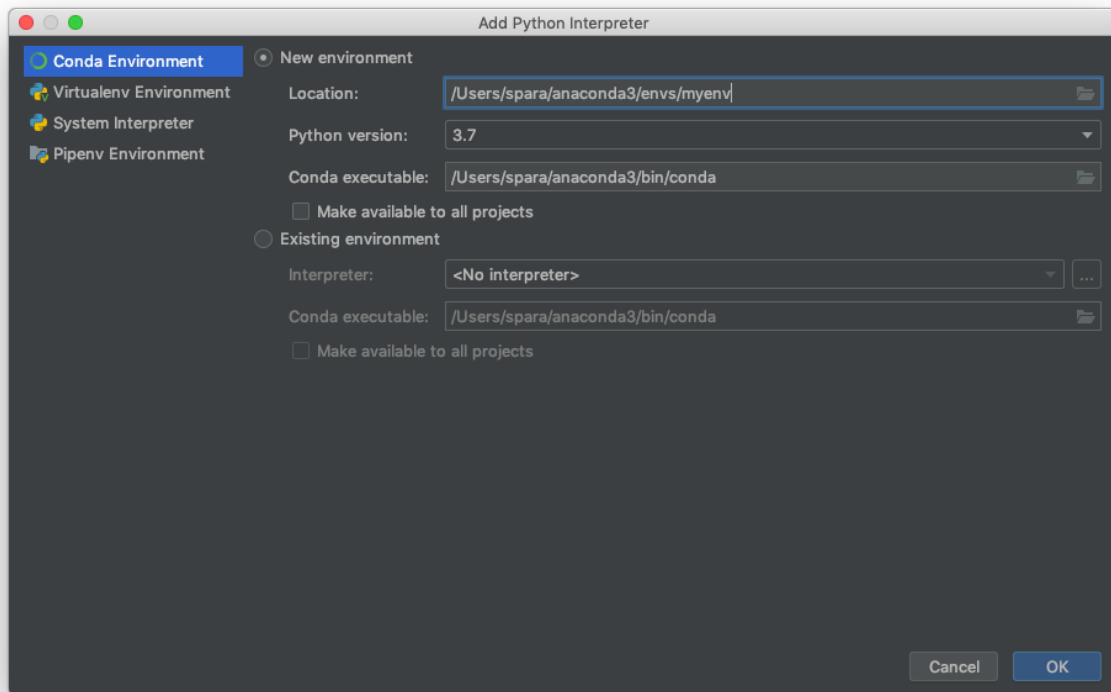
1. In the Settings/Preferences dialog (,), select Project: <project name> | Project Interpreter.



2. Alternatively, from the Welcome screen, select Configure.
3. Select Preferences.
4. Select Project Interpreter.
5. In the Project Interpreter page, click the gear icon and select Add.
6. In the left-hand pane of the Add Python Interpreter dialog box, select Conda Environment. The following actions depend on whether the conda environment existed before.
7. **If New environment is selected:**







1. Specify the location of the new conda environment in the text field or click the folder icon and find the location in your file system.

---

**Note:** The directory where the new conda environment should be located must be empty.

---

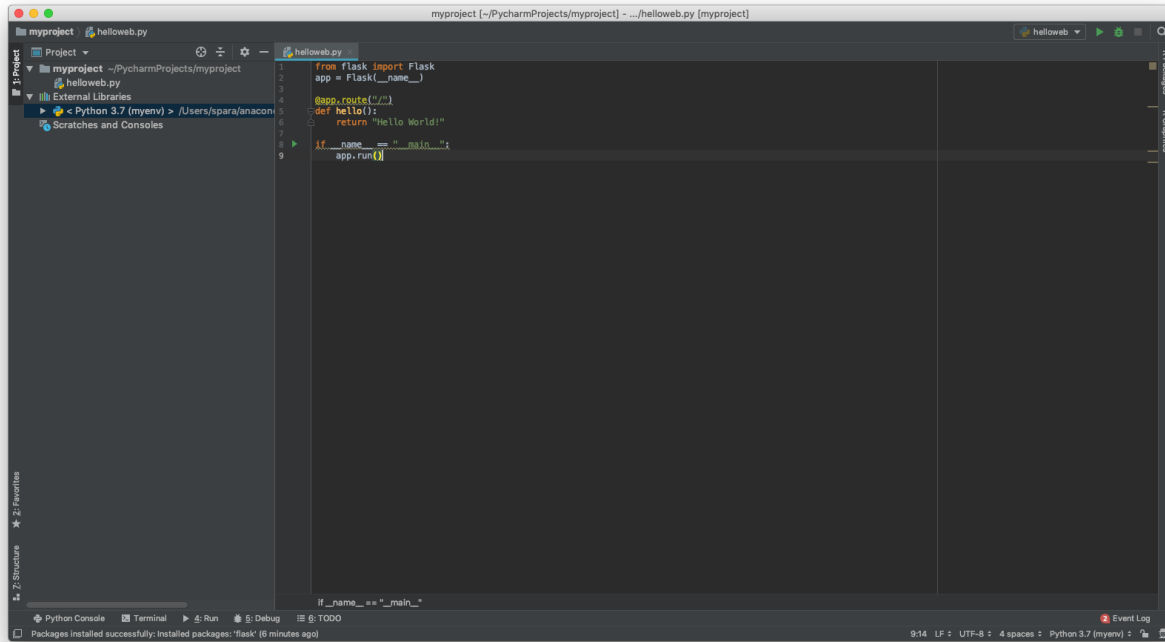
2. Select the Python version from the drop-down list.
3. Specify the location of the conda executable file in the text field or click the ellipsis and find the location in the conda installation directory.
4. If needed, select the Make available to all projects check box.

**8. If Existing environment is selected:**

1. Specify the required interpreter: use the drop-down list or click and find one in your file system (for example, `C:\Users\jetbrains\Anaconda3\python.exe`).
  2. Select the check box Make available to all projects (if needed).
9. Click OK to complete the task.

### Adding a package to a project

The project uses the flask package, which is available on the [Anaconda defaults channel](#).



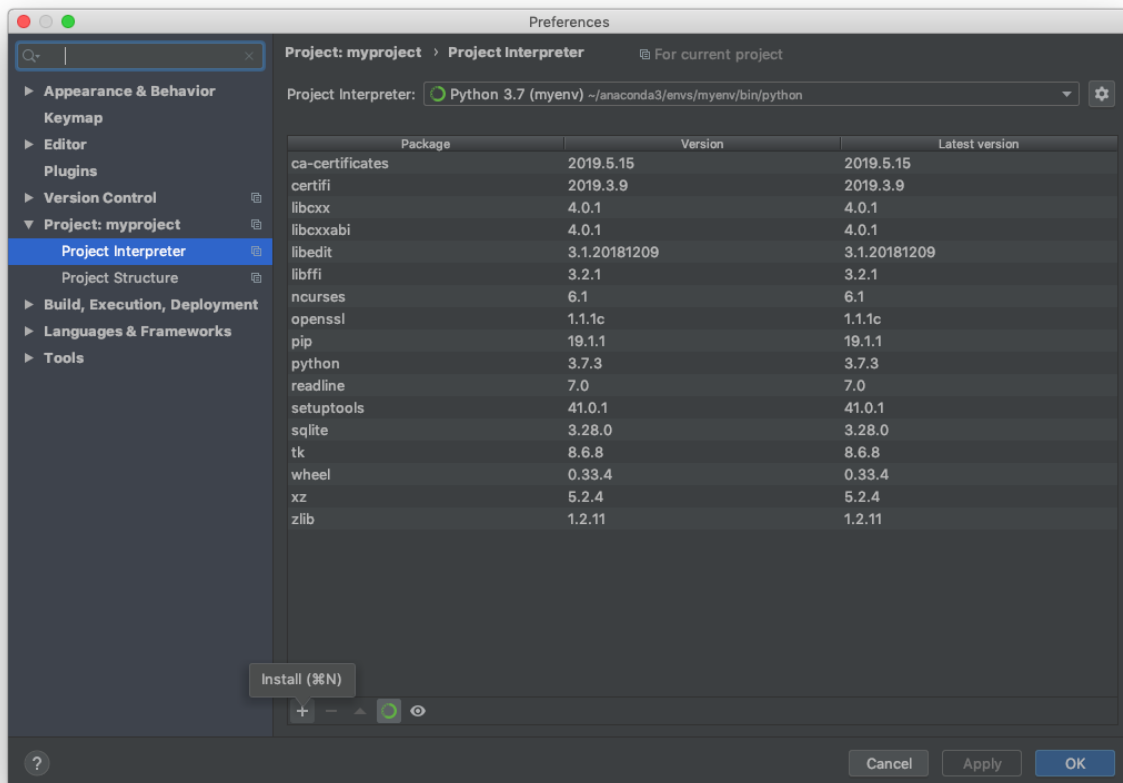
1. To add flask, select Preferences (,).
2. Select + to display the packages available in the defaults channel.
3. The packages in the defaults channel are displayed. Type “flask” into the search bar and select Install.
4. After flask is installed, it will be displayed in the project environment.

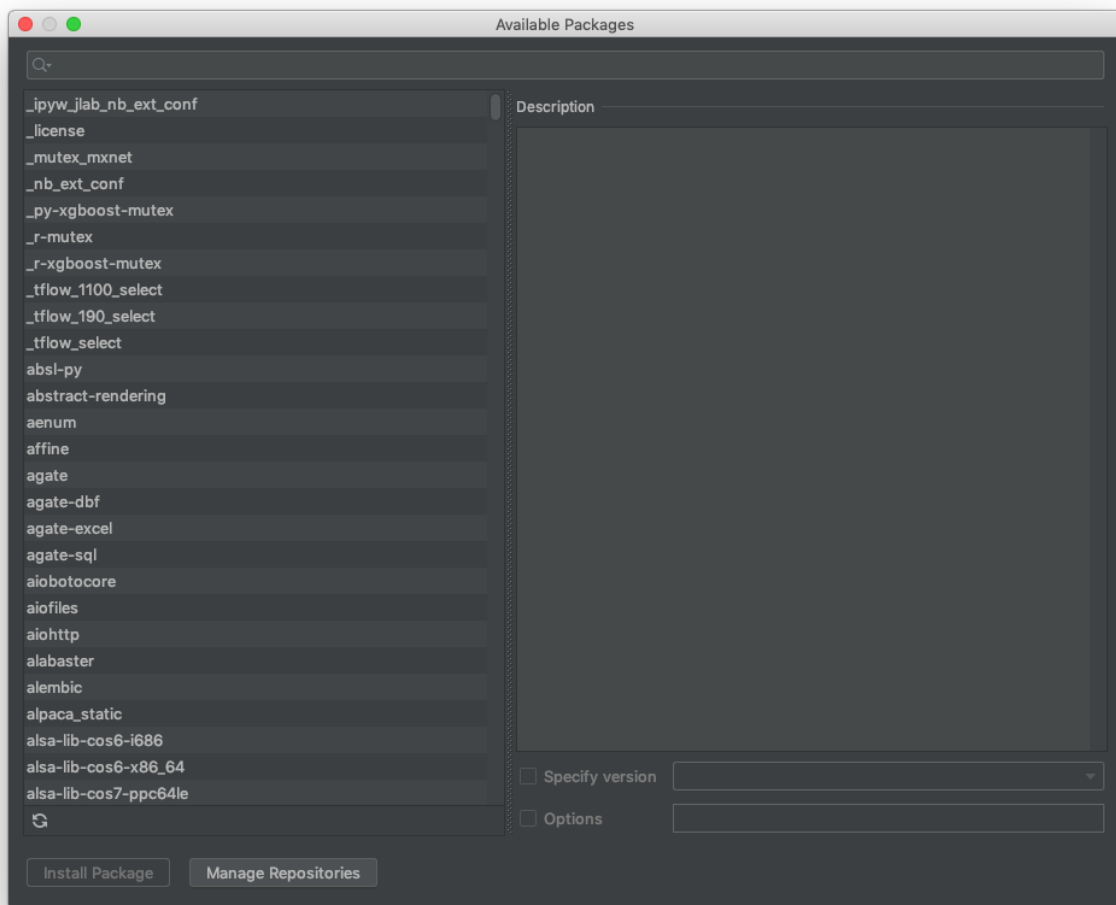
## Adding a repository to a project

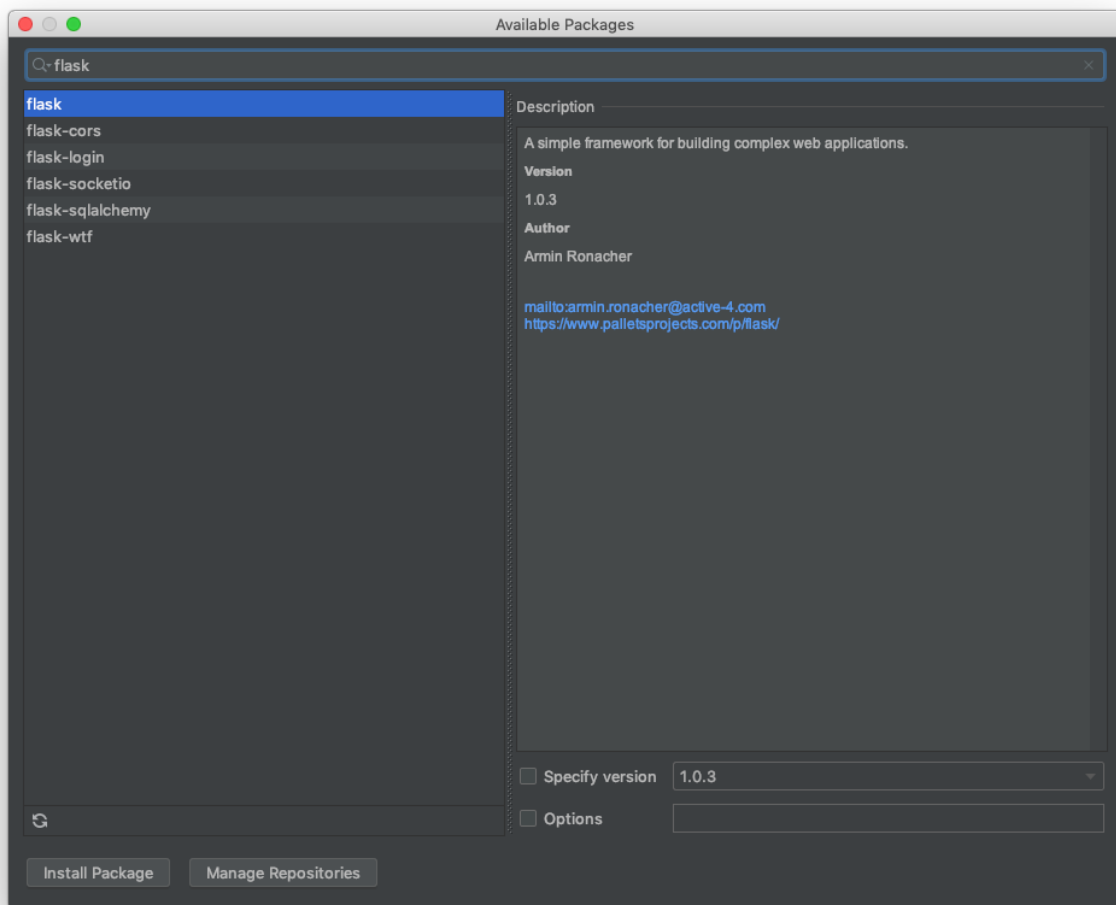
This project uses the bottle package, which is available on the [conda-forge channel](#).

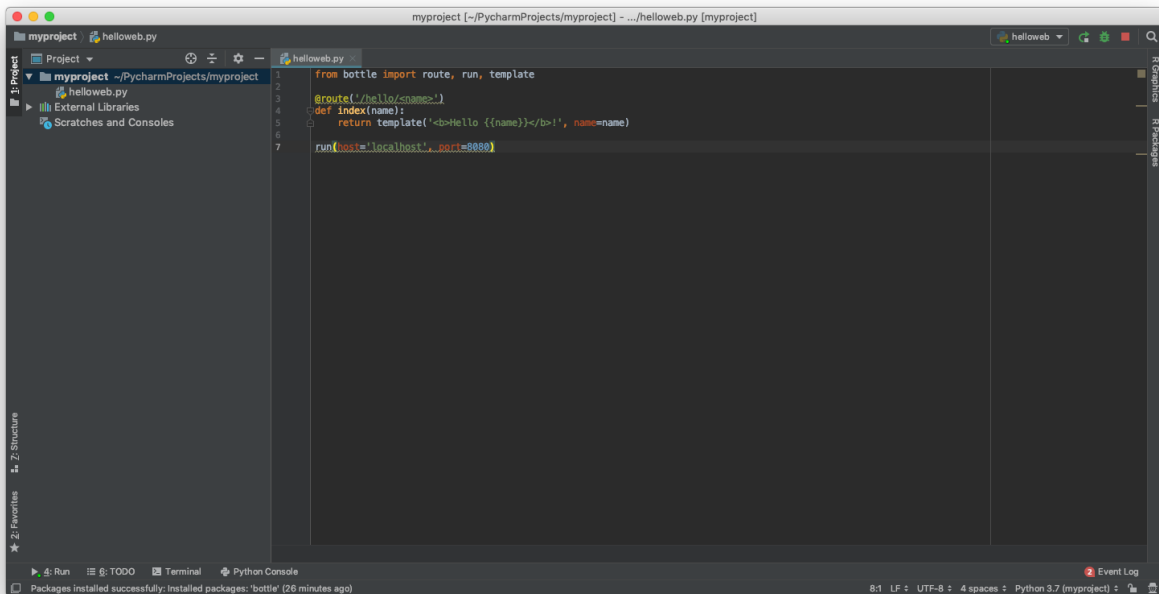
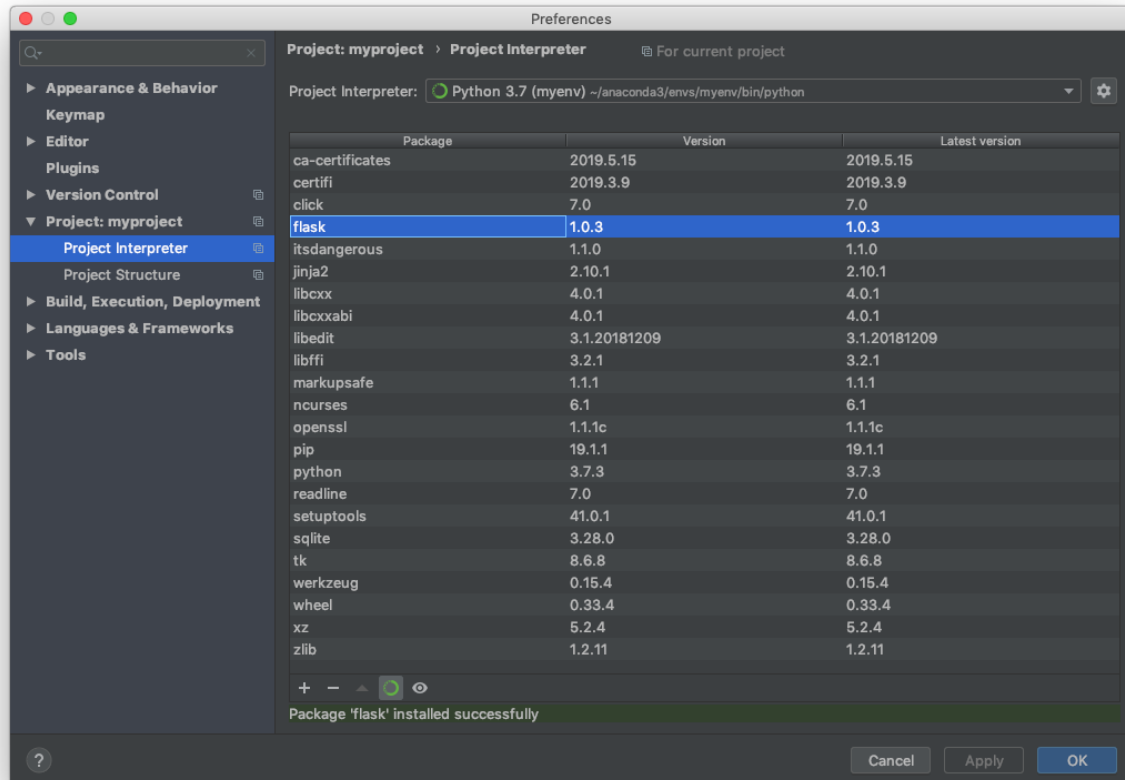
1. To add the conda-forge channel, select Preferences (,).
2. Select + to display the packages available in the defaults channel.
3. To add a repository, select Manage Repositories, select +, and enter “conda-forge”. Select OK.

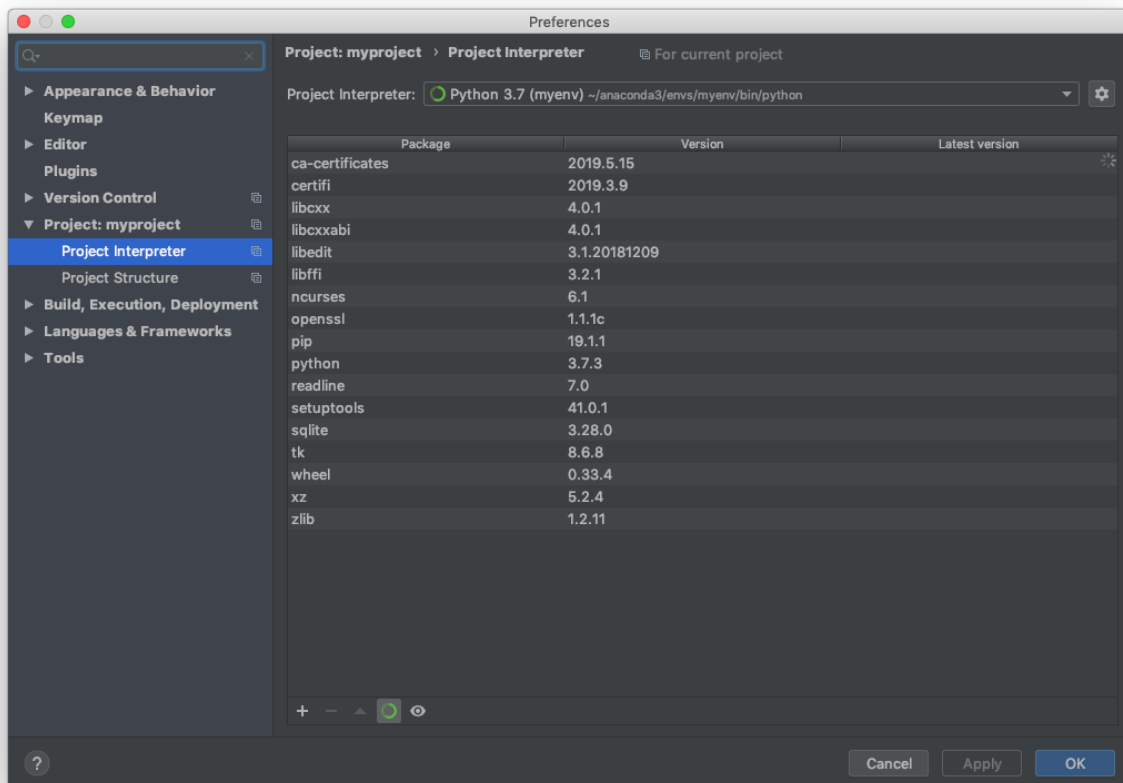


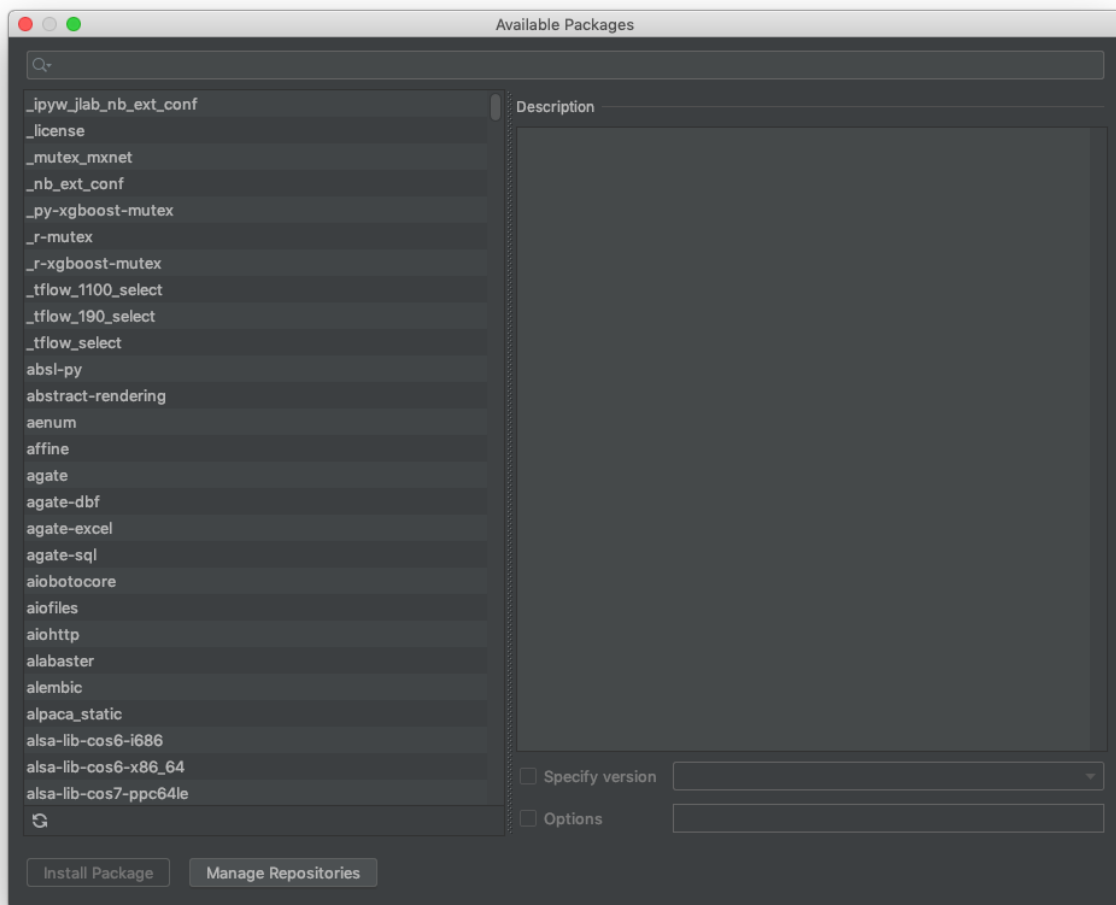


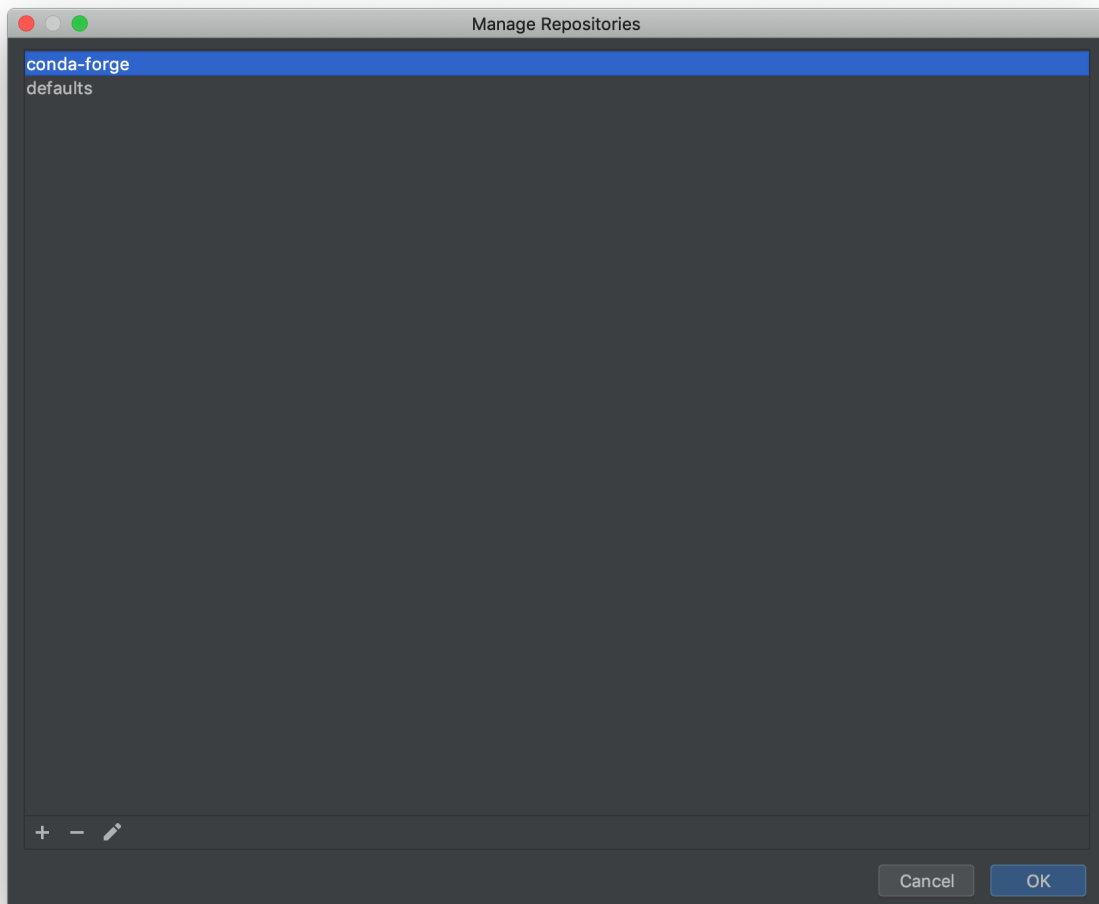






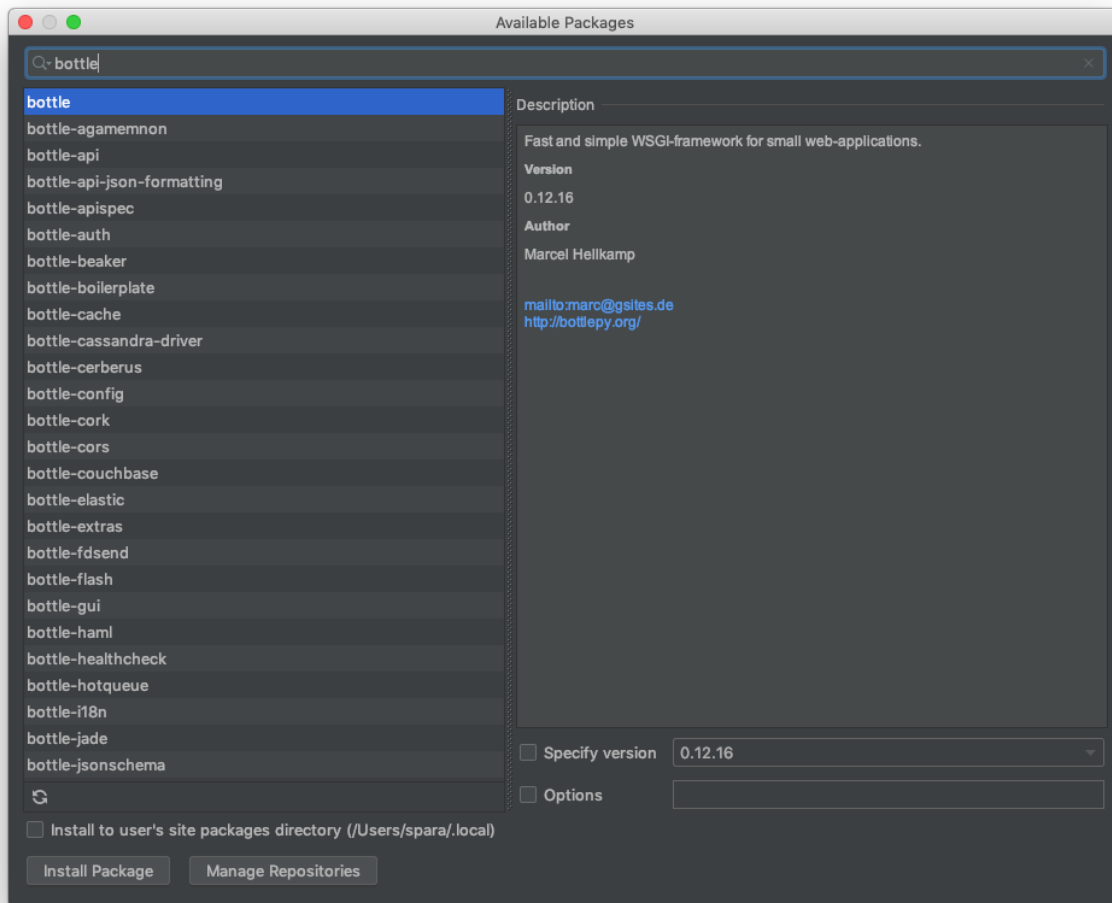






The packages from both defaults and conda-forge will be displayed.

4. Type “bottle” into the search bar and select Install Package.



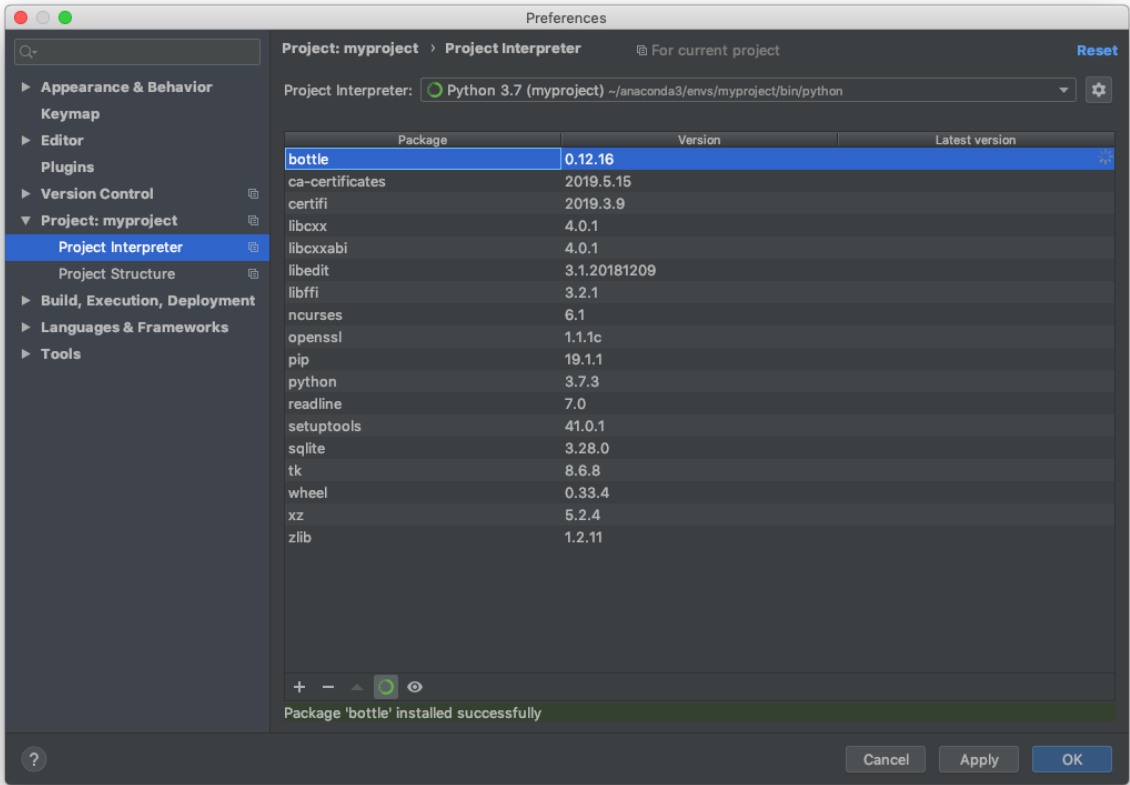
5. After bottle is installed, it will be displayed in the project environment.

### Using Anaconda behind a company proxy

When using Anaconda with a company proxy, you may encounter an HTTP and SSL error due to custom security profiles managed by corporate IT departments.

There are 3 potential ways to resolve this. Start with updating the .condarc file before trying the other methods.





### Update the .condarc file

We recommend updating your .condarc file to include the `proxy_servers` key. This is the preferred method because this will affect only conda and not the system environment variables.

Read more about the [.condarc file and using proxies](#).

For example:

```
proxy_servers:  
  http: http://username:password@corp.com:8080  
  https: https://username:password@corp.com:8080
```

You can see if your proxy is set by running `conda info --all`.

### Environment variables

You can also resolve this error by updating the system environment variables. This can affect all CLI software across the whole system.

### Windows

To change environment variables on Windows:

1. In the Start menu, search for “env”.
2. Select “Edit Environment Variables for your account”
3. Select “Environment Variables...”
4. Press “New...”
5. Add two variables `http_proxy` and `https_proxy` both with the same value: [http://proxy-XX:XXX](#)

### MacOS

To change environment variables on macOS:

1. Check the current environment variable settings by running `printenv` in the terminal.
2. To check a specific environment variable, use `echo $variable_name`.
3. Temporarily change the environment variables by running `export variable_name=variable_value`.  
You can check if it's there by running `conda info --all`.

To change your environment variables on macOS permanently, review this [guide](#).

### Linux

To change environment variables on Linux:

1. Run `export variable_name=variable_value`
2. To output the value of the environment variable from the shell, run `echo $variable_name`.

Read more about [unsetting, listing, and persisting environment variables](#).

## Netrc authentication

A `.netrc` file is an alternate way to accomplish the same goal of setting the `*_PROXY` environment variables or configuring things only for conda in the `.condarc` file. The risk in this approach is that changing the environment variables here will affect the system settings as a whole.

[Read more about the `.netrc` file.](#)

## TensorFlow

Anaconda makes it easy to install TensorFlow, enabling your data science, machine learning, and artificial intelligence workflows.

This page shows how to install [TensorFlow](#) with the conda package manager included in Anaconda and Miniconda.

TensorFlow with conda is supported on 64-bit Windows 7 or later, 64-bit Ubuntu Linux 14.04 or later, 64-bit CentOS Linux 6 or later, and macOS 10.10 or later.

The instructions are the same for all operating systems. No `apt install` or `yum install` commands are required.

## Install TensorFlow

1. Download and install [Anaconda](#) or the smaller [Miniconda](#).
2. On Windows open the Start menu and open an Anaconda Command Prompt. On macOS or Linux open a terminal window. Use the default bash shell on macOS or Linux.
3. Choose a name for your TensorFlow environment, such as “tf”.
4. To install the current release of CPU-only TensorFlow, recommended for beginners:

```
conda create -n tf tensorflow
conda activate tf
```

Or, to install the current release of GPU TensorFlow on Linux or Windows:

```
conda create -n tf-gpu tensorflow-gpu
conda activate tf-gpu
```

TensorFlow is now installed and ready to use.

For using TensorFlow with a GPU, refer to the [TensorFlow documentation](#) on the topic, specifically the section on [device placement](#).

## CUDA versions

GPU TensorFlow uses CUDA. On Windows and Linux only CUDA 10.0 is supported for the TensorFlow 2.0 release. Previous versions of TensorFlow support other version of CUDA.

To install GPU TensorFlow with a non-default CUDA version such as 9.0 run:

```
conda create -n tf-gpu-cuda8 tensorflow-gpu cudatoolkit=9.0
conda activate tf-gpu-cuda8
```

### Python 2

We recommend Python 3, but it is possible to use TensorFlow with Python 2 on Linux and macOS.

CPU-only TensorFlow on Python 2 on Linux or macOS:

```
conda create -n tf-2 tensorflow python=2
conda activate tf-2
```

GPU TensorFlow on Python 2 on Linux:

```
conda create -n tf-2-gpu tensorflow python=2
conda activate tf-2-gpu
```

### Nightly builds

Advanced users may wish to install the latest nightly build of TensorFlow. These nightly builds are unstable and are only available as pip packages on PyPI.

To install the nightly build of CPU-only TensorFlow:

```
conda create -n tf-n python
conda activate tf-n
pip install tf-nightly
```

Or, to install the nightly build of GPU TensorFlow on Linux or Windows:

```
conda create -n tf-n-gpu python
conda activate tf-n-gpu
pip install tf-nightly-gpu
```

Nightly build of CPU-only TensorFlow on Python 2 on Linux or macOS:

```
conda create -n tf-2-n python=2
conda activate tf-2-n
pip install tf-nightly
```

Nightly build of GPU TensorFlow on Python 2 on Linux:

```
conda create -n tf-2-n-gpu python=2
conda activate tf-2-n-gpu
pip install tf-nightly-gpu
```

### Cloudera CDH



Cloudera provides Apache Hadoop-based software, support and services, as well as training to business customers. Their open-source Apache Hadoop distribution, CDH (Cloudera Distribution Including Apache Hadoop), targets enterprise-class deployments of that technology.

There are two methods of using Anaconda on an existing cluster with [Cloudera CDH](#), Cloudera's distribution including Apache Hadoop:

- Use the Anaconda parcel for Cloudera CDH. The following procedure describes how to install the Anaconda parcel on a CDH cluster using Cloudera Manager. The Anaconda parcel provides a static installation of Anaconda, based on Python 2.7, that can be used with Python and PySpark jobs on the cluster.
- Use Anaconda Scale, which provides additional functionality, including the ability to manage multiple conda environments and packages, including Python and R, alongside an existing CDH cluster. For more information, see [Using Anaconda with Cloudera CDH](#).

See the blog post [Self-service Open Data Science: Custom Anaconda parcels for Cloudera](#).

## Install the Anaconda parcel

1. In the Cloudera Manager Admin Console, in the top navigation bar, click the Parcels icon.
2. At the top right of the parcels page, click the Edit Settings button.
3. In the Remote Parcel Repository URLs section, click the plus symbol, and then add the following repository URL for the Anaconda parcel:

```
https://repo.anaconda.com/pkg/misc/parcels/
```

4. At the top of the page, click the Save Changes button.
5. In the top navigation bar, click the Parcels icon to return to the list of available parcels, where you should see the latest version of the Anaconda parcel that is available.
6. To the right of the Anaconda parcel listing, click the Download button.
7. After the parcel is downloaded, click the Distribute button to distribute the parcel to all of the cluster nodes.
8. After the parcel is distributed, click the Activate button to activate the parcel on all of the cluster nodes.
9. When prompted, confirm the activation.

After the parcel is activated, Anaconda is available on all of the cluster nodes.

You can submit Spark jobs along with the `PYSPARK_PYTHON` environment variable that refers to the location of Anaconda. For example, enter the following command all on one line:

```
PYSPARK_PYTHON=/opt/cloudera/parcels/Anaconda/bin/ python spark-submit pyspark_script.  
↪py
```

---

**Note:** The repository URL shown above installs the most recent version of the Anaconda parcel. To install an older version of the Anaconda parcel, add <https://repo.anaconda.com/pkg/misc/parcels/archive/> to the Remote Parcel Repository URLs in Cloudera manager, and then follow the above steps with your desired version of the Anaconda parcel.

---

### Parcel updates

Anaconda builds new Cloudera parcels at least once a year each spring and also offers custom parcel creation for our enterprise customers. The Anaconda parcel provided at the repository URL shown above is based on Python 2.7. To use the Anaconda parcel with other versions of Python or with additional packages, contact [sales@anaconda.com](mailto:sales@anaconda.com) for more information about custom Anaconda parcel builds or other enterprise solutions for using Anaconda with cluster computing.

Anaconda Workgroup and Anaconda Enterprise subscribers can also use Anaconda Repository to *create and distribute their own custom Anaconda parcels for Cloudera Manager*.

For more information about managing Cloudera parcels, see the [Cloudera documentation](#).

### Amazon AWS



Amazon Web Services (AWS) is a collection of cloud-computing services that make up a cloud-computing platform offered by Amazon.com.

To see the currently available official Anaconda or Miniconda AMIs please go to [AWS marketplace](#)

### Docker

Docker is an open platform for developers and system administrators to build, ship, and run distributed applications, whether on laptops, data center virtual machines, or the cloud. Anaconda, Inc. provides Anaconda and Miniconda Docker images.

Read the [official Docker documentation](#) and specifically the information related to [Docker images](#).

Begin by browsing the available Anaconda images [on our Docker profile](#).

To obtain a fully working Anaconda image:

1. In a terminal window, run this command to display a list of available images:

```
docker search continuumio
```

2. Pull the desired image:

```
docker pull continuumio/miniconda
```

3. Create a container using the image:

```
docker run -t -i continuumio/miniconda /bin/bash
```

This gives you direct access to the container where the conda tool is already available.

4. Test the container:

```
conda info
```

You now have a fully working Anaconda image.

To install and launch the Jupyter Notebook, execute the following command all on one line from the host machine:

```
docker run -i -t -p 8888:8888 continuumio/miniconda /bin/bash
-c "/opt/conda/bin/conda install jupyter -y --quiet && mkdir
/opt/notebooks && /opt/conda/bin/jupyter notebook
--notebook-dir=/opt/notebooks --ip='*' --port=8888
--no-browser"
```

---

**Note:** Line breaks in the example above are for readability only. Enter the command all on one line.

---

To access the Jupyter notebook open <http://localhost:8888> in your browser, or open <http://<DOCKER-MACHINE-IP>:8888> if you are using a Docker Machine VM.

---

**Note:** Replace <DOCKER-MACHINE-IP> with your Docker Machine VM IP address.

---

## Using IDEs

Data science is a team sport, so we have built the Anaconda platform to be language-agnostic as well as extensible.

You can use the following IDEs with Anaconda:

- *Eclipse and PyDev*
- *IDLE*
- *IntelliJ*

- *Ninja IDE*
- *Python Tools for Visual Studio (PTVS)*
- *Python for Visual Studio Code*
- *Spyder*
- *Sublime Text*
- *Microsoft Visual Studio Code (VS Code)*
- *Wing IDE*

---

**Note:** IDEs often require you to specify the path to your Python interpreter. See [Finding your Anaconda Python interpreter path](#).

---

*Microsoft Excel*—Anaconda on Windows comes ready to bring the power of Python into Excel. Use one of the many packages included in Anaconda or connect to an outside integration tool.

### Eclipse and PyDev

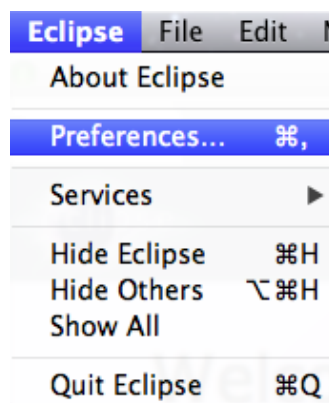
**Eclipse** is an open-source platform that provides an array of convenient and powerful code-editing and debugging tools. **PyDev** is a Python IDE that runs on top of Eclipse.

If you do not already have Eclipse and PyDev installed:

- [Download Eclipse](#) and read the [Eclipse resources](#).
- You may need to install the latest [Java JDK/JRE](#) before installing PyDev in order for PyDev to show up in the Eclipse Preferences menu after PyDev installation.
- [Install PyDev](#).

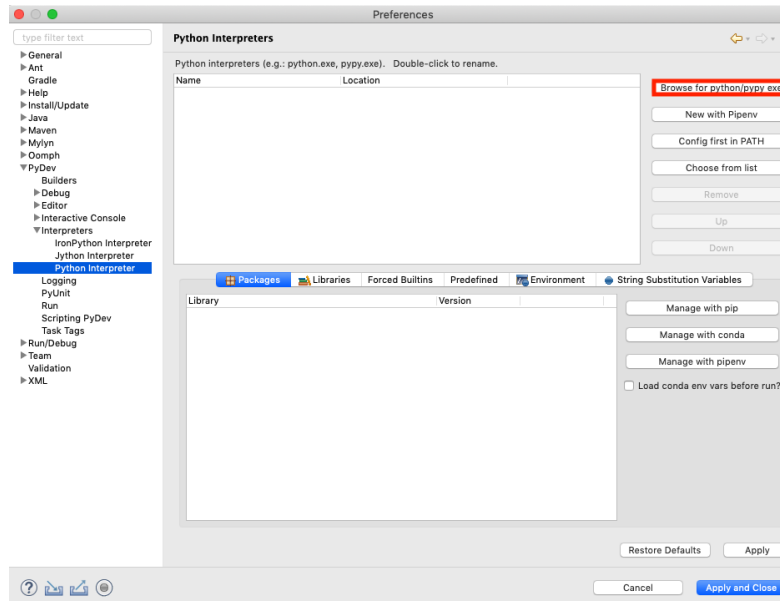
After you have Eclipse, PyDev, and Anaconda installed, set Anaconda Python as your default:

1. Open the Eclipse Preferences window:

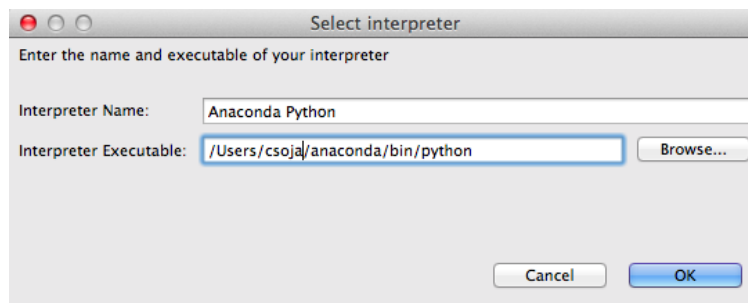




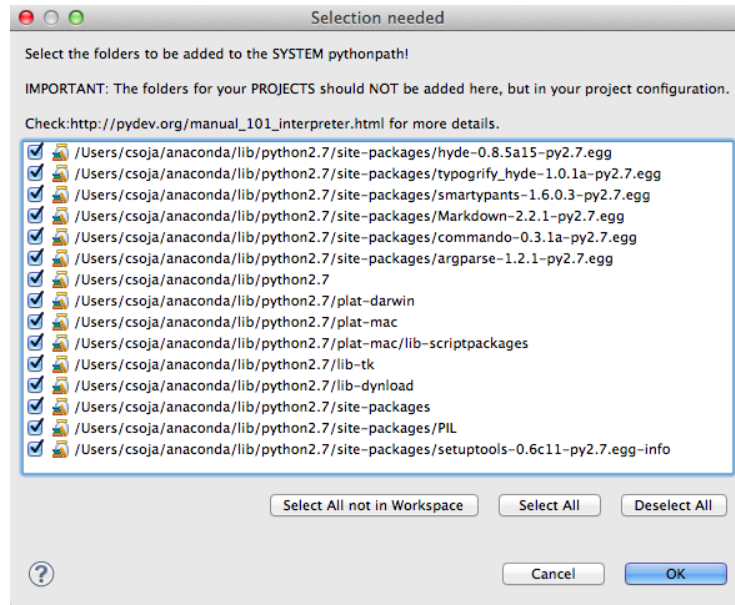
2. In the PyDev list, select Interpreters, and then select Python Interpreter.
3. Click the Browse for python/pypy exe button:



4. In the Interpreter Name box, type `Anaconda Python`.
5. Browse to your *Anaconda Python interpreter path*. The interpreter you choose is related to your environment, so Eclipse will have access to all of the packages in that environment. To add new packages, you may need to `conda install package-name` in your Anaconda Prompt or terminal.
6. Click the OK button:

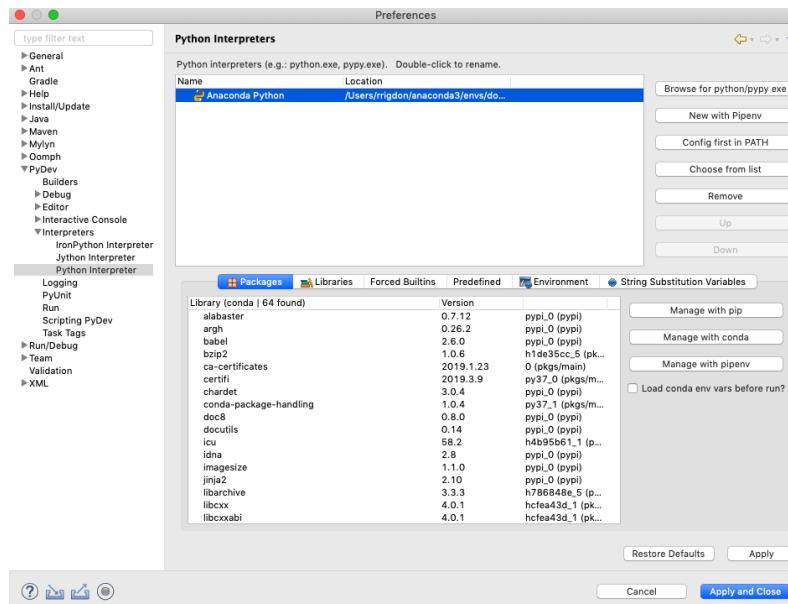


7. In the next window, select the folders to add to the SYSTEM Python path:
  1. Select all the folders:



2. Click the OK button.

The Python Interpreters window now displays Anaconda Python:



3. Click the Apply and Close button.

You are now ready to use Anaconda Python with your Eclipse and PyDev installation.

## IDLE

IDLE is a very small and simple cross-platform IDE that is included free with Python and is released under the open-source Python Software Foundation License.

Anaconda and Miniconda include IDLE.

To use IDLE:

1. Find the IDLE program file:

EXAMPLES for Miniconda with Python 3 and user name “jsmith”:

- On macOS, the full path may be `/Users/jsmith/miniconda3/bin/idle3.5`
- On Windows, the full path may be `C:\Users\jsmith\Miniconda3\Scripts\idle`

2. Run IDLE from file explorer or from the command line by entering the full path.

---

**Tip:** You can make a shortcut to the IDLE program file on your desktop.

---

## IntelliJ

IntelliJ IDEA Community Edition is the open-source version of [IntelliJ IDEA](#), an IDE (Integrated Development Environment) for Java, Groovy, and other programming languages such as Scala or Clojure. It is made by JetBrains, maker of *PyCharm Python IDE*.

### Before you start

You should have both Miniconda and IntelliJ installed and working.

### Set up IntelliJ using Miniconda

Find location of Miniconda Python executable:

```
which python
```

The system responds with your path to Python. You need this in the next step.

### Within IntelliJ

1. Go to `File > Project Structure > Platform Settings > SDKs`
2. Click the Add (+) icon
3. Choose `Python SDK`

4. Enter location of Miniconda Python executable `/Users/UserName/miniconda3/bin/python`

---

**Note:** Substitute your actual path to Miniconda that you found in the previous step.

---

5. Go to `File > Project Settings > Project > Project SDK`
6. Select from the drop-down: `Python 3.6.0 (~/.miniconda3/bin/python...)`
7. Go to `Run > Debug`
8. Click the Add (+) icon
9. Select `Python` and then enter the following:  
Name: `MyProject`  
Script: `/Users/UserName/MyProject/my_file.py`  
Use Specified Interpreter: `Python 3.6.0 (~/.miniconda3/bin/python...)`

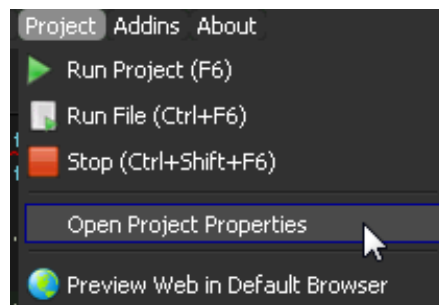
For more information, see the [IntelliJ IDEA documentation](#).

## Ninja IDE

[Ninja IDE](#) is a cross-platform, free, open-source IDE specially designed for Python application development.

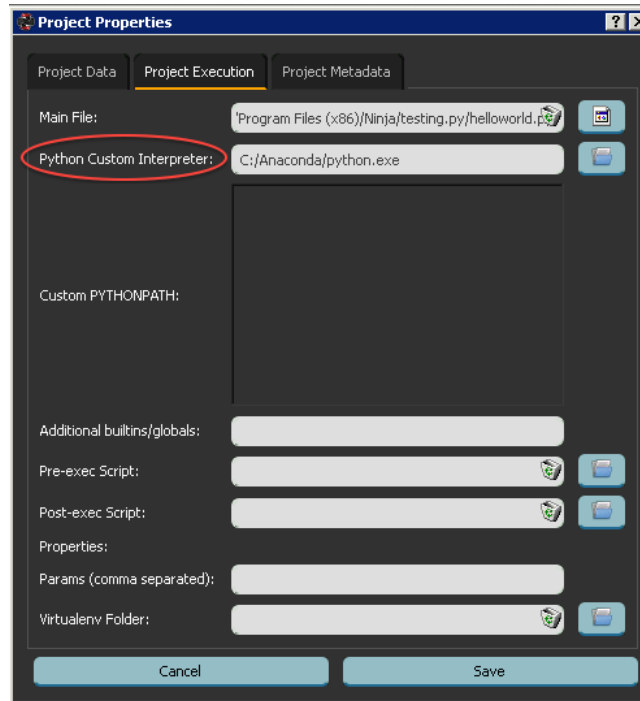
To use Anaconda Python with the Ninja IDE:

1. In the **Project** menu, select Open Project Properties:



2. On the **Project Execution** tab, in the Python Custom Interpreter box, enter *the Anaconda Python interpreter path* to select Anaconda Python:

3. Verify the setup with a test script:



- a. To create the test script, enter this code:

```
import sys
print(sys.version)
```

- b. Run your test script.

In the command output, your Anaconda Python version is listed:

For more information, see the [Ninja-IDE documentation](#).

## Python Tools for Visual Studio (PTVS)

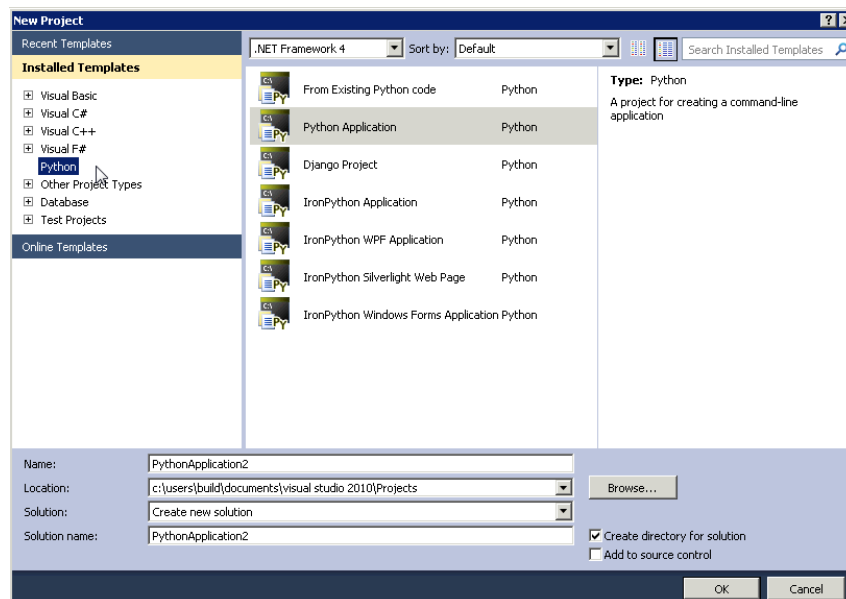
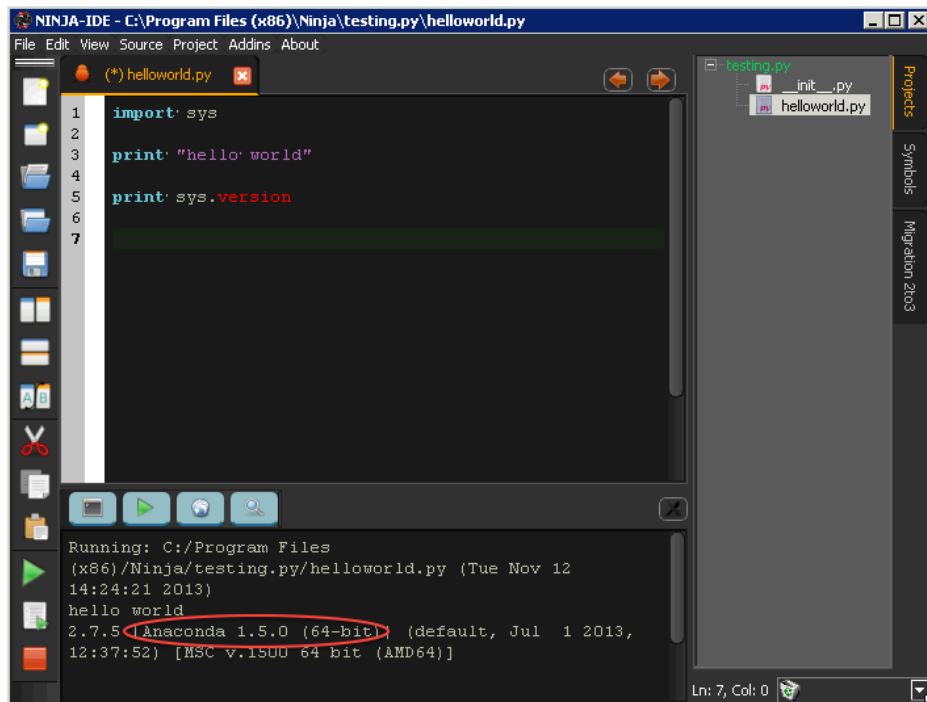
Python Tools for Visual Studio is a free, open source plugin that turns Visual Studio into a Python IDE.

If you have installed Anaconda as your default Python installation and installed PTVS, your Visual Studio installation is already set to use Anaconda's Python interpreter in PTVS.

To verify this, create a new Python project and then check whether Anaconda is the Python that it uses.

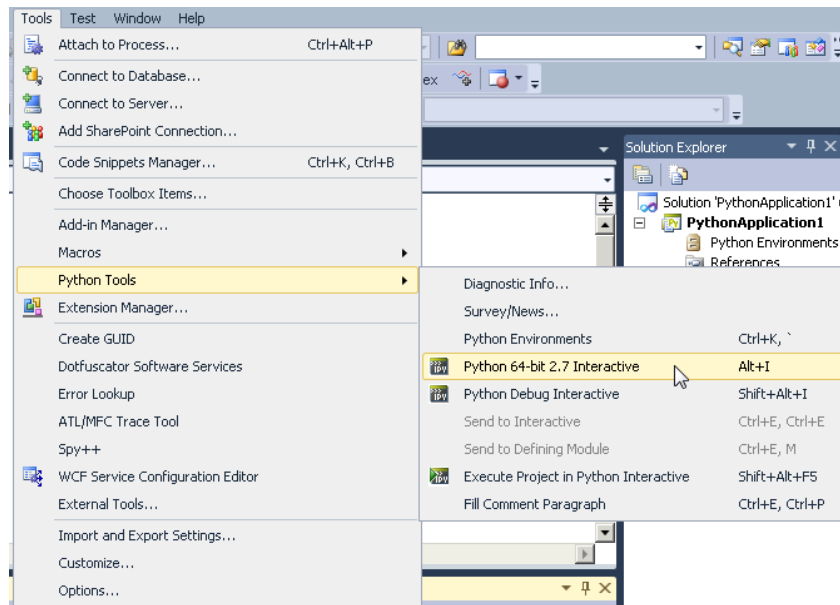
To create a new Python project:

1. In the **File** menu, select New, and then select Project. The keyboard shortcut is Ctrl-Shift-N.
2. Select Python Application:



To check which Python the project uses:

1. From the **Tools** menu, select Python Tools, and then select Python Interactive. The keyboard shortcut is Alt+I:



2. In the **Python Interactive** window, type `import sys` and then press Enter.
3. Type `sys.version` and then press Enter.

If PTVS is using Anaconda, your Anaconda Python version is displayed. In the example below, it is Anaconda 1.5.0 (64-bit):

```
Python 64-bit 2.7 Interactive
__main__
Python interactive window. Type $help for a list of commands.
>>> import sys
>>> sys.version
'2.7.5 |Anaconda 1.5.0 (64-bit)| (default, Jul 1 2013, 12:37:52) [MSC v.1500 64 bit (AMD64)]'
>>>
```

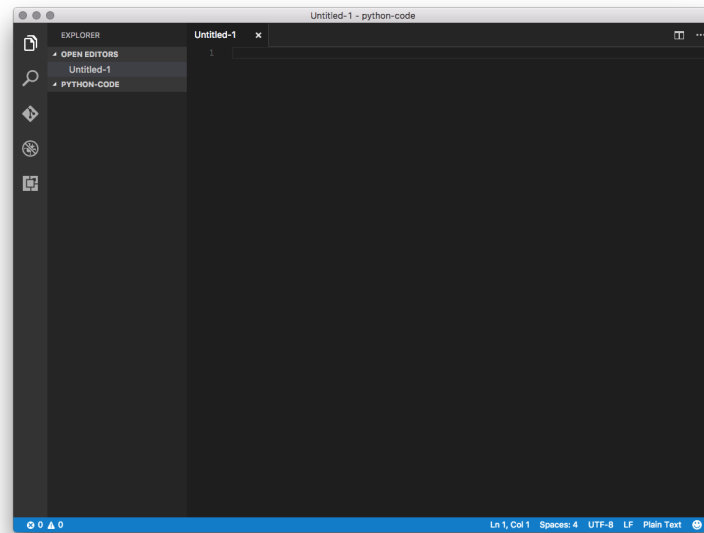
If PTVS does not automatically discover Anaconda, see the [official PTVS documentation](#), especially the section on [Selecting and Installing Python Interpreters](#) and the [PTVS installation instructions](#).

## Python for Visual Studio Code

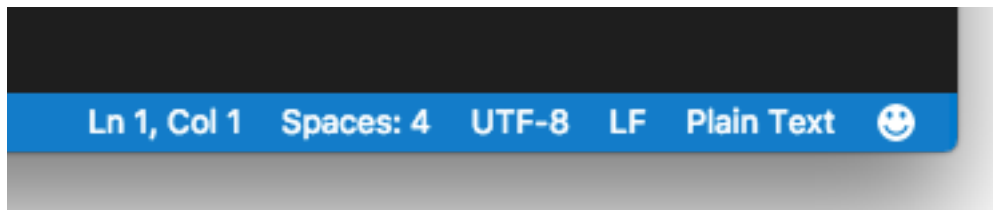
**Visual Studio Code (VSC)** is a free cross-platform source code editor. The **Python for Visual Studio Code extension** allows VSC to connect to Python distributions installed on your computer.

If you've installed Anaconda as your default Python installation and installed Python for Visual Studio Code, your VSC installation is already set to use Anaconda's Python interpreter.

1. Create a new Python source code file:
  1. In the **File** menu, select Open to choose a directory to place the code.
  2. In the **File** menu, select New File. Your screen will now look like this:

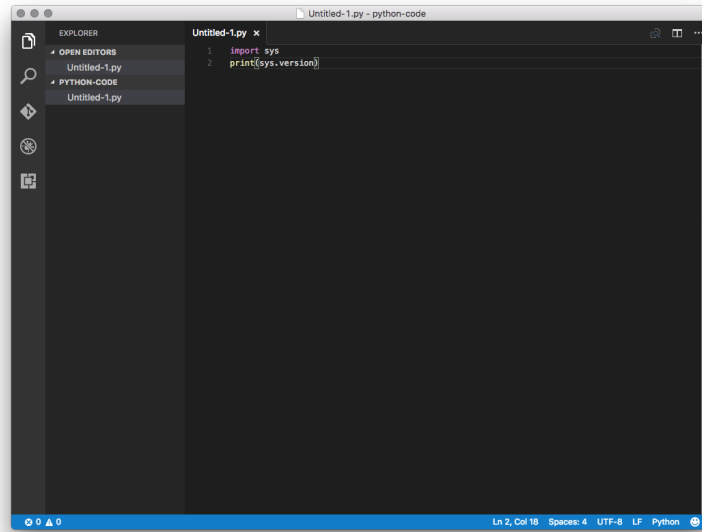


2. Click Plain Text at the bottom of the window to associate the new file with the Python interpreter.

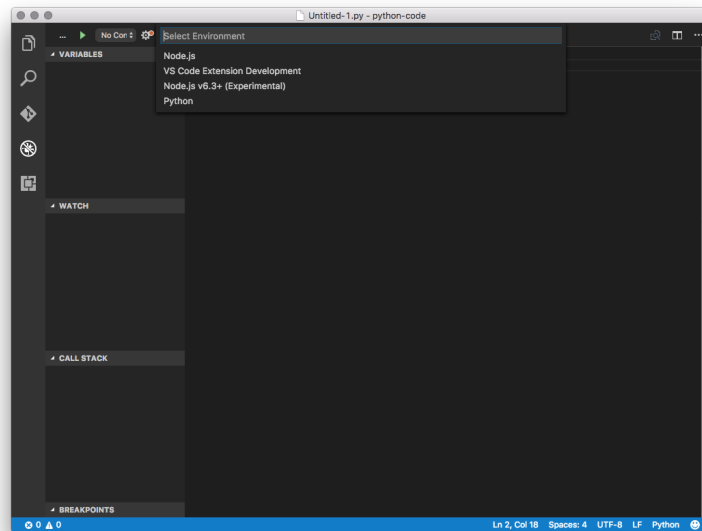


3. In the menu that displays, type or select Python.
4. In the pane on the right, add source code:

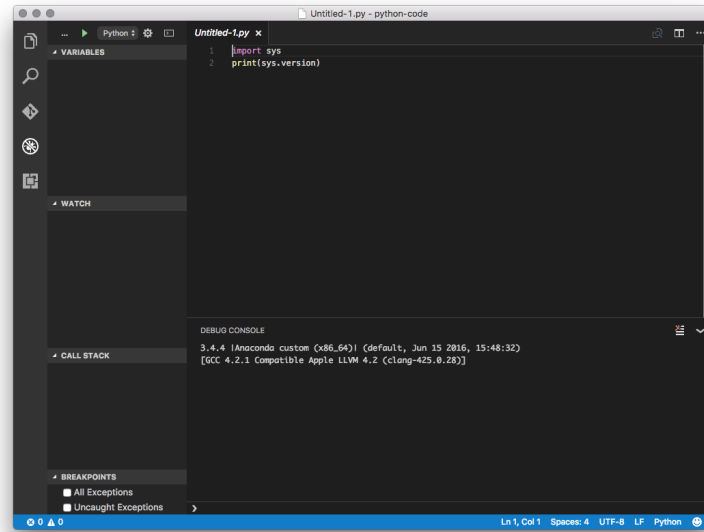




5. To save the file, in the **File** menu, select Save.
6. To open the Debug pane, click the bug icon. Click the gear icon, and then select Python:



7. At the top-right, click the green run arrow next to Python.
- The source code is run using your Anaconda Python interpreter:



### Spyder

Spyder, the Scientific Python Development Environment, is a free integrated development environment (IDE) that is included with Anaconda. It includes editing, interactive testing, debugging, and introspection features.

After you have installed Anaconda, start Spyder on Windows, macOS, or Linux by running the command `spyder`.

Spyder is also pre-installed in *Anaconda Navigator*, which is included in Anaconda. On the Navigator **Home** tab, click the Spyder icon.

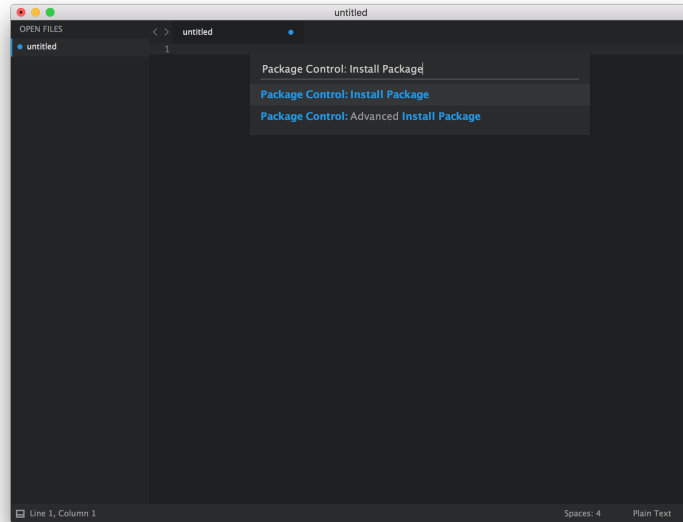
For more information about Spyder, see the [Spyder web page](#) or the [Spyder documentation](#).

### Sublime Text

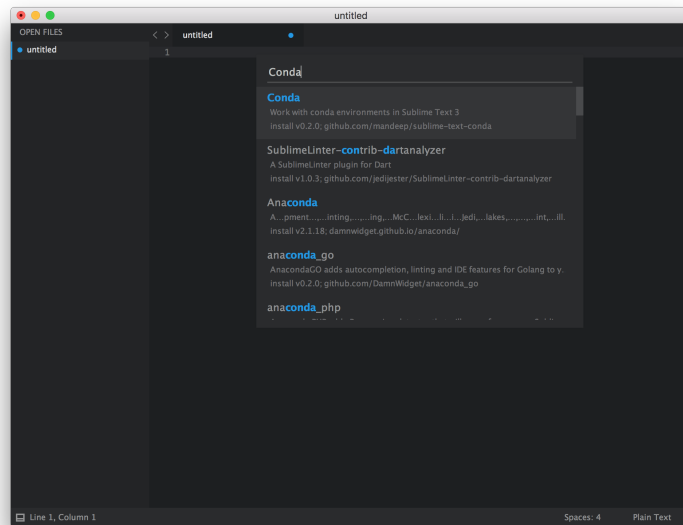
Sublime Text is a cross-platform text editor for code, markup, and prose. [Download and Install Sublime Text](#).

To use your Anaconda installation with Sublime Text:

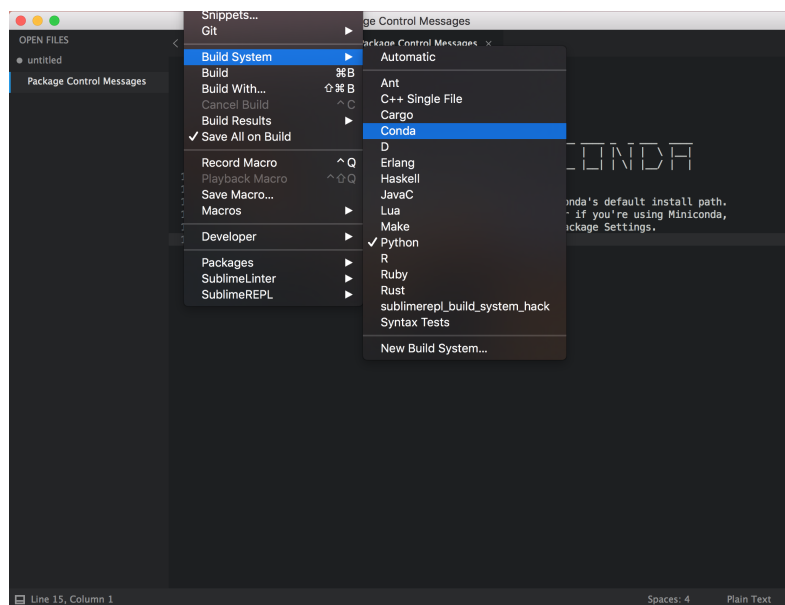
1. [Download Package control](#).
2. Open the Sublime Text command palette by pressing CTRL+Shift+p (Windows, Linux) or CMD+Shift+p (macOS).
3. All Package Control commands begin with “Package Control:”. Start by typing “Package”.
4. Select “Package Control: Install Package”.



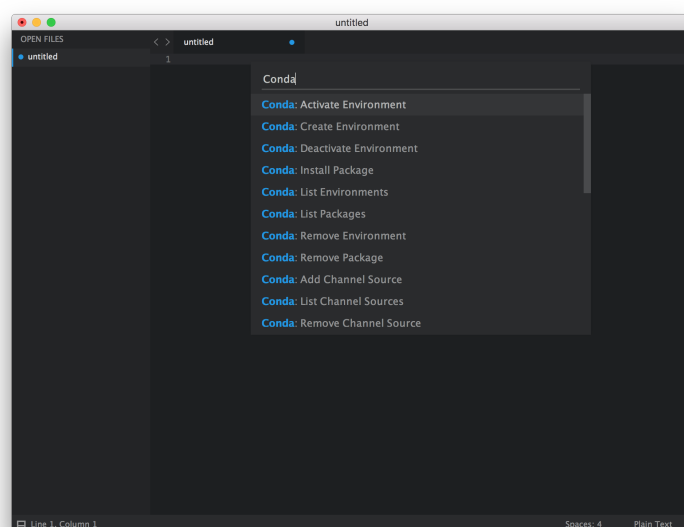
5. Search for `conda` in the command palette and select the conda plugin. When the plugin is installed, a Package Control Message will open in the Sublime Text window.



6. Change the current Build System to conda by accessing Tools -> Build System -> Conda in the menu bar.



7. Access the conda Commands with the Command Palette by searching for conda.



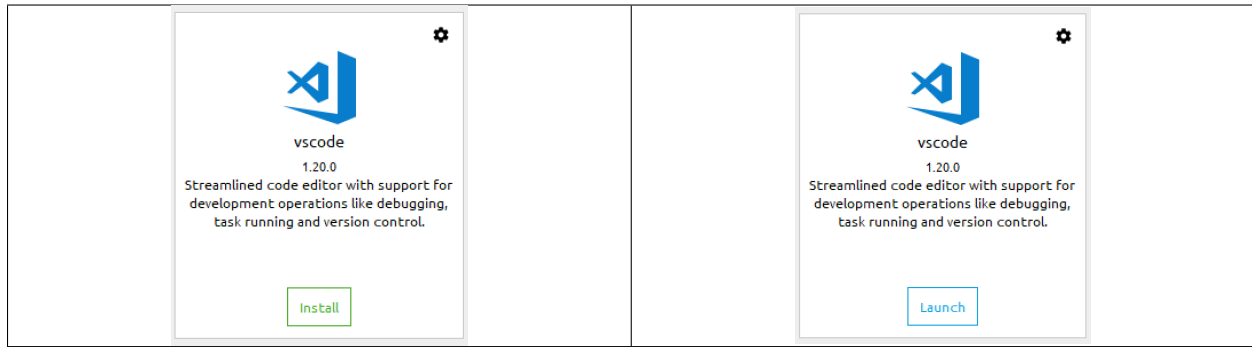
## Microsoft Visual Studio Code (VS Code)

Anaconda Distribution works with Visual Studio Code (VS Code), Microsoft's lightweight and fast open-source code editor.

VS Code is free for both private and commercial use, runs on Windows, macOS, and Linux, and includes support for linting, debugging, task running, version control and Git integration, IntelliSense code completion, and conda environments.

VS Code is openly extensible and [many extensions](#) are available.

In Anaconda Navigator version 1.7 or higher, use the VS Code tile on the home screen to install or launch VS Code.



When you launch VS Code from Navigator, VS Code is configured to use the Python interpreter in the currently selected environment.

In addition to VS Code, Anaconda fully supports *Spyder*, Jupyter Notebook, and other IDEs.

## Wing IDE

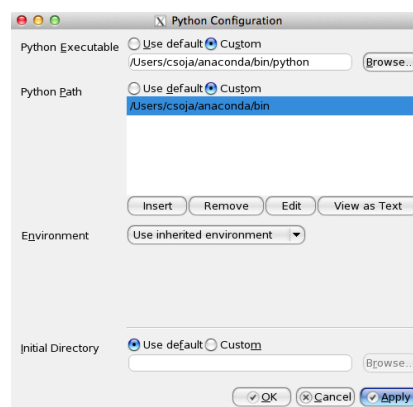
**Wing IDE** is an IDE designed specifically for the Python programming language. Wing IDE is offered in a paid Pro version and in free Personal and 101 versions.

To set up your Wing IDE installation to use Anaconda:

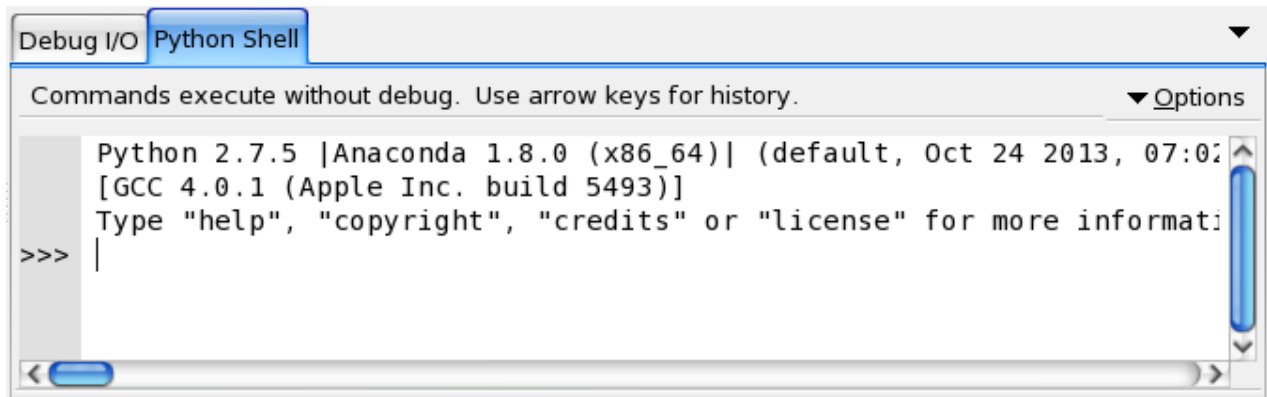
1. Navigate to the Python configuration window:
  - In Wing 101, in the **Edit** menu, select Configure Python.
  - In Wing Personal and Wing Pro, in the **Project** menu, select Project Properties.

The Wing 101 menu looks like this:

2. Next to Python Executable, click the Custom radio button.
3. Click the Browse button and navigate to your *Anaconda Python interpreter path*.
4. For Python Path, click the Custom radio button.
5. Click the Insert button and browse to your *Anaconda Python interpreter path*.
6. Click the OK button:



7. If you are prompted to reload your Python shell, do so. After the reload, Anaconda is displayed on the **Python Shell** tab:



Wing IDE is now set up to Anaconda's Python.

For more information, see the [Wing IDE documentation](#).

### Finding your Anaconda Python interpreter path

IDEs often require you to specify the path to your Python interpreter.

This path varies according to which operating system version and which Anaconda version you use, so you will need to search your file system to find the correct path to your Python interpreter.

You can search for the Python interpreter with your operating system's file manager, such as File Explorer on Windows, Finder on macOS, or Nautilus on Ubuntu Linux.

You can also use the command line to show the location of the Python interpreter in the active conda environment.

### Windows

1. From the Start Menu open the Anaconda Prompt.
2. If you want the location of a Python interpreter for a conda environment other than the root conda environment, run `activate environment-name`.
3. Run `where python`.

### macOS and Linux

1. Open a terminal window.
2. If you want the location of a Python interpreter for a conda environment other than the root conda environment, run `conda activate environment-name`.
3. Run `which python`.

### Examples

- Windows 10 with Anaconda3 and username “jsmith”— `C:\Users\jsmith\Anaconda3\python.exe`.  
The Python image in a conda environment called “my-env” might be in a location such as `C:\Users\jsmith\Anaconda3\envs\my-env\python.exe`
- macOS— `~/anaconda/bin/python` or `/Users/jsmith/anaconda/bin/python`
- Linux— `~/anaconda/bin/python` or `/home/jsmith/anaconda/bin/python`

Instead of `anaconda`, the folder in your home directory might be named one of the following:

- `anaconda2`
- `anaconda3`

If you have installed Miniconda instead of Anaconda, the folder might be named:

- `miniconda`
- `miniconda2`
- `miniconda3`

### Excel plug-ins for Anaconda

Anaconda on Windows comes ready to interact with Microsoft Excel—quickly, intuitively, and powerfully. You can use one of the many included packages in Anaconda or you can connect to an outside integration tool to bring the power of Python into Excel.

The packages described here are available only on Windows unless otherwise noted. Like most Anaconda packages, this software is written by third-party open-source development teams around the world. Anaconda collects and curates these programs, builds them into conda packages, and distributes them through the Anaconda platform so our users can enjoy the benefits of easy installation, version control, package management, and environment management.

### What tool should I use?

For a versatile, all-purpose tool, Anaconda includes `xlwings`, which incorporates the following features:

- Drives Excel interactively from an IPython Session/Notebook.
- Performs one-line conversion to and from a NumPy array or pandas DataFrame.
- Uses Python as Excel’s computation backend by wrapping Python function calls in VBA macros.



- Easily shares Python-integrated Excel workbooks with collaborators who are also running Anaconda, with no additional installation needed.

---

**Note:** The `xlwings` package is in active development. Additional features may be added in the future. This package is available for Windows and macOS platforms.

---

To export data from a Python object into Excel or import the contents of an Excel spreadsheet to perform calculations or visualizations in Python, Anaconda includes the following libraries and modules:

- `openpyxl`—Read/write Excel 2007 `xlsx/xlsm` files.
- `xlrd`—Extract data from Excel spreadsheets—`.xls` and `.xlsx`, versions 2.0 onwards—on any platform.
- `xlsxwriter`—Write files in the Excel 2007+ `XLSX` file format.
- `xlwt`—Generate spreadsheet files that are compatible with Excel 97/2000/XP/2003, OpenOffice.org Calc, and Gnumeric.

To determine which one best suits your needs, see the documentation for each library or module.

### Python-Excel tools not included in Anaconda

- `ExcelPython`—A free, open-source library that lets you write UDFs and macros in Python, as well as load Python modules, call methods, and manipulate objects from VBA without modifying the original Python code.
- `XLLoop`—Open-source software that implements UDFs that are hosted from a server in a variety of languages, including Python, Java, C++, and R. Installation requires multiple steps to set up the provided Excel add-in and configure the UDF server.
- `ExPy`—Freely available demonstration software that is simple to install. Once installed, Excel users have access to built-in Excel functions that wrap Python code. Documentation and examples are provided at the site.
- `PyXLL`—A widely used tool that is free for personal or educational use. It implements UDFs written in Python as add-in functions for Excel.

### Using default repositories

When you use a `conda` command that involves looking for a package to install or upgrade, by default `conda` searches the default repository located at <https://repo.anaconda.com/pkg>.

### Main channel

<https://repo.anaconda.com/pkg/main>

Added Sept 26, 2017 with the release of Anaconda 5.0 and `conda` 4.3.27, the main channel includes packages built by Anaconda, Inc. with the new compiler stack. The majority of all new Anaconda, Inc. package builds are hosted here. This is the top priority channel in `conda`'s default channel list.

### More info

Utilizing the New Compilers in Anaconda Distribution 5

### Free channel

<https://repo.anaconda.com/pkgsg/free>

As of conda 4.7, the `free` channel was removed from conda's default channels.

The `free` channel contains packages built without the new compiler stack. It includes packages built as far back as Fall 2012. The majority of these packages are compatible with the packages in `main`. Learn more about the `free` channel.

### R Language channel

<https://repo.anaconda.com/pkgsg/r>

Mirror: <https://anaconda.org/r>

Anaconda, Inc.'s R conda packages and Microsoft R Open conda packages. This channel is included in conda's "defaults" channel. When creating new environments, R is the default R implementation.

### MRO channel

<https://repo.anaconda.com/pkgsg/mro>

Mirror: <https://anaconda.org/mro>

As of Dec. 19, 2017, this is an empty channel. Packages in this channel have been moved to `pkgsg/mro-archive`. New MRO packages are in the `pkgsg/r` channel.

### Pro channel

<https://repo.anaconda.com/pkgsg/pro>

Now deprecated, though still available in conda's default channels. Packages in this channel were once sold commercially, but are now open source and available without charge. The last package was updated Feb. 2017. Includes MKL Optimizations, IOPro, and Accelerate.

### More info

- [Open sourcing Anaconda Accelerate](#)

### Anaconda Extras channel

<https://anaconda.org/anaconda-extras>

This channel contains packages custom built for customers by Anaconda, Inc.

### Archive channel

<https://repo.anaconda.com/pkgsg/archive>

Sometimes a package that is released onto one of the other channels has an issue that forces Anaconda, Inc. to remove it from the channel. In these cases, the package is archived to this channel for anyone who still needs it.

## MSYS2 channel

<https://repo.anaconda.com/pkgms/msys2>

Mirror: <https://anaconda.org/msys2>

Windows only - included in conda's default channels. Necessary for Anaconda, Inc.'s R conda packages and some others in /main and /free. It provides a bash shell, Autotools, revision control systems and the like for building native Windows applications using MinGW-w64 toolchains.

## Anaconda channel on anaconda.org

<https://anaconda.org/anaconda>

The Anaconda channel on anaconda.org is a mirror of the packages available in <https://repo.anaconda.com/pkgms/main>, <https://repo.anaconda.com/pkgms/free>, and <https://repo.anaconda.com/pkgms/pro>.

## Working with GPU packages

The Anaconda Distribution includes several packages that use the GPU as an accelerator to increase performance, sometimes by a factor of five or more. These packages can dramatically improve machine learning and simulation use cases, especially deep learning. Read more about [getting started with GPU computing in Anaconda](#).

While both AMD and NVIDIA are major vendors of GPUs, NVIDIA is currently the most common GPU vendor for machine learning and cloud computing. The information on this page applies only to NVIDIA GPUs. As of August 27th, 2018, experimental AMD GPU packages for Anaconda are in progress but not yet officially supported.

## GPU compatibility

GPU acceleration requires the author of a project such as TensorFlow to implement GPU-specific code paths for algorithms that can be executed on the GPU. A GPU-accelerated project will call out to NVIDIA-specific libraries for standard algorithms or use the NVIDIA GPU compiler to compile custom GPU code. Only the algorithms specifically modified by the project author for GPU usage will be accelerated, and the rest of the project will still run on the CPU.

For most packages, GPU support is either a compile-time or run-time choice, allowing a variant of the package to be available for CPU-only usage. When GPU support is a compile-time choice, Anaconda will typically need to build two versions of the package, to allow the user to choose between the “regular” version of the project that runs on CPU only and the “GPU-enabled” version of the project that runs on GPU.

Due to the different ways that CUDA support is enabled by project authors, there is no universal way to detect GPU support in a package. For many GPU-enabled packages, there is a dependency on the `cuda-toolkit` package. Other packages such as Numba do not have a `cuda-toolkit` dependency, because they can be used without the GPU.

## Hardware requirements

NVIDIA released the CUDA API for GPU programming in 2006, and all new NVIDIA GPUs released since that date have been CUDA-capable regardless of market. Although any NVIDIA GPU released in the last 5 years will technically work with Anaconda, these are the best choices for machine learning and specifically model training use cases:

- Tesla P100 or V100
- Titan Xp or V

- GeForce 1080 or 1080 Ti
- Various recent Quadro models

Deployed models do not always require a GPU. When a GPU is required for a deployed model, there are other Tesla GPU models that are more optimized for inference than training, such as the Tesla M4, M40, P4, and P40.

Cloud and on-premise data center deployments require Tesla cards, whereas the GeForce, Quadro, and Titan options are suitable for use in workstations.

Most users will have an Intel or AMD 64-bit CPU. We recommend having at least two to four times more CPU memory than GPU memory, and at least 4 CPU cores to support data preparation before model training. There are a limited number of Anaconda packages with GPU support for IBM POWER 8/9 systems as well.

## Software requirements

The best performance and user experience for CUDA is on Linux systems. Windows is also supported. No Apple computers have been released with an NVIDIA GPU since 2014, so they generally lack the memory for machine learning applications and only have support for Numba on the GPU.

Anaconda requires that the user has installed a recent NVIDIA driver that meets the version requirements in the table below. Anaconda does not require the installation of the CUDA SDK.

Ubuntu and some other Linux distributions ship with a third party open-source driver for NVIDIA GPUs called Nouveau. CUDA requires replacing the Nouveau driver with the official closed source NVIDIA driver.

All other CUDA libraries are supplied as conda packages.

GPU-enabled packages are built against a specific version of CUDA. Currently supported versions include CUDA 8, 9.0 and 9.2. The NVIDIA drivers are designed to be backward compatible to older CUDA versions, so a system with NVIDIA driver version 384.81 can support CUDA 9.0 packages and earlier. As a result, if a user is not using the latest NVIDIA driver, they may need to manually pick a particular CUDA version by selecting the version of the `cuda-toolkit` conda package in their environment. To select a `cuda-toolkit` version, add a selector such as `cuda-toolkit=8.0` to the version specification.

Required NVIDIA driver versions, excerpted from the [NVIDIA CUDA Toolkit Release Notes](#):

CUDA Version	Linux x86_64 Driver Version	Windows x86_64 Driver Version
CUDA 8.0 (8.0.61 GA2)	>= 375.26	>= 376.51
CUDA 9.0 (9.0.76)	>= 384.81	>= 385.54
CUDA 9.2 (9.2.88)	>= 396.26	>= 397.44
CUDA 9.2 (9.2.148 Update 1)	>= 396.37	>= 398.26

Sometimes specific GPU hardware generations have a minimum CUDA version. As of August 27th, 2018, the only relevant constraint is that the Tesla V100 and Titan V (using the “Volta” GPU architecture) require CUDA 9 or later.

## Available packages

### TensorFlow

TensorFlow is a general machine learning library, but most popular for deep learning applications. There are three supported variants of the `tensorflow` package in Anaconda, one of which is the NVIDIA GPU version. This is selected by installing the meta-package `tensorflow-gpu`:

```
conda install tensorflow-gpu
```

Other packages such as Keras depend on the generic `tensorflow` package name and will use whatever version of TensorFlow is installed. This makes it easy to switch between variants in an environment.

## PyTorch

PyTorch is another machine learning library with a deep learning focus. PyTorch detects GPU availability at run-time, so the user does not need to install a different package for GPU support.

```
conda install pytorch
```

## Caffe

Caffe was one of the first popular deep learning libraries.

```
conda install caffe-gpu
```

## Chainer/CuPy (Linux only)

Chainer is a deep learning library that uses NumPy or CuPy for computations.

```
conda install chainer
```

Chainer's companion project CuPy is a GPU-accelerated clone of the NumPy API that can be used as a drop-in replacement for NumPy with a few changes to user code. When CuPy is installed, Chainer is GPU-accelerated. CuPy can also be used on its own for general array computation.

```
conda install cupy
```

## XGBoost

XGBoost is a machine learning library that implements gradient-boosted decision trees. Training several forms of trees is GPU-accelerated.

```
conda install py-xgboost-gpu
```

## MXNet

MXNet is a machine learning library supported by various industry partners, most notably Amazon. Like TensorFlow, it comes in three variants, with the GPU variant selected by the `mxnet-gpu` meta-package.

```
conda install mxnet-gpu
```

## Numba

Numba is a general-purpose JIT compiler for Python functions. It provides a way to implement custom GPU algorithms in purely Python syntax when the `cuda-toolkit` package is present.

```
conda install numba cudatoolkit
```

### GPU support in Anaconda Enterprise

GPU-enabled conda packages can be used in AE 5 projects when the cluster has resource profiles which include GPUs. For more details see [the GPU support section of the AE 5 FAQ](#).

### Using Jupyter Notebook extensions

You can open Jupyter Notebook by running `jupyter notebook`, or by opening Anaconda Navigator and clicking the Jupyter Notebook icon.

- *Obtaining the extensions*
- *Uninstalling the extensions*
- *RISE*
- *Notebook Anaconda Cloud*
- *Notebook conda*
- *Notebook Conda Kernels*

With Anaconda you can download and install 4 extensions for the Jupyter Notebook which make the notebook easier to use:

- RISE
- Notebook Anaconda Cloud (nb\_anacondacloud)
- Notebook Conda (nb\_conda)
- Notebook Conda Kernels (nb\_conda\_kernels)

Installing any of the 4 installs all of them. The `_nb_ext_conf` package is also installed, which activates the extensions.

### Obtaining the extensions

To get the extensions using Anaconda Navigator:

1. Install and manage notebook extensions packages like any other packages. See [Navigator user guide](#).
2. To use the new extensions, on the Navigator **Home** tab, open Jupyter Notebook.

To install all Jupyter Notebook extensions from the command line, run:

```
conda install nb_conda
```

**Note:** These extensions were already installed in Anaconda versions 4.1 and 4.2. If you have Anaconda v4.1 or v4.2 installed, there is no need to install them separately. To begin using them, open a new or existing notebook.

## Uninstalling the extensions

To remove all Jupyter Notebook extensions, run:

```
conda remove nb_conda
```

Uninstalling nb\_conda or any other 1 of the 4 extensions uninstalls all 4.

To disable Jupyter Notebook extensions individually without uninstalling them, run:

```
python -m nb_conda_kernels.install --disable --prefix=<ENV_PREFIX>

jupyter-nbextension disable nb_conda --py --sys-prefix
jupyter-serverextension disable nb_conda --py --sys-prefix

jupyter-nbextension disable nb_anacondacloud --py --sys-prefix
jupyter-serverextension disable nb_anacondacloud --py --sys-prefix

jupyter-nbextension disable nbpresent --py --sys-prefix
jupyter-serverextension disable nbpresent --py --sys-prefix
```

**Note:** Replace <ENV\_PREFIX> with your root environment or another conda environment where the extensions have been installed.

## RISE

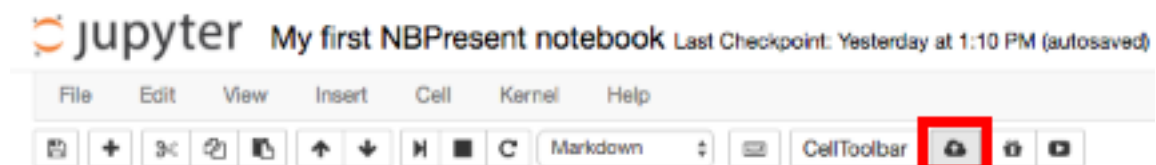
You can access the install instructions for the RISE extension from [Anaconda Cloud](#).

In-depth documentation can be found there as well.

## Notebook Anaconda Cloud

You must have an Anaconda Cloud account for this extension to work. You can sign up for a free account at [Anaconda Cloud](#).

1. You can upload your notebook to your Cloud account with a simple button push:



You can use the Attach conda environment option described below to embed a copy of your conda environment as an `environment.yml` file in the notebook metadata.

2. Sign in to Cloud:

- If you are not signed in to Cloud, a dialog box appears asking for your Cloud username and password.
- You may instead log in at the command line:

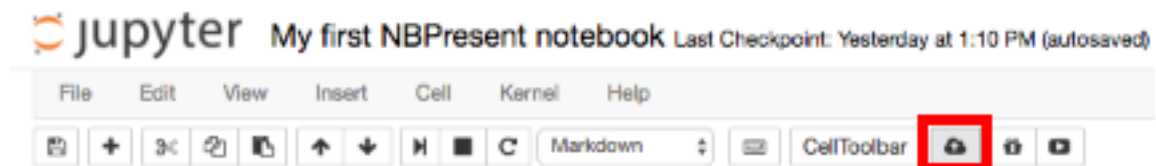
```
anaconda login
```

---

**Note:** This is recommended if you do not have a secure connection.

---

3. Open Jupyter Notebook, then open the notebook you wish to upload to Cloud.
4. In the top navigation bar, click the Publish to Anaconda Cloud button:



5. In the dialog box that appears, select your username.
6. Type a description of the notebook for display on Cloud:
7. If you want the identical environment to be included when the notebook is downloaded and opened, select the Attach conda environment checkbox.
8. Click the Publish button.
9. After publishing, you can view the notebook or play the presentation on Cloud from the top navigation bar by clicking the Cloud button:

Your notebook on Anaconda Cloud will look similar to this one:

For more information on Cloud, see [Anaconda Cloud](#).



### Publish My first NBPresent notebook to ANACONDA CLOUD

User/Organization


ContinuumCrew (Continuum Crew)

Summary

This is a description of the notebook I am uploading

Environment

☒ Attach conda environment

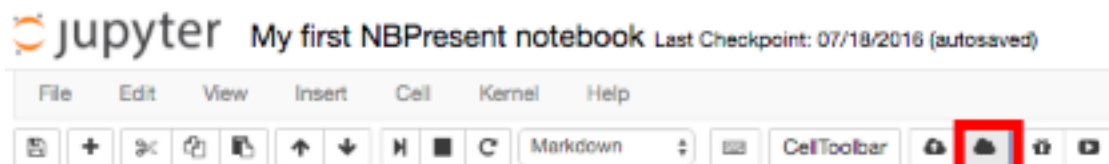
 Publish

This notebook was previously published as <https://anaconda.org/continuumcrew/my-first-nbpresent-notebook>

Initially, all published notebooks will be **public**.

Make **My first NBPresent notebook** **private** or **authenticated** on the [Anaconda Cloud settings page](#).

Close



The screenshot shows the Anaconda Cloud web interface. At the top is a dark navigation bar with the Anaconda Cloud logo, a search bar, and links for Docs, Contact, and a user profile. Below the navigation bar, the breadcrumb path is 'ContinuumCrew / Notebooks / my-first-nbpresent-notebook'. To the right of the title are a star icon and a count of '0'. A subtitle reads 'This is a description of the notebook I am uploading'. Below this is a horizontal tab bar with 'Notebook' (selected), 'Files', 'Labels', 'Badges', and 'Settings'. Under the 'Notebook' tab, there's a status bar showing 'You are viewing 2016.08.04.1612' and a 'Download' button. The main content area displays a Jupyter Notebook interface with a 'Presentation View' button in the top right. The notebook content shows a heading 'Hello, nbpresent!' followed by two code input cells. The first cell contains the code: `import nbpresent` and `nbpresent.__version__`. The second cell is empty.

## Notebook conda

This extension provides conda environment and package access from within Jupyter Notebook.

To manage all environments:

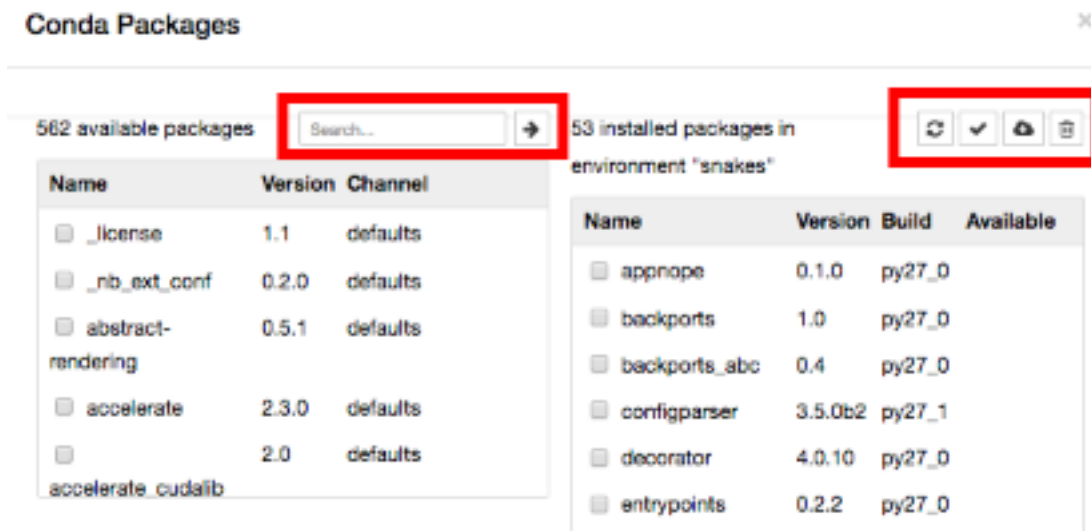
1. While viewing the dashboard file manager, select the **Conda** tab, which shows your current conda environments:

The screenshot shows the Anaconda Cloud interface with the 'Conda' tab selected. The header shows 'Files', 'Running', 'Clusters', and 'Conda'. Below the header, it says '4 Conda environments' with a '+ -' icon. A table lists the environments:

Action	Name	Default?	Directory
	root		/opt/wakari/anaconda
	default	✓	/projects/TestUser/screenshottest/envs/default
	flowers		/projects/TestUser/screenshottest/envs/flowers
	snakes		/projects/TestUser/screenshottest/envs/snakes

**Note:** To add a new conda environment, click the + button above the environments list on the right side.

2. Select an environment by clicking its name.
3. In the package management section that displays, the icons from left to right have the following meanings:
  - Search for packages in your current environment.
  - Refresh your packages list.
  - Update selected packages.
  - Remove selected packages.



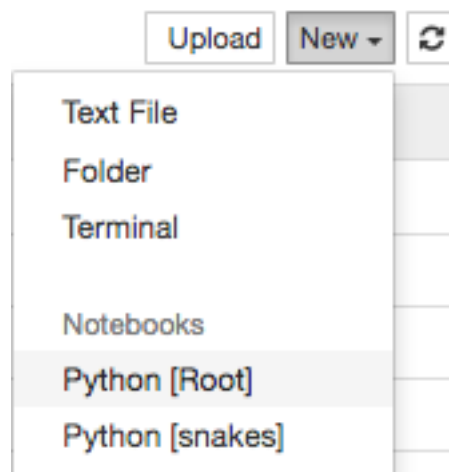
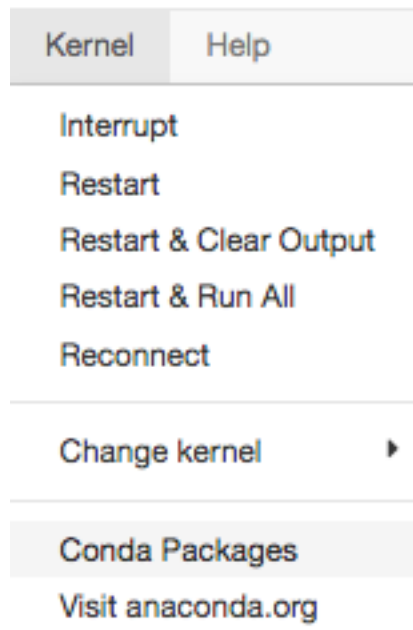
To manage the current kernel environment, in the **Kernel** menu, select Conda Packages, which displays a list of conda packages in the current environment:

For more information on using and managing conda packages, see [Managing packages](#).

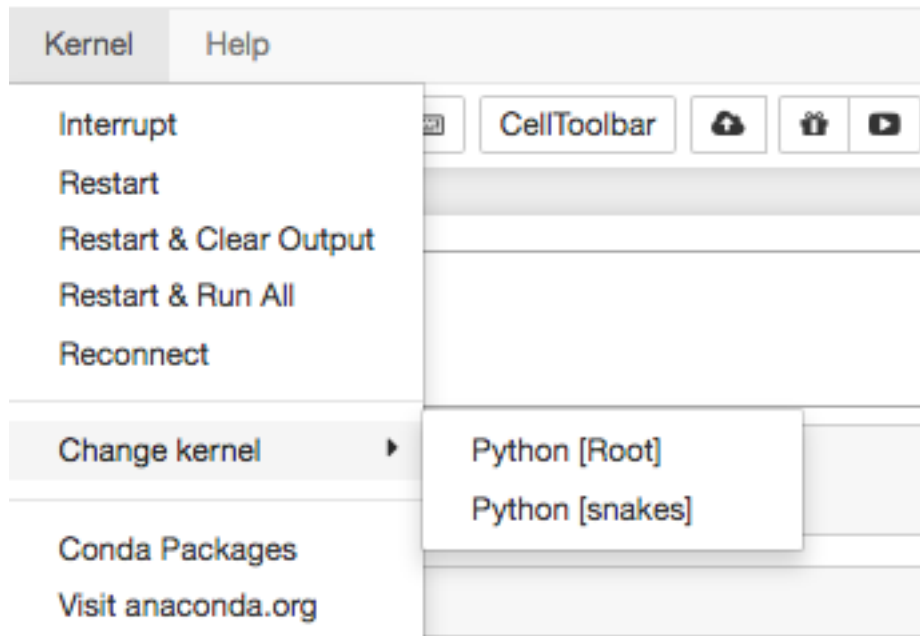
## Notebook Conda Kernels

This extension allows you to use conda environment-based kernels from the dashboard and the notebook's **Kernel** menu. It makes the notebook aware of your conda environments, and it is required for Notebook Anaconda Cloud and Notebook Conda.

When creating a new notebook on the **Files** tab, you can pick any of the Python or R language kernels in any of your environments:



You can also change to those kernels on a current notebook:



## Running Jupyter Notebook on a remote server

Follow the following steps to use Jupyter Notebook launched from remote server.

1. Launch Jupyter Notebook from remote server using port 8080: `jupyter notebook --no-browser --port=8080`

Or run the following command to launch with default port: `jupyter notebook --no-browser`

Please note the port setting. You will need it in the next step.

2. You can access the notebook from your remote machine over SSH by setting up a SSH tunnel. Run the following command from your local machine: `ssh -L 8080:localhost:<port> <remote_user>@<remote_host>`

---

**Note:** Replace `<port>` with your port number used in the above step, `<remote_user>` with remote server username, and `<remote_host>` with your remote server address.

---

The above command opens up a new SSH session in the terminal.

3. Open a browser from your local machine and navigate to <http://localhost:8080/>, the Jupyter Notebook web interface. Replace 8080 with your port number used in step 1.

### Moving Anaconda from one directory to another

Anaconda environment management requires known paths, and Anaconda must know the exact path where it is installed at installation time.

If you simply copy the Anaconda files to a new directory, Anaconda will not work.

To move Anaconda from one directory to another:

1. OPTIONAL: Save your environments using the conda [managing environments](#) instructions.
2. *Uninstall Anaconda.*
3. Go to the new directory and install it there following the [Anaconda installation instructions](#).
4. OPTIONAL: Restore your environments using the conda [managing environments](#) instructions.

### Cheat sheet

Download the [Anaconda Cheat Sheet](#) for a quick guide to using Anaconda.

### Frequently asked questions

- [Getting Anaconda](#)
- [Installing Anaconda](#)
- [Using conda packages](#)
- [General](#)

### Getting Anaconda

#### How do I get Anaconda with Python 3.5 or 3.6?

There are three ways to get Anaconda with Python 3.5 or 3.6:

- We recommend that you download the latest version of Anaconda and then [make a Python 3.5 \(or 3.6\) environment](#).
- Or download the latest version of Anaconda and run the following command to install Python 3.5 (or 3.6) in the root environment: `conda install python=3.5` or `conda install python=3.6`.
- Or download the most recent Anaconda installer that included Python 3.5 (Anaconda 4.2.0) or Python 3.6 (Anaconda 5.2.0). You can download either of these from our [archive](#). Scroll down the page until you find the version you need for your platform.

**How do I get previous versions of Anaconda or older versions of packages?**

You can download previous versions of Anaconda from the [Anaconda installer archive](#).

The installation procedures for previous versions are the same as the installation for the current version. For graphical installs, double click the downloaded installer file and follow the prompts. For command line installs, run “`bash filename.sh`” and follow the prompts. The installer filenames and hashes for previous versions will be different.

Older versions of packages can usually be downloaded from the [package repository](#) or from <https://anaconda.org/anaconda/PackageName>.

---

**Note:** Replace `PackageName` with the name of the desired package.

---

EXAMPLE: At <https://anaconda.org/anaconda/beautifulsoup4>, previous versions of beautifulsoup4 are shown on the **Files** tab.

You can also search for packages from the command line with `conda search PackageName`.

**I am behind a firewall. How can I download Anaconda?**

If your corporate security settings do not allow you to download a Windows .exe executable file, download our [zipped file](#).

**Installing Anaconda****How can I install Anaconda on an air-gapped computer?**

After you have the file, it's the same as any other install. Save a local copy of the appropriate Anaconda installer for the non-networked computer. You can copy the Anaconda installer using many different methods including a portable hard drive, USB drive, or CD.

After copying the installer to the air-gapped machine, follow the installation instructions for your operating system.

**In what folder should I install Anaconda on Windows?**

We recommend installing Anaconda or Miniconda into a directory that contains only 7-bit ASCII characters and no spaces, such as `C:\anaconda`. Do not install into paths that contain spaces such as `C:\Program Files` or that include Unicode characters outside the 7-bit ASCII character set. This helps ensure correct operation and no errors when using any open-source tools in either Python 3 or Python 2 conda environments.

### Should I add Anaconda to the Windows PATH?

When installing Anaconda, we recommend that you do not add Anaconda to the Windows PATH because this can interfere with other software. Instead, open Anaconda with the Start Menu and select Anaconda Prompt, or use Anaconda Navigator (Start Menu - Anaconda Navigator).

### Should I add Anaconda to the macOS or Linux PATH?

We do not recommend adding Anaconda to the PATH manually. During installation, you will be asked “Do you wish the installer to initialize Anaconda3 by running `conda init`?” We recommend “yes”. If you enter “no”, then `conda` will not modify your shell scripts at all. In order to initialize after the installation process is done, first run `source <path to conda>/bin/activate` and then run `conda init`.

---

**Note:** Replace `<path-to-anaconda>` with the actual path of your installed Anaconda file.

---

### What is the default path for installing Anaconda?

If you accept the default option to install Anaconda on the “default path” Anaconda is installed in your user home directory:

- Windows 10: `C:\Users\<your-username>\Anaconda3\`
- macOS: `/Users/<your-username>/anaconda3` for the shell install, `~/opt` for the graphical install. See [installing on macOS](#).
- Linux: `/home/<your-username>/anaconda3`

---

**Note:** If your username includes spaces, as is common on Windows systems, you should not accept the default path. See [In what folder should I install Anaconda on Windows?](#)

---

### I already have Python installed. Can I install Anaconda?

You do not need to uninstall other Python installations or packages before installing Anaconda. Even if you already have a system Python, another Python installation from a source such as the macOS Homebrew package manager and globally installed packages from pip such as pandas and NumPy, you do not need to uninstall, remove, or change any of them.

Install Anaconda or Miniconda normally. There is no need to set the `PYTHONPATH` environment variable.

To see if the `conda` installation of Python is in your `PATH` variable:

- On macOS and Linux, open the terminal and run `echo $PATH`.
- On Windows, open an Anaconda Prompt and run `echo %PATH%`.



To see which Python installation is currently set as the default:

- On macOS and Linux, open the terminal and run `which python`.
- On Windows, open an Anaconda Prompt and run `where python`.

To see which packages are installed in your current conda environment and their version numbers, in your terminal window or an Anaconda Prompt, run `conda list`.

### How can I use Anaconda on older systems?

See [Outdated operating system support](#).

## Using conda packages

### How can I configure or opt out of the Intel Math Kernel Library (MKL)?

For information on configuring and uninstalling MKL, see the [Anaconda MKL documentation](#).

### How can I use TKinter?

Make sure the conda package `tk` is installed:

```
conda list tk
```

If it is not installed, run:

```
conda install tk
```

Python programs can use TKinter with `import Tkinter` on Python 2 or `import tkinter` on Python 3.

### How can I use Cython on macOS?

Cython needs a C compiler, so you need to install [Xcode](#).

### How can I use Theano?

Theano requires [gcc](#) for acceleration.

To install Theano with acceleration:

- On Windows, run `conda install theano`.

- On Linux and macOS run `conda install gcc theano`.

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**Note:** Theano is available from the default Anaconda channels for Windows, macOS, and Linux with the command `conda install theano`.

---

### How can I use GPUs with Anaconda?

See *Working with GPU packages*.

## General

### How is CPython compiled?

- Python 2.6 and 2.7 were compiled with Visual Studio 2008.
- Python 3.3 and 3.4 were compiled with VS 2010.
- Python 3.5 was compiled with VS 2015.

### How do I cite Anaconda in an academic paper?

To cite Anaconda in an academic paper, use the recommended format. Example:

*Anaconda Software Distribution*. Computer software. Vers. 2-2.4.0. Anaconda, Nov. 2016. Web. <<https://anaconda.com>>.

## 4.2.3 Reference

The following information is provided for your reference, to help you understand some of the *core terminology* used in Anaconda Distribution as well as information about the various *packages* available.

Consult the *release notes* to see what changes were made between releases. We also include several *support resources*, and workarounds for *known issues* you may encounter while using the product.

## Glossary

### Anaconda Cloud

A cloud package repository hosting service at <https://www.anaconda.org>. With a free account, you can publish packages you create to be used publicly.

## Anaconda Distribution

Open-source repository of hundreds of popular data science packages, along with the conda package and virtual environment manager for Windows, macOS, and Linux. Conda makes it quick and easy to install, run, and upgrade complex data science and machine learning environments like scikit-learn, TensorFlow, and SciPy.

## Anaconda Enterprise

A software platform for developing, governing, and automating data science and AI pipelines from laptop to production. Enterprise enables collaboration between teams of thousands of data scientists running large-scale model deployments on high-performance production clusters.

## Anaconda metapackage

A collection of packages at specific versions that are associated with Distribution installers. Anaconda metapackage is used to pull all of the other packages into the installer. It contains several core, low-level libraries, including compression, encryption, linear algebra, and some GUI libraries.

The Anaconda metapackage is useful for creating environments that have all of the Anaconda Distribution packages in them and it has strong effects on conda's solver behavior.

Read more about the [Anaconda metapackage](#). Read more about the distinctions between [Anaconda Distribution](#) and the [Anaconda metapackage](#).

## Anaconda Navigator

A desktop Graphical User Interface (GUI) included in Anaconda Distribution that allows you to easily use and manage IDEs, conda packages, environments, channels, and notebooks without the need to use the Command Line Interface (CLI).

## channel

A location in a repository where conda looks for packages. Channels may point to a Cloud repository or a private location on a remote or local repository that you or your organization created. The `conda channel` command has a default set of channels to search beginning with <https://repo.anaconda.com/pkg/>. You may override the default channels to, for example, maintain a private or internal channel. In conda commands and in the `.condarc` file, these default channels are referred to by the channel name `defaults`.

### **conda**

An open-source package and environment manager bundled with Anaconda Distribution that finds, installs, and updates conda packages and their dependencies. Conda also lets you easily switch between conda environments on your local computer.

### **conda-build**

A tool used to build conda packages from recipes.

### **conda environment**

A superset of Python virtual environments, conda environments make it easy to create projects with different versions of Python and avoid issues related to dependencies and version requirements. A conda environment maintains its own files, directories, and paths so that you can work with specific versions of libraries and/or Python itself without affecting other Python projects. For example, you may use one conda environment for only Python 2.7 and Python 2.7 packages, and maintain another conda environment with only Python 3.5 and Python 3.5 packages.

### **conda package**

A binary tarball file containing system-level libraries, Python and R modules, executable programs, or other components. Conda tracks dependencies between specific packages and platforms, making it simple to create operating system-specific environments using different combinations of packages.

### **conda recipe**

Instructions used to tell conda-build how to build a package.

### **Miniconda**

A minimal installer for conda. Like Anaconda Distribution, Miniconda is a free software package that includes the Anaconda Distribution and conda. Miniconda does not include any packages other than those dependencies needed to install it. After installing Miniconda, you can install additional conda packages directly from the command line using `conda install`.

**package**

Software files and information about the software, such as its name, the specific version, and a description, that are bundled into a file that can be installed and managed by a package manager. While packages are generally used for files, they can also be used for metadata alone. When it is, it is called a metapackage.

**repository**

Any storage location from which software or software assets may be retrieved and installed on a local computer.

**How to contribute to Anaconda**

Community engagement makes Anaconda Distribution, conda, and conda-build better. We value our open-source community and encourage all users to contribute to the Anaconda ecosystem. The best contributions start by helping and encouraging others, especially newcomers who are struggling with something you've overcome. See below for other ways you can contribute.

- *Social*
- *Mailing lists*
- *GitHub issues*
- *Stack Overflow*
- *Documentation*
- *Conda-forge feedstocks*
- *Anaconda Enterprise*

**Social**

The easiest way to contribute is to tell your friends about all of the things you can do with Anaconda. Be sure to mention that Anaconda provides package and environment management and over 7,500+ open source packages—completely free.

Check our social media to keep up with what's happening at Anaconda and add to the conversation.

[Twitter](#) | [Facebook](#) | [LinkedIn](#) | [SlideShare](#)

### Mailing lists

Join the mailing lists to help other users answer questions, debug issues, and suggest solutions.

- [Anaconda mailing list](#).
- [Conda mailing list](#).
- [Documentation mailing list](#).

### GitHub issues

If you want to get involved in contributing code for Anaconda, conda, or conda-build, we recommend collaborating with others, resolving bug issues, and submitting pull requests with those resolutions.

- [Conda issues](#).
- [Conda-build issues](#).
- [Anaconda issues](#).

### Stack Overflow

Answer questions and suggest resolutions and workarounds on [Stack Overflow](#).

### Documentation

Notice an error or gap in our documentation? We welcome pull requests for conda and conda-build documentation improvements and additions.

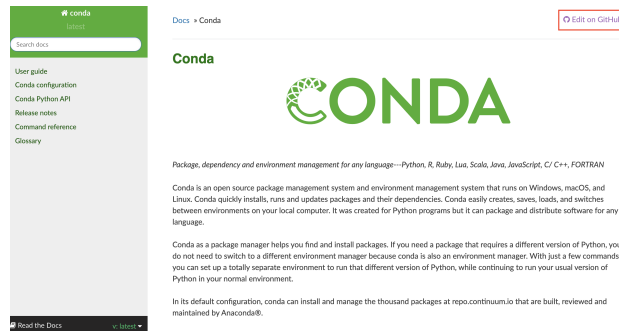
- [Conda documentation](#).
- [Conda GitHub](#).
- [Conda-build documentation](#).
- [Conda-build GitHub](#).

If a documentation change is needed in Distribution, open a ticket on [anaconda-issues](#).

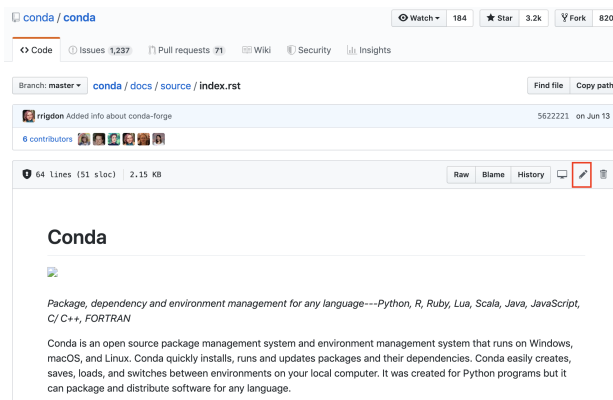
## Example documentation contribution

Follow the directions below to submit a documentation PR using the GitHub interface.

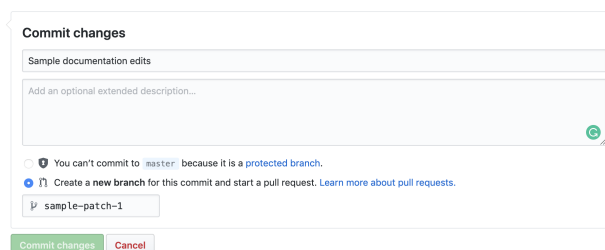
1. Start in the [conda](#) or [conda-build](#) documentation.
2. Select “Edit on GitHub” on the page needing the edit.



3. Edit the file in GitHub.



4. Commit your changes.



5. PR review process

- PR is submitted.
- Anaconda community members and/or staff review the PR, providing comments and revisions.
- New contributors sign the CLA.
- PR is merged.

### Conda-forge feedstocks

Contribute to [conda-forge feedstocks](#) where you can improve, update, and/or add new conda-build recipes to conda-forge. See our [tutorials](#) on how to build conda-build recipes.

The recipes here are often used as the base of recipes used to build packages for defaults/repo.anaconda.com. Helping conda-forge increases the number and quality of packages available to install with conda, as well as helping Anaconda do the same for packages shipped in defaults.

---

**Tip:** A good way to find feedstocks to work on is to look at the [staged recipes](#) issues with the “Package request” label.

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### Anaconda Enterprise

Ready to scale up your projects? Anaconda Enterprise is an enterprise-ready, secure, and scalable data science platform that empowers teams to govern data science assets, collaborate, and deploy their data science projects.

Read more about [Anaconda Enterprise](#) to see if it’s the right option for you and your team.

### Release notes

#### Anaconda 2020.07 (July 23, 2020)

##### User-facing changes

- The installer and base environment now use Python 3.8. Meta-packages for Python 3.6, 3.7, and 3.8 are also available.
- Fixed an issue where the win-32 installer would install win-64 executables in the base environment.
- Fixed an issue where the Windows installer would hang on systems with >64 cores.
- Update PyCharm text and links in the GUI installers.
- Update EULA to reflect terms-of-service change for repo.anaconda.com

##### Backend improvements (non-visible changes)

- Fixed signing of PyCharm bundle for macOS 10.15

##### Changes for all x86 platforms

##### Updated:

- astroid 2.3.3 -> 2.4.2
- astropy 4.0 -> 4.0.1.post1
- atomicwrites 1.3.0 -> 1.4.0



- autopep8 1.4.4 -> 1.5.3
- backcall 0.1.0 -> 0.2.0
- beautifulsoup4 4.8.2 -> 4.9.1
- bitarray 1.2.1 -> 1.4.0
- bleach 3.1.0 -> 3.1.5
- blosc 1.16.3 -> 1.19.0
- bokeh 1.4.0 -> 2.1.1
- ca-certificates 2020.1.1 -> 2020.6.24
- certifi 2019.11.28 -> 2020.6.20
- click 7.0 -> 7.1.2
- cloudpickle 1.3.0 -> 1.5.0
- cryptography 2.8 -> 2.9.2
- curl 7.68.0 -> 7.71.1
- cython 0.29.15 -> 0.29.21
- dask 2.11.0 -> 2.20.0
- dask-core 2.11.0 -> 2.20.0
- decorator 4.4.1 -> 4.4.2
- diff-match-patch 20181111 -> 20200713
- distributed 2.11.0 -> 2.20.0
- flake8 3.7.9 -> 3.8.3
- flask 1.1.1 -> 1.1.2
- freetype 2.9.1 -> 2.10.2
- fsspec 0.6.2 -> 0.7.4
- gevent 1.4.0 -> 20.6.2
- greenlet 0.4.15 -> 0.4.16
- html5lib 1.0.1 -> 1.1
- idna 2.8 -> 2.10
- imageio 2.6.1 -> 2.9.0
- ipykernel 5.1.4 -> 5.3.2
- ipython 7.12.0 -> 7.16.1
- jedi 0.14.1 -> 0.17.1
- jinja2 2.11.1 -> 2.11.2
- joblib 0.14.1 -> 0.16.0
- json5 0.9.1 -> 0.9.5
- jupyter\_client 5.3.4 -> 6.1.6
- jupyter\_core 4.6.1 -> 4.6.3

- jupyterlab 1.2.6 -> 2.1.5
- jupyterlab\_server 1.0.6 -> 1.2.0
- keyring 21.1.0 -> 21.2.1
- kiwisolver 1.1.0 -> 1.2.0
- krb5 1.17.1 -> 1.18.2
- libarchive 3.3.3 -> 3.4.2
- libcurl 7.68.0 -> 7.71.1
- liblief 0.9.0 -> 0.10.1
- libsodium 1.0.16 -> 1.0.18
- libxml2 2.9.9 -> 2.9.10
- libxslt 1.1.33 -> 1.1.34
- llvmlite 0.31.0 -> 0.33.0
- lxml 4.5.0 -> 4.5.2
- lz4-c 1.8.1.2 -> 1.9.2
- matplotlib 3.1.3 -> 3.2.2
- matplotlib-base 3.1.3 -> 3.2.2
- mkl\_fft 1.0.15 -> 1.1.0
- mkl\_random 1.1.0 -> 1.1.1
- mock 4.0.1 -> 4.0.2
- more-itertools 8.2.0 -> 8.4.0
- msgpack-python 0.6.1 -> 1.0.0
- nbformat 5.0.4 -> 5.0.7
- nltk 3.4.5 -> 3.5
- numba 0.48.0 -> 0.50.1
- numpy 1.18.1 -> 1.18.5
- numpy-base 1.18.1 -> 1.18.5
- numpydoc 0.9.2 -> 1.1.0
- openpyxl 3.0.3 -> 3.0.4
- openssl 1.1.1d -> 1.1.1g
- packaging 20.1 -> 20.4
- pandas 1.0.1 -> 1.0.5
- parso 0.5.2 -> 0.7.0
- pillow 7.0.0 -> 7.2.0
- pip 20.0.2 -> 20.1.1
- prometheus\_client 0.7.1 -> 0.8.0
- prompt\_toolkit 3.0.3 -> 3.0.5

- psutil 5.6.7 -> 5.7.0
- py 1.8.1 -> 1.9.0
- py-lief 0.9.0 -> 0.10.1
- pycodestyle 2.5.0 -> 2.6.0
- pycparser 2.19 -> 2.20
- pydocstyle 4.0.1 -> 5.0.2
- pyflakes 2.1.1 -> 2.2.0
- pygments 2.5.2 -> 2.6.1
- pylint 2.4.4 -> 2.5.3
- pyparsing 2.4.6 -> 2.4.7
- pyrsistent 0.15.7 -> 0.16.0
- pytest 5.3.5 -> 5.4.3
- python 3.8.1 -> 3.8.3
- python-language-server 0.31.7 -> 0.34.1
- python-libarchive-c 2.8 -> 2.9
- pytz 2019.3 -> 2020.1
- pyyaml 5.3 -> 5.3.1
- pyzmq 18.1.1 -> 19.0.1
- qdarkstyle 2.8 -> 2.8.1
- qtawesome 0.6.1 -> 0.7.2
- qtconsole 4.6.0 -> 4.7.5
- requests 2.22.0 -> 2.24.0
- rope 0.16.0 -> 0.17.0
- rtree 0.9.3 -> 0.9.4
- scikit-learn 0.22.1 -> 0.23.1
- scipy 1.4.1 -> 1.5.0
- seaborn 0.10.0 -> 0.10.1
- six 1.14.0 -> 1.15.0
- snappy 1.1.7 -> 1.1.8
- sortedcollections 1.1.2 -> 1.2.1
- sortedcontainers 2.1.0 -> 2.2.2
- soupsieve 1.9.5 -> 2.0.1
- sphinx 2.4.0 -> 3.1.2
- sphinxcontrib-applehelp 1.0.1 -> 1.0.2
- sphinxcontrib-devhelp 1.0.1 -> 1.0.2
- sphinxcontrib-htmlhelp 1.0.2 -> 1.0.3

- sphinxcontrib-qthelp 1.0.2 -> 1.0.3
- sphinxcontrib-serializinghtml 1.1.3 -> 1.1.4
- sphinxcontrib-websupport 1.2.0 -> 1.2.3
- spyder 4.0.1 -> 4.1.4
- spyder-kernels 1.8.1 -> 1.9.2
- sqlalchemy 1.3.13 -> 1.3.18
- sqlite 3.31.1 -> 3.32.3
- statsmodels 0.11.0 -> 0.11.1
- sympy 1.5.1 -> 1.6.1
- tk 8.6.8 -> 8.6.10
- tornado 6.0.3 -> 6.0.4
- tqdm 4.42.1 -> 4.47.0
- urllib3 1.25.8 -> 1.25.9
- watchdog 0.10.2 -> 0.10.3
- wcwidth 0.1.8 -> 0.2.5
- werkzeug 1.0.0 -> 1.0.1
- xlswriter 1.2.7 -> 1.2.9
- xz 5.2.4 -> 5.2.5
- yaml 0.1.7 -> 0.2.5
- yapf 0.28.0 -> 0.30.0
- zeromq 4.3.1 -> 4.3.2
- zict 1.0.0 -> 2.0.0
- zipp 2.2.0 -> 3.1.0
- zstd 1.3.7 -> 1.4.5

**Added:**

- brotlipy 0.7.0
- contextvars 2.4
- immutables 0.14
- libllvm9 9.0.1
- prompt-toolkit 3.0.5
- regex 2020.6.8
- threadpoolctl 2.1.0
- toml 0.10.1
- typing\_extensions 3.7.4.2
- zope 1.0
- zope.event 4.4

- zope.interface 4.7.1

**Removed:**

- hypothesis
- pytest-arraydiff
- pytest-astropy
- pytest-astropy-header
- pytest-doctestplus
- pytest-openfiles
- pytest-remotedata

**More changes specific to linux-64****Updated:**

- dbus 1.13.12 -> 1.13.16
- expat 2.2.6 -> 2.2.9
- fribidi 1.0.5 -> 1.0.9
- glib 2.63.1 -> 2.65.0
- graphite2 1.3.13 -> 1.3.14
- harfbuzz 1.8.8 -> 2.4.0
- importlib\_metadata 1.5.0 -> 1.7.0
- intel-openmp 2020.0 -> 2020.1
- jeepney 0.4.2 -> 0.4.3
- libedit 3.1.20181209 -> 3.1.20191231
- libffi 3.2.1 -> 3.3
- libssh2 1.8.2 -> 1.9.0
- libxcb 1.13 -> 1.14
- mkl 2020.0 -> 2020.1
- mpfr 4.0.1 -> 4.0.2
- pandoc 2.2.3.2 -> 2.10
- pango 1.42.4 -> 1.45.3
- patchelf 0.10 -> 0.11
- pcre 8.43 -> 8.44
- pixman 0.38.0 -> 0.40.0
- readline 7.0 -> 8.0
- setuptools 45.2.0 -> 49.2.0
- wurlitzer 2.0.0 -> 2.0.1

**Added:**

- importlib-metadata 1.7.0
- lcms2 2.11

### More changes specific to linux-ppc64le

#### Updated:

- expat 2.2.6 -> 2.2.9
- glib 2.63.1 -> 2.65.0
- importlib\_metadata 1.5.0 -> 1.7.0
- jedi 0.16.0 -> 0.17.1
- libedit 3.1.20181209 -> 3.1.20191231
- libffi 3.2.1 -> 3.3
- libopenblas 0.3.6 -> 0.3.10
- libssh2 1.8.2 -> 1.9.0
- libxcb 1.13 -> 1.14
- mpfr 4.0.1 -> 4.0.2
- openblas 0.3.6 -> 0.3.10
- openblas-devel 0.3.6 -> 0.3.10
- pandoc 2.0.0.1 -> 2.2.1
- parso 0.6.1 -> 0.7.0
- patchelf 0.10 -> 0.11
- pcre 8.43 -> 8.44
- pixman 0.34.0 -> 0.40.0
- readline 7.0 -> 8.0
- setuptools 45.2.0 -> 49.2.0
- zeromq 4.2.5 -> 4.3.2

#### Added:

- importlib-metadata 1.7.0
- lcms2 2.11
- liblief 0.10.1
- py-lief 0.10.1

### More changes specific to win-32

#### Updated:

- importlib\_metadata 1.5.0 -> 1.6.1
- intel-openmp 2020.0 -> 2020.1

- mkl 2020.0 -> 2020.1
- pandoc 2.2.3.2 -> 2.9.2.1
- pynacl 1.3.0 -> 1.4.0
- setuptools 46.0.0 -> 49.2.0
- xlwings 0.17.1 -> 0.19.5

**Added:**

- gmpy2 2.0.8
- importlib-metadata 1.6.1
- mpc 1.1.0
- mpfr 4.0.2
- mpir 3.0.0

**More changes specific to win-64****Updated:**

- importlib\_metadata 1.5.0 -> 1.7.0
- intel-openmp 2020.0 -> 2020.1
- libssh2 1.8.2 -> 1.9.0
- mkl 2020.0 -> 2020.1
- pandoc 2.2.3.2 -> 2.10
- pynacl 1.3.0 -> 1.4.0
- setuptools 45.2.0 -> 49.2.0
- xlwings 0.17.1 -> 0.19.5

**Added:**

- gmpy2 2.0.8
- importlib-metadata 1.7.0
- mpc 1.1.0
- mpfr 4.0.2
- mpir 3.0.0

**More changes specific to osx-64****Updated:**

- appscript 1.1.0 -> 1.1.1
- dbus 1.13.12 -> 1.13.16
- expat 2.2.6 -> 2.2.9
- glib 2.63.1 -> 2.65.0

- `importlib_metadata` 1.5.0 -> 1.7.0
- `libcxx` 4.0.1 -> 10.0.0
- `libedit` 3.1.20181209 -> 3.1.20191231
- `libffi` 3.2.1 -> 3.3
- `libiconv` 1.15 -> 1.16
- `llvm-openmp` 4.0.1 -> 10.0.0
- `mpfr` 4.0.1 -> 4.0.2
- `pandoc` 2.2.3.2 -> 2.10
- `pcre` 8.43 -> 8.44
- `readline` 7.0 -> 8.0
- `setuptools` 46.0.0 -> 49.2.0
- `wurlitzer` 2.0.0 -> 2.0.1
- `xlwings` 0.17.1 -> 0.19.5

### Added:

- `importlib-metadata` 1.7.0
- `lcms2` 2.11

### Removed:

- `libcxxabi`

## Anaconda 2020.02 (March 11, 2020)

### User-facing changes

- Name changed to Anaconda Individual Edition.
- The previous 2019.10 release was the last for Python 2.7, and Python 2 will not be supported going forward.
- Python 3.6, 3.7 and 3.8 meta-packages available, installer is Python 3.7.
- Last official release to support Windows 7.
- Updated links to in GUI installer.
- Anaconda Navigator updated to 1.9.12.

### Backend improvements (non-visible changes)

- Deadlock fixes on single core computers.
- Improved menu removal on Windows.



## Changes for all x86 platforms

### Updated:

- anaconda-project 0.8.3 -> 0.8.4
- asn1crypto 1.0.1 -> 1.3.0
- astroid 2.3.1 -> 2.3.3
- astropy 3.2.2 -> 4.0
- attrs 19.2.0 -> 19.3.0
- babel 2.7.0 -> 2.8.0
- beautifulsoup4 4.8.0 -> 4.8.2
- bitarray 1.0.1 -> 1.2.1
- bokeh 1.3.4 -> 1.4.0
- bottleneck 1.2.1 -> 1.3.2
- ca-certificates 2019.8.28 -> 2020.1.1
- certifi 2019.9.11 -> 2019.11.28
- cffi 1.12.3 -> 1.14.0
- cloudpickle 1.2.2 -> 1.3.0
- colorama 0.4.1 -> 0.4.3
- contextlib2 0.6.0 -> 0.6.0.post1
- cryptography 2.7 -> 2.8
- curl 7.65.3 -> 7.68.0
- cython 0.29.13 -> 0.29.15
- cytoolz 0.10.0 -> 0.10.1
- dask 2.5.2 -> 2.11.0
- dask-core 2.5.2 -> 2.11.0
- decorator 4.4.0 -> 4.4.1
- distributed 2.5.2 -> 2.11.0
- docutils 0.15.2 -> 0.16
- fsspec 0.5.2 -> 0.6.2
- h5py 2.9.0 -> 2.10.0
- imageio 2.6.0 -> 2.6.1
- imagesize 1.1.0 -> 1.2.0
- importlib\_metadata 0.23 -> 1.5.0
- ipykernel 5.1.2 -> 5.1.4
- ipython 7.8.0 -> 7.12.0
- jinja2 2.10.3 -> 2.11.1
- joblib 0.13.2 -> 0.14.1

- json5 0.8.5 -> 0.9.1
- jsonschema 3.0.2 -> 3.2.0
- jupyter\_client 5.3.3 -> 5.3.4
- jupyter\_console 6.0.0 -> 6.1.0
- jupyter\_core 4.5.0 -> 4.6.1
- jupyterlab 1.1.4 -> 1.2.6
- keyring 18.0.0 -> 21.1.0
- krb5 1.16.1 -> 1.17.1
- lazy-object-proxy 1.4.2 -> 1.4.3
- libcurl 7.65.3 -> 7.68.0
- libtiff 4.0.10 -> 4.1.0
- llvmlite 0.29.0 -> 0.31.0
- lxml 4.4.1 -> 4.5.0
- matplotlib 3.1.1 -> 3.1.3
- mkl\_fft 1.0.14 -> 1.0.15
- mock 3.0.5 -> 4.0.1
- more-itertools 7.2.0 -> 8.2.0
- nbconvert 5.6.0 -> 5.6.1
- nbformat 4.4.0 -> 5.0.4
- networkx 2.3 -> 2.4
- notebook 6.0.1 -> 6.0.3
- numexpr 2.7.0 -> 2.7.1
- numpydoc 0.9.1 -> 0.9.2
- openpyxl 3.0.0 -> 3.0.3
- packaging 19.2 -> 20.1
- pandas 0.25.1 -> 1.0.1
- parso 0.5.1 -> 0.5.2
- partd 1.0.0 -> 1.1.0
- path.py 12.0.1 -> 12.4.0
- pillow 6.2.0 -> 7.0.0
- pip 19.2.3 -> 20.0.2
- pluggy 0.13.0 -> 0.13.1
- prompt\_toolkit 2.0.10 -> 3.0.3
- psutil 5.6.3 -> 5.6.7
- py 1.8.0 -> 1.8.1
- pycurl 7.43.0.3 -> 7.43.0.5

- `pygments` 2.4.2 -> 2.5.2
- `pylint` 2.4.2 -> 2.4.4
- `pyodbc` 4.0.27 -> 4.0.30
- `pyopenssl` 19.0.0 -> 19.1.0
- `pyparsing` 2.4.2 -> 2.4.6
- `pyrsistent` 0.15.4 -> 0.15.7
- `pytables` 3.5.2 -> 3.6.1
- `pytest` 5.2.1 -> 5.3.5
- `pytest-astropy` 0.5.0 -> 0.8.0
- `pytest-doctestplus` 0.4.0 -> 0.5.0
- `python` 3.7.4 -> 3.7.6
- `python-dateutil` 2.8.0 -> 2.8.1
- `pywavelets` 1.0.3 -> 1.1.1
- `pyyaml` 5.1.2 -> 5.3
- `pyzmq` 18.1.0 -> 18.1.1
- `qtawesome` 0.6.0 -> 0.6.1
- `qtconsole` 4.5.5 -> 4.6.0
- `rope` 0.14.0 -> 0.16.0
- `ruamel_yaml` 0.15.46 -> 0.15.87
- `scikit-image` 0.15.0 -> 0.16.2
- `scipy` 1.3.1 -> 1.4.1
- `seaborn` 0.9.0 -> 0.10.0
- `six` 1.12.0 -> 1.14.0
- `soupsieve` 1.9.3 -> 1.9.5
- `sphinx` 2.2.0 -> 2.4.0
- `sphinxcontrib-websupport` 1.1.2 -> 1.2.0
- `spyder` 3.3.6 -> 4.0.1
- `spyder-kernels` 0.5.2 -> 1.8.1
- `sqlalchemy` 1.3.9 -> 1.3.13
- `sqlite` 3.30.0 -> 3.31.1
- `statsmodels` 0.10.1 -> 0.11.0
- `sympy` 1.4 -> 1.5.1
- `tblib` 1.4.0 -> 1.6.0
- `terminado` 0.8.2 -> 0.8.3
- `testpath` 0.4.2 -> 0.4.4
- `tqdm` 4.36.1 -> 4.42.1

- typed-ast 1.4.0 -> 1.4.1
- urllib3 1.24.2 -> 1.25.8
- wcwidth 0.1.7 -> 0.1.8
- werkzeug 0.16.0 -> 1.0.0
- wheel 0.33.6 -> 0.34.2
- xlswriter 1.2.1 -> 1.2.7
- zipp 0.6.0 -> 2.2.0

### Added:

- argh 0.26.2
- autopep8 1.4.4
- diff-match-patch 20181111
- flake8 3.7.9
- future 0.18.2
- hypothesis 5.5.4
- intervaltree 3.0.2
- matplotlib-base 3.1.3
- path 13.1.0
- pathtools 0.1.2
- pydocstyle 4.0.1
- pytest-astropy-header 0.1.2
- python-jsonrpc-server 0.3.4
- python-language-server 0.31.7
- qdarkstyle 2.8
- rtree 0.9.3
- ujson 1.35
- watchdog 0.10.2
- yapf 0.28.0

### Removed:

- backports.os

## More changes specific to linux-64

### Updated:

- dbus 1.13.6 -> 1.13.12
- glib 2.56.2 -> 2.63.1
- intel-openmp 2019.4 -> 2020.0
- jeepney 0.4.1 -> 0.4.2

- mkl 2019.4 -> 2020.0
- ncurses 6.1 -> 6.2
- numba 0.45.1 -> 0.48.0
- numpy 1.17.2 -> 1.18.1
- numpy-base 1.17.2 -> 1.18.1
- patchelf 0.9 -> 0.10
- pexpect 4.7.0 -> 4.8.0
- ripgrep 0.10.0 -> 11.0.2
- scikit-learn 0.21.3 -> 0.22.1
- secretstorage 3.1.1 -> 3.1.2
- setuptools 41.4.0 -> 45.2.0
- tbb 2019.4 -> 2020.0
- wurlitzer 1.0.3 -> 2.0.0

**Added:**

- ld\_impl\_linux-64 2.33.1
- libspatialindex 1.9.3
- pyxdg 0.26

**More changes specific to linux-ppc64le****Updated:**

- glib 2.56.2 -> 2.63.1
- h5py 2.8.0 -> 2.10.0
- hdf5 1.10.2 -> 1.10.4
- jedi 0.15.1 -> 0.16.0
- ncurses 6.1 -> 6.2
- numpy 1.17.2 -> 1.18.1
- numpy-base 1.17.2 -> 1.18.1
- parso 0.5.1 -> 0.6.1
- patchelf 0.9 -> 0.10
- pexpect 4.7.0 -> 4.8.0
- pytables 3.4.4 -> 3.6.1
- scikit-learn 0.21.3 -> 0.22.1
- scipy 1.3.0 -> 1.4.1
- setuptools 41.4.0 -> 45.2.0

**Added:**

- ld\_impl\_linux-ppc64le 2.33.1

- mock 4.0.1

### Removed:

- atomicwrites

### More changes specific to win-32

#### Updated:

- intel-openmp 2019.4 -> 2020.0
- mkl 2019.4 -> 2020.0
- numba 0.45.0 -> 0.48.0
- numpy 1.16.5 -> 1.18.1
- numpy-base 1.16.5 -> 1.18.1
- pywin32 223 -> 227
- pywinpty 0.5.5 -> 0.5.7
- setuptools 41.4.0 -> 45.2.0
- tbb 2019.4 -> 2020.0
- xlwings 0.15.10 -> 0.17.1

#### Added:

- bcrypt 3.1.7
- libspatialindex 1.8.5
- paramiko 2.7.1
- pexpect 4.8.0
- pynacl 1.3.0
- pywin32-ctypes 0.2.0

### More changes specific to win-64

#### Updated:

- intel-openmp 2019.4 -> 2020.0
- mkl 2019.4 -> 2020.0
- numba 0.45.1 -> 0.48.0
- numpy 1.16.5 -> 1.18.1
- numpy-base 1.16.5 -> 1.18.1
- pywin32 223 -> 227
- pywinpty 0.5.5 -> 0.5.7
- scikit-learn 0.21.3 -> 0.22.1
- setuptools 41.4.0 -> 45.2.0

- tbb 2019.4 -> 2020.0
- xlwings 0.15.10 -> 0.17.1

**Added:**

- bcrypt 3.1.7
- libspatialindex 1.9.3
- paramiko 2.7.1
- pexpect 4.8.0
- pynacl 1.3.0
- pywin32-ctypes 0.2.0

**More changes specific to osx-64****Updated:**

- dbus 1.13.6 -> 1.13.12
- glib 2.56.2 -> 2.63.1
- libssh2 1.8.2 -> 1.9.0
- ncurses 6.1 -> 6.2
- numba 0.45.1 -> 0.48.0
- numpy 1.17.2 -> 1.18.1
- numpy-base 1.17.2 -> 1.18.1
- pexpect 4.7.0 -> 4.8.0
- ripgrep 0.10.0 -> 11.0.2
- scikit-learn 0.21.3 -> 0.22.1
- setuptools 41.4.0 -> 46.0.0
- tbb 2019.8 -> 2020.0
- wurlitzer 1.0.3 -> 2.0.0
- xlwings 0.15.10 -> 0.17.1

**Added:**

- applaunchservices 0.2.1
- libspatialindex 1.9.3

**Anaconda 2019.10 (October 15, 2019)****User-facing changes**

- Updated packages.
- For macOS Catalina, we have notarized the package installers and changed the default install directory to /opt/anaconda{2,3}.

**Backend improvements (non-visible changes)**

- Added a new Cython-based Python wrapper to clear up library loading problems with libarchive.
- Extraction scripts work better with older operating systems.

**Changes for all x86 platforms****Updated:**

- asn1crypto 0.24.0 -> 1.0.1
- astroid 2.2.5 -> 2.3.1
- astropy 3.2.1 -> 3.2.2
- attrs 19.1.0 -> 19.2.0
- beautifulsoup4 4.7.1 -> 4.8.0
- bitarray 0.9.3 -> 1.0.1
- ca-certificates 2019.5.15 -> 2019.8.28
- certifi 2019.6.16 -> 2019.9.11
- cloudpickle 1.2.1 -> 1.2.2
- configparser 3.7.4 -> 4.0.2
- contextlib2 0.5.5 -> 0.6.0
- curl 7.65.2 -> 7.65.3
- cython 0.29.12 -> 0.29.13
- dask 2.1.0 -> 2.5.2
- dask-core 2.1.0 -> 2.5.2
- distributed 2.1.0 -> 2.5.2
- docutils 0.14 -> 0.15.2
- heapdict 1.0.0 -> 1.0.1
- imageio 2.5.0 -> 2.6.0
- importlib\_metadata 0.17 -> 0.23
- ipykernel 5.1.1 -> 5.1.2
- ipython 7.6.1 -> 7.8.0
- ipywidgets 7.5.0 -> 7.5.1
- jedi 0.13.3 -> 0.15.1
- jinja2 2.10.1 -> 2.10.3
- json5 0.8.4 -> 0.8.5
- jsonschema 3.0.1 -> 3.0.2
- jupyter\_client 5.3.1 -> 5.3.3
- jupyterlab 1.0.2 -> 1.1.4



- jupyterlab\_server 1.0.0 -> 1.0.6
- lazy-object-proxy 1.4.1 -> 1.4.2
- libcurl 7.65.2 -> 7.65.3
- lxml 4.3.4 -> 4.4.1
- matplotlib 3.1.0 -> 3.1.1
- mkl-service 2.0.2 -> 2.3.0
- mkl\_fft 1.0.12 -> 1.0.14
- mkl\_random 1.0.2 -> 1.1.0
- more-itertools 7.0.0 -> 7.2.0
- nbconvert 5.5.0 -> 5.6.0
- nltk 3.4.4 -> 3.4.5
- notebook 6.0.0 -> 6.0.1
- numexpr 2.6.9 -> 2.7.0
- openpyxl 2.6.2 -> 3.0.0
- packaging 19.0 -> 19.2
- pandas 0.24.2 -> 0.25.1
- parso 0.5.0 -> 0.5.1
- pathlib2 2.3.4 -> 2.3.5
- pillow 6.1.0 -> 6.2.0
- pip 19.1.1 -> 19.2.3
- pluggy 0.12.0 -> 0.13.0
- prompt\_toolkit 2.0.9 -> 2.0.10
- pylint 2.3.1 -> 2.4.2
- pyodbc 4.0.26 -> 4.0.27
- pyparsing 2.4.0 -> 2.4.2
- pyrsistent 0.14.11 -> 0.15.4
- pysocks 1.7.0 -> 1.7.1
- pytest 5.0.1 -> 5.2.1
- pytest-doctestplus 0.3.0 -> 0.4.0
- pytest-openfiles 0.3.2 -> 0.4.0
- pytest-remotedata 0.3.1 -> 0.3.2
- python 3.7.3 -> 3.7.4
- pytz 2019.1 -> 2019.3
- pyyaml 5.1.1 -> 5.1.2
- pyzmq 18.0.0 -> 18.1.0
- qtawesome 0.5.7 -> 0.6.0

- qtpy 1.8.0 -> 1.9.0
- setuptools 41.0.1 -> 41.4.0
- snowballstemmer 1.9.0 -> 2.0.0
- soupsieve 1.8 -> 1.9.3
- sphinx 2.1.2 -> 2.2.0
- spyder-kernels 0.5.1 -> 0.5.2
- sqlalchemy 1.3.5 -> 1.3.9
- sqlite 3.29.0 -> 3.30.0
- statsmodels 0.10.0 -> 0.10.1
- tqdm 4.32.1 -> 4.36.1
- traitlets 4.3.2 -> 4.3.3
- typed-ast 1.3.4 -> 1.4.0
- typing 3.7.4 -> 3.7.4.1
- werkzeug 0.15.4 -> 0.16.0
- wheel 0.33.4 -> 0.33.6
- widgetsnbextension 3.5.0 -> 3.5.1
- xlswriter 1.1.8 -> 1.2.1
- zipp 0.5.1 -> 0.6.0

**Added:**

- fsspec 0.5.2

### More changes specific to linux-64

**Updated:**

- bokeh 1.2.0 -> 1.3.4
- jeepney 0.4 -> 0.4.1
- numba 0.45.0 -> 0.45.1
- numpy 1.16.4 -> 1.17.2
- numpy-base 1.16.4 -> 1.17.2
- qtconsole 4.5.1 -> 4.5.5
- scikit-learn 0.21.2 -> 0.21.3
- scipy 1.3.0 -> 1.3.1
- wurlitzer 1.0.2 -> 1.0.3

**Added:**

- ripgrep 0.10.0
- tbb 2019.4

### More changes specific to linux-ppc64le

#### Updated:

- bokeh 1.2.0 -> 1.3.4
- libopenblas 0.2.20 -> 0.3.6
- numexpr 2.6.7 -> 2.7.0
- numpy 1.14.5 -> 1.17.2
- numpy-base 1.14.5 -> 1.17.2
- openblas 0.2.20 -> 0.3.6
- openblas-devel 0.2.20 -> 0.3.6
- pytest-openfiles 0.3.1 -> 0.4.0
- scikit-learn 0.19.1 -> 0.21.3
- scipy 1.1.0 -> 1.3.0

#### Added:

- joblib 0.13.2
- nomkl 3.0

### More changes specific to win-32

#### Updated:

- bokeh 1.3.0 -> 1.3.4
- numpy 1.16.4 -> 1.16.5
- numpy-base 1.16.4 -> 1.16.5
- qtconsole 4.5.2 -> 4.5.5
- scipy 1.3.0 -> 1.3.1
- vs2015\_runtime 14.15.26706 -> 14.16.27012
- xlwings 0.15.8 -> 0.15.10

#### Added:

- tbb 2019.4

### More changes specific to win-64

#### Updated:

- bokeh 1.3.0 -> 1.3.4
- numba 0.45.0 -> 0.45.1
- numpy 1.16.4 -> 1.16.5
- numpy-base 1.16.4 -> 1.16.5
- qtconsole 4.5.2 -> 4.5.5

- scikit-learn 0.21.2 -> 0.21.3
- scipy 1.2.1 -> 1.3.1
- vs2015\_runtime 14.15.26706 -> 14.16.27012
- xlwings 0.15.8 -> 0.15.10

### Added:

- tbb 2019.4

## More changes specific to osx-64

### Updated:

- bokeh 1.2.0 -> 1.3.4
- numba 0.45.0 -> 0.45.1
- numpy 1.16.4 -> 1.17.2
- numpy-base 1.16.4 -> 1.17.2
- qtconsole 4.5.1 -> 4.5.5
- scikit-learn 0.21.2 -> 0.21.3
- scipy 1.3.0 -> 1.3.1
- wurlitzer 1.0.2 -> 1.0.3
- xlwings 0.15.8 -> 0.15.10

### Added:

- ripgrep 0.10.0
- tbb 2019.8

## Anaconda 2019.07 (July 24, 2019)

### User-facing changes

- Conda install times have decreased by more than half for large packages.
- Conda 4.7.10 improves environment management and error messages.
- Conda constructor now supports building installers with the new .conda file format as well as noarch packages.
- Documentation has been updated for our integration with PyCharm, including more tutorials and improved navigation for easier use.
- Updated packages, including R packages and ML/AI packages.

### Backend improvements (non-visible changes)

- Conda is moving to a quarterly release cycle.
- Conda build 3.18 works with the new .conda file format.

## Changes for all x86 platforms

### Updated:

- anaconda-project 0.8.2 -> 0.8.3
- astropy 3.1.2 -> 3.2.1
- babel 2.6.0 -> 2.7.0
- bitarray 0.8.3 -> 0.9.3
- blosc 1.15.0 -> 1.16.3
- bzip2 1.0.6 -> 1.0.8
- ca-certificates 2019.1.23 -> 2019.5.15
- certifi 2019.3.9 -> 2019.6.16
- cffi 1.12.2 -> 1.12.3
- cloudpickle 0.8.0 -> 1.2.1
- configparser 3.7.3 -> 3.7.4
- cryptography 2.6.1 -> 2.7
- curl 7.64.0 -> 7.65.2
- cython 0.29.6 -> 0.29.12
- cytoolz 0.9.0.1 -> 0.10.0
- dask 1.1.4 -> 2.1.0
- dask-core 1.1.4 -> 2.1.0
- defusedxml 0.5.0 -> 0.6.0
- distributed 1.26.0 -> 2.1.0
- fastcache 1.0.2 -> 1.1.0
- filelock 3.0.10 -> 3.0.12
- flask 1.0.2 -> 1.1.1
- futures 3.2.0 -> 3.3.0
- glob2 0.6 -> 0.7
- importlib\_metadata 0.8 -> 0.17
- intel-openmp 2019.3 -> 2019.4
- ipykernel 5.1.0 -> 5.1.1
- ipython 7.4.0 -> 7.6.1
- ipywidgets 7.4.2 -> 7.5.0
- isort 4.3.16 -> 4.3.21
- jdcal 1.4 -> 1.4.1
- jinja2 2.10 -> 2.10.1
- jupyter\_client 5.2.4 -> 5.3.1
- jupyter\_core 4.4.0 -> 4.5.0

- jupyterlab 0.35.4 -> 1.0.2
- jupyterlab\_server 0.2.0 -> 1.0.0
- kiwisolver 1.0.1 -> 1.1.0
- lazy-object-proxy 1.3.1 -> 1.4.1
- libcurl 7.64.0 -> 7.65.2
- libpng 1.6.36 -> 1.6.37
- libssh2 1.8.0 -> 1.8.2
- llvmlite 0.28.0 -> 0.29.0
- lxml 4.3.2 -> 4.3.4
- matplotlib 3.0.3 -> 3.1.0
- mkl 2019.3 -> 2019.4
- mkl-service 1.1.2 -> 2.0.2
- mkl\_fft 1.0.10 -> 1.0.12
- more-itertools 6.0.0 -> 7.0.0
- nbconvert 5.4.1 -> 5.5.0
- networkx 2.2 -> 2.3
- nltk 3.4 -> 3.4.4
- notebook 5.7.8 -> 6.0.0
- numba 0.43.1 -> 0.45.0
- numpy 1.16.2 -> 1.16.4
- numpy-base 1.16.2 -> 1.16.4
- numpydoc 0.8.0 -> 0.9.1
- openpyxl 2.6.1 -> 2.6.2
- openssl 1.1.1b0 -> 1.1.1rc0
- parso 0.3.4 -> 0.5.0
- partd 0.3.10 -> 1.0.0
- path.py 11.5.0 -> 12.0.1
- pathlib2 2.3.3 -> 2.3.4
- pillow 5.4.1 -> 6.1.0
- pip 19.0.3 -> 19.1.1
- pluggy 0.9.0 -> 0.12.0
- prometheus\_client 0.6.0 -> 0.7.1
- psutil 5.6.1 -> 5.6.3
- pycurl 7.43.0.2 -> 7.43.0.3
- pygments 2.3.1 -> 2.4.2
- pyparsing 2.3.1 -> 2.4.0

- pysocks 1.6.8 -> 1.7.0
- pytables 3.5.1 -> 3.5.2
- pytest 4.3.1 -> 5.0.1
- pytz 2018.9 -> 2019.1
- pywavelets 1.0.2 -> 1.0.3
- pyyaml 5.1 -> 5.1.1
- qtpy 1.7.0 -> 1.8.0
- requests 2.21.0 -> 2.22.0
- rope 0.12.0 -> 0.14.0
- scikit-image 0.14.2 -> 0.15.0
- setuptools 40.8.0 -> 41.0.1
- snowballstemmer 1.2.1 -> 1.9.0
- sphinx 1.8.5 -> 2.1.2
- sphinxcontrib-websupport 1.1.0 -> 1.1.2
- spyder 3.3.3 -> 3.3.6
- spyder-kernels 0.4.2 -> 0.5.1
- sqlalchemy 1.3.1 -> 1.3.5
- sqlite 3.27.2 -> 3.29.0
- statsmodels 0.9.0 -> 0.10.0
- subprocess32 3.5.3 -> 3.5.4
- sympy 1.3 -> 1.4
- tblib 1.3.2 -> 1.4.0
- terminado 0.8.1 -> 0.8.2
- toolz 0.9.0 -> 0.10.0
- tornado 6.0.2 -> 6.0.3
- tqdm 4.31.1 -> 4.32.1
- typed-ast 1.3.1 -> 1.3.4
- typing 3.6.6 -> 3.7.4
- urllib3 1.24.1 -> 1.24.2
- werkzeug 0.14.1 -> 0.15.4
- wheel 0.33.1 -> 0.33.4
- widgetsnbextension 3.4.2 -> 3.5.0
- wrapt 1.11.1 -> 1.11.2
- xlswriter 1.1.5 -> 1.1.8
- zict 0.1.4 -> 1.0.0
- zipp 0.3.3 -> 0.5.1

### Added:

- joblib 0.13.2
- json5 0.8.4
- mock 3.0.5
- sphinxcontrib-applehelp 1.0.1
- sphinxcontrib-devhelp 1.0.1
- sphinxcontrib-htmlhelp 1.0.2
- sphinxcontrib-jsmath 1.0.1
- sphinxcontrib-qthelp 1.0.2
- sphinxcontrib-serializinghtml 1.1.3

### More changes specific to linux-64

#### Updated:

- bokeh 1.0.4 -> 1.2.0
- libgcc-ng 8.2.0 -> 9.1.0
- libstdcxx-ng 8.2.0 -> 9.1.0
- pexpect 4.6.0 -> 4.7.0
- pycairo 1.18.0 -> 1.18.1
- qtconsole 4.4.3 -> 4.5.1
- scikit-learn 0.20.3 -> 0.21.2
- scipy 1.2.1 -> 1.3.0

#### Added:

- \_libgcc\_mutex 0.1

### More changes specific to linux-ppc64le

#### Updated:

- bokeh 1.0.4 -> 1.2.0
- pexpect 4.6.0 -> 4.7.0
- pillow 5.3.0 -> 6.1.0
- pycairo 1.18.0 -> 1.18.1
- scikit-image 0.14.1 -> 0.15.0

#### Added:

- \_libgcc\_mutex 0.1



### More changes specific to win-32

#### Updated:

- bokeh 1.0.4 -> 1.3.0
- qtconsole 4.4.3 -> 4.5.2
- scikit-learn 0.20.3 -> 0.21.1
- scipy 1.2.1 -> 1.3.0
- xlwings 0.15.4 -> 0.15.8

#### Added:

- liblief 0.9.0
- py-lief 0.9.0

### More changes specific to win-64

#### Updated:

- bokeh 1.0.4 -> 1.3.0
- qtconsole 4.4.3 -> 4.5.2
- scikit-learn 0.20.3 -> 0.21.2
- xlwings 0.15.4 -> 0.15.8

### More changes specific to osx-64

#### Updated:

- bokeh 1.0.4 -> 1.2.0
- pexpect 4.6.0 -> 4.7.0
- qtconsole 4.4.3 -> 4.5.1
- scikit-learn 0.20.3 -> 0.21.2
- scipy 1.2.1 -> 1.3.0
- xlwings 0.15.4 -> 0.15.8

#### Added:

- llvm-openmp 4.0.1

### Anaconda 2019.03 (April 4, 2019)

#### User-facing changes

- Full conda integration with Windows Powershell.
- The Windows Python package includes an optional feature that, when enabled, will improve DLL handling of library conflicts.

- This is the first release which includes conda 4.6.
- A link is added to the installer so you have the option to easily install PyCharm for Anaconda.

### Backend improvements (non-visible changes)

- Anaconda uninstalls faster on Windows.

### Changes for all x86 platforms

#### Updated:

- astroid 2.1.0 -> 2.2.5
- astropy 3.1 -> 3.1.2
- atomicwrites 1.2.1 -> 1.3.0
- attrs 18.2.0 -> 19.1.0
- beautifulsoup4 4.6.3 -> 4.7.1
- bleach 3.0.2 -> 3.1.0
- blosc 1.14.4 -> 1.15.0
- bokeh 1.0.2 -> 1.0.4
- ca-certificates 2018.3.7 -> 2019.1.23
- certifi 2018.11.29 -> 2019.3.9
- cffi 1.11.5 -> 1.12.2
- cloudpickle 0.6.1 -> 0.8.0
- configparser 3.5.0 -> 3.7.3
- cryptography 2.4.2 -> 2.6.1
- curl 7.63.0 -> 7.64.0
- cython 0.29.2 -> 0.29.6
- dask 1.0.0 -> 1.1.4
- dask-core 1.0.0 -> 1.1.4
- decorator 4.3.0 -> 4.4.0
- distributed 1.25.1 -> 1.26.0
- entrypoints 0.2.3 -> 0.3
- gevent 1.3.7 -> 1.4.0
- h5py 2.8.0 -> 2.9.0
- hdf5 1.10.2 -> 1.10.4
- imageio 2.4.1 -> 2.5.0
- importlib\_metadata 0.6 -> 0.8
- intel-openmp 2019.1 -> 2019.3

- ipython 7.2.0 -> 7.4.0
- isort 4.3.4 -> 4.3.16
- jedi 0.13.2 -> 0.13.3
- jsonschema 2.6.0 -> 3.0.1
- jupyterlab 0.35.3 -> 0.35.4
- keyring 17.0.0 -> 18.0.0
- libcurl 7.63.0 -> 7.64.0
- libpng 1.6.35 -> 1.6.36
- libtiff 4.0.9 -> 4.0.10
- libxml2 2.9.8 -> 2.9.9
- libxslt 1.1.32 -> 1.1.33
- llvmlite 0.26.0 -> 0.28.0
- lxml 4.2.5 -> 4.3.2
- markupsafe 1.1.0 -> 1.1.1
- matplotlib 3.0.2 -> 3.0.3
- mkl 2019.1 -> 2019.3
- mkl\_fft 1.0.6 -> 1.0.10
- more-itertools 4.3.0 -> 6.0.0
- msgpack-python 0.5.6 -> 0.6.1
- nbconvert 5.4.0 -> 5.4.1
- notebook 5.7.4 -> 5.7.8
- numba 0.41.0 -> 0.43.1
- numexpr 2.6.8 -> 2.6.9
- numpy 1.15.4 -> 1.16.2
- numpy-base 1.15.4 -> 1.16.2
- openpyxl 2.5.12 -> 2.6.1
- openssl 1.1.1a0 -> 1.1.1b0
- packaging 18.0 -> 19.0
- pandas 0.23.4 -> 0.24.2
- pandoc 1.19.2.1 -> 2.2.3.2
- parso 0.3.1 -> 0.3.4
- partd 0.3.9 -> 0.3.10
- pillow 5.3.0 -> 5.4.1
- pip 18.1 -> 19.0.3
- pkginfo 1.4.2 -> 1.5.0.1
- pluggy 0.8.0 -> 0.9.0

- prometheus\_client 0.5.0 -> 0.6.0
- prompt\_toolkit 2.0.7 -> 2.0.9
- psutil 5.4.8 -> 5.6.1
- py 1.7.0 -> 1.8.0
- pycodestyle 2.4.0 -> 2.5.0
- pyflakes 2.0.0 -> 2.1.1
- pylint 2.2.2 -> 2.3.1
- pyodbc 4.0.25 -> 4.0.26
- pyopenssl 18.0.0 -> 19.0.0
- pyparsing 2.3.0 -> 2.3.1
- pytables 3.4.4 -> 3.5.1
- pytest 4.0.2 -> 4.3.1
- pytest-doctestplus 0.2.0 -> 0.3.0
- pytest-openfiles 0.3.1 -> 0.3.2
- python 3.7.1 -> 3.7.3
- python-dateutil 2.7.5 -> 2.8.0
- pytz 2018.7 -> 2018.9
- pywavelets 1.0.1 -> 1.0.2
- pyyaml 3.13 -> 5.1
- pyzmq 17.1.2 -> 18.0.0
- qtawesome 0.5.3 -> 0.5.7
- qtpy 1.5.2 -> 1.7.0
- rope 0.11.0 -> 0.12.0
- scandir 1.9.0 -> 1.10.0
- scikit-image 0.14.1 -> 0.14.2
- scikit-learn 0.20.1 -> 0.20.3
- scipy 1.1.0 -> 1.2.1
- setuptools 40.6.3 -> 40.8.0
- sortedcollections 1.0.1 -> 1.1.2
- sphinx 1.8.2 -> 1.8.5
- spyder 3.3.2 -> 3.3.3
- spyder-kernels 0.3.0 -> 0.4.2
- sqlalchemy 1.2.15 -> 1.3.1
- sqlite 3.26.0 -> 3.27.2
- ssl\_match\_hostname 3.5.0.1 -> 3.7.0.1
- tornado 5.1.1 -> 6.0.2

- tqdm 4.28.1 -> 4.31.1
- typed-ast 1.1.0 -> 1.3.1
- wheel 0.32.3 -> 0.33.1
- wrapt 1.10.11 -> 1.11.1
- xlswriter 1.1.2 -> 1.1.5
- zeromq 4.2.5 -> 4.3.1
- zict 0.1.3 -> 0.1.4

**Added:**

- pyrsistent 0.14.11
- soupsieve 1.8
- zipp 0.3.3

**Removed:**

- blaze
- conda
- conda-build
- conda-env
- datashape
- flask-cors
- odo

**More changes specific to linux-64****Updated:**

- dbus 1.13.2 -> 1.13.6
- graphite2 1.3.12 -> 1.3.13
- libedit 3.1.20170329 -> 3.1.20181209
- pcre 8.42 -> 8.43
- pixman 0.34.0 -> 0.38.0
- secretstorage 3.1.0 -> 3.1.1

**More changes specific to linux-ppc64le****Updated:**

- libedit 3.1.20170329 -> 3.1.20181209
- nbconvert 5.3.1 -> 5.4.1
- pcre 8.42 -> 8.43

**Added:**

- defusedxml 0.5.0

### More changes specific to win-32

#### Updated:

- menuinst 1.4.14 -> 1.4.16
- win\_inet\_pton 1.0.1 -> 1.1.0
- xlwings 0.15.1 -> 0.15.4

#### Added:

- powershell\_shortcut 0.0.1
- pyreadline 2.1

### More changes specific to win-64

#### Updated:

- menuinst 1.4.14 -> 1.4.16
- win\_inet\_pton 1.0.1 -> 1.1.0
- xlwings 0.15.1 -> 0.15.4

#### Added:

- liblief 0.9.0
- powershell\_shortcut 0.0.1
- py-lief 0.9.0
- pyreadline 2.1

### More changes specific to osx-64

#### Updated:

- appscript 1.0.1 -> 1.1.0
- dbus 1.13.2 -> 1.13.6
- libedit 3.1.20170329 -> 3.1.20181209
- pcre 8.42 -> 8.43
- xlwings 0.15.1 -> 0.15.4

### Anaconda 2018.12 (December 21, 2018)

#### User-facing changes

- Anaconda version numbers now follow a year.month format.
- OpenSSL 1.1.1 is installed on all platforms and versions except for the Python 2.7 on win-32 and win-64.
- This is the last Anaconda release for the linux-32 platform.

## Backend improvements (non-visible changes)

- Improvements have been made to conda which will decrease the time it takes to solve and install packages.

## Changes for all x86 platforms

### Updated:

- alabaster 0.7.11 -> 0.7.12
- astroid 2.0.4 -> 2.1.0
- astropy 3.0.4 -> 3.1
- bleach 2.1.4 -> 3.0.2
- bokeh 0.13.0 -> 1.0.2
- certifi 2018.8.24 -> 2018.11.29
- click 6.7 -> 7.0
- cloudpickle 0.5.5 -> 0.6.1
- colorama 0.3.9 -> 0.4.1
- cryptography 2.3.1 -> 2.4.2
- curl 7.61.0 -> 7.63.0
- cython 0.28.5 -> 0.29.2
- dask 0.19.1 -> 1.0.0
- dask-core 0.19.1 -> 1.0.0
- distributed 1.23.1 -> 1.25.1
- filelock 3.0.8 -> 3.0.10
- flask-cors 3.0.6 -> 3.0.7
- gevent 1.3.6 -> 1.3.7
- idna 2.7 -> 2.8
- intel-openmp 2019.0 -> 2019.1
- ipython 6.5.0 -> 7.2.0
- ipywidgets 7.4.1 -> 7.4.2
- itsdangerous 0.24 -> 1.1.0
- jedi 0.12.1 -> 0.13.2
- jupyter\_client 5.2.3 -> 5.2.4
- jupyter\_console 5.2.0 -> 6.0.0
- jupyterlab 0.34.9 -> 0.35.3
- keyring 13.2.1 -> 17.0.0
- libcurl 7.61.0 -> 7.63.0
- libpng 1.6.34 -> 1.6.35

- llvmlite 0.24.0 -> 0.26.0
- markupsafe 1.0 -> 1.1.0
- matplotlib 2.2.3 -> 3.0.2
- mistune 0.8.3 -> 0.8.4
- mkl 2019.0 -> 2019.1
- mkl\_fft 1.0.4 -> 1.0.6
- mkl\_random 1.0.1 -> 1.0.2
- mpmath 1.0.0 -> 1.1.0
- networkx 2.1 -> 2.2
- nltk 3.3.0 -> 3.4
- notebook 5.6.0 -> 5.7.4
- numba 0.39.0 -> 0.41.0
- numpy 1.15.1 -> 1.15.4
- numpy-base 1.15.1 -> 1.15.4
- openpyxl 2.5.6 -> 2.5.12
- openssl 1.0.2p -> 1.1.1a0
- packaging 17.1 -> 18.0
- partd 0.3.8 -> 0.3.9
- path.py 11.1.0 -> 11.5.0
- pathlib2 2.3.2 -> 2.3.3
- patsy 0.5.0 -> 0.5.1
- pickleshare 0.7.4 -> 0.7.5
- pillow 5.2.0 -> 5.3.0
- pip 10.0.1 -> 18.1
- pluggy 0.7.1 -> 0.8.0
- prometheus\_client 0.3.1 -> 0.5.0
- prompt\_toolkit 1.0.15 -> 2.0.7
- psutil 5.4.7 -> 5.4.8
- py 1.6.0 -> 1.7.0
- pycparser 2.18 -> 2.19
- pygments 2.2.0 -> 2.3.1
- pylint 2.1.1 -> 2.2.2
- pyodbc 4.0.24 -> 4.0.25
- pyparsing 2.2.0 -> 2.3.0
- pytest 3.8.0 -> 4.0.2
- pytest-arraydiff 0.2 -> 0.3



- pytest-astropy 0.4.0 -> 0.5.0
- pytest-doctestplus 0.1.3 -> 0.2.0
- pytest-openfiles 0.3.0 -> 0.3.1
- pytest-remotedata 0.3.0 -> 0.3.1
- python 3.7.0 -> 3.7.1
- python-dateutil 2.7.3 -> 2.7.5
- pytz 2018.5 -> 2018.7
- pywavelets 1.0.0 -> 1.0.1
- qt 5.9.6 -> 5.9.7
- qtawesome 0.4.4 -> 0.5.3
- qtconsole 4.4.1 -> 4.4.3
- qtpy 1.5.0 -> 1.5.2
- requests 2.19.1 -> 2.21.0
- scikit-image 0.14.0 -> 0.14.1
- scikit-learn 0.19.2 -> 0.20.1
- setuptools 40.2.0 -> 40.6.3
- six 1.11.0 -> 1.12.0
- sortedcontainers 2.0.5 -> 2.1.0
- sphinx 1.7.9 -> 1.8.2
- spyder 3.3.1 -> 3.3.2
- spyder-kernels 0.2.6 -> 0.3.0
- sqlalchemy 1.2.11 -> 1.2.15
- sqlite 3.24.0 -> 3.26.0
- subprocess32 3.5.2 -> 3.5.3
- sympy 1.2 -> 1.3
- testpath 0.3.1 -> 0.4.2
- tornado 5.1 -> 5.1.1
- tqdm 4.26.0 -> 4.28.1
- urllib3 1.23 -> 1.24.1
- wheel 0.31.1 -> 0.32.3
- widgetsnbextension 3.4.1 -> 3.4.2
- xlrd 1.1.0 -> 1.2.0
- xlswriter 1.1.0 -> 1.1.2

**Added:**

- backports.os 0.1.1
- conda 4.5.12

- conda-build 3.17.6
- conda-env 2.6.0
- future 0.17.1
- importlib\_metadata 0.6
- jupyterlab\_server 0.2.0
- krb5 1.16.1
- libarchive 3.3.3
- lz4-c 1.8.1.2
- python-libarchive-c 2.8
- zstd 1.3.7

### Removed:

- appdirs
- automat
- constantly
- hyperlink
- incremental
- pyasn1
- pyasn1-modules
- service\_identity
- twisted
- zope
- zope.interface

### More changes specific to linux-64

#### Updated:

- ipykernel 4.9.0 -> 5.1.0
- jeepney 0.3.1 -> 0.4
- pycairo 1.17.1 -> 1.18.0

#### Added:

- liblief 0.9.0
- py-lief 0.9.0
- wurlitzer 1.0.2

### More changes specific to linux-32

**Updated:**

- ipykernel 4.9.0 -> 5.1.0
- jeepney 0.3.1 -> 0.4
- pycairo 1.17.1 -> 1.18.0

**Added:**

- liblief 0.9.0
- py-lief 0.9.0
- wurlitzer 1.0.2

### More changes specific to linux-ppc64le

**Updated:**

- conda 4.5.11 -> 4.5.12
- conda-build 3.15.1 -> 3.16.3
- ipykernel 4.9.0 -> 5.1.0
- libpng 1.6.32 -> 1.6.35
- pycairo 1.17.1 -> 1.18.0
- tqdm 4.25.0 -> 4.28.1

**Added:**

- libssh2 1.8.0

### More changes specific to win-32

**Updated:**

- backports.shutil\_which 3.5.1 -> 3.5.2
- icc\_rt 2017.0.4 -> 2019.0.0
- ipykernel 4.10.0 -> 5.1.0
- pywinpty 0.5.4 -> 0.5.5
- xlwings 0.11.8 -> 0.15.1

**Added:**

- xz 5.2.4

### More changes specific to win-64

**Updated:**

- backports.shutil\_which 3.5.1 -> 3.5.2
- icc\_rt 2017.0.4 -> 2019.0.0

- ipykernel 4.10.0 -> 5.1.0
- pywinpty 0.5.4 -> 0.5.5
- xlwings 0.11.8 -> 0.15.1

### Added:

- xz 5.2.4

## Anaconda 5.3.1 (Nov 19, 2018)

### User-facing changes

- The Anaconda Installers are shipped with a fix for VSCode Installation. xref: <https://github.com/ContinuumIO/anaconda-issues/issues/10286>

## Anaconda 5.3.0 (Sept 28, 2018)

### User-facing changes

- The Anaconda3 installers ship with python 3.7 instead of python 3.6
- Windows installers disallow the character , in installation path to prevent usability issues.
- Instructions in the macOS pkg installer for choice of initializing installation has been improved.

### Backend improvements (non-visible changes)

- Installers mimic the functionality of “conda init” (a highly anticipated feature in conda 4.6) instead of just adding \$PREFIX/bin to PATH in bash profile.
- The repodata\_record.json file for each package in the package cache directory is populated correctly, which will assist in offline installation of packages in new environments.

### Changes for all x86 platforms

### Updated:

- alabaster 0.7.10 -> 0.7.11
- anaconda-client 1.6.14 -> 1.7.2
- astroid 1.6.3 -> 2.0.4
- astropy 3.0.2 -> 3.0.4
- attrs 18.1.0 -> 18.2.0
- babel 2.5.3 -> 2.6.0
- beautifulsoup4 4.6.0 -> 4.6.3
- bitarray 0.8.1 -> 0.8.3
- bleach 2.1.3 -> 2.1.4
- blosc 1.14.3 -> 1.14.4

- bokeh 0.12.16 -> 0.13.0
- boto 2.48.0 -> 2.49.0
- certifi 2018.4.16 -> 2018.8.24
- cloudpickle 0.5.3 -> 0.5.5
- cryptography 2.2.2 -> 2.3.1
- curl 7.60.0 -> 7.61.0
- cython 0.28.2 -> 0.28.5
- dask 0.17.5 -> 0.19.1
- dask-core 0.17.5 -> 0.19.1
- distributed 1.21.8 -> 1.23.1
- filelock 3.0.4 -> 3.0.8
- flask-cors 3.0.4 -> 3.0.6
- freetype 2.8 -> 2.9.1
- gevent 1.3.0 -> 1.3.6
- greenlet 0.4.13 -> 0.4.15
- h5py 2.7.1 -> 2.8.0
- idna 2.6 -> 2.7
- imageio 2.3.0 -> 2.4.1
- imagesize 1.0.0 -> 1.1.0
- intel-openmp 2018.0.0 -> 2019.0
- ipython 6.4.0 -> 6.5.0
- ipywidgets 7.2.1 -> 7.4.1
- jedi 0.12.0 -> 0.12.1
- jupyterlab 0.32.1 -> 0.34.9
- jupyterlab\_launcher 0.10.5 -> 0.13.1
- libcurl 7.60.0 -> 7.61.0
- llvmlite 0.23.1 -> 0.24.0
- lxml 4.2.1 -> 4.2.5
- matplotlib 2.2.2 -> 2.2.3
- mkl 2018.0.2 -> 2019.0
- mkl\_fft 1.0.1 -> 1.0.4
- more-itertools 4.1.0 -> 4.3.0
- multipledispatch 0.5.0 -> 0.6.0
- nbconvert 5.3.1 -> 5.4.0
- notebook 5.5.0 -> 5.6.0
- numba 0.38.0 -> 0.39.0

- numexpr 2.6.5 -> 2.6.8
- numpy 1.14.3 -> 1.15.1
- numpy-base 1.14.3 -> 1.15.1
- olefile 0.45.1 -> 0.46
- openpyxl 2.5.3 -> 2.5.6
- openssl 1.0.2o -> 1.0.2p
- pandas 0.23.0 -> 0.23.4
- parso 0.2.0 -> 0.3.1
- path.py 11.0.1 -> 11.1.0
- pillow 5.1.0 -> 5.2.0
- pluggy 0.6.0 -> 0.7.1
- psutil 5.4.5 -> 5.4.7
- py 1.5.3 -> 1.6.0
- pycurl 7.43.0.1 -> 7.43.0.2
- pyflakes 1.6.0 -> 2.0.0
- pylint 1.8.4 -> 2.1.1
- pyodbc 4.0.23 -> 4.0.24
- pytables 3.4.3 -> 3.4.4
- pytest 3.5.1 -> 3.8.0
- pytest-astropy 0.3.0 -> 0.4.0
- pytest-remotedata 0.2.1 -> 0.3.0
- python 3.6.5 -> 3.7.0
- pytz 2018.4 -> 2018.5
- pywavelets 0.5.2 -> 1.0.0
- pyyaml 3.12 -> 3.13
- pyzmq 17.0.0 -> 17.1.2
- qt 5.9.5 -> 5.9.6
- qtconsole 4.3.1 -> 4.4.1
- qtpy 1.4.1 -> 1.5.0
- requests 2.18.4 -> 2.19.1
- rope 0.10.7 -> 0.11.0
- ruamel\_yaml 0.15.35 -> 0.15.46
- scandir 1.7 -> 1.9.0
- scikit-image 0.13.1 -> 0.14.0
- scikit-learn 0.19.1 -> 0.19.2
- seaborn 0.8.1 -> 0.9.0

- setuptools 39.1.0 -> 40.2.0
- sortedcollections 0.6.1 -> 1.0.1
- sortedcontainers 1.5.10 -> 2.0.5
- sphinx 1.7.4 -> 1.7.9
- sphinxcontrib-websupport 1.0.1 -> 1.1.0
- spyder 3.2.8 -> 3.3.1
- sqlalchemy 1.2.7 -> 1.2.11
- sqlite 3.23.1 -> 3.24.0
- subprocess32 3.5.0 -> 3.5.2
- sympy 1.1.1 -> 1.2
- tk 8.6.7 -> 8.6.8
- tornado 5.0.2 -> 5.1
- typing 3.6.4 -> 3.6.6
- urllib3 1.22 -> 1.23
- widetsnbextension 3.2.1 -> 3.4.1
- xlsxwriter 1.0.4 -> 1.1.0

**Added:**

- appdirs 1.4.3
- atomicwrites 1.2.1
- automat 0.7.0
- constantly 15.1.0
- defusedxml 0.5.0
- hyperlink 18.0.0
- incremental 17.5.0
- keyring 13.2.1
- linecache2 1.0.0
- prometheus\_client 0.3.1
- pyasn1 0.4.4
- pyasn1-modules 0.2.2
- service\_identity 17.0.0
- spyder-kernels 0.2.6
- tqdm 4.26.0
- traceback2 1.4.0
- twisted 18.7.0
- typed-ast 1.1.0
- unittest2 1.1.0

- zope 1.0
- zope.interface 4.5.0

### More changes specific to linux-64

#### Updated:

- expat 2.2.5 -> 2.2.6
- fontconfig 2.12.6 -> 2.13.0
- glib 2.56.1 -> 2.56.2
- graphite2 1.3.11 -> 1.3.12
- harfbuzz 1.7.6 -> 1.8.8
- ipykernel 4.8.2 -> 4.9.0
- libgcc-ng 7.2.0 -> 8.2.0
- libgfortran-ng 7.2.0 -> 7.3.0
- libstdcxx-ng 7.2.0 -> 8.2.0
- mpc 1.0.3 -> 1.1.0
- mpfr 3.1.5 -> 4.0.1
- pango 1.41.0 -> 1.42.4
- pexpect 4.5.0 -> 4.6.0
- ptyprocess 0.5.2 -> 0.6.0
- pycairo 1.15.4 -> 1.17.1
- unixodbc 2.3.6 -> 2.3.7

#### Added:

- fribidi 1.0.5
- jeepney 0.3.1
- libuuid 1.0.3
- secretstorage 3.1.0

### More changes specific to linux-32

#### Updated:

- expat 2.2.5 -> 2.2.6
- fontconfig 2.12.6 -> 2.13.0
- glib 2.56.1 -> 2.56.2
- graphite2 1.3.11 -> 1.3.12
- harfbuzz 1.7.6 -> 1.8.8
- ipykernel 4.8.2 -> 4.9.0



- libgcc-ng 7.2.0 -> 8.2.0
- libgfortran-ng 7.2.0 -> 7.3.0
- libstdcxx-ng 7.2.0 -> 8.2.0
- mpc 1.0.3 -> 1.1.0
- mpfr 3.1.5 -> 4.0.1
- pango 1.41.0 -> 1.42.4
- pexpect 4.5.0 -> 4.6.0
- ptyprocess 0.5.2 -> 0.6.0
- pycairo 1.15.4 -> 1.17.1
- sip 4.19.8 -> 4.19.12
- unixodbc 2.3.6 -> 2.3.7

**Added:**

- fribidi 1.0.5
- jeepney 0.3.1
- libuuid 1.0.3
- secretstorage 3.1.0

**More changes specific to linux-ppc64le****Updated:**

- asn1crypto 0.23.0 -> 0.24.0
- astroid 1.6.2 -> 2.0.4
- babel 2.5.0 -> 2.6.0
- backports.functools\_lru\_cache 1.4 -> 1.5
- bokeh 0.12.15 -> 0.13.0
- conda 4.5.4 -> 4.5.11
- conda-build 3.10.5 -> 3.15.1
- curl 7.55.1 -> 7.61.0
- cython 0.28.1 -> 0.28.5
- decorator 4.1.2 -> 4.3.0
- expat 2.2.5 -> 2.2.6
- filelock 2.0.13 -> 3.0.8
- flask 0.12.2 -> 1.0.2
- fontconfig 2.12.6 -> 2.13.0
- glib 2.56.1 -> 2.56.2
- greenlet 0.4.12 -> 0.4.15
- imageio 2.2.0 -> 2.4.1

- image size 0.7.1 -> 1.1.0
- ipykernel 4.8.0 -> 4.9.0
- ipywidgets 7.2.0 -> 7.4.1
- isort 4.2.15 -> 4.3.4
- jedi 0.11.0 -> 0.12.1
- libgcc-ng 7.2.0 -> 8.2.0
- libgfortran-ng 7.2.0 -> 7.3.0
- libstdc++-ng 7.2.0 -> 8.2.0
- numexpr 2.6.5 -> 2.6.7
- numpy 1.13.3 -> 1.14.5
- parso 0.1.1 -> 0.3.1
- patsy 0.4.1 -> 0.5.0
- pep8 1.7.0 -> 1.7.1
- pexpect 4.3.0 -> 4.6.0
- pillow 5.0.0 -> 5.2.0
- pkginfo 1.4.1 -> 1.4.2
- ply 3.10 -> 3.11
- psutil 5.4.1 -> 5.4.7
- ptyprocess 0.5.2 -> 0.6.0
- pycairo 1.13.3 -> 1.17.1
- pycurl 7.43.0 -> 7.43.0.2
- pysocks 1.6.7 -> 1.6.8
- pytz 2017.3 -> 2018.5
- scandir 1.6 -> 1.9.0
- send2trash 1.4.2 -> 1.5.0
- toolz 0.8.2 -> 0.9.0
- typing 3.6.2 -> 3.6.6
- unixodbc 2.3.6 -> 2.3.7
- werkzeug 0.12.2 -> 0.14.1
- zeromq 4.2.3 -> 4.2.5

**Added:**

- blas 1.0
- gmpy2 2.0.8
- libcurl 7.61.0
- libuuid 1.0.3
- mpc 1.1.0

- mpfr 4.0.1
- numpy-base 1.14.5
- tqdm 4.25.0
- twisted 18.4.0

**Removed:**

- conda-verify
- libssh2

**More changes specific to win-32****Updated:**

- comtypes 1.1.4 -> 1.1.7
- ipykernel 4.8.2 -> 4.10.0
- pywinpty 0.5.1 -> 0.5.4
- vc 14 -> 14.1
- vs2015\_runtime 14.0.25123 -> 14.15.26706

**More changes specific to win-64****Updated:**

- comtypes 1.1.4 -> 1.1.7
- ipykernel 4.8.2 -> 4.10.0
- pywinpty 0.5.1 -> 0.5.4
- vc 14 -> 14.1
- vs2015\_runtime 14.0.25123 -> 14.15.26706

**Anaconda 5.2.0 (May 30, 2018)****User-facing changes**

- Windows installers disallow the characters ! % ^ = in installation path to prevent later usability issues
- Improved Windows multi-user installations by providing more dynamic shortcut working directory behavior
- Default channels point to repo.anaconda.com instead of anaconda.com

**Backend improvements (non-visible changes)**

- Security fixes for more than 20 packages based on a deep-dive of CVE vulnerabilities
- Windows installer uses a trimmed down value for PATH env var, to avoid DLL hell with existing software
- History file in the conda-meta directory is populated correctly to improve behavior of `--prune`

- Developer certificate for macOS pkg installers has been updated to Anaconda, Inc.

### Changes for all x86 platforms

#### Updated:

- anaconda-client 1.6.9 -> 1.6.14
- astroid 1.6.1 -> 1.6.3
- astropy 2.0.3 -> 3.0.2
- attrs 17.4.0 -> 18.1.0
- backports.functools\_lru\_cache 1.4 -> 1.5
- bleach 2.1.2 -> 2.1.3
- bokeh 0.12.13 -> 0.12.16
- ca-certificates 2017.8.26 -> 2018.3.7
- certifi 2018.1.18 -> 2018.4.16
- cffi 1.11.4 -> 1.11.5
- cloudpickle 0.5.2 -> 0.5.3
- cryptography 2.1.4 -> 2.2.2
- curl 7.58.0 -> 7.60.0
- cython 0.27.3 -> 0.28.2
- cytoolz 0.9.0 -> 0.9.0.1
- dask 0.16.1 -> 0.17.5
- dask-core 0.16.1 -> 0.17.5
- decorator 4.2.1 -> 4.3.0
- distributed 1.20.2 -> 1.21.8
- filelock 2.0.13 -> 3.0.4
- flask 0.12.2 -> 1.0.2
- flask-cors 3.0.3 -> 3.0.4
- gevent 1.2.2 -> 1.3.0
- greenlet 0.4.12 -> 0.4.13
- hdf5 1.10.1 -> 1.10.2
- imageio 2.2.0 -> 2.3.0
- imagesize 0.7.1 -> 1.0.0
- ipaddress 1.0.19 -> 1.0.22
- ipykernel 4.8.0 -> 4.8.2
- ipython 6.2.1 -> 6.4.0
- ipywidgets 7.1.1 -> 7.2.1
- isort 4.2.15 -> 4.3.4

- jdcal 1.3 -> 1.4
- jedi 0.11.1 -> 0.12.0
- jupyter\_client 5.2.2 -> 5.2.3
- jupyterlab 0.31.5 -> 0.32.1
- jupyterlab\_launcher 0.10.2 -> 0.10.5
- libcurl 7.58.0 -> 7.60.0
- libxml2 2.9.7 -> 2.9.8
- llvmlite 0.21.0 -> 0.23.1
- lxml 4.1.1 -> 4.2.1
- matplotlib 2.1.2 -> 2.2.2
- mkl 2018.0.1 -> 2018.0.2
- msgpack-python 0.5.1 -> 0.5.6
- multipledispatch 0.4.9 -> 0.5.0
- nltk 3.2.5 -> 3.3.0
- notebook 5.4.0 -> 5.5.0
- numba 0.36.2 -> 0.38.0
- numexpr 2.6.4 -> 2.6.5
- numpy 1.14.0 -> 1.14.3
- numpydoc 0.7.0 -> 0.8.0
- openpyxl 2.4.10 -> 2.5.3
- openssl 1.0.2n -> 1.0.2o
- packaging 16.8 -> 17.1
- pandas 0.22.0 -> 0.23.0
- parso 0.1.1 -> 0.2.0
- path.py 10.5 -> 11.0.1
- pathlib2 2.3.0 -> 2.3.2
- pillow 5.0.0 -> 5.1.0
- pip 9.0.1 -> 10.0.1
- pkginfo 1.4.1 -> 1.4.2
- ply 3.10 -> 3.11
- psutil 5.4.3 -> 5.4.5
- py 1.5.2 -> 1.5.3
- pycodestyle 2.3.1 -> 2.4.0
- pylint 1.8.2 -> 1.8.4
- pyodbc 4.0.22 -> 4.0.23
- pyopenssl 17.5.0 -> 18.0.0

- pyqt 5.6.0 -> 5.9.2
- pysocks 1.6.7 -> 1.6.8
- pytables 3.4.2 -> 3.4.3
- pytest 3.3.2 -> 3.5.1
- python 3.6.4 -> 3.6.5
- python-dateutil 2.6.1 -> 2.7.3
- pytz 2017.3 -> 2018.4
- pyzmq 16.0.3 -> 17.0.0
- qt 5.6.2 -> 5.9.5
- qtpy 1.3.1 -> 1.4.1
- scandir 1.6 -> 1.7
- scipy 1.0.0 -> 1.1.0
- send2trash 1.4.2 -> 1.5.0
- setuptools 38.4.0 -> 39.1.0
- sip 4.18.1 -> 4.19.8
- sortedcollections 0.5.3 -> 0.6.1
- sortedcontainers 1.5.9 -> 1.5.10
- sphinx 1.6.6 -> 1.7.4
- spyder 3.2.6 -> 3.2.8
- sqlalchemy 1.2.1 -> 1.2.7
- sqlite 3.22.0 -> 3.23.1
- statsmodels 0.8.0 -> 0.9.0
- subprocess32 3.2.7 -> 3.5.0
- tornado 4.5.3 -> 5.0.2
- typing 3.6.2 -> 3.6.4
- wheel 0.30.0 -> 0.31.1
- widgetsnbextension 3.1.0 -> 3.2.1
- xlswriter 1.0.2 -> 1.0.4

**Added:**

- backcall 0.1.0
- blas 1.0
- blosc 1.14.3
- kiwisolver 1.0.1
- mkl\_fft 1.0.1
- mkl\_random 1.0.1
- more-itertools 4.1.0

- numpy-base 1.14.3
- pytest-arraydiff 0.2
- pytest-astropy 0.3.0
- pytest-doctestplus 0.1.3
- pytest-openfiles 0.3.0
- pytest-remotedata 0.2.1
- snappy 1.1.7

### More changes specific to linux-64

#### Updated:

- dbus 1.12.2 -> 1.13.2
- fontconfig 2.12.4 -> 2.12.6
- glib 2.53.6 -> 2.56.1
- graphite2 1.3.10 -> 1.3.11
- gst-plugins-base 1.12.4 -> 1.14.0
- gstreamer 1.12.4 -> 1.14.0
- harfbuzz 1.7.4 -> 1.7.6
- libedit 3.1 -> 3.1.20170329
- libsodium 1.0.15 -> 1.0.16
- libxcb 1.12 -> 1.13
- ncurses 6.0 -> 6.1
- pcre 8.41 -> 8.42
- pexpect 4.3.1 -> 4.5.0
- unixodbc 2.3.4 -> 2.3.6
- xz 5.2.3 -> 5.2.4
- zeromq 4.2.2 -> 4.2.5

### More changes specific to linux-32

#### Updated:

- dbus 1.12.2 -> 1.13.2
- fontconfig 2.12.4 -> 2.12.6
- glib 2.53.6 -> 2.56.1
- graphite2 1.3.10 -> 1.3.11
- gst-plugins-base 1.12.4 -> 1.14.0
- gstreamer 1.12.4 -> 1.14.0

- harfbuzz 1.7.4 -> 1.7.6
- libedit 3.1 -> 3.1.20170329
- libsodium 1.0.15 -> 1.0.16
- libxcb 1.12 -> 1.13
- ncurses 6.0 -> 6.1
- pcre 8.41 -> 8.42
- pexpect 4.3.1 -> 4.5.0
- unixodbc 2.3.4 -> 2.3.6
- xz 5.2.3 -> 5.2.4
- zeromq 4.2.2 -> 4.2.5

### **More changes specific to linux-ppc64le**

#### **Updated:**

- anaconda-client 1.6.6 -> 1.6.14
- astroid 1.6.1 -> 1.6.2
- bokeh 0.12.13 -> 0.12.15
- cairo 1.14.10 -> 1.14.12
- cffi 1.11.2 -> 1.11.5
- conda 4.4.9 -> 4.5.4
- conda-build 3.4.1 -> 3.10.5
- cython 0.27.3 -> 0.28.1
- cytoolz 0.8.2 -> 0.9.0.1
- dask 0.16.0 -> 0.17.5
- dask-core 0.16.0 -> 0.17.5
- fontconfig 2.12.4 -> 2.12.6
- glib 2.53.6 -> 2.56.1
- ipaddress 1.0.18 -> 1.0.22
- ipywidgets 7.1.1 -> 7.2.0
- libsodium 1.0.15 -> 1.0.16
- libxcb 1.12 -> 1.13
- libxml2 2.9.4 -> 2.9.8
- libxslt 1.1.29 -> 1.1.32
- mistune 0.8.1 -> 0.8.3
- msgpack-python 0.4.8 -> 0.5.6
- ncurses 6.0 -> 6.1
- pcre 8.41 -> 8.42



- pytest 3.2.5 -> 3.5.1
- setuptools 36.5.0 -> 39.1.0
- sortedcontainers 1.5.7 -> 1.5.10
- sphinx 1.6.3 -> 1.7.4
- sqlite 3.21.0 -> 3.23.1
- tornado 4.5.2 -> 5.0.2
- unixodbc 2.3.4 -> 2.3.6
- xz 5.2.3 -> 5.2.4
- zeromq 4.2.2 -> 4.2.3

**Added:**

- attrs 18.1.0
- pluggy 0.6.0

**Removed:**

- gmpy2
- mpc
- mpfr

**More changes specific to win-32****Updated:**

- menuinst 1.4.11 -> 1.4.14
- pywin32 222 -> 223
- pywinpty 0.5 -> 0.5.1
- xlwings 0.11.5 -> 0.11.8

**Added:**

- libsodium 1.0.16
- m2w64-gcc-libgfortran 5.3.0
- m2w64-gcc-libs 5.3.0
- m2w64-gcc-libs-core 5.3.0
- m2w64-gmp 6.1.0
- m2w64-libwinpthread-git 5.0.0.4634.697f757
- msys2-conda-epoch 20160418
- zeromq 4.2.5

### More changes specific to win-64

#### Updated:

- menuinst 1.4.11 -> 1.4.14
- pywin32 222 -> 223
- pywinpty 0.5 -> 0.5.1
- xlwings 0.11.5 -> 0.11.8

#### Added:

- libsodium 1.0.16
- m2w64-gcc-libgfortran 5.3.0
- m2w64-gcc-libs 5.3.0
- m2w64-gcc-libs-core 5.3.0
- m2w64-gmp 6.1.0
- m2w64-libwinpthread-git 5.0.0.4634.697f757
- msys2-conda-epoch 20160418
- zeromq 4.2.5

### Anaconda 5.1.0 (Feb 15, 2018)

#### User-facing changes

- Microsoft Visual Studio Code added as an install option
- Anaconda Navigator has install and launch options for VS Code
- The installer support link has been replaced with the [Getting Started](#) page

#### Backend improvements (non-visible changes)

- Power packages are built with [same recipes](#) as rest of distribution
- Fixed some incomplete Windows installations due to interactions with antivirus software
- Fixed spaces in paths problems on Windows
- Anaconda Navigator was removed from the anaconda metapackage (but not the Anaconda installer)
- Installers present warnings when executed on the wrong platform

#### Changes for all x86 platforms

#### Updated:

- anaconda-client 1.6.5 -> 1.6.9
- anaconda-project 0.8.0 -> 0.8.2
- anaconda-navigator 1.6.9 -> 1.7.0

- asn1crypto 0.22.0 -> 0.24.0
- astroid 1.5.3 -> 1.6.1
- astropy 2.0.2 -> 2.0.3
- babel 2.5.0 -> 2.5.3
- bleach 2.0.0 -> 2.1.2
- bokeh 0.12.10 -> 0.12.13
- certifi 2017.7.27.1 -> 2018.1.18
- cffi 1.10.0 -> 1.11.4
- cloudpickle 0.4.0 -> 0.5.2
- conda 4.3.27 -> 4.4.10
- conda-build 3.0.27 -> 3.4.1
- cryptography 2.0.3 -> 2.1.4
- curl 7.55.1 -> 7.58.0
- cython 0.26.1 -> 0.27.3
- cytoolz 0.8.2 -> 0.9.0
- dask 0.15.3 -> 0.16.1
- dask-core 0.15.3 -> 0.16.1
- decorator 4.1.2 -> 4.2.1
- distributed 1.19.1 -> 1.20.2
- filelock 2.0.12 -> 2.0.13
- futures 3.1.1 -> 3.2.0
- glob2 0.5 -> 0.6
- h5py 2.7.0 -> 2.7.1
- html5lib 0.999999999 -> 1.0.1
- ipaddress 1.0.18 -> 1.0.19
- ipykernel 4.6.1 -> 4.8.0
- ipython 6.1.0 -> 6.2.1
- ipywidgets 7.0.0 -> 7.1.1
- jedi 0.10.2 -> 0.11.1
- jinja2 2.9.6 -> 2.10
- jupyter\_client 5.1.0 -> 5.2.2
- jupyter\_core 4.3.0 -> 4.4.0
- jupyterlab\_launcher 0.4.0 -> 0.10.2
- libpng 1.6.32 -> 1.6.34
- libtiff 4.0.8 -> 4.0.9
- libxml2 2.9.4 -> 2.9.7

- libxslt 1.1.29 -> 1.1.32
- llvmlite 0.20.0 -> 0.21.0
- lxml 4.1.0 -> 4.1.1
- matplotlib 2.1.0 -> 2.1.2
- mistune 0.7.4 -> 0.8.3
- mkl 2018.0.0 -> 2018.0.1
- mpmath 0.19 -> 1.0.0
- msgpack-python 0.4.8 -> 0.5.1
- networkx 2.0 -> 2.1
- nltk 3.2.4 -> 3.2.5
- notebook 5.0.0 -> 5.4.0
- numba 0.35.0 -> 0.36.2
- numexpr 2.6.2 -> 2.6.4
- numpy 1.13.3 -> 1.14.0
- olefile 0.44 -> 0.45.1
- openpyxl 2.4.8 -> 2.4.10
- openssl 1.0.2l -> 1.0.2n
- pandas 0.20.3 -> 0.22.0
- path.py 10.3.1 -> 10.5
- patsy 0.4.1 -> 0.5.0
- pep8 1.7.0 -> 1.7.1
- pillow 4.2.1 -> 5.0.0
- psutil 5.4.0 -> 5.4.3
- py 1.4.34 -> 1.5.2
- pycosat 0.6.2 -> 0.6.3
- pycurl 7.43.0 -> 7.43.0.1
- pylint 1.7.4 -> 1.8.2
- pyodbc 4.0.17 -> 4.0.22
- pyopenssl 17.2.0 -> 17.5.0
- pytest 3.2.1 -> 3.3.2
- python 3.6.3 -> 3.6.4
- pytz 2017.2 -> 2017.3
- pyzmq 16.0.2 -> 16.0.3
- rope 0.10.5 -> 0.10.7
- ruamel\_yaml 0.11.14 -> 0.15.35
- scikit-image 0.13.0 -> 0.13.1

- scipy 0.19.1 -> 1.0.0
- seaborn 0.8.0 -> 0.8.1
- setuptools 36.5.0 -> 38.4.0
- sortedcontainers 1.5.7 -> 1.5.9
- sphinx 1.6.3 -> 1.6.6
- spyder 3.2.4 -> 3.2.6
- sqlalchemy 1.1.13 -> 1.2.1
- sqlite 3.20.1 -> 3.22.0
- toolz 0.8.2 -> 0.9.0
- tornado 4.5.2 -> 4.5.3
- werkzeug 0.12.2 -> 0.14.1
- wheel 0.29.0 -> 0.30.0
- widgetsnbextension 3.0.2 -> 3.1.0

**Added:**

- attrs 17.4.0
- libcurl 7.58.0
- parso 0.1.1
- pluggy 0.6.0
- send2trash 1.4.2

**More changes specific to win-64****Updated:**

- comtypes 1.1.2 -> 1.1.4
- jupyterlab 0.27.0 -> 0.31.4
- menuinst 1.4.10 -> 1.4.11
- pywin32 221 -> 222
- xlwings 0.11.4 -> 0.11.5

**Added:**

- backports.shutil\_which 3.5.1
- pywinpty 0.5
- terminado 0.8.1
- winpty 0.4.3

**Removed:**

- cachecontrol
- distlib
- lockfile

- progress

### More changes specific to win-32

#### Updated:

- comtypes 1.1.2 -> 1.1.4
- jupyterlab 0.27.0 -> 0.31.5
- menuinst 1.4.10 -> 1.4.11
- pywin32 221 -> 222
- xlwings 0.11.4 -> 0.11.5

#### Added:

- backports.shutil\_which 3.5.1
- pywinpty 0.5
- terminado 0.8.1
- winpty 0.4.3

#### Removed:

- cachecontrol
- distlib
- lockfile
- progress

### More changes specific to osx-64

#### Updated:

- dbus 1.10.22 -> 1.12.2
- expat 2.2.4 -> 2.2.5
- jupyterlab 0.27.0 -> 0.31.5
- libsodium 1.0.13 -> 1.0.15
- pexpect 4.2.1 -> 4.3.1
- terminado 0.6 -> 0.8.1
- xlwings 0.11.4 -> 0.11.5

### More changes specific to linux-64

#### Updated:

- cairo 1.14.10 -> 1.14.12
- dbus 1.10.22 -> 1.12.2
- expat 2.2.4 -> 2.2.5

- gst-plugins-base 1.12.2 -> 1.12.4
- gstreamer 1.12.2 -> 1.12.4
- harfbuzz 1.5.0 -> 1.7.4
- jupyterlab 0.27.0 -> 0.31.5
- libsodium 1.0.13 -> 1.0.15
- pango 1.40.11 -> 1.41.0
- pexpect 4.2.1 -> 4.3.1
- pycairo 1.13.3 -> 1.15.4
- terminado 0.6 -> 0.8.1

### More changes specific to linux-32

#### Updated:

- cairo 1.14.10 -> 1.14.12
- dbus 1.10.22 -> 1.12.2
- expat 2.2.4 -> 2.2.5
- gst-plugins-base 1.12.2 -> 1.12.4
- gstreamer 1.12.2 -> 1.12.4
- harfbuzz 1.5.0 -> 1.7.4
- jupyterlab 0.27.0 -> 0.31.5
- libsodium 1.0.13 -> 1.0.15
- pango 1.40.11 -> 1.41.0
- pexpect 4.2.1 -> 4.3.1
- pycairo 1.13.3 -> 1.15.4
- terminado 0.6 -> 0.8.1

### Changes for linux-ppc64le

#### Updated:

- anaconda-client 1.6.3 -> 1.6.6
- anaconda-project 0.6.0 -> 0.8.2
- asn1crypto 0.22.0 -> 0.23.0
- astroid 1.5.3 -> 1.6.1
- astropy 2.0.1 -> 2.0.3
- bleach 1.5.0 -> 2.1.2
- bokeh 0.12.7 -> 0.12.13
- cairo 1.14.8 -> 1.14.10

- certifi 2016.2.28 -> 2018.1.18
- cffi 1.10.0 -> 1.11.2
- cloudpickle 0.4.0 -> 0.5.2
- cryptography 1.8.1 -> 2.1.4
- curl 7.52.1 -> 7.55.1
- cython 0.26 -> 0.27.3
- dask 0.15.2 -> 0.16.0
- distributed 1.18.1 -> 1.20.2
- expat 2.1.0 -> 2.2.5
- filelock 2.0.7 -> 2.0.13
- fontconfig 2.12.1 -> 2.12.4
- freetype 2.5.5 -> 2.8
- futures 3.1.1 -> 3.2.0
- glob2 0.5 -> 0.6
- h5py 2.7.0 -> 2.7.1
- hdf5 1.8.17 -> 1.10.1
- html5lib 0.9999999 -> 1.0.1
- ipykernel 4.6.1 -> 4.8.0
- ipython 5.3.0 -> 5.4.1
- ipython 6.1.0 -> 6.2.1
- ipywidgets 6.0.0 -> 7.1.1
- jedi 0.10.2 -> 0.11.0
- jinja2 2.9.6 -> 2.10
- jupyter\_client 5.1.0 -> 5.2.2
- jupyter\_core 4.3.0 -> 4.4.0
- libpng 1.6.30 -> 1.6.32
- libsodium 1.0.10 -> 1.0.15
- libtiff 4.0.6 -> 4.0.9
- lxml 3.7.3 -> 4.1.1
- matplotlib 2.0.2 -> 2.1.2
- mistune 0.7.4 -> 0.8.1
- mpmath 0.19 -> 1.0.0
- nbconvert 5.2.1 -> 5.3.1
- networkx 1.11 -> 2.1
- nltk 3.2.4 -> 3.2.5
- notebook 5.0.0 -> 5.4.0



- numexpr 2.6.2 -> 2.6.4
- numpy 1.13.1 -> 1.13.3
- olefile 0.44 -> 0.45.1
- openblas 0.2.19 -> 0.2.20
- openpyxl 2.4.8 -> 2.4.10
- openssl 1.0.2l -> 1.0.2n
- pandas 0.20.3 -> 0.22.0
- path.py 10.3.1 -> 10.5
- pcre 8.39 -> 8.41
- pexpect 4.2.1 -> 4.3.0
- pillow 4.2.1 -> 5.0.0
- psutil 5.2.2 -> 5.4.1
- py 1.4.34 -> 1.5.2
- pycairo 1.10.0 -> 1.13.3
- pycosat 0.6.2 -> 0.6.3
- pylint 1.7.2 -> 1.8.2
- pyodbc 4.0.16 -> 4.0.22
- pyopenssl 17.0.0 -> 17.5.0
- pytest 3.2.1 -> 3.2.5
- python 2.7.13 -> 2.7.14
- python 3.6.2 -> 3.6.4
- pytz 2017.2 -> 2017.3
- pyzmq 16.0.2 -> 16.0.3
- requests 2.14.2 -> 2.18.4
- ruamel\_yaml 0.11.14 -> 0.15.35
- scandir 1.5 -> 1.6
- scikit-image 0.13.0 -> 0.13.1
- scikit-learn 0.19.0 -> 0.19.1
- scipy 0.19.1 -> 1.0.0
- seaborn 0.8 -> 0.8.1
- setuptools 36.4.0 -> 36.5.0
- six 1.10.0 -> 1.11.0
- sqlalchemy 1.1.13 -> 1.2.1
- sqlite 3.13.0 -> 3.21.0
- terminado 0.6 -> 0.8.1
- tk 8.5.18 -> 8.6.7

- wheel 0.29.0 -> 0.30.0
- widgetsnbextension 3.0.2 -> 3.1.0
- xlswriter 0.9.8 -> 1.0.2
- yaml 0.1.6 -> 0.1.7
- zeromq 4.1.5 -> 4.2.2
- zict 0.1.2 -> 0.1.3

### Added:

- backports.functools\_lru\_cache 1.4
- backports.shutil\_get\_terminal\_size 1.0.0
- bzip2 1.0.6
- ca-certificates 2017.08.26
- conda 4.4.9
- conda-build 3.4.1
- conda-env 2.6.0
- conda-verify 3.0.0
- dask-core 0.16.0
- glib 2.53.6
- gmp 6.1.2
- gmpy2 2.0.8
- icu 58.2
- imageio 2.2.0
- libedit 3.1.20170329
- libgcc-ng 7.2.0
- libgfortran-ng 7.2.0
- libopenblas 0.2.20
- libssh2 1.8.0
- libstdcxx-ng 7.2.0
- libxcb 1.12
- lzo 2.10
- mccabe 0.6.1
- mpc 1.0.3
- mpfr 3.1.5
- ncurses 6.0
- openblas-devel 0.2.20
- pandoc 2.0.0.1
- parso 0.1.1

- pysocks 1.6.7
- readline 7.0
- send2trash 1.4.2
- typing 3.6.2
- urllib3 1.22
- webencodings 0.5.1

**Removed:**

- functools\_lru\_cache
- libgfortran
- libiconv

**Anaconda 5.0.1 (Oct 25, 2017)**

The changes detailed here are based on an upgrade from Anaconda 5.0.0.

- R has been updated to version 3.4.2. All R packages (including RStudio) have been rebuilt to be compatible with the new Anaconda 5.0 compilers.
- Updated many packages, including Python, Numpy, Spyder, Navigator, and Bokeh.
- The MKL library load path has been modified to address issue for Julia users.
- Fixed an OpenSSL issue with WSL on Windows.
- Fixed Anaconda Installer Configuration (AIC) feature for Unix installers.
- Re-enabled spaces in installation paths on Windows (temporarily disabled in 5.0.0).

**Changes for all x86 platforms****Updated:**

- anaconda-navigator 1.6.8 -> 1.6.9
- bokeh 0.12.7 -> 0.12.10
- conda 4.3.27 -> 4.3.30
- conda-build 3.0.22 -> 3.0.27
- dask 0.15.2 -> 0.15.3
- dask-core 0.15.2 -> 0.15.3
- distributed 1.18.3 -> 1.19.1
- lxml 3.8.0 -> 4.1.0
- matplotlib 2.0.2 -> 2.1.0
- networkx 1.11 -> 2.0
- numpy 1.13.1 -> 1.13.3
- psutil 5.2.2 -> 5.4.0
- pyflakes 1.5.0 -> 1.6.0

- pylint 1.7.2 -> 1.7.4
- python 2.7.13 -> 2.7.14
- python 3.6.2 -> 3.6.3
- scandir 1.5 -> 1.6
- scikit-learn 0.19.0 -> 0.19.1
- six 1.10.0 -> 1.11.0
- spyder 3.2.3 -> 3.2.4
- xlswriter 0.9.8 -> 1.0.2
- zict 0.1.2 -> 0.1.3

### More changes specific to win-64

#### Updated:

- menuinst 1.4.8 -> 1.4.10

#### Added:

- lzo 2.10

### More changes specific to win-32

#### Updated:

- menuinst 1.4.8 -> 1.4.10

#### Added:

- lzo 2.10

### More changes specific to macOS-64

#### Added:

- bzip2 1.0.6
- lzo 2.10

### More changes specific to linux-64

#### Added:

- bzip2 1.0.6

### More changes specific to linux-32

#### Added:

- bzip2 1.0.6

### Anaconda 5.0.0.1 (Oct 2, 2017)

- Fixes Python & C compiler fallback path for all cases on x86/x86\_64 Linux. Without this fix, people were required to use our new compilers, which is not something we want to enforce at this time. This was affecting travis-ci builds and pip installs of packages that require compilation for extensions.

### What's new in Anaconda 5.0?

Anaconda 5.0 was released on Sept 26, 2017.

- Over 100 packages updated and added. MKL is updated to 2018.0.0. JupyterLab alpha preview 0.27.0 is included.
- All new compilers on macOS and Linux, giving substantial security and performance improvements.
- Where possible, all build recipes use conda-forge as a base, using <https://github.com/AnacondaRecipes>.
- A new channel, `pkgs/main`, has been added to `defaults`. The new channel is given top priority within `defaults` and holds packages built with the new compiler stack.
- Continuum Analytics has been renamed to Anaconda, Inc. See [this blog post](#) for more.
- Spaces are no longer allowed in the installation path on Windows.
- Transitioned to more flexible dependency pinning of numpy packages, giving wider ranges of compatibility.

### Changes for all x86 platforms

#### Updated:

- anaconda-client 1.6.3 -> 1.6.5
- anaconda-navigator 1.6.2 -> 1.6.8
- anaconda-project 0.6.0 -> 0.8.0
- astroid 1.4.9 -> 1.5.3
- astropy 1.3.2 -> 2.0.2
- babel 2.4.0 -> 2.5.0
- blaze 0.10.1 -> 0.11.3
- bleach 1.5.0 -> 2.0.0
- bokeh 0.12.5 -> 0.12.7
- boto 2.46.1 -> 2.48.0
- chardet 3.0.3 -> 3.0.4
- cloudpickle 0.2.2 -> 0.4.0
- conda 4.3.21 -> 4.3.27
- cryptography 1.8.1 -> 2.0.3
- curl 7.52.1 -> 7.55.1
- cython 0.25.2 -> 0.26.1
- dask 0.14.3 -> 0.15.2

- decorator 4.0.11 -> 4.1.2
- distributed 1.16.3 -> 1.18.3
- docutils 0.13.1 -> 0.14
- entrypoints 0.2.2 -> 0.2.3
- flask-cors 3.0.2 -> 3.0.3
- freetype 2.5.5 -> 2.8
- gevent 1.2.1 -> 1.2.2
- html5lib 0.999 -> 0.999999999
- idna 2.5 -> 2.6
- ipywidgets 6.0.0 -> 7.0.0
- isort 4.2.5 -> 4.2.15
- jupyter\_client 5.0.1 -> 5.1.0
- jupyter\_console 5.1.0 -> 5.2.0
- lazy-object-proxy 1.2.2 -> 1.3.1
- libpng 1.6.27 -> 1.6.32
- libtiff 4.0.6 -> 4.0.8
- llvmlite 0.18.0 -> 0.20.0
- lxml 3.7.3 -> 3.8.0
- markupsafe 0.23 -> 1.0
- mkl 2017.0.1 -> 2018.0.0
- nbconvert 5.1.1 -> 5.3.1
- nbformat 4.3.0 -> 4.4.0
- nltk 3.2.3 -> 3.2.4
- numba 0.33.0 -> 0.35.0
- numpy 1.12.1 -> 1.13.1
- numpydoc 0.6.0 -> 0.7.0
- odo 0.5.0 -> 0.5.1
- openpyxl 2.4.7 -> 2.4.8
- pandas 0.20.1 -> 0.20.3
- pandocfilters 1.4.1 -> 1.4.2
- pathlib2 2.2.1 -> 2.3.0
- pillow 4.1.1 -> 4.2.1
- prompt\_toolkit 1.0.14 -> 1.0.15
- py 1.4.33 -> 1.4.34
- pycparser 2.17 -> 2.18
- pylint 1.6.4 -> 1.7.2

- pyodbc 4.0.16 -> 4.0.17
- pyopenssl 17.0.0 -> 17.2.0
- pyparsing 2.1.4 -> 2.2.0
- pytest 3.0.7 -> 3.2.1
- python-dateutil 2.6.0 -> 2.6.1
- qtconsole 4.3.0 -> 4.3.1
- qtpy 1.2.1 -> 1.3.1
- requests 2.14.2 -> 2.18.4
- rope 0.9.4 -> 0.10.5
- scikit-learn 0.18.1 -> 0.19.0
- scipy 0.19.0 -> 0.19.1
- seaborn 0.7.1 -> 0.8.0
- setuptools 27.2.0 -> 36.5.0
- sip 4.18 -> 4.18.1
- sphinx 1.5.6 -> 1.6.3
- spyder 3.1.4 -> 3.2.3
- sqlalchemy 1.1.9 -> 1.1.13
- sympy 1.0 -> 1.1.1
- testpath 0.3 -> 0.3.1
- tk 8.5.18 -> 8.6.7
- tornado 4.5.1 -> 4.5.2
- widgetsnbextension 2.0.0 -> 3.0.2
- wrapt 1.10.10 -> 1.10.11
- xlrd 1.0.0 -> 1.1.0
- xlswriter 0.9.6 -> 0.9.8
- zlib 1.2.8 -> 1.2.11

**Added:**

- backports.shutil\_get\_terminal\_size 1.0.0
- bkcharts 0.2
- ca-certificates 2017.08.26
- certifi 2017.7.27.1
- conda-build 3.0.22
- dask-core 0.15.2
- filelock 2.0.12
- glob2 0.5
- imageio 2.2.0

- intel-openmp 2018.0.0
- jupyterlab 0.27.0
- jupyterlab\_launcher 0.4.0
- libssh2 1.8.0
- mccabe 0.6.1
- pkginfo 1.4.1
- pycodestyle 2.3.1
- pysocks 1.6.7
- sphinxcontrib 1.0
- sphinxcontrib-websupport 1.0.1
- typing 3.6.2
- urllib3 1.22
- webencodings 0.5.1

### Removed:

- \_license

### More changes specific to win-64

### Updated:

- hdf5 1.8.15.1 -> 1.10.1
- icu 57.1 -> 58.2
- ipython 5.3.0 -> 5.4.1
- ipython 5.3.0 -> 6.1.0
- menuinst 1.4.7 -> 1.4.8
- pytables 3.2.2 -> 3.4.2
- python 3.5.3 -> 3.5.4
- python 3.6.1 -> 3.6.2
- pywin32 220 -> 221
- ssl\_match\_hostname 3.4.0.2 -> 3.5.0.1
- vs2008\_runtime 9.00.30729.5054 -> 9.00.30729.1
- xlwings 0.10.4 -> 0.11.4
- xlwt 1.2.0 -> 1.3.0

### Added:

- backports.functools\_lru\_cache 1.4
- cachecontrol 0.12.3
- distlib 0.2.5
- icc\_rt 2017.0.4



- libiconv 1.15
- libxml2 2.9.4
- libxslt 1.1.29
- lockfile 0.12.2
- pandoc 1.19.2.1
- progress 1.3
- sqlite 3.20.1
- vc 14
- vc 9
- win\_inet\_pton 1.0.1
- wincertstore 0.2
- yaml 0.1.7

### More changes specific to win-32

#### Updated:

- hdf5 1.8.15.1 -> 1.10.1
- icu 57.1 -> 58.2
- ipython 5.3.0 -> 5.4.1
- ipython 5.3.0 -> 6.1.0
- menuinst 1.4.7 -> 1.4.8
- pytables 3.2.2 -> 3.4.2
- python 3.5.3 -> 3.5.4
- python 3.6.1 -> 3.6.2
- pywin32 220 -> 221
- ssl\_match\_hostname 3.4.0.2 -> 3.5.0.1
- vs2008\_runtime 9.00.30729.5054 -> 9.00.30729.1
- xlwings 0.10.4 -> 0.11.4
- xlwt 1.2.0 -> 1.3.0

#### Added:

- backports.functools\_lru\_cache 1.4
- cachecontrol 0.12.3
- distlib 0.2.5
- icc\_rt 2017.0.4
- libiconv 1.15
- libxml2 2.9.4
- libxslt 1.1.29

- lockfile 0.12.2
- pandoc 1.19.2.1
- progress 1.3
- sqlite 3.20.1
- vc 14
- vc 9
- win\_inet\_pton 1.0.1
- wincertstore 0.2
- yaml 0.1.7

### More changes specific to macOS-64

#### Updated:

- hdf5 1.8.17 -> 1.10.1
- icu 54.1 -> 58.2
- ipython 5.3.0 -> 5.4.1
- ipython 5.3.0 -> 6.1.0
- libiconv 1.14 -> 1.15
- ptyprocess 0.5.1 -> 0.5.2
- pytables 3.3.0 -> 3.4.2
- python 3.5.3 -> 3.5.4
- python 3.6.1 -> 3.6.2
- python.app 1.2 -> 2
- readline 6.2 -> 7.0
- sqlite 3.13.0 -> 3.20.1
- ssl\_match\_hostname 3.4.0.2 -> 3.5.0.1
- xlwings 0.10.4 -> 0.11.4
- xz 5.2.2 -> 5.2.3
- yaml 0.1.6 -> 0.1.7

#### Added:

- backports.functools\_lru\_cache 1.4
- dbus 1.10.22
- expat 2.2.4
- gettext 0.19.8.1
- glib 2.53.6
- gmp 6.1.2
- gmpy2 2.0.8

- libcxx 4.0.1
- libcxxabi 4.0.1
- libedit 3.1
- libffi 3.2.1
- libgfortran 3.0.1
- libsodium 1.0.13
- mpc 1.0.3
- mpfr 3.1.5
- ncurses 6.0
- pandoc 1.19.2.1
- pcre 8.41
- zeromq 4.2.2

### More changes specific to linux-64

#### Updated:

- cairo 1.14.8 -> 1.14.10
- dbus 1.10.10 -> 1.10.22
- expat 2.1.0 -> 2.2.4
- fontconfig 2.12.1 -> 2.12.4
- glib 2.50.2 -> 2.53.6
- gst-plugins-base 1.8.0 -> 1.12.2
- gstreamer 1.8.0 -> 1.12.2
- harfbuzz 0.9.39 -> 1.5.0
- hdf5 1.8.17 -> 1.10.1
- icu 54.1 -> 58.2
- ipython 5.3.0 -> 5.4.1
- ipython 5.3.0 -> 6.1.0
- libsodium 1.0.10 -> 1.0.13
- libtool 2.4.2 -> 2.4.6
- pango 1.40.3 -> 1.40.11
- pcre 8.39 -> 8.41
- ptyprocess 0.5.1 -> 0.5.2
- pycairo 1.10.0 -> 1.13.3
- pytables 3.3.0 -> 3.4.2
- python 3.5.3 -> 3.5.4
- python 3.6.1 -> 3.6.2

- readline 6.2 -> 7.0
- sqlite 3.13.0 -> 3.20.1
- ssl\_match\_hostname 3.4.0.2 -> 3.5.0.1
- xlwt 1.2.0 -> 1.3.0
- xz 5.2.2 -> 5.2.3
- yaml 0.1.6 -> 0.1.7
- zeromq 4.1.5 -> 4.2.2

### Added:

- backports.functools\_lru\_cache 1.4
- gmp 6.1.2
- gmpy2 2.0.8
- graphite2 1.3.10
- libedit 3.1
- libgcc-ng 7.2.0
- libgfortran-ng 7.2.0
- libstdcxx-ng 7.2.0
- lzo 2.10
- mpc 1.0.3
- mpfr 3.1.5
- ncurses 6.0
- pandoc 1.19.2.1
- patchelf 0.9

### Removed:

- libgcc
- libgfortran
- libiconv

## More changes specific to linux-32

### Updated:

- cairo 1.14.8 -> 1.14.10
- dbus 1.10.10 -> 1.10.22
- expat 2.1.0 -> 2.2.4
- fontconfig 2.12.1 -> 2.12.4
- glib 2.50.2 -> 2.53.6
- gst-plugins-base 1.8.0 -> 1.12.2
- gstreamer 1.8.0 -> 1.12.2

- harfbuzz 0.9.39 -> 1.5.0
- hdf5 1.8.17 -> 1.10.1
- icu 54.1 -> 58.2
- ipython 5.3.0 -> 5.4.1
- ipython 5.3.0 -> 6.1.0
- libsodium 1.0.10 -> 1.0.13
- libtool 2.4.2 -> 2.4.6
- pango 1.40.3 -> 1.40.11
- pcre 8.39 -> 8.41
- ptyprocess 0.5.1 -> 0.5.2
- pycairo 1.10.0 -> 1.13.3
- pytables 3.3.0 -> 3.4.2
- python 3.5.3 -> 3.5.4
- python 3.6.1 -> 3.6.2
- readline 6.2 -> 7.0
- sqlite 3.13.0 -> 3.20.1
- ssl\_match\_hostname 3.4.0.2 -> 3.5.0.1
- xlwt 1.2.0 -> 1.3.0
- xz 5.2.2 -> 5.2.3
- yaml 0.1.6 -> 0.1.7
- zeromq 4.1.5 -> 4.2.2

**Added:**

- backports.functools\_lru\_cache 1.4
- gmp 6.1.2
- gmpy2 2.0.8
- graphite2 1.3.10
- libedit 3.1
- libgcc-ng 7.2.0
- libgfortran-ng 7.2.0
- libstdcxx-ng 7.2.0
- lzo 2.10
- mpc 1.0.3
- mpfr 3.1.5
- ncurses 6.0
- pandoc 1.15.0.6
- patchelf 0.9

### Removed:

- libgcc
- libgfortran
- libiconv

### Changes for linux-ppc64le

### Updated:

- astroid 1.4.9 -> 1.5.3
- astropy 1.3.2 -> 2.0.1
- babel 2.4.0 -> 2.5.0
- bokeh 0.12.5 -> 0.12.7
- boto 2.46.1 -> 2.48.0
- chardet 3.0.3 -> 3.0.4
- cloudpickle 0.2.2 -> 0.4.0
- cython 0.25.2 -> 0.26
- dask 0.14.3 -> 0.15.2
- decorator 4.0.11 -> 4.1.2
- distributed 1.16.3 -> 1.18.1
- docutils 0.13.1 -> 0.14
- entrypoints 0.2.2 -> 0.2.3
- flask-cors 3.0.2 -> 3.0.3
- gevent 1.2.1 -> 1.2.2
- html5lib 0.999 -> 0.9999999
- idna 2.5 -> 2.6
- ipython 5.3.0 -> 6.1.0
- isort 4.2.5 -> 4.2.15
- jupyter\_client 5.0.1 -> 5.1.0
- jupyter\_console 5.1.0 -> 5.2.0
- lazy-object-proxy 1.2.2 -> 1.3.1
- libpng 1.6.27 -> 1.6.30
- markupsafe 0.23 -> 1.0
- nbconvert 5.1.1 -> 5.2.1
- nbformat 4.3.0 -> 4.4.0
- nltk 3.2.3 -> 3.2.4
- numpy 1.12.1 -> 1.13.1
- numpydoc 0.6.0 -> 0.7.0

- `odo` 0.5.0 -> 0.5.1
- `openpyxl` 2.4.7 -> 2.4.8
- `pandas` 0.20.1 -> 0.20.3
- `pandocfilters` 1.4.1 -> 1.4.2
- `pathlib2` 2.2.1 -> 2.3.0
- `pillow` 4.1.1 -> 4.2.1
- `prompt_toolkit` 1.0.14 -> 1.0.15
- `ptyprocess` 0.5.1 -> 0.5.2
- `py` 1.4.33 -> 1.4.34
- `pycparser` 2.17 -> 2.18
- `pyflakes` 1.5.0 -> 1.6.0
- `pylint` 1.6.4 -> 1.7.2
- `pyparsing` 2.1.4 -> 2.2.0
- `pytables` 3.2.2 -> 3.4.2
- `pytest` 3.0.7 -> 3.2.1
- `python` 3.5.3 -> 3.5.4
- `python` 3.6.1 -> 3.6.2
- `python-dateutil` 2.6.0 -> 2.6.1
- `scikit-learn` 0.18.1 -> 0.19.0
- `scipy` 0.19.0 -> 0.19.1
- `seaborn` 0.7.1 -> 0.8
- `setuptools` 27.2.0 -> 36.4.0
- `sphinx` 1.5.6 -> 1.6.3
- `sqlalchemy` 1.1.9 -> 1.1.13
- `ssl_match_hostname` 3.4.0.2 -> 3.5.0.1
- `sympy` 1.0 -> 1.1.1
- `testpath` 0.3 -> 0.3.1
- `tornado` 4.5.1 -> 4.5.2
- `widgetsnbextension` 2.0.0 -> 3.0.2
- `wrapt` 1.10.10 -> 1.10.11
- `xlrd` 1.0.0 -> 1.1.0
- `xlsxwriter` 0.9.6 -> 0.9.8
- `xlwt` 1.2.0 -> 1.3.0
- `xz` 5.2.2 -> 5.2.3
- `zlib` 1.2.8 -> 1.2.11

**Added:**

- bkcharts 0.2
- certifi 2016.2.28
- filelock 2.0.7
- functools\_lru\_cache 1.4
- glob2 0.5
- jedi 0.10.2
- patchelf 0.9
- pkginfo 1.4.1
- pycodestyle 2.3.1
- sphinxcontrib 1.0
- sphinxcontrib-websupport 1.0.1
- typing 3.6.2

### What's new in Anaconda 4.4?

Anaconda 4.4 was released on May 31, 2017 and includes the following:

- Support added for the “ppc64le” machine type, for the POWER8 LE architecture used by IBM Power Systems and OpenPOWER servers.
- On Windows, the PATH environment variable is no longer changed by default, as this can cause trouble with other software. Instead, use Anaconda Navigator or the Anaconda Prompt in the Start Menu under “Anaconda” to use Anaconda software. If a user does choose to change the PATH variable, Anaconda is no longer appended to the PATH in system mode, and is now always added to the front of PATH in either system mode or user mode.
- Python 3.5 is updated from 3.5.2 to 3.5.3 and Python 3.6 from 3.6.0 to 3.6.1. Anaconda 4.4 supports Python 2.7, 3.5, and 3.6. Anaconda 4.3 was the last release to support Python 3.4.
- Minimum supported version of CentOS is now CentOS 6. Anaconda 4.3 was the last release to support CentOS 5.
- Applied pycrypto patch for CVE-2013-7439.
- Improved cp\_acp support for install paths with non-ASCII characters on Windows.
- conda is updated from 4.3.14 to 4.3.21.
- Navigator is updated from 1.5.0 to 1.6.2.
- Project is updated from 0.4.1 to 0.6.0.
- Added distributed and pyodbc to the installers.
- Updated EULA.
- Conda packages with “mkl” in the package name now contain a file license.txt with a copy of the [Intel Simplified Software License](#) that applies to the Intel Math Kernel Library (MKL).
- Over 90 packages are updated or added.



**2017-05-31 4.4.0:****Highlights:**

- add support for the ppc64le (POWER8 LE used by IBM Power Systems and OpenPOWER servers) machine types

**Other changes:**

- On Windows, the PATH environment variable is no longer changed by default, as this can cause trouble with other software. The recommended approach is to instead use Anaconda Navigator or the Anaconda Prompt (located in the Start Menu under “Anaconda”) when you wish to use Anaconda software. Also, Anaconda will always be added to the front of PATH, for either system or user mode. (Previously it was appended to the system path.)
- improve cp\_acp support for install path on Windows
- updated 80 packages in the installer (and their dependencies)
- added distributed and pyodbc to the installers
- apply pycrypto patch for CVE-2013-7439
- end support for CentOS 5. CentOS 6 is now the minimum supported version.

**Updates:**

- alabaster from 0.7.9 to 0.7.10
- anaconda-client from 1.6.0 to 1.6.3
- anaconda-navigator from 1.5.0 to 1.6.2
- anaconda-project from 0.4.1 to 0.6.0
- astropy from 1.3 to 1.3.2
- babel from 2.3.4 to 2.4.0
- beautifulsoup4 from 4.5.3 to 4.6.0
- bokeh from 0.12.4 to 0.12.5
- boto from 2.45.0 to 2.46.1
- bottleneck from 1.2.0 to 1.2.1
- cffi from 1.9.1 to 1.10.0
- chardet from 2.3.0 to 3.0.3
- colorama from 0.3.7 to 0.3.9
- conda from 4.3.14 to 4.3.21
- contextlib2 from 0.5.4 to 0.5.5
- cryptography from 1.7.1 to 1.8.1
- dask from 0.13.0 to 0.14.3
- flask from 0.12 to 0.12.2
- futures from 3.0.5 to 3.1.1
- greenlet from 0.4.11 to 0.4.12
- h5py from 2.6.0 to 2.7.0

- hdf5 from 1.8.15.1 to 1.8.17
- idna from 2.2 to 2.5
- ipykernel from 4.5.2 to 4.6.1
- ipython from 5.1.0 to 5.3.0
- ipython\_genutils from 0.1.0 to 0.2.0
- ipywidgets from 5.2.2 to 6.0.0
- jedi from 0.9.0 to 0.10.2
- jinja2 from 2.9.4 to 2.9.6
- jsonschema from 2.5.1 to 2.6.0
- jupyter\_client from 4.4.0 to 5.0.1
- jupyter\_console from 5.0.0 to 5.1.0
- jupyter\_core from 4.2.1 to 4.3.0
- llvmlite from 0.15.0 to 0.18.0
- lxml from 3.7.2 to 3.7.3
- matplotlib from 2.0.0 to 2.0.2
- menuinst from 1.4.4 to 1.4.7
- mistune from 0.7.3 to 0.7.4
- nbconvert from 4.2.0 to 5.1.1
- nbformat from 4.2.0 to 4.3.0
- nltk from 3.2.2 to 3.2.3
- notebook from 4.3.1 to 5.0.0
- numba from 0.30.1 to 0.33.0
- numpy from 1.11.3 to 1.12.1
- numexpr from 2.6.1 to 2.6.2
- openpyxl from 2.4.1 to 2.4.7
- openssl from 1.0.2k to 1.0.2l
- pandas from 0.19.2 to 0.20.1
- partd from 0.3.7 to 0.3.8
- path.py from 10.0 to 10.3.1
- pathlib2 from 2.2.0 to 2.2.1
- pillow from 4.0.0 to 4.1.1
- ply from 3.9 to 3.10
- prompt\_toolkit from 1.0.9 to 1.0.14
- psutil from 5.0.1 to 5.2.2
- py from 1.4.32 to 1.4.33
- pycosat from 0.6.1 to 0.6.2

- pygments from 2.1.3 to 2.2.0
- pyopenssl from 16.2.0 to 17.0.0
- pytables from 3.2.2 to 3.3.0
- pytest from 3.0.5 to 3.0.7
- python 3.5 from 3.5.2 to 3.5.3
- python 3.6 from 3.6.0 to 3.6.1
- pytz from 2016.10 to 2017.2
- qtawesome from 0.4.3 to 0.4.4
- qtconsole from 4.2.1 to 4.3.0
- requests from 2.12.4 to 2.14.2
- scandir from 1.4 to 1.5
- scikit-image from 0.12.3 to 0.13.0
- scipy from 0.18.1 to 0.19.0
- sphinx from 1.5.1 to 1.5.6
- spyder from 3.1.2 to 3.1.4
- sqlalchemy from 1.1.5 to 1.1.9
- statsmodels from 0.6.1 to 0.8.0
- tornado from 4.4.2 to 4.5.1
- traitlets from 4.3.1 to 4.3.2
- werkzeug from 0.11.15 to 0.12.2
- widgetsnbextension from 1.2.6 to 2.0.0
- wrapt from 1.10.8 to 1.10.10
- xlwings from 0.10.2 to 0.10.4

**Added:**

- asn1crypto 0.22.0
- bleach 1.5.0
- distributed 1.16.3
- html5lib 0.999
- msgpack-python 0.4.8
- navigator-updater 0.1.0
- olefile 0.44
- packaging 16.8
- pandocfilters 1.4.1
- pyodbc 4.0.16
- pywavelets 0.5.2
- sortedcollections 0.5.3

- sortedcontainers 1.5.7
- tblib 1.3.2
- testpath 0.3
- zict 0.1.2

### Removed (from installers only):

- argcomplete
- chest
- configobj
- dill
- pyasn1
- redis
- redis-py
- sockjs-tornado

### 2017-03-10 4.3.1:

This patch release fixes problems with Anaconda Navigator not starting correctly on some versions of Mac OS X when using the GUI installers.

#### Fixes:

- removed creation of `~/ .continuum` folder during install process on all platforms
- fixed `'/'` showing up in prefix when installing system wide on Mac OS using the GUI installer
- fixed OpenSSL not being installable into a path which contains spaces
- allow Unicode characters in install path on Windows (cp\_acp fix)

#### Updates:

- anaconda-navigator from 1.4.3 to 1.5.0
- conda from 4.3.8 to 4.3.14

#### Added:

- anaconda-project 0.4.1

### 2017-02-03 4.3.0.1:

In this “mirco” patch release, we fixed a problem with the Windows installers which was causing problems with Qt applications when the install prefix exceeds 30 characters. No new Anaconda meta-packages correspond to this release (only new Windows installers).

### 2017-01-31 4.3.0:

#### Highlights:

- The Anaconda3 installers are based on Python 3.6. Anaconda 4.3 supports Python 2.7, 3.4, 3.5 and 3.6. Anaconda 4.3 will be the last release which supports Python 3.4. We will discontinue regular Python 3.4 package updates in the next release.
- The Intel Math Kernel Library (MKL) is updated from 11.3.3 to 2017.0.1.
- Over 90 packages are updated.
- seaborn is now installed by default.

**Other changes:**

- Updates jpeg and libpng to increase compatibility with conda-forge.
- Warns about possible errors if installing on Windows into an install path with spaces, and does not allow installation if the install path contains unicode characters.
- Fixes many Windows menu uninstallation issues and some other often reported uninstallation issues on Windows.
- Anaconda 4.2 is the last release that supports macOS 10.7 and macOS 10.8. Anaconda 4.3 supports macOS versions from 10.9 through the current version 10.12.
- conda-build, anaconda-clean and the Jupyter Notebook extensions are no longer installed by default but can be installed with a single conda command.

**Updates:**

- anaconda-client from 1.5.1 to 1.6.0
- anaconda-navigator from 1.3.1 to 1.4.3
- astroid from 1.4.7 to 1.4.9
- astropy from 1.2.1 to 1.3
- backports\_abc from 0.4 to 0.5
- beautifulsoup4 from 4.5.1 to 4.5.3
- bokeh from 0.12.2 to 0.12.4
- boto from 2.42.0 to 2.45.0
- bottleneck from 1.1.0 to 1.2.0
- cairo from 1.12.18 to 1.14.8
- cffi from 1.7.0 to 1.9.1
- click from 6.6 to 6.7
- cloudpickle from 0.2.1 to 0.2.2
- conda from 4.2.9 to 4.3.8
- contextlib2 from 0.5.3 to 0.5.4
- cryptography from 1.5 to 1.7.1
- curl from 7.49.0 to 7.52.1
- cython from 0.24.1 to 0.25.2
- cytoolz from 0.8.0 to 0.8.2
- dask from 0.11.0 to 0.13.0
- datashape from 0.5.2 to 0.5.4

- decorator from 4.0.10 to 4.0.11
- docutils from 0.12 to 0.13.1
- flask from 0.11.1 to 0.12
- flask-cors from 2.1.2 to 3.0.2
- fontconfig from 2.11.1 to 2.12.1
- gevent from 1.1.2 to 1.2.1
- glib from 2.43.0 to 2.50.2
- greenlet from 0.4.10 to 0.4.11
- hdf5 from 1.8.15.1 to 1.8.17
- idna from 2.1 to 2.2
- ipaddress from 1.0.16 to 1.0.18
- ipykernel from 4.5.0 to 4.5.2
- jdcal from 1.2 to 1.3
- jinja2 from 2.8 to 2.9.4
- jpeg from 8d to 9b
- jupyter\_core from 4.2.0 to 4.2.1
- lazy-object-proxy from 1.2.1 to 1.2.2
- libpng from 1.6.22 to 1.6.27
- libxml2 from 2.9.2 to 2.9.4
- libxslt from 1.1.28 to 1.1.29
- llvmlite from 0.13.0 to 0.15.0
- lxml from 3.6.4 to 3.7.2
- matplotlib from 1.5.3 to 2.0.0
- menuinst from 1.4.1 to 1.4.4
- mkl from 11.3.3 to 2017.0.1
- multipledispatch from 0.4.8 to 0.4.9
- nbformat from 4.1.0 to 4.2.0
- nltk from 3.2.1 to 3.2.2
- notebook from 4.2.3 to 4.3.1
- numba from 0.28.1 to 0.30.1
- numpy from 1.11.1 to 1.11.3
- openpyxl from 2.3.2 to 2.4.1
- openssl from 1.0.2j to 1.0.2k
- pandas from 0.18.1 to 0.19.2
- partd from 0.3.6 to 0.3.7
- path.py from 8.2.1 to 10.0

- pathlib2 from 2.1.0 to 2.2.0
- pexpect from 4.0.1 to 4.2.1
- pillow from 3.3.1 to 4.0.0
- pip from 8.1.2 to 9.0.1
- pixman from 0.32.6 to 0.34.0
- prompt\_toolkit from 1.0.3 to 1.0.9
- psutil from 4.3.1 to 5.0.1
- py from 1.4.31 to 1.4.32
- pycparser from 2.14 to 2.17
- pyflakes from 1.3.0 to 1.5.0
- pylint from 1.5.4 to 1.6.4
- pyopenssl from 16.0.0 to 16.2.0
- pytables from 3.2.2 to 3.3.0
- pytest from 2.9.2 to 3.0.5
- python from 2.7.12 to 2.7.13
- python-dateutil from 2.5.3 to 2.6.0
- pytz from 2016.6.1 to 2016.10
- pyzmq from 15.4.0 to 16.0.2
- qt from 5.6.0 to 5.6.2
- qtawesome from 0.3.3 to 0.4.3
- qtpy from 1.1.2 to 1.2.1
- requests from 2.11.1 to 2.12.4
- scikit-learn from 0.17.1 to 0.18.1
- sphinx from 1.4.6 to 1.5.1
- spyder from 3.0.0 to 3.1.2
- sqlalchemy from 1.0.13 to 1.1.5
- toolz from 0.8.0 to 0.8.2
- tornado from 4.4.1 to 4.4.2
- traitlets from 4.3.0 to 4.3.1
- werkzeug from 0.11.11 to 0.11.15
- wrapt from 1.10.6 to 1.10.8
- xlswriter from 0.9.3 to 0.9.6
- xlwings from 0.10.0 to 0.10.2
- xlwt from 1.1.2 to 1.2.0
- zeromq from 4.1.4 to 4.1.5

**Added:**

- chardet 2.3.0
- isort 4.2.5
- libiconv 1.14
- numpydoc 0.6.0
- pcre 8.39 (on Linux)
- scandir 1.4
- seaborn 0.7.1
- subprocess32 3.2.7 (Python 2)

### Removed (from installer only):

- anaconda-clean
- dynd-python
- filelock
- libdynd
- nb\_anacondacloud
- nb\_conda
- nb\_conda\_kernels
- nbpresent
- patchelf
- pkginfo

### 2016-09-28 4.2.0:

#### Highlights:

- updated Qt from major version 4 to 5
- updated IPython from 4.2 to 5.1
- added anaconda-clean, a tool for cleaning up Anaconda related configuration files and directories

#### Fixes:

- fixed Windows Outlook crash in silent install mode
- updated OpenSSL to 1.0.2j which contains important security fixes

#### Updates:

- alabaster from 0.7.8 to 0.7.9
- anaconda-client from 1.4.0 to 1.5.1
- anaconda-navigator from 1.2.1 to 1.3.1
- babel from 2.3.3 to 2.3.4
- beautifulsoup4 from 4.4.1 to 4.5.1
- bokeh from 0.12.0 to 0.12.2
- boto from 2.40.0 to 2.42.0



- cffi from 1.6.0 to 1.7.0
- conda from 4.1.4 to 4.2.9
- conda-build from 1.21.2 to 2.0.2
- configparser from 3.5.0b2 to 3.5.0
- cryptography from 1.4 to 1.5
- cython from 0.24 to 0.24.1
- dask from 0.10.0 to 0.11.0
- gevent from 1.1.1 to 1.1.2
- hdf5 from 1.8.15.1 to 1.8.17
- ipykernel from 4.3.1 to 4.5.0
- ipython from 4.2.0 to 5.1.0
- ipywidgets from 4.1.1 to 5.2.2
- jupyter\_client from 4.3.0 to 4.4.0
- jupyter\_console from 4.1.1 to 5.0.0
- jupyter\_core from 4.1.0 to 4.2.0
- llvmlite from 0.11.0 to 0.13.0
- lxml from 3.6.0 to 3.6.4
- matplotlib from 1.5.1 to 1.5.3
- mistune from 0.7.2 to 0.7.3
- nb\_anacondacloud from 1.1.0 to 1.2.0
- nb\_conda from 1.1.0 to 2.0.0
- nb\_conda\_kernels from 1.0.3 to 2.0.0
- nbformat from 4.0.1 to 4.1.0
- notebook from 4.2.1 to 4.2.3
- numba from 0.26.0 to 0.28.1
- numexpr from 2.6.0 to 2.6.1
- openssl from 1.0.2h to 1.0.2j
- partd from 0.3.4 to 0.3.6
- pickleshare from 0.7.2 to 0.7.4
- pillow from 3.2.0 to 3.3.1
- ply from 3.8 to 3.9
- psutil from 4.3.0 to 4.3.1
- pyflakes from 1.2.3 to 1.3.0
- pyopenssl from 0.16.0 to 16.0.0
- pyqt from 4.11.4 to 5.6.0
- pytables from 3.2.2 to 3.2.3.1

- pytz from 2016.4 to 2016.6.1
- pyyaml from 3.11 to 3.12
- pyzmq from 15.2.0 to 15.4.0
- qt from 4.8.7 to 5.6.0
- qtpy from 1.0.2 to 1.1.2
- requests from 2.10.0 to 2.11.1
- ruamel\_yaml from 0.11.7 to 0.11.14
- scipy from 0.17.1 to 0.18.1
- setuptools from 23.0.0 to 27.2.0
- sip from 4.16.9 to 4.18
- sphinx from 1.4.1 to 1.4.6
- spyder from 2.3.9 to 3.0.0
- tornado from 4.3 to 4.4.1
- traitlets from 4.2.1 to 4.3.0
- werkzeug from 0.11.10 to 0.11.11
- xlswriter from 0.9.2 to 0.9.3
- xlwings from 0.7.2 to 0.10.0

**Added:**

- anaconda-clean 1.0.0
- astroid 1.4.7
- dbus 1.10.10 (Linux)
- expat 2.1.0 (Linux)
- filelock 2.0.6
- glib 2.43.0 (Linux)
- gst-plugins-base 1.8.0 (Linux)
- gstreamer 1.8.0 (Linux)
- harfbuzz 0.9.39 (Linux)
- icu 57.1
- lazy-object-proxy 1.2.1
- libgcc 4.8.5 (Linux)
- libxcb 1.12 (Linux)
- pkginfo 1.3.2
- prompt\_toolkit 1.0.3
- pylint 1.5.4
- qtawesome 0.3.3
- wcwidth 0.1.7

- widgetsnbextension 1.2.6
- win\_unicode\_console 0.5 (Windows)
- wrapt 1.10.6

**Removed (from installer only):**

- pyreadline
- sphinx\_rtd\_theme
- conda-env (now part of conda itself)

**2016-07-08 4.1.1:****Fixes:**

- Running the shell installer on some older system, would print out (harmless) tracebacks during the install process, see: <https://github.com/ContinuumIO/anaconda-issues/issues/860>
- We added blaze 0.10.1 back into the installer, which was accidentally missing in 4.1.0

**Updates:**

- bokeh from 0.11.1 to 0.12.0
- bottleneck from 1.0.0 to 1.1.0
- conda from 4.1.4 to 4.1.6
- conda-build from 1.21.2 to 1.21.3
- numpy from 1.11.0 to 1.11.1
- Python 2.7 from 2.7.11 to 2.7.12
- Python 3.4 from 3.4.4 to 3.4.5
- Python 3.5 from 3.5.1 to 3.5.2

**2016-06-28 4.1.0:****Highlights:**

- added Jupyter Notebook Extensions
- Windows installation: silent mode fixes & now compatible with SCCM (System Center Configuration Manager)
- updated MKL to 11.3.3, numpy to 1.11.0, as well as over 80 other updates, see below
- update Navigator from 1.1 to 1.2, in particular it no longer installs a desktop shortcut on macOS
- conda-recipes used to build the vast majority of the packages in the Anaconda installer have been published at: <https://github.com/ContinuumIO/anaconda-recipes>

**Updates:**

- alabaster from 0.7.7 to 0.7.8
- anaconda-navigator from 1.1.0 to 1.2.1
- astropy from 1.1.2 to 1.2.1

- babel from 2.2.0 to 2.3.3
- boto from 2.39.0 to 2.40.0
- cffi from 1.5.2 to 1.6.0
- cloudpickle from 0.1.1 to 0.2.1
- clyent from 1.2.1 to 1.2.2
- conda from 4.0.5 to 4.1.4
- conda-build from 1.20.0 to 1.21.2
- conda-env from 2.4.5 to 2.5.1
- cryptography from 1.3 to 1.4
- curl from 7.45.0 to 7.49.0
- cython from 0.23.4 to 0.24
- cytoolz from 0.7.5 to 0.8.0
- dask from 0.8.1 to 0.10.0
- datashape from 0.5.1 to 0.5.2
- decorator from 4.0.9 to 4.0.10
- dill from 0.2.4 to 0.2.5
- enum34 from 1.1.2 to 1.1.6
- flask from 0.10.1 to 0.11.1
- funcsigs from 0.4 to 1.0.2
- futures from 3.0.3 to 3.0.5
- gevent from 1.1.0 to 1.1.1
- greenlet from 0.4.9 to 0.4.10
- h5py from 2.5.0 to 2.6.0
- hdf5 from 1.8.15.1 to 1.8.16
- idna from 2.0 to 2.1
- ipaddress from 1.0.14 to 1.0.16
- ipython from 4.1.2 to 4.2.0
- jsonschema from 2.4.0 to 2.5.1
- jupyter\_client from 4.2.2 to 4.3.0
- libffi from 3.0.13 to 3.2.1
- libgfortran from 3.0 to 3.0.0
- libpng from 1.6.17 to 1.6.22
- libsodium from 1.0.3 to 1.0.10
- llvmlite from 0.9.0 to 0.11.0
- menuinst from 1.3.2 to 1.4.1
- mkl from 11.3.1 to 11.3.3

- nbconvert from 4.1.0 to 4.2.0
- nltk from 3.2 to 3.2.1
- notebook from 4.1.0 to 4.2.1
- numba from 0.24.0 to 0.26.0
- numexpr from 2.5 to 2.6.0
- numpy from 1.10.4 to 1.11.0
- odo from 0.4.2 to 0.5.0
- openssl from 1.0.2g to 1.0.2h
- pandas from 0.18.0 to 0.18.1
- partd from 0.3.2 to 0.3.4
- patchelf from 0.8 to 0.9
- path.py from 8.1.2 to 8.2.1
- patsy from 0.4.0 to 0.4.1
- pickleshare from 0.5 to 0.7.2
- pillow from 3.1.1 to 3.2.0
- pip from 8.1.1 to 8.1.2
- psutil from 4.1.0 to 4.3.0
- ptyprocess from 0.5 to 0.5.1
- pycurl from 7.19.5.3 to 7.43.0
- pyflakes from 1.1.0 to 1.2.3
- pygments from 2.1.1 to 2.1.3
- pyopenssl from 0.15.1 to 0.16.0
- pyparsing from 2.0.3 to 2.1.4
- pytest from 2.8.5 to 2.9.2
- python-dateutil from 2.5.1 to 2.5.3
- pytz from 2016.2 to 2016.4
- qtconsole from 4.2.0 to 4.2.1
- qtpy from 1.0 to 1.0.2
- redis from 2.6.9 to 3.2.0
- redis-py from 2.10.3 to 2.10.5
- requests from 2.9.1 to 2.10.0
- scipy from 0.17.0 to 0.17.1
- setuptools from 20.3 to 23.0.0
- sockjs-tornado from 1.0.1 to 1.0.3
- sphinx from 1.3.5 to 1.4.1
- spyder from 2.3.8 to 2.3.9

- sqlalchemy from 1.0.12 to 1.0.13
- sqlite from 3.9.2 to 3.13.0
- terminado from 0.5 to 0.6
- toolz from 0.7.4 to 0.8.0
- werkzeug from 0.11.4 to 0.11.10
- xlrd from 0.9.4 to 1.0.0
- xlswriter from 0.8.4 to 0.9.2
- xlwings from 0.7.0 to 0.7.2
- xlwt from 1.0.0 to 1.1.2
- xz from 5.0.5 to 5.2.2
- zeromq from 4.1.3 to 4.1.4

### Added:

- click 6.6
- configparser 3.5.0b2
- contextlib2 0.5.3
- entrypoints 0.2.2
- functools32 3.2.3.2
- get\_terminal\_size 1.0.0
- imagesize 0.7.1
- nb\_anacondacloud 1.1.0
- nb\_conda 1.1.0
- nb\_conda\_kernels 1.0.3
- nbpresent 3.0.2
- pathlib2 2.1.0
- ruamel\_yaml 0.11.7

### Removed:

- conda-manager
- qtawesome

### 2016-03-29 4.0.0:

The reason for jumping the Anaconda version from 2.5 to 4.0 is to avoid any possible confusion with the versions of Python included in Anaconda.

### Highlights:

- this release of Anaconda includes the new Navigator, which is a graphical tool developed by Continuum Analytics to manage conda environments, applications and much more.

### Enhancements:

- much improved package resolving in the new conda 4.0

**Fixes:**

- updated OpenSSL to 1.0.2g which contains important security fixes

**Updates:**

- anaconda-client from 1.2.2 to 1.4.0
- astropy from 1.1.1 to 1.1.2
- blaze from 0.9.0 to 0.9.1
- bokeh from 0.11.0 to 0.11.1
- cffi from 1.2.1 to 1.5.2
- clyent from 1.2.0 to 1.2.1
- colorama from 0.3.6 to 0.3.7
- conda from 3.19.1 to 4.0.5
- conda-build from 1.19.0 to 1.20.0
- cryptography from 1.0.2 to 1.3
- cycler from 0.9.0 to 0.10.0
- datashape from 0.5.0 to 0.5.1
- decorator from 4.0.6 to 4.0.9
- dynd-python from 0.7.1 to 0.7.2
- gevent from 1.0.2 to 1.1.0
- ipykernel from 4.2.2 to 4.3.1
- ipython from 4.0.3 to 4.1.2
- jupyter\_client from 4.1.1 to 4.2.2
- jupyter\_console from 4.1.0 to 4.1.1
- jupyter\_core from 4.0.6 to 4.1.0
- libdynd from 0.7.1 to 0.7.2
- libgfortran from 1.0 to 3.0
- llvmlite from 0.8.0 to 0.9.0
- lxml from 3.5.0 to 3.6.0
- mistune from 0.7.1 to 0.7.2
- nltk from 3.1 to 3.2
- numba from 0.23.1 to 0.24.0
- numexpr from 2.4.6 to 2.5
- odo from 0.4.0 to 0.4.2
- openssl from 1.0.2f to 1.0.2g
- pandas from 0.17.1 to 0.18.0
- pexpect from 3.3 to 4.0.1

- pillow from 3.1.0 to 3.1.1
- pip from 8.0.2 to 8.1.1
- psutil from 3.4.2 to 4.1.0
- pyflakes from 1.0.0 to 1.1.0
- pygments from 2.1 to 2.1.1
- python-dateutil from 2.4.2 to 2.5.1
- pytz from 2015.7 to 2016.2
- pywin32 from 219 to 220
- qtconsole from 4.1.1 to 4.2.0
- scikit-image from 0.11.3 to 0.12.3
- scikit-learn from 0.17 to 0.17.1
- setuptools from 19.6.2 to 20.3
- sqlalchemy from 1.0.11 to 1.0.12
- sympy from 0.7.6.1 to 1.0
- traitlets from 4.1.0 to 4.2.1
- werkzeug from 0.11.3 to 0.11.4
- wheel from 0.26.0 to 0.29.0
- xlwings from 0.6.4 to 0.7.0

### **Added:**

- anaconda-navigator 1.1.0
- chest 0.2.3
- cloudpickle 0.1.1
- conda-manager 0.3.1
- dask 0.8.1
- dill 0.2.4
- flask-cors 2.1.2
- heapdict 1.0.0
- locket 0.2.0
- mpmath 0.19
- partd 0.3.2
- qtawesome 0.3.2
- qtpy 1.0

### **Removed (from installer only, the packages are still available):**

- abstract-rendering
- gevent-websocket
- launcher



- node-webkit

## 2016-02-05 2.5.0:

### Highlights:

- add MKL (runtime, version 11.3.1) and make it the default backend for numpy, scipy, scikit-learn and numexpr on all platforms

### Enhancements:

- added Windows debug information files, more precisely program database (.pdb files) files for Python by default
- added NoRegistry option to Windows installers, passing /NoRegistry=1 makes the installer not touch the registry

### Fixes:

- in some cases start menu items were not created on Windows, due to a race condition, which we fixed in menuinst
- fixed the -f option of the Unix bash installers
- updated OpenSSL to 1.0.2f which contains important security fixes

### Updates:

- alabaster from 0.7.6 to 0.7.7
- anaconda-client from 1.2.1 to 1.2.2
- astropy from 1.0.6 to 1.1.1
- babel from 2.1.1 to 2.2.0
- blaze-core from 0.8.3 to 0.9.0
- bokeh from 0.10.0 to 0.11.0
- boto from 2.38.0 to 2.39.0
- colorama from 0.3.3 to 0.3.6
- conda from 3.18.8 to 3.19.1
- conda-build from 1.18.2 to 1.19.0
- cytoolz from 0.7.4 to 0.7.5
- datashape from 0.4.7 to 0.5.0
- decorator from 4.0.4 to 4.0.6
- dynd-python from 0.7.0 to 0.7.1
- enum34 from 1.0.4 to 1.1.2
- gevent from 1.0.1 to 1.0.2
- gevent-websocket from 0.9.3 to 0.9.5
- ipykernel from 4.1.1 to 4.2.2
- ipython from 4.0.1 to 4.0.3
- ipywidgets from 4.1.0 to 4.1.1

- `jdcal` from 1.0 to 1.2
- `jupyter_console` from 4.0.3 to 4.1.0
- `libdynd` from 0.7.0 to 0.7.1
- `lxml` from 3.4.4 to 3.5.0
- `matplotlib` from 1.5.0 to 1.5.1
- `menuinst` from 1.3.1 to 1.3.2
- `nbconvert` from 4.0.0 to 4.1.0
- `networkx` from 1.10 to 1.11
- `notebook` from 4.0.6 to 4.1.0
- `numba` from 0.22.1 to 0.23.1
- `numexpr` from 2.4.4 to 2.4.6
- `numpy` from 1.10.1 to 1.10.4
- `odo` from 0.3.4 to 0.4.0
- `openpyxl` from 2.2.6 to 2.3.2
- `openssl` from 1.0.2d to 1.0.2f
- `patchelf` from 0.6 to 0.8
- `pep8` from 1.6.2 to 1.7.0
- `pillow` from 3.0.0 to 3.1.0
- `pip` from 7.1.2 to 8.0.2
- `psutil` from 3.3.0 to 3.4.2
- `py` from 1.4.30 to 1.4.31
- `pycurl` from 7.19.5.1 to 7.19.5.3
- `pygments` from 2.0.2 to 2.1
- `pytest` from 2.8.1 to 2.8.5
- `python 3.4` from 3.4.3 to 3.4.4
- `pyzmq` from 14.7.0 to 15.2.0
- `requests` from 2.8.1 to 2.9.1
- `scipy` from 0.16.0 to 0.17.0
- `setuptools` from 18.5 to 19.6.2
- `snowballstemmer` from 1.2.0 to 1.2.1
- `sphinx` from 1.3.1 to 1.3.5
- `sphinx_rtd_theme` from 0.1.7 to 0.1.9
- `sqlalchemy` from 1.0.9 to 1.0.11
- `sqlite` from 3.8.4.1 to 3.9.2
- `traitlets` from 4.0.0 to 4.1.0
- `werkzeug` from 0.11.2 to 0.11.3

- xlswriter from 0.7.7 to 0.8.4
- xlwings from 0.5.0 to 0.6.4

**Added:**

- et\_xmlfile 1.0.1
- futures 3.0.3
- mkl 11.3.1
- mkl-service 1.1.1

**Removed (from installer only, the packages are still maintained and available):**

- openblas 0.2.14 (Linux)
- theano 0.7.0 (Linux)
- ujson 1.33

**2015-12-08 2.4.1:****Fixes:**

- added missing Windows process elevation when creating menu items
- added libdynd and dynd-python, which was missing in the last release
- fixed Cython on Mac OS X reporting missing libgcc\_s.10.5.dylib
- fixed default channels being shown correctly in “conda list” after installing using Anaconda installer

**Updates:**

- anaconda-client from 1.1.0 to 1.2.1
- astropy from 1.0.5 to 1.0.6
- clyent from 0.4.0 to 1.2.0
- conda from 3.18.3 to 3.18.8
- conda-build 1.18.1 to 1.18.2
- conda-env from 2.4.4 to 2.4.5
- ipython from 4.0.0 to 4.0.1
- llvmlite from 0.7.0 to 0.8.0
- matplotlib from 1.4.3 to 1.5.0
- menuinst from 1.2.1 to 1.3.1
- numba from 0.21.0 to 0.22.1
- pandas from 0.17.0 to 0.17.1
- pixman from 0.26.2 to 0.32.6
- psutil from 3.2.2 to 3.3.0
- python 2.7 from 2.7.10 to 2.7.11
- python 3.5 from 3.5.0 to 3.5.1
- pytz from 2015.6 to 2015.7

- qtconsole from 4.1.0 to 4.1.1
- scikit-learn from 0.16.1 to 0.17
- setuptools from 18.4 to 18.5
- spyder from 2.3.7 to 2.3.8
- tornado from 4.2.1 to 4.3
- werkzeug from 0.10.4 to 0.11.2
- xlwings from 0.4.1 to 0.5.0

### Added:

- backports\_abc 0.4
- cycler 0.9.0
- libdynd and dynd-python 0.7.0
- jbig 2.1
- pycairo 1.10.0

### 2015-11-02 2.4.0:

#### Highlights:

- add Python 3.5 support
- updated NumPy to 1.10
- added OpenBLAS support on Linux
- made drastic speed improvements to conda
- moved from IPython to Jupyter
- improved Start Menus on Windows
- updated Qt to 4.8.7 on all platforms
- updates to more than 60 other packages

#### Known issues:

- numba and llvmlite are missing for Python 3.5 (because they don't support this Python version yet)
- numpy 1.10 has performance regression for record array access, see <https://github.com/numpy/numpy/issues/6467>
- Python 3.5 does not work on Windows XP

#### Updates:

- alabaster from 0.7.3 to 0.7.6
- argcomplete from 0.8.9 to 1.0.0
- astropy from 1.0.3 to 1.0.5
- babel from 1.3 to 2.1.1
- blaze-core from 0.8.0 to 0.8.3
- bokeh from 0.9.0 to 0.10.0

- cffi from 1.1.0 to 1.2.1
- clyent from 0.3.4 to 0.4.0
- cryptography from 0.9.1 to 1.0.2
- curl from 7.43.0 to 7.45.0
- conda from 3.14.1 to 3.18.3
- conda-build from 1.14.1 to 1.18.1
- conda-env from 2.2.3 to 2.4.4
- cython from 0.22.1 to 0.23.4
- cytoolz from 0.7.3 to 0.7.4
- datashape from 0.4.5 to 0.4.7
- decorator from 3.4.2 to 4.0.4
- freetype from 2.5.2 to 2.5.5
- greenlet from 0.4.7 to 0.4.9
- ipaddress from 1.0.7 to 1.0.14
- ipython from 3.2.0 to 4.0.0
- ipython-notebook from 3.2.0 to 4.0.4
- ipython-qtconsole from 3.2.0 to 4.0.1
- jedi from 0.8.1 to 0.9.0
- jinja2 from 2.7.3 to 2.8
- libsodium from 0.4.5 to 1.0.3
- libtiff from 4.0.2 to 4.0.6
- llvmlite from 0.5.0 to 0.7.0
- menuinst from 1.0.4 to 1.2.1
- mistune from 0.5.1 to 0.7.1
- multipledispatch from 0.4.7 to 0.4.8
- networkx from 1.9.1 to 1.10
- nltk from 3.0.3 to 3.1
- numba from 0.19.1 to 0.21.0
- numexpr from 2.4.3 to 2.4.4
- numpy from 1.9.2 to 1.10.1
- odo from 0.3.2 to 0.3.4
- openpyxl from 1.8.5 to 2.2.6
- openssl from 1.0.1k to 1.0.2d
- pandas from 0.16.2 to 0.17.0
- patsy from 0.3.0 to 0.4.0
- pillow from 2.8.2 to 3.0.0

- pip from 7.0.3 to 7.1.2
- ply from 3.6 to 3.8
- psutil from 2.2.1 to 3.2.2
- ptyprocess from 0.4 to 0.5
- py from 1.4.27 to 1.4.30
- pyasn1 from 0.1.7 to 0.1.9
- pyflakes from 0.9.2 to 1.0.0
- pyqt from 4.11.3 to 4.11.4
- pytables from 3.2.0 to 3.2.2
- pytest from 2.7.1 to 2.8.1
- pytz from 2015.4 to 2015.6
- qt from 4.8.6 to 4.8.7
- requests from 2.7.0 to 2.8.1
- scipy from 0.15.1 to 0.16.0
- setuptools from 17.1.1 to 18.4
- sip from 4.16.5 to 4.16.9
- six from 1.9.0 to 1.10.0
- spyder from 2.3.5.2 to 2.3.7
- spyder-app from 2.3.5.2 to 2.3.7
- sqlalchemy from 1.0.5 to 1.0.9
- sympy from 0.7.6 to 0.7.6.1
- toolz from 0.7.2 to 0.7.4
- tornado from 4.2 to 4.2.1
- unicodesv from 0.9.4 to 0.14.1
- xlrd from 0.9.3 to 0.9.4
- xlswriter from 0.7.3 to 0.7.7
- xlwings from 0.3.5 to 0.4.1
- zeromq from 4.0.5 to 4.1.3

**Added:**

- anaconda-client 1.1.0
- beautifulsoup4 4.4.1
- ipykernel 4.1.1
- ipython\_genutils 0.1.0
- ipywidgets 4.1.0
- jupyter 1.0.0
- jupyter\_client 4.1.1

- jupyter\_console 4.0.3
- jupyter\_core 4.0.6
- libgfortran 1.0
- nbconvert 4.0.0
- nbformat 4.0.1
- notebook 4.0.6
- openblas 0.2.14
- patchelf 0.6
- path.py 8.1.2
- pexpect 3.3
- pickleshare 0.5
- qtconsole 4.1.0
- simplegeneric 0.8.1
- singledispatch 3.4.0.3
- traitlets 4.0.0
- wheel 0.26.0

**Removed (from installer only, the packages are still maintained and available):**

- bcolz
- blz
- certifi
- dynd-python
- libdynd
- mock
- runipy

## **2015-07-02 2.3.0:**

### **Highlights:**

- updates to 60 packages, including Python 2.7.10 and Pandas 0.16.2
- support for signed packages in conda

### **Fixes:**

- fixed the extra space in IPython terminal being created when typing the tab key on Linux
- added missing zope.interface.common sub-package
- fixed Sphinx package being included in Spyder package

### **Enhancements:**

- added support for signed packages in conda
- added curl on Windows, and kerberos authentication support

- added Windows support for libnetcdf and hdf5
- split gdal into libgdal and gdal (python-bindings)

### Known issues:

- when opening some HDF5 files, pytables will crash on Windows and Python 3

### Updates:

- argcomplete from 0.8.4 to 0.8.9
- astropy from 1.0.1 to 1.0.3
- bcolz from 0.8.1 to 0.9.0
- binstar from 0.10.1 to 0.11.0
- blaze-core from 0.7.3 to 0.8.0
- bokeh from 0.8.1 to 0.9.0
- boto from 2.36.0 to 2.38.0
- cffi from 0.9.2 to 1.1.0
- cryptography from 0.8 to 0.9.1
- conda from 3.10.0 to 3.14.1
- conda-build from 1.11.0 to 1.14.1
- conda-env from 2.1.3 to 2.2.3
- curl from 7.38.0 to 7.43.0
- cython from 0.22 to 0.22.1
- cytoolz from 0.7.2 to 0.7.3
- datashape from 0.4.4 to 0.4.5
- decorator from 3.4.0 to 3.4.2
- greenlet from 0.4.5 to 0.4.7
- h5py from 2.4.0 to 2.5.0
- hdf5 from 1.8.14 to 1.8.15.1
- ipython from 3.0.0 to 3.2.0
- libpng from 1.5.13 to 1.6.17
- libxml2 from 2.9.0 to 2.9.2
- llvmlite from 0.2.2 to 0.5.0
- lxml from 3.4.2 to 3.4.4
- nltk from 3.0.2 to 3.0.3
- nose from 1.3.4 to 1.3.7
- numba from 0.17.0 to 0.19.1
- numexpr from 2.3.1 to 2.4.3
- odo from 0.3.1 to 0.3.2
- pandas from 0.15.2 to 0.16.2



- pillow from 2.7.0 to 2.8.2
- pip from 6.0.8 to 7.0.3
- ply from 3.4 to 3.6
- py from 1.4.26 to 1.4.27
- pycparser from 2.10 to 2.14
- pyflakes from 0.8.1 to 0.9.2
- pyopenssl from 0.14 to 0.15.1
- pytables from 3.1.1 to 3.2.0
- pytest from 2.6.4 to 2.7.1
- python from 2.7.9 to 2.7.10
- python-dateutil from 2.4.1 to 2.4.2
- pytz from 2015.2 to 2015.4
- pyzmq from 14.5.0 to 14.7.0
- requests from 2.6.0 to 2.7.0
- scikit-image from 0.11.2 to 0.11.3
- scikit-learn from 0.15.2 to 0.16.1
- setuptools from 14.3 to 17.1.1
- sphinx from 1.2.3 to 1.3.1
- spyder from 2.3.4 to 2.3.5.2
- sqlalchemy from 0.9.9 to 1.0.5
- theano from 0.6.0 to 0.7.0
- toolz from 0.7.1 to 0.7.2
- tornado from 4.1 to 4.2
- werkzeug from 0.10.1 to 0.10.4
- xlswriter from 0.6.7 to 0.7.3
- xlwt from 0.7.5 to 1.0.0
- yaml from 0.1.4 to 0.1.6
- zeromq from 4.0.4 to 4.0.5

**Added to Anaconda installers:**

- alabaster 0.7.3
- babel 1.3
- bottleneck 1.0.0
- idna 2.0
- ipaddress 1.0.7
- snowballstemmer 1.2.0
- sphinx\_rtd\_theme 0.1.7

**Removed (from installer only, the packages are still maintained and available):**

- futures

**Added (repository) support for:**

- ansi2html
- azure
- blockspring
- boost
- btrees
- cloudpickle
- chest
- cligj
- csvkit
- dbf
- dill
- essbasepy
- flask-login
- heapdict
- holoviews
- ldap3
- line\_profiler
- locket
- lockfile
- markdown
- markdown2
- meld3
- msgpack-python
- mysql-connector-python
- nano (Unix)
- param
- partd
- plac
- pyopengl
- pywget
- rasterio
- sas7bdat
- seaborn

- semantic\_version
- snuggs
- spacy
- stripe
- supervisor (Unix)
- thinc
- unxutils (Windows)
- xray

## 2015-03-31 2.2.0:

### Highlights:

- updates to 61 packages, including: Python, NumPyBokeh, pandas and blaze
- added 16 new packages
- added HTTPS support for default conda packages repo

### Fixes:

- fixed cython command on Windows
- fixed untgz NSIS plugin to install files with exactly 100 characters

### Enhancements:

- added https support for default conda packages repo
- renamed dateutil to python-dateutil to reflect the official name
- added HDF5 and netcdf support for GDAL
- switched to using Pillow instead of PIL
- changed ipython-notebook to start directory to home directory on Windows

### Updates:

- argcomplete from 0.8.1 to 0.8.4
- astropy from 0.4.2 to 1.0.1
- binstar from 0.7.1 to 0.10.1
- blaze from 0.6.3 to 0.7.3
- bokeh from 0.6.1 to 0.8.1
- boto from 2.32.1 to 2.36.0
- cairo from 1.12.2 to 1.12.18
- cffi from 0.8.6 to 0.9.2
- colorama from 0.3.1 to 0.3.3
- conda from 3.7.0 to 3.10.0
- conda-build from 1.8.2 to 1.11.0
- cryptography from 0.5.4 to 0.8

- cython from 0.21 to 0.22
- cytoolz from 0.7.0 to 0.7.2
- datashape from 0.3.0 to 0.4.4
- freetype from 2.4.10 to 2.5.2
- futures from 2.1.6 to 2.2.0
- greenlet from 0.4.4 to 0.4.5
- h5py from 2.3.1 to 2.4.0
- hdf5 from 1.8.13 to 1.8.14
- ipython from 2.2.0 to 3.0.0
- ipython-notebook from 2.2.0 to 3.0.0
- ipython-qtconsole from 2.2.0 to 3.0.0
- lxml from 3.4.0 to 3.4.2
- matplotlib from 1.4.0 to 1.4.3
- nltk from 3.0.0 to 3.0.2
- numba from 0.14.0 to 0.17.0
- numpy from 1.9.0 to 1.9.2
- openssl from 1.0.1h to 1.0.1k
- pandas from 0.14.1 to 0.15.2
- pep8 from 1.5.7 to 1.6.2
- pip from 1.5.6 to 6.0.8
- psutil from 2.1.1 to 2.2.1
- py from 1.4.25 to 1.4.26
- pycurl from 7.19.5 to 7.19.5.1
- pygments from 1.6 to 2.0.2
- pyparsing from 2.0.1 to 2.0.3
- pyqt from 4.10.4 to 4.11.3
- pytest from 2.6.3 to 2.6.4
- python from 2.7.8 to 2.7.9
- python-dateutil from 2.1 to 2.4.1
- pytz from 2014.7 to 2015.2
- pyzmq from 14.3.1 to 14.5.0
- qt from 4.8.5 to 4.8.6
- redis-py from 2.9.1 to 2.10.3
- requests from 2.4.1 to 2.6.0
- runipy from 0.1.1 to 0.1.3
- scikit-image from 0.10.1 to 0.11.2

- scipy from 0.14.0 to 0.15.1
- setuptools from 5.8 to 14.3
- sip from 4.15.5 to 4.16.5
- six from 1.8.0 to 1.9.0
- spyder from 2.3.1 to 2.3.4
- spyder-app from 2.3.1 to 2.3.4
- sqlalchemy from 0.9.7 to 0.9.9
- statsmodels from 0.5.0 to 0.6.1
- sympy from 0.7.5 to 0.7.6
- tk from 8.5.15 to 8.5.18
- toolz from 0.7.0 to 0.7.1
- tornado from 4.0.2 to 4.1
- werkzeug from 0.9.6 to 0.10.1
- xlswriter from 0.5.7 to 0.6.7
- zlib from 1.2.7 to 1.2.8

**Added:**

- bcolz 0.8.1
- certifi 14.05.14
- clyent 0.3.4
- enum34 1.0.4 (on Python 2.6, 2.7 and 3.3)
- fastcache 1.0.2
- fontconfig 2.11.1
- funcsigs 0.4
- jedi 0.8.1
- jsonschema 2.4.0
- llvmlite 0.2.2
- mistune 0.5.1
- odo 0.3.1
- pillow 2.7.0
- ptyprocess 0.4
- pyasn1 0.1.7
- terminado 0.5

**Removed (from installer only, the packages are still maintained and available):**

- atom
- casuarius
- chaco

- enable
- enaml
- future
- kiwisolver
- llvmpy
- mingw (on Windows)
- mpi4py
- pil (in favor of pillow)
- pyface
- traits
- traitsui

### 2014-09-30 2.1.0:

#### Fixes:

- fixed the ability to compile C extensions in Python 3 using MinGW
- added missing lzma module to Python 3.3 and 3.4 (links to xz)
- added missing werkzeug/debug/shared package data to Werkzeug package

#### Enhancements:

- added statsmodel support for Python 3.4
- added LZO support for pytables on Linux
- added scikit-learn support for Python 3.4
- added Windows cffi support (in repository)
- added bsddb conda package on Linux to support Berkeley DB

#### Updates:

- argcomplete from 0.6.7 to 0.8.1
- astropy from 0.3.2 to 0.4.2
- atom from 0.3.7 to 0.3.9
- beautiful-soup from 4.3.1 to 4.3.2
- binstar from 0.5.3 to 0.7.1
- blaze from 0.5.0 to 0.6.3
- bokeh from 0.4.4 to 0.6.1
- boto from 0.28.0 to 2.32.1
- conda from 3.5.2 to 3.7.0
- conda-build from 1.3.3 to 1.8.2
- configobj from 5.0.5 to 5.0.6
- colorama from 0.2.7 to 0.3.1

- curl from 7.30.0 to 7.38.0
- cython from 0.20.1 to 0.20.2
- datashape from 0.2.0 to 0.3.0
- docutils from 0.11 to 0.12
- dynd from 0.6.2 to 0.6.5
- enaml from 0.9.1 to 0.9.8
- future from 0.12.1 to 0.13.1
- greenlet from 0.4.2 to 0.4.4
- h5py from 2.3.0 to 2.3.1
- hdf5 from 1.8.9 to 1.8.13
- ipython from 2.1.0 to 2.2.0
- jinja2 from 2.7.2 to 2.7.3
- kiwisolver from 0.1.2 to 0.1.3
- launcher from 0.1.5 to 1.0.0
- libnetcdf from 4.2.1.1 to 4.3.2
- llvmpy from 0.12.6 to 0.12.7
- lxml from 3.3.5 to 3.4.0
- markupsafe from 0.18 to 0.23
- matplotlib from 1.3.1 to 1.4.0
- multipledispatch from 0.4.3 to 0.4.7
- networkx from 1.8.1 to 1.9.1
- nltk from 2.0.4 to 3.0.0
- nose from 1.3.3 to 1.3.4
- numba from 0.13.2 to 0.14.0
- numpy from 1.8.2 to 1.9.0
- pandas from 0.14.0 to 0.14.1
- patsy from 0.2.1 to 0.3.0
- pep8 from 1.5.6 to 1.5.7
- py from 1.4.20 to 1.4.25
- pycurl from 7.19.3.1 to 7.19.5
- pytest from 2.5.2 to 2.6.3
- python from 2.7.7 to 2.7.8
- pytz from 2014.3 to 2014.7
- pyzmq from 14.3.0 to 14.3.1
- requests from 2.3.0 to 2.4.1
- runipy from 0.1.0 to 0.1.1

- scikit-image from 0.10.0 to 0.10.1
- scikit-learn from 0.14.1 to 0.15.2
- setuptools from 3.6 to 5.8
- six 1.6.1 to 1.8.0
- sphinx from 1.2.2 to 1.2.3
- spyder from 2.3.0rc1 to 2.3.1
- sqlalchemy from 0.9.4 to 0.9.7
- tornado from 3.2.1 to 4.0.2
- xlswriter from 0.5.5 to 0.5.7

### Added:

- abstract-rendering 0.5.1 (on Unix and Python 2)
- cffi 0.8.6
- cryptography 0.5.4
- cytoolz 0.7.0
- decorator 3.4.0
- futures-2.1.6 (for Python 2)
- pyopenssl 0.14
- sockjs-tornado 1.0.1
- toolz 0.7.0
- unicodecsv 0.9.4
- xz 5.0.5

### 2014-06-12 2.0.1:

#### Fixes:

- added missing libpython (the so-called MinGW import library) for Python 3.4
- in order to make pandas.io.excel work, we downgraded openpyxl from 2.0.2 to 1.8.5
- added missing idle script on Windows

#### Updates:

- conda from 3.5.2 to 3.5.5
- conda-build from 1.3.3 to 1.3.5
- numba from 0.13.1 to 0.13.2
- openssl from 1.0.1g to 1.0.1h
- pandas from 0.13.1 to 0.14.0
- python from 2.7.6 to 2.7.7
- scikit-image from 0.9.3 to 0.10.0
- werkzeug from 0.9.4 to 0.9.6



**2014-05-28: 2.0.0:****Fixes:**

- on Windows the /D option of the executable installer is now working
- added missing TkAgg matplotlib backend on Windows
- added missing osgeo.\_gdal\_array extension to GDAL
- fixed rope on Python 3

**Known issues:**

- even though the matplotlib tkagg backend is now supported on all platforms and with all Python versions now, there might be problems on Windows with Python 3.4
- the Windows file association (‘.py’-files being executed by the Anaconda Python interpreter) is not working

**Enhancements:**

- switched from using PySide to PyQt as the default Qt binding
- added lcms to PIL on Unix
- added ability to copy files upon install when filesystem fails to create hard links
- added netCDF4 support on 64-bit Windows
- on macOS, Tk in now linked to Cocoa (instead of X11)

**Updated:**

- astropy from 0.3.0 to 0.3.2
- binstar from 0.4.4 to 0.5.3
- blz from 0.6.1 to 0.6.2
- bokeh from 0.4.1 to 0.4.4
- boto from 2.25.0 to 2.28.0
- conda from 3.0.6 to 3.5.2
- conda-build from 1.2.0 to 1.3.3
- configobj from 4.7.2 to 5.0.5
- datashape from 0.1.1 to 0.2.0
- dynd-python gtom 0.6.1 to 0.6.2
- future from 0.11.2 to 0.12.1
- gevent from 1.0 to 1.0.1
- gevent-websocket from 0.9.2 to 0.9.3
- h5py from 2.2.1 to 2.3.0
- ipython from 1.1.0 to 2.1.0
- itsdangerous from 0.23 to 0.24
- launcher from 0.1.2 to 0.1.5
- llvmpy from 0.12.3 to 0.12.4
- lxml from 3.3.1 to 3.3.5

- nose from 1.3.0 to 1.3.3
- numba from 0.12.1 to 0.13.1
- numpy from 1.8.0 to 1.8.1
- openpyxl 1.8.2 to 2.0.2
- openssl from 1.0.1c to 1.0.1g
- pep8 gtom 1.4.6 to 1.5.6
- pip from 1.5.2 to 1.5.6
- psutil from 1.2.1 to 2.1.1
- pycosat from 0.6.0 to 0.6.1
- pycurl from 7.19.0 to 7.19.3.1
- pyflakes from 0.7.3 to 0.8.1
- pytables from 3.1.0 to 3.1.1
- pytz from 2013b to 2014.3
- pyyaml 3.10 to 3.11
- pyzmq from 2.2.0.1 to 14.3.0
- requests from 2.2.1 to 2.3.0
- scipy from 0.13.3 to 0.14.0
- setuptools from 2.2 to 3.6
- six from 1.5.2 to 1.6.1
- sphinx form 1.2.1 to 1.2.2
- spyder from 2.2.5 to 2.3.0rc1
- sqlalchemy from 0.9.2 to 0.9.4
- sqlite from 3.7.13 to 3.8.4.1
- sympy from 0.7.4.1 to 0.7.5
- tk from 8.5.13 to 8.5.15
- tornado from 3.2.0 to 3.2.1
- xlrd from 0.9.2 to 0.9.3
- xlswriter from 0.5.2 to 0.5.5
- zeromq from 2.2.0 to 4.0.4

**Added:**

- conda-launch 0.1
- jdcals 1.0
- multipledispatch 0.4.0
- python 3.4.1
- pyqt 4.10.4
- runipy 0.1.0

- sip 4.15.5
- xlwings 0.1.0 (Windows only)

**Removed (from installer, packages are still supported and available in repo):**

- apptools
- biopython
- envisage
- disco and erlang (from 64-bit Linux)
- gevent\_zeromq
- keyring
- mayavi
- mdp
- netcdf4
- pykit
- pysal
- pysam
- vtk

**2014-04-09: 1.9.2:**

**Fixes:**

- updated to openssl 1.0.1g on Unix to fix the “Heartbleed bug” of the TLS Heartbeat Extension problem (reported in the news)
- fixed /D option in silent mode for Windows installer

**Updates:**

- openssl from 1.0.1c to 1.0.1g
- conda from 3.0.6 to 3.4.1
- conda-build from 1.2.0 to 1.3.1

**2014-02-20: 1.9.1:**

**Fixes:**

- openpyxl to depend on up-to-date version of lxml
- added missing MSVCP (both for 2008 and 2010) DLLs to Windows installers which fixes issues with the user install mode on some systems

**Updates:**

- atom from 0.3.6 to 0.3.7
- blaze from 0.4.1 to 0.4.2
- bokeh from 0.4 to 0.4.1

- boto 2.24.0 to 2.25.0
- conda from 3.0.3 to 3.0.6
- conda-build from 1.1.0 to 1.2.0
- cython from 0.20 to 0.20.1
- datashape from 0.1.0 to 0.1.1
- dynd-python 0.6.0 to 0.6.1
- enaml from 0.9.0 to 0.9.1
- llvmpy from 0.12.2 to 0.12.3
- lxml from 3.2.3 to 3.3.1
- netcdf4 from 1.0.7 to 1.0.8
- numba from 0.12.0 to 0.12.1
- numexpr from 2.3.0 to 2.3.1
- pandas from 0.13.0 to 0.13.1
- pykit from 0.1.0 to 0.2.0
- python from 3.3.3 to 3.3.4
- setuptools from 2.1 to 2.2

### Added:

- added Py3k support for h5py
- netcdf4 on 32-bit Windows
- xlsxwriter 0.5.2

### 2014-02-10: 1.9.0:

#### Highlights:

- NumPy updated to version 1.8
- updates to about 35 packages, including Bokeh and Blaze
- added 10 new packages

#### Enhancements:

- use MSVC 2010 to compile Python 3 and C extensions on Windows
- remove distribute in favor of setuptools
- enable threadsafe when building HDF5 on Linux
- renamed the Python Imaging Library (PIL) from imaging to pil
- updated EULA

#### Fixes:

- ssl bindings in Python standard library on macOS
- Windows installers not working properly when PYTHONHOME is set

#### Updated:

- apptools from 4.2.0 to 4.2.1
- astropy from 0.2.5 to 0.3.0
- atom from 0.3.4 to 0.3.6
- binstar from 0.3.1 to 0.4.4
- biopython from 1.62 to 1.63
- blaze from 0.3.0 to 0.4.1
- boto from 2.15.0 to 2.24.0
- bokeh from 0.2 to 0.4
- chaco from 4.3.0 to 4.4.1
- conda from 2.0.4 to 3.0.3
- cython from 0.19.2 to 0.20
- dynd-python 0.5.0 to 0.6.0
- enaml from 0.8.3 to 0.9.0
- envisage from 4.3.0 to 4.4.1
- gevent from 0.13.8 to 1.0
- gevent-websocket from 0.3.6 to 0.9.2
- greenlet from 0.4.1 to 0.4.2
- h5py from 2.2.0 to 2.2.1
- jinja2 from 2.7.1 to 2.7.2
- keyring from 3.2 to 3.3
- llvmmath from 0.1.1 to 0.1.2
- llvmpy from 0.12.0 to 0.12.1
- netcdf4 from 1.0.6 to 1.0.7
- numexpr from 2.2.2 to 2.3.0
- numba from 0.11.0 to 0.12.0
- numpy from 1.7.1 to 1.8.0
- openpyxl from 1.6.2 to 1.8.2
- pandas from 0.12.0 to 0.13.0
- pip from 1.4.1 to 1.5.2
- psutil from 1.1.2 to 1.2.1
- py from 1.4.17 to 1.4.20
- pycparser from 2.9.1 to 2.10
- pyface from 4.3.0 to 4.4.0
- pyparsing from 1.5.6 to 2.0.1
- pyreadline from 2.0.dev to 2.0
- pytables from 3.0.0 to 3.1.0

- pytest from 2.4.2 to 2.5.2
- python from 2.7.5 to 2.7.6, and 3.3.2 to 3.3.3
- redis-py from 2.7.2 to 2.9.1
- requests 1.2.3 to 2.2.1
- scipy from 0.13.0 to 0.13.2
- six from 1.4.1 to 1.5.2
- sphinx from 1.1.3 to 1.2.1
- sqlalchemy from 0.8.3 to 0.9.2
- sympy from 0.7.3 to 0.7.4.1
- tornado from 3.1.1 to 3.2.0
- theano from 0.5.0 to 0.6.0
- traits from 4.3.0 to 4.4.0
- traitsui from 4.3.0 to 4.4.0

### Added:

- argcomplete 0.6.7
- blz 0.6.1
- cdecimal 2.3
- conda-build 1.1.0
- datashape 0.1.0
- future 0.11.2
- kiwisolver 0.1.2
- mock 1.0.1
- setuptools 2.1
- ssl\_match\_hostname 3.4.0.2
- ujson 1.33
- scikit-learn and redis-py support for Python 3
- added traits and unittest2 support for Python 2.6

### Removed:

- distribute
- llvmmath
- meta

### 2013-11-05: 1.8.0:

#### Enhancements:

- on Windows the installer now allows installing in user mode without having system administrator privileges

- use RPATH (instead of RUNPATH) on Linux, which fixes link problems when LD\_LIBRARY\_PATH is set
- added ipython-notebook meta package for all supported Python versions
- removed curl binary on macOS, to avoid superseding system curl

**Fixes:**

- wrong location of VTK libraries in VTKTargets-debug.cmake on Linux
- fix python.app problem related to adding the symlink to lib, which also appears to create problems with %%cython magic in ipython
- apply patch to Mayavi, which fixes running mlab scripts

**Updated:**

- astropy from 0.2.4 to 0.2.5
- atom from 0.3.2 to 0.3.4
- biopython from 1.61 to 1.62
- boto from 2.12.0 to 2.15.0
- bokeh from 0.1.1 to 0.2
- conda from 1.9.1 to 2.0.4
- cython from 0.19.1 to 0.19.2
- dynd from 0.4.2 to 0.5.0
- enaml from 0.7.19 to 0.8.3
- ipython 1.0.0 to 1.1.0
- keyring from 3.0.1 to 3.2
- matplotlib from 1.3.0 to 1.3.1
- netcdf4 from 1.0.5 to 1.0.6
- numba from 0.10.2 to 0.11.0
- numexpr from 2.0.1 to 2.2.2
- psutil from 1.0.1 to 1.1.2
- pycrypto from 2.6 to 2.6.1
- pytables from 2.4.0 to 3.0.0
- python 2.6.8 to 2.6.9
- pytest from 2.3.5 to 2.4.2
- scikit-image from 0.8.2 to 0.9.3
- scipy from 0.12.0 to 0.13.0
- sqlalchemy from 0.8.2 to 0.8.3
- sympy from 2.2.4 to 2.2.5

**Added:**

- blaze 0.3
- pykit 0.1

- beautiful-soup 4.3.1
- openpyxl 1.6.2

### 2013-09-10: 1.7.0:

#### Highlights:

- added VTK, Mayavi and Bokeh
- updated to new ipython 1.0 and matplotlib 1.3, and llvm 3.3
- many improvements and bug fixes to conda

#### Enhancements:

- removed conda as a direct anaconda dependency
- add MinGW runtime DLLs to Scripts directory on Windows
- fixed python-dateutil for Python 2

#### Updated:

- astropy from 0.2.3 to 0.2.4
- atom from 0.2.3 to 0.3.2
- binstar from 0.1.2 to 0.3.1
- boto from 2.9.6 to 2.12.0
- conda from 1.7.2 to 1.9.1
- docutils from 0.10 to 0.11
- enaml from 0.7.6 to 0.7.19
- h5py from 2.1.1 to 2.2.0
- ipython from 0.13.2 to 1.0.0
- itsdangerous from 0.21 to 0.23
- jinja2 from 2.6 to 2.7.1
- libdynd and dynd-python from 0.4.0 to 0.4.2
- llvm from 3.2 to 3.3
- llvmmath from 0.1.0 to 0.1.1
- llvmpy from 0.11.3 to 0.12.0
- lxml from 3.2.1 to 3.2.3
- keyring from 1.4 to 3.0.1
- matplotlib from 1.2.1 to 1.3.0
- netcdf4 from 1.0.4 to 1.0.5
- networkx fomr 1.7 to 1.8.1
- numba from 0.9.0 to 0.10.2
- opencv from 2.4.2 to 2.4.6
- pandas from 0.11.0 to 0.12.0



- pep8 from 1.4.5 to 1.4.6
- pip from 1.3.1 to 1.4.1
- psutil from 0.7.1 to 1.0.1
- pyflakes from 0.7.2 to 0.7.3
- pysal 1.5.0 to 1.6.0
- pyside from 1.1.2 to 1.2.1 (not macOS)
- qt from 4.7.4 to 4.8.5 (not macOS)
- scikit-learn from 0.13.1 to 0.14.1
- six from 1.3.0 to 1.4.1
- spyder from 2.2.0 to 2.2.4
- sqlalchemy 0.8.1 to 0.8.2
- statsmodels from 0.4.3 to 0.5.0
- sympy from 0.7.2 to 0.7.3
- tornado from 3.1 to 3.1.1
- werkzeug from 0.9.1 to 0.9.4

**Added:**

- bokeh 0.1.1
- chaco 4.3.0
- configobj 4.7.2
- markupsafe 0.18
- mayavi 4.3.0
- patsy 0.2.1
- traits 4.3.0
- vtk 5.10.1

**2013-07-09: 1.6.2: (Windows only)**

- Fixed path being incorrectly appended on Windows during install

**2013-07-03: 1.6.1:**

- fixed .pkg installer
- updated binstar from 0.1.1 to 0.1.2 (fixes upload on Windows)
- updated conda from 1.7.1 to 1.7.2 (fixes updating python.app on macOS)
- updated dynd from 0.3.0 to 0.4.0
- updated launcher from 0.1.1 to 0.1.2
- added missing pydoc command on Unix

- macOS: fix hard coded build prefix in .dylib files for may other libraries
- Windows: append instead of prepend path on Windows

### 2013-06-21: 1.6.0:

#### Highlights:

- the “Launcher”, which allows users to start up applications
- conda has now the ability to build conda packages, which can be uploaded to binstar.org
- conda now uses a SAT solver to solve the install dependency problem

#### Enhancements:

- added a .pkg installer for macOS, such that installing Anaconda does not require command line access
- create copy of .bashrc (.bash\_profile on macOS) before appending the PATH setting upon install
- Windows Menu items should are now installed system wide

#### Fixes:

- removed Lib/test/testbz2\_bigmem.bz2 from Windows, this (harmless) file was triggering Trojan-ArcBomb.BZip.Agent warning, see: <http://bugs.python.org/issue17843>
- json.decoder in Python 2.7 standard library not using .decode('hex'), this was (mysteriously) causing install problems on macOS
- fixed PIL.\_imagedtk on Linux

#### Updated:

- python from 2.7.4 to 2.7.5, and 3.3.1 to 3.3.2
- astropy from 0.2.1 to 0.2.3
- boto from 2.9.2 to 2.9.6
- conda from 1.5.2 to 1.7.1
- cython from 0.19 to 0.19.1
- distribute from 0.6.36 to 0.6.45
- flask from 0.9 to 0.10.1
- greenlet from 0.4.0 to 0.4.1
- llvmpy from 0.11.2 to 0.11.3
- lxml form 3.2.0 to 3.2.1
- numba from 0.8.1 to 0.9.0
- py from 1.4.12 to 1.4.14
- pytest from 2.3.4 to 2.3.5
- requests from 1.2.0 to 1.2.3
- tornado from 3.0.1 to 3.1
- werkzeug from 0.8.3 to 0.9.1

#### Added:

- launcher 0.1.1
- binstar 0.1.1
- itsdangerous 0.21
- keyring 1.4
- llvmmath 0.1.0
- pep8 1.4.5
- pywin32 218.4 on Windows

#### **2013-05-09: 1.5.1: (macOS only)**

- fixed pip command
- replace spaces by underscore in user install location
- shared libraries now link to /usr/lib/libgcc\_s.1.dylib (instead of /usr/local/lib/libgcc\_s.1.dylib)

#### **2013-05-08: 1.5.0:**

##### **Highlights:**

- updates to all important packages: python, numpy, scipy, ipython, matplotlib, pandas, cython
- added netCDF4 (with OpenDAP support) on Linux and macOS

##### **Fixed:**

- Cython on macOS on Python 2.6, due to a problem with Pyhton's config/Makefile
- py.test command (all platforms)
- python-config command not using correct interpreter on macOS
- added missing MSVC 2008 and 2010 runtime to Windows installers
- removed hard-coded build location from identification name of dynamic shared libraries on macOS, to allow easier building against libraries in Anaconda

##### **Enhancements:**

- **The Windows installers has a new dialog box with the following options:**
  - “Add Anaconda to the System Path”
  - “Register Anaconda as default Python version of the system”
- The Unix installers have an option to add Anaconda to the path in the ~/.bashrc (on Linux) or ~/.bash\_profile (on macOS). On macOS the default is ‘yes’, on Linux the default is ‘no’.
- added armv6l supports (only Python 2.7 and selected packages)
- link pycurl and libnetcdf dynamically against curl library on Unix
- add configure option –with-pgm for zeromq on Unix

##### **Added:**

- netCDF4 (with OpenDAP support) 1.0.4 on Linux and macOS
- ordereddict 1.1 (on Python 2.6)

- pycosat 0.6.0
- atom 0.2.3
- enaml 0.7.6
- casuarius 1.1
- dynd-python 0.3.0
- rope 0.9.4

**Updates:**

- python from 2.7.3 to 2.7.4, and 3.3.0 to 3.3.1
- numpy from 1.7.0 to 1.7.1
- scipy from 0.11.0 to 0.12.0
- ipython from 0.13.1 to 0.13.2
- matplotlib from 1.2.0 to 1.2.1
- astropy from 0.2 to 0.2.1
- biopython from 1.60 to 1.61
- bitarray from 0.8.0 to 0.8.1
- boto from 2.8.0 to 2.9.2
- conda from 1.4.4 to 1.5.2
- curl from 7.26.0 to 7.30.0
- cython from 0.18 to 0.19
- distribute from 0.6.34 to 0.6.36
- llvmpy from 0.11.1 to 0.11.2
- lxml from 3.0.2 to 3.2.0
- nose from 1.2.1 to 1.3.0
- numba from 0.7.0 to 0.8.1
- pandas from 0.10.1 to 0.11.0
- psutil from 0.6.1 to 0.7.1
- pyflakes from 0.6.1 to 0.7.2
- pytz from 2012j to 2013b
- requests from 0.13.9 to 1.2.0
- scikit-learn from 0.13 to 0.13.1
- six from 1.2.0 to 1.3.0
- spyder from 2.1.13 to 2.2.0
- sqlalchemy from 0.7.8 to 0.8.1
- sympy from 0.7.1 to 0.7.2
- tornado from 2.4.1 to 3.0.1
- xlrd from 0.9.0 to 0.9.2

- xlwt from 0.7.4 to 0.7.5

**Removed (from installer only, still available with conda):**

- bitey
- gdata (conflicts with atom (which is required by enaml))
- googlecl (requires gdata)

**2013-03-12: 1.4.0:**

Many more packages are now supported on Python 3.3. In addition, we have added Python 3 support on Windows, such that now Python 2.6, 2.7 and 3.3 is supported across all platforms. In addition, we have redesigned the Windows installer, which was suffering from a number of problems, in particular the lack of uninstall functionality and the GUI not working on some systems.

**added:**

- astropy 0.2
- lxml 3.0.2
- pycparser 2.9.1
- six 1.2.0
- xlrd 0.9.0
- xlwt 0.7.4

**updated:**

- boto from 2.7.0 to 2.8.0
- conda from 1.3.5 to 1.4.2
- cubes from 0.10.1 to 0.10.2
- cython from 0.17.4 to 0.18
- dateutil from 1.5 to 2.1
- llvmpy from 0.10.2 to 0.11.1
- numba from 0.6.0 to 0.7.0
- numpy from 1.7rc1 to 1.7.0
- pyflakes from 0.5.0 to 0.6.1
- pygments from 1.5 to 1.6
- pysal from 1.4.0 to 1.5.0
- pyreadline from 1.7.1 to 2.0.dev
- pytz from 2012d to 2012j
- scikit-image from 0.7.1 to 0.8.2

**fixed:**

- pytables on Windows

**other notes:**

- Linux: a ATLAS package is now available (conda install atlas). In addition the site.cfg in the numpy.distutils has been updated, such that other packages (e.g. scipy) which use the atlas build configuration can be build against the (non-MKL linked) numpy in Anaconda.

### 2013-02-06: 1.3.1:

#### added:

- Python 2.6 support for iopro, numba and numbapro
- Python 2.6 support on Windows (Python 2.6 is now supported on all platforms)
- added pythonw (the command to run Python GUI applications) on macOS
- added chaco on Windows

#### updates:

- conda from 1.3.2 to 1.3.5
- iopro from 1.3.0 to 1.3.2
- llvmpy from 0.10.0 to 0.10.2
- numba from 0.5.0 to 0.6.0
- numbapro from 0.8.1 to 0.8.1

#### other changes:

- removed anaconda-launcher

### 2013-01-23: 1.3.0:

#### fixes:

- fixed missing Grammar.txt in Sphinx
- recompiled llvm and llvmpy using gcc 4.4.6 on Linux, this fixes a problem with the mandel.py example in numba
- made Windows installer dialog box resizable
- fixed problem that importing numbapro or iopro removed sys from the namespace

#### updates:

- LLVM from 3.1 to 3.2
- llvmpy from 0.9 to 0.10.0
- numba from 0.3.2 to 0.5.0
- numbapro from 0.7.3 to 0.8.0
- iopro from 1.2.3 to 1.3.0
- conda from 1.2.1 to 1.3.0
- pandas from 0.9.0 to 0.10.1
- cython from 0.17.1 to 0.17.4
- iopro from 1.2.2 to 1.2.3

- spyder from 2.1.11 to 2.1.13
- h5py from 2.1.0 to 2.1.1
- distribute from 0.6.30 to 0.6.34
- nose from 1.1.2 to 1.2.1
- tornado from 2.3 to 2.4.1
- docutils from 0.9.1 to 0.10
- nltk from 2.0.3 to 2.0.4
- gevent from 0.13.7 to 0.13.8
- numpy from 1.7.0b2 to 1.7.0rc1
- boto from 2.6.0 to 2.7.0
- scikit-learn from 0.11 to 0.12.1
- scikits-image from 0.6.1 to 0.7.1
- pyaudio from 0.2.6 to 0.2.7
- pytest from 2.3.3 to 2.3.4
- redis from 2.4.15 to 2.6.9
- redis-py from 2.4.13 to 2.7.2
- disco from 0.4.2 to 0.4.4

**added:**

- Tkinter support on all platforms
- redis support on macOS
- cubes 0.10.1
- ply 3.4
- pycrypto 2.6
- pyparsing 1.5.6
- googlecl 0.9.12
- gdata 2.0.17
- biopython 1.60

**2012-11-21: 1.2.1:**

- pucurl on macOS
- anaconda-launcher envs by updating to conda 1.2.1
- add missing pyodbc numpy\_tests in iopro/tests/pyodbc
- updated wiseRF to version 1.1
- add creation of .continuum directory (if not created yet) on Windows
- minor fixes in numba, numbapro, and iopro
- fixed version of “py” package

- add missing Windows manifest to Windows executable installer
- fixed Windows Menu install and making Anaconda the default Python
- on 2012-12-06 we released a 32-bit Linux version

### **2012-11-13: 1.2.0:**

- performance and feature enhancements to Numba Pro
- performance and feature enhancements to IOPro
- improved conda command (package management)
- added Qt to the Linux Version (Qt is now on all platforms)
- added MDP, NLTK and py, pytest
- update matplotlib from 1.1.1 to 1.2.0
- update h5py from 2.0.1 to 2.1.0
- update IOPro to 1.2.1
- update libpng to 1.5.13

### **2012-10-05: 1.1.0:**

- add GUI to Windows installer
- IDE Spyder (Qt) for Mac Version
- add conda 1.0
- update llvmpy to 0.8.3
- add MinGW on Windows

### **2012-09-06: 1.0.0:**

- add Windows support
- installer can now install into different locations
- enable building free and permium version
- enable termcap in erlang
- add MKL support to permium version
- add networkx, pysal, pycurl, gevent\_zeromq, requests, pip, distribute
- add iopro to permium version
- update scipy from 0.11.0b1 to 0.11.0rc2
- update scikits-image form 0.6 to 0.6.1
- update pytables from 2.4.0b1 to 2.4.0
- update pandas from 0.8.0 to 0.8.1
- add patch to disco to always use the anaconda erl



- remove useless files (Python) from being installed

**2012-08-21: 0.9.0:**

- add macOS (x86\_64 10.5 or higher) support
- add bitey and other packages
- update several other packages

**2012-07-18: 0.8.3:**

- update changes to etc/init.d/disco script
- add patch, fixes disco and ddfs listdir misfeature
- add `-packages` option to `anaconda` command
- add missing `h5py`
- improve ease of testing

**2012-07-18: 0.8.2:**

- fixed `theano.sparse`
- removed (broken) `scikits` namespace
- add disco config and setup files
- add `anaconda` command, for version information

**2012-07-17: 0.8.1:**

- fixed `libm.so` ctypes error in `scipy` tests
- added import tests to all C extension modules
- fixed lzo support in `pytables`

**2012-07-17: 0.8.0:**

- initial release

## Help and support

The following resources are available to help you:

- Free community support is available from the [Anaconda Support Group](#).
- Anaconda offers [support and training](#).
- Package creators or maintainers may be able to help you with installing a package or building and publishing an updated version. Package creators may also contact Anaconda to submit their package for consideration to be included in Anaconda.

- Report bugs on the [Anaconda GitHub issue tracker](#).

### Security practices

Anaconda maintains the following security and provenance/chain-of-custody practices:

- The engineers whose purpose is to build and maintain the Anaconda Distribution have curated the packages contained within based on their relevance to the data science community. These open-source packages are vetted for their widespread adoption and community support, which allows any security vulnerabilities to be addressed quickly and completely in a transparent manner.
- Source code and built artifacts are maintained with strict chain-of-control and are built, scanned, and hashed on a separate secure network within Anaconda. Only a small number of developers and IT team members have access to this network and the associated servers.
- All versions of the Anaconda Distribution and all packages that are made available at <https://repo.anaconda.com/> have published SHA256 checksums. We recommend you *verify your install*.
- A Quality Assurance team performs exhaustive testing on each release of Anaconda and Miniconda, including all installers and packages. This includes the use of multiple commercial anti-malware products, as well as custom in-house security tools, for all supported operating systems - Windows, macOS, and Linux. When there are issues, they are followed up on for remediation or noted in the documentation.
- Anaconda maintains a team of IT leaders that works with software engineers to monitor all active security events through various channels of information, which results in fast response times and, whenever necessary, direct communication to our customers through Customer Support.
- Developers use controlled machines with the latest security patches.
- Especially security-minded customers may implement the functionality of the Anaconda Repository as part of an Anaconda Enterprise subscription to only allow a small set of packages to come onto their site at their control and block all others from entering their network. Due to the open-source nature of the enclosed packages, they may perform advanced code reviews or other associated activities to ensure their desired level of risk management and/or compliance.

### Troubleshooting

If you have a troubleshooting issue that is not listed here, obtain free support for Anaconda through the [Anaconda mailing list](#). For Anaconda installation or technical support options, visit our [support offerings page](#).

You may also wish to see the [Anaconda Navigator Troubleshooting guide](#).

- *[Anaconda installer download problems](#)*
- *[Cannot open Anaconda Prompt after installation](#)*
- *[Cannot see Anaconda menu shortcuts after installation on Windows](#)*
- *[Windows error: Failed to create Anaconda menus or Failed to add Anaconda to the system PATH](#)*
- *[I'm having trouble with the Anaconda installer on Windows. How can I debug my issue?](#)*
- *[Cannot get conda to run after installing](#)*
- *[Recovering your Anaconda installation](#)*
- *[Using Anaconda behind a firewall or proxy](#)*
- *[.zshrc not updated under macOS Catalina](#)*

- *Insecure Platform Warning*
- *Conda: command not found on macOS or Linux*
- *Anaconda interfering with other software on Windows*
- *Windows error: no environment named “search” exists*
- *MKL Trial warning is displayed even though MKL-linked packages are now free and installed by default*
- *Error message: Permission denied, when loading MKL shared libraries*
- *Error message on Miniconda install: Already installed*
- *Conda update anaconda command does not install the latest version of Anaconda*
- *Linking problems when Python extensions are compiled with gcc*
- *Error message: Unable to remove files*
- *Files left behind after uninstalling Anaconda on Windows*
- *Spyder errors or failure to launch on Windows*
- *Problems running Anaconda on macOS 10.12.2*
- *“execution error: localhost doesn’t understand the “open location” message. (-1708)” when opening a Jupyter notebook on macOS 10.12.5*
- *Missing libgfortran on Power8*
- *Missing libgomp on Power8*
- *Anaconda on Power8 reports “can not execute binary file”*
- *Uninstaller requests admin privileges on Windows*
- *Windows permission errors when installing from Favorites folder*
- *Trouble with activation on PowerShell on Windows*
- *Cannot install Distribution 2019.07 on a webfaction server*
- *Segmentation fault on package import with macOS Python 3.7 interpreter*
- *Using 32- and 64-bit libraries and CONDA\_FORCE\_32BIT*

## Anaconda installer download problems

### Cause

The Anaconda installer files are large (over 300 MB), and some users have problems with errors and interrupted downloads when downloading large files.

### Solution

One option is to download and install the smaller [Miniconda](#) (under 60MB) and then use the command `conda install anaconda` to download and install all the remaining packages in Anaconda. If the package downloads

are interrupted, just run `conda install anaconda` again. Conda only downloads the packages that were not finished in any previous attempts.

A second option is to download the large Anaconda installer file, and restart it if the download is interrupted or you need to pause it.

### Windows

If you use Internet Explorer:

1. Click the Settings icon.
2. Click “View Downloads” to open the Download Manager.
3. Click on the “Resume” button next to the stopped download to restart downloading. The download resumes at the point where it stopped.

If you use Edge browser:

1. In Windows Explorer, open your downloads folder. There will be temporary files there associated with the partial downloads. Delete all of the temporary files except for the download you want to resume.
2. In Edge, click the file to download it again. Pause the download but do not cancel it.
3. In Windows Explorer, open your downloads folder. You will see two files: the partially downloaded file from earlier, and the paused download you just started. Copy the name of the file you just started, delete this file, and rename the other file with the copied name.
4. In Edge, resume the download.

If you use Chrome browser:

Download the plugin for Chrome called Chrono Download manager. In your Chrome browser, go to <https://chrome.google.com/webstore/category/extensions>, search on “Chrono Download” and select, “Add to Chrome.”

To resume the download using Chrono Download, from your top browser menu, click on the Chrome menu button, then click “Downloads.” Select the filename, then click “Resume” to restart your download.

### macOS and Linux

- In your terminal window, download the file with the command `curl -O FILENAME`.

---

**Note:** Replace FILENAME with the full path and name of the file, including `http://` or `https://`.

---

- To pause the download, use `CTRL-C`.

---

**Note:** While a download is paused, you can shut down or restart your computer.

---

- When ready to resume your download, use `curl -O -C FILENAME`.

Where “-C” is the option for “continue”. You can pause and restart a download as many times as you wish.

### Cannot open Anaconda Prompt after installation

I get an error message that says “activate.bat is not a recognized file or command”.

#### Cause

Anaconda 5.0.1 sometimes does not install completely on Windows.

## Solution

Until a new version is released, you can install Miniconda, and then use conda to install the rest of the packages in Anaconda with these instructions:

Open the command prompt (Windows key + the R key on your keyboard) which brings up the Run... dialog box. Enter `cmd.exe` and then press enter)

Copy the following text:

```
cd %UserProfile%
powershell -command "& { (New-Object Net.WebClient).DownloadFile('https://repo.
↪anaconda.com/miniconda/Miniconda3-latest-Windows-x86_64.exe', 'mc3.exe') }"
start /wait "" mc3.exe /InstallationType=JustMe /AddToPath=0 /RegisterPython=0 /
↪NoRegistry=0 /S /D=%UserProfile%\anaconda3
%UserProfile%\anaconda3\Scripts\activate.bat
conda install -y anaconda=5.0.1 conda-build _ipyw_jlab_nb_ext_conf
```

Then paste it into the command prompt window.

---

**Note:** This installs to a subdirectory in your User directory named `anaconda3`. If you use a different directory, replace `anaconda3` with the actual name.

---

## Cannot see Anaconda menu shortcuts after installation on Windows

After installing on Windows, in the Windows Start menu I cannot see Anaconda prompt, Anaconda Cloud and Navigator shortcuts.

### Cause

This may be caused by the way Windows updates the Start menu, or by having multiple versions of Python installed, where they are interfering with one another. Existing Python installations, installations of Python modules in global locations, or libraries that have the same names as Anaconda libraries can all prevent Anaconda from working properly.

## Solution

If start menu shortcuts are missing, Microsoft recommends rebooting your computer or [restarting Windows Explorer](#).

If that doesn't work, clear `$PYTHONPATH` and re-install Anaconda. Other potential solutions are covered in the “Conflicts with system state” section of [this blog post](#).

## Windows error: Failed to create Anaconda menus or Failed to add Anaconda to the system PATH

During installation on a Windows system, a dialog box appears that says “Failed to create Anaconda menus, Abort Retry Ignore” or “Failed to add Anaconda to the system PATH.” There are many possible Windows causes for this.

## Solution

Try these solutions, in order:

- Do not install on a PATH longer than 1024 characters.
- Turn off anti-virus programs during install, then turn back on.
- Uninstall all previous Python installations.
- Clear all PATHs related to Python in sysdm.cpl file.
- Delete any previously set up Java PATHs.
- If JDK is installed, uninstall it.

### I'm having trouble with the Anaconda installer on Windows. How can I debug my issue?

#### Cause

The cause could be any number of issues.

#### Solution

Anaconda 4.4 added a feature to the Windows installer so that the “verbose” install information is printed out to a special debug stream via the Win32 API function OutputDebugStream. To see these messages, during installation you need to run the Microsoft utility <https://technet.microsoft.com/en-us/sysinternals/debugview.aspx>. This may provide useful clues for troubleshooting or submitting bug reports.

### Cannot get conda to run after installing

You may get “conda not found” or “conda is not recognized as an internal or external command” or a similar message, and you cannot execute conda in a terminal window regardless of what path you are on.

#### Cause

Most likely when you were installing Anaconda or Miniconda, you answered “NO” to the question whether or not to prepend the conda prompt to your path.

#### Solution

Uninstall and then reinstall Anaconda or Miniconda, answering “YES” to the question about prepending the conda prompt.

Or, you can manually edit your .bashrc file to prepend the Anaconda or Miniconda install location. Open a text editor and in your home directory, locate the hidden file .bashrc. Add this line to it and save:

```
export PATH=/Users/your-username/anaconda3/bin:$PATH
```

Close your terminal window and re-open before running a conda command.

### Recovering your Anaconda installation

If your Anaconda installation is in a state where normal conda commands are not functioning, use the following steps to repair Anaconda and preserve your installed packages and environments.

## Step 1

Download a [new installer](#), then follow the instructions for your system Windows, macOS, or Linux.

---

**Note:** Use the actual path, filename, and directory name for your installation.

---

### Windows

Change your original installer's name so you do not overwrite it:

```
move Anaconda Anaconda_old
```

Run the Anaconda.exe installer as usual and use robocopy to sync the directories:

```
robocopy Anaconda_old Anaconda /S  
rd /s Anaconda_old
```

### macOS

Change your original installer's name so you do not overwrite it:

```
mv anaconda anaconda_orig
```

Install to same directory as your original installer:

```
bash Anaconda3-4.0.0-MacOSX-x86_64.sh  
rsync -a anaconda_orig/ anaconda/  
rm -rf anaconda_orig
```

### Linux

Change your original installer's name so you do not overwrite it:

```
mv anaconda anaconda_orig
```

Install to same directory as your original installer:

```
bash Anaconda3-4.0.0-Linux-x86_64.sh  
rsync -a anaconda_orig/ anaconda/
```

## Step 2

Run `conda list` to view the packages from the previous installation.

Run `conda info -e` to list the environments created in the previous installation which are now available in the new installation.

### Using Anaconda behind a firewall or proxy

Corporate security policies may prevent a new Anaconda installation from downloading packages and other functionality that requires connecting to an external server. To make external connections you may need to connect to a firewall/proxy. Additionally, your IT team may need to allow connections to <https://anaconda.org> and <https://repo.anaconda.com> as these are the main package repositories.

#### Solution

To add the proxy information you will need to add two entries to your `.condarc` file located in the user's home directory. This information should be made available by your IT team and may contain a username and password that is included in the URL. Read more about the [.condarc configuration](#).

Example configuration:

```
channels:
- defaults

proxy_servers:
- http: http://username:password@proxyurl.com:8080
- https: https://username:password@proxyurl.com:8443
```

In some situations it may be necessary to export the `HTTP_PROXY` and `HTTPS_PROXY` environment variables.

#### MacOS/Linux

```
export HTTP_PROXY=http://username:password@proxyurl.com:8080
export HTTPS_PROXY=https://username:password@proxyurl.com:8443
```

#### Windows

```
set HTTP_PROXY=http://username:password@proxyurl.com:8080
set HTTPS_PROXY=https://username:password@proxyurl.com:8443
```

If these steps have not allowed connections you should speak to your IT team to verify that security policies are not blocking connections to <https://anaconda.com> and <https://repo.continuum.io>.

### .zshrc not updated under macOS Catalina

#### Cause

MacOS Catalina changed the default shell from Bash to zsh.

#### Solution

Run `bash -c "conda init zsh"` and then restart your shell to initialize conda for zsh.

### Insecure Platform Warning



## Cause

“InsecurePlatformWarning” appears only when the installed version of Python is older than version 2.7.9. This message warns only that the validity of the SSL connection is not being verified. It should not affect your package downloads.

## Solution

To resolve this on Windows, install the updated package `ndg-httpsclient`:

```
conda install ndg-httpsclient
```

---

**Note:** When initially installing this package, you receive the SSL warning again. Once it is installed, the package will prevent the warnings.

---

## Conda: command not found on macOS or Linux

### Cause

The conda shell function is not available, or is not working properly. Some causes:

- You have set `conda_auto_activate_base` to false. You need to run `conda activate [env]`. Env is optional, the default if not provided is base.
- You haven’t started a new shell after installing Anaconda/Miniconda (assuming you allow it to modify your startup script)
- You didn’t allow the installer to modify your startup script
- Conda has been corrupted, usually by a change in the Python package (e.g. 3.6->3.7)

### Solution

Run `/full/path/to/bin/conda init` to modify `~/.bashrc`.

Either start a new shell or source the modified `~/.bash_profile` (Windows/MSYS2, Windows/Cygwin and macOS) or `~/.bashrc` (Linux and Windows Subsystem for Linux). Source them via `. ~/.bash_profile`.

You may prefer that conda not automatically activate your base environment when a new shell is started. This behavior shadows your system Python, and some users prefer to have their conda environment be inactive until they need it. To achieve this, you can set a `.condarc` setting:

```
conda config --set auto_activate_base false
```

If you have this set, the conda command will still be available as a shell function, but your base environment will not be active when a new shell is started. To activate your base environment, run `conda activate`.

## Anaconda interfering with other software on Windows

### Cause

If a user chooses to add Anaconda to the Windows PATH, this can cause programs to use the new Anaconda versions of software such as Python and not the versions that were already in place. In some cases this can cause incompatibility and errors.

### Solution

We recommend not adding Anaconda to the Windows PATH. Instead, use Anaconda software by opening Anaconda Navigator or the Anaconda Prompt from the Start Menu.

### Windows error: no environment named “search” exists

If `anaconda-client` is not installed and you search for a package on `anaconda.org` using the Anaconda search command:  
`anaconda search -t conda packagename`

You will receive the following error message:

```
C:\Users\username>anaconda search -t conda packagename
No environment named "search" exists in C:\Anaconda\envs
Solution
```

Anaconda on Windows contains an `anaconda.bat` file, which is used for setting environment paths and switching environments. If `anaconda-client` is not installed, this batch file is called instead and produces the error.

To resolve the error, install `anaconda-client`:

```
conda install anaconda-client
```

And then search for a package:

```
anaconda search -t conda packagename
```

### MKL Trial warning is displayed even though MKL-linked packages are now free and installed by default

See [Dismissing MKL Trial warnings](#).

### Error message: Permission denied, when loading MKL shared libraries

See [Resolving MKL shared library permission denied errors](#).

### Error message on Miniconda install: Already installed

### Cause

This situation can occur if you are getting a conda error and you want to reinstall Miniconda to fix it.

## Solution

For macOS and Linux, download and install the appropriate Miniconda for your operating system from the [Miniconda download page](#) using the force or -f option:

```
bash Miniconda3-latest-MacOSX-x86_64.sh -f
```

---

**Note:** For `Miniconda3-latest-MacOSX-x86_64`, substitute the appropriate filename and version for your operating system.

Be sure that you install to the same location as your existing install so it overwrites the core conda files and does not install a duplicate in a new folder.

---

## Conda update anaconda command does not install the latest version of Anaconda

### Cause

For users who have installed packages that are not compatible with the latest version of the Anaconda metapackage, running `conda update anaconda` updates the Anaconda metapackage to the latest compatible version, but this may not be the latest version.

### Solution

Obtain a list of the conflicting packages by running `conda update anaconda` or `conda install anaconda=5.2`.

---

**Note:** Replace `5.2` with the latest version number.

---

Once you know which packages are conflicting, you can update all current packages without upgrading to the latest version of Anaconda, or you can remove the conflicting packages and then upgrade to the latest version of Anaconda.

To update all current packages without upgrading to the latest version of Anaconda:

1. Use `conda remove anaconda` to remove the Anaconda metapackage itself. (This will not remove any of the packages included with Anaconda.)
2. Use `conda update --all` to update all currently installed packages.

To remove the conflicting packages and upgrade to the latest version of Anaconda:

1. Remove the conflicting packages by running `conda remove package-name` for each one.

---

**Note:** Replace `package-name` with the name of the package.

---

2. Run `conda update anaconda`.

## Linking problems when Python extensions are compiled with gcc

### Cause

When compiling Python extensions with gcc on Windows, linking problems may result.

### Solution

To resolve these linking problems, use the mingw import library—the conda package libpython—which Anaconda builds and includes with the Anaconda Distribution.

### Error message: Unable to remove files

When trying to update or install packages with conda, you may see an error message such as:

```
Error: Unable to remove files for package: <package-name>
Please close all processes running code from conda and try again.
```

### Cause

This may be caused by a file lock issue.

### Solution

Before updating or installing any packages with conda, be sure to terminate any running Anaconda processes such as Spyder or IPython.

You can also force the installation of the package: `conda install -f package-name`.

---

**Note:** Replace `package-name` with the name of the package that you want to install.

---

## Files left behind after uninstalling Anaconda on Windows

### Cause

Some users may need to keep settings files and other users may need to delete them, so Anaconda leaves some settings files in place when it is uninstalled. Specifically, the directories `.spyder2`, `.ipython`, `.matplotlib`, and `.astropy` remain. Depending on your version of Windows these may be in `C:\Documents and Settings\Your_User_Name` or in `C:\Users\Your_User_Name`.

---

**Note:** Replace `Your_User_Name` with your Windows user name as it appears in the Documents and Settings or Users folder.

---

### Solution

Manually delete any unneeded settings files.

## Spyder errors or failure to launch on Windows

### Cause

This may be caused by errors in the Spyder setting and configuration files.

### Solution

1. Close and relaunch Spyder and see if the problem remains.
2. On the menu, select Start, then select Reset Spyder Settings and see if the problem remains.
3. Close Spyder and relaunch it from the Anaconda Prompt:
  1. From the Start menu, open the Anaconda Prompt.
  2. At the Anaconda Prompt, enter `Spyder`.
  3. See if the problem remains.
4. Delete the directory `.spyder2` and then repeat the previous steps from Step 1. Depending on your version of Windows, `.spyder2` may be in `C:\Documents and Settings\Your_User_Name` or in `C:\Users\Your_User_Name`.

---

**Note:** Replace `Your_User_Name`, with your Windows user name as it appears in the *Documents and Settings* folder.

---

## Problems running Anaconda on macOS 10.12.2

### Cause

Some installations of Anaconda on macOS 10.12.2 experienced incorrect file and directory permissions, which caused a range of errors with Navigator and other parts of Anaconda.

### Solution

We recommend that any users with Anaconda on macOS 10.12.2 follow these steps:

1. Uninstall Anaconda. Open the Terminal.app or iTerm2 terminal application and remove your Anaconda directory, which will have a name such as “anaconda2” or “anaconda3”, by entering a command such as this: `rm -rf ~/anaconda3`
2. Use a text editor such as TextEdit to open the file named `.bash_profile` in your home directory. If you see a line that adds Anaconda or Miniconda to your PATH environment variable, remove this line, and then save and close the file. For example, if you see a line such as `export PATH="/Users/jsmith/anaconda3/bin:$PATH"`, remove that line.
3. Update to macOS 10.12.3 or later.
4. [Reinstall Anaconda](#).

### “execution error: localhost doesn’t understand the “open location” message. (-1708)” when opening a Jupyter notebook on macOS 10.12.5

#### Cause

This version of macOS seems to have a bug affecting some of the ways for a program to open a web page in a browser.

#### Solution

Several possible workarounds have been found for this bug.

You can explicitly set the browser in `~/ .jupyter/jupyter_notebook_config.py` with a line such as this:

```
c.NotebookApp.browser = u'Safari'
```

Or you can copy the Jupyter notebook URL from the log messages on the command line and paste it into your browser.

Or you can set the `BROWSER` environment variable: `export BROWSER=/Applications/Google\ Chrome.app/Contents/MacOS/Google\ Chrome`

Further information is available at the [Jupyter bug tracker](#), the [Python bug tracker](#), and [this blog post](#).

### Missing libgfortran on Power8

#### Cause

Anaconda 4.4.0.0 for Power8 did not include libgfortran.

#### Solution

Anaconda 4.4.0.1 and later for Power8 do include libgfortran.

Upgrade to the latest version of Anaconda:

```
conda update anaconda
```

Anaconda 4.4.0.0 users who do not wish to upgrade may instead install libgfortran with this command:

```
conda install libgfortran
```

### Missing libgomp on Power8

If the Python command “`import numpy`” fails, the system is likely missing the libgomp system library.

#### Cause

Most Power8 Linux distributions include libgomp, but some may not.

## Solution

Check whether the system is missing libgomp with this command:

```
conda inspect linkages -n root numpy
```

If libgomp.so.1 is listed in the “not found:” section, it must be installed.

Install libgomp on Ubuntu with this command:

```
apt install libgomp1
```

Install libgomp on Red Hat Enterprise Linux (RHEL) or CentOS with this command:

```
yum install libgomp
```

## Anaconda on Power8 reports “can not execute binary file”

### Cause

Anaconda on Power8 only supports little endian mode. The little endian Python binary will not execute on a big endian operating system.

### Solution

Install Anaconda on Power8 on a little endian Linux installation or VM.

## Uninstaller requests admin privileges on Windows

### Cause

After installing Anaconda or Miniconda as a non-administrative user on Windows, uninstalling may prompt for administrative privileges.

This occurs when running the uninstaller by choosing Control Panel, System, Apps & features, Python x.x.x (Miniconda3 4.3.xx 64-bit), Uninstall.

### Solution

Open the Anaconda or Miniconda installation folder and run the `.exe` file uninstaller from that location. Uninstallation will complete without prompting for administrative privileges.

EXAMPLE: If you installed Miniconda3, the uninstall file will be `Uninstall-Miniconda3.exe`. Users who installed Miniconda2 or Anaconda will find a similar file with the appropriate name.

## Windows permission errors when installing from Favorites folder

### Cause

The Windows Favorites folder has unusual permissions and may cause permission errors with installers of any software. If you try launching the installer from the Favorites folder you may see errors such as “Setup was unable to create the directory”, “Access is denied”, or “Error opening file for writing”.

### Solution

Move the installer to a different folder and run the installer from the new folder.

### Trouble with activation on PowerShell on Windows

#### Solution

If you run into the following backtrace on Windows:

```
File "C:\Users\damia\Miniconda3\lib\site-packages\conda\activate.py", line 550, in _
    ↪replace_prefix_in_path
assert last_idx is not None
AssertionError
```

Open a cmd.exe prompt. cd to where you installed conda and run:

```
python -m conda init
```

Close the cmd.exe prompt and the Anaconda Prompt or the Anaconda PowerShell Prompt as usual.

If this doesn't work, try running:

```
conda update conda
```

### Cannot install Distribution 2019.07 on a webfaction server

You may receive an error when trying to install Distribution 2019.07 for Linux on a webfaction server:

```
PREFIX=/home/myname/anaconda3
Unpacking payload ...
[13822] Error loading Python lib '/tmp/_MEI<randomstring>/libpython3.6m.so.1.0':
    ↪dlopen /tmp/_MEI<randomstring>/libpython3.6m.so.1.0: failed to map segment from
    ↪shared object: Operation not permitted
ERROR: could not extract tar starting at offset 00000000000020980+9231072+2
```

### Cause

This is caused by having TMP as a noexec.

### Solution

To enable installation, you can temporarily set TMP to somewhere else from which you can execute software.

For example:



```
cd
mkdir TMPconda
TMP=~ /TMPconda bash Anaconda3-2019.07-Linux-x86_64.sh
```

After installing, set the TMP folder back to its initial location.

### Segmentation fault on package import with macOS Python 3.7 interpreter

In CPython < 3.8, using `python3-config` to determine a linking command line to compile an extension module will cause that extension module to segfault upon import. `python3-config` does provide command-line flags but for the different purpose of embedding a Python interpreter.

#### Cause

This is because of the command-line flags returned by `python3-config`. Before Python 3.8, those are needed to embed the core Python interpreter into a different project altogether and not those that should be used when linking a Python extension module.

Python modules should never link to the core Python interpreter library directly, either statically at build time or dynamically at runtime. This is because the Python executable itself provides all the necessary functions and symbols.

#### Solution

You should only use `python*-config --ldflags` when linking to an interpreter library (either static or shared).

Action	Python < 3.8	Python >= 3.8
Get command line to link to extension module	<code>python -c "import sysconfig; print(sysconfig.get_config_var('LD_SHARED'))"</code>	<code>python3-config --ldflags</code>
Get command line to embed Python interpreter	<code>python3-config --ldflags</code>	<code>python3-config --ldflags --embed</code>

`python3-config` doesn't include the command/compiler name whereas the `sysconfig` way does. This works provided none of your arguments have spaces:

```
python -c "import sysconfig; print(' '.join(sysconfig.get_config_var('LD_SHARED').
↳split(' ')[1:]))"
```

### Using 32- and 64-bit libraries and CONDA\_FORCE\_32BIT

To work with both 32- and 64-bit libraries, we recommend that you have two separate installs: Anaconda32 and Anaconda64 or Miniconda32 and Miniconda64.

When working with both versions, add the path to your installer files to the PATH.

**Note:** Always specify which version you want to work with because mixing 32- and 64-bit packages can cause problems in your environment.

To get the information about conda including your PATH, run: `conda info -a`

Using `CONDA_FORCE_32BIT` is not recommended because it forces 32-bit packages to be installed in the environment, but does not force 32-bit libraries to load at runtime.

`CONDA_FORCE_32BIT` should be used only when running `conda-build` to build 32-bit packages on a 64-bit system.

## Packages

### Anaconda package lists

All packages available in the latest release of Anaconda are listed on the pages linked below. These packages may be installed with the command `conda install PACKAGENAME` and are located in the [package repository](#).

Click the links below to see which packages are available for each version of Python (3.7, 3.6, or 2.7) and each operating system and architecture.

Anaconda is available for 64 and 32 bit Windows, macOS, and 64 Linux on the Intel and AMD x86, x86-64 CPU, and IBM Power CPU architectures.

An [RSS feed](#) is updated each time a new package is added to the Anaconda package repository.

To request a package not listed on this page, please create an issue on the [Anaconda issues page](#).

	Python 3.8	Python 3.7	Python 3.6
64-bit Windows	<a href="#">64-bit Windows, Py3.8</a>	<a href="#">64-bit Windows, Py3.7</a>	<a href="#">64-bit Windows, Py3.6</a>
32-bit Windows	<a href="#">32-bit Windows, Py3.8</a>	<a href="#">32-bit Windows, Py3.7</a>	<a href="#">32-bit Windows, Py3.6</a>
macOS	<a href="#">macOS, Py3.8</a>	<a href="#">macOS, Py3.7</a>	<a href="#">macOS, Py3.6</a>
64-bit Linux	<a href="#">64-bit Linux, Py3.8</a>	<a href="#">64-bit Linux, Py3.7</a>	<a href="#">64-bit Linux, Py3.6</a>
64-bit Linux on IBM Power CPUs	<a href="#">Linux on IBM Power, Py3.8</a>	<a href="#">Linux on IBM Power, Py3.7</a>	<a href="#">Linux on IBM Power, Py3.6</a>

### Packages for 64-bit Windows with Python 3.6

### Packages for 64-bit Windows with Python 3.7

### Packages for 64-bit Windows with Python 3.8

### Packages for 32-bit Windows with Python 3.6

### Packages for 32-bit Windows with Python 3.7

### Packages for 32-bit Windows with Python 3.8

### Packages for macOS with Python 3.6

### Packages for macOS with Python 3.7

### Packages for macOS with Python 3.8

## Packages for 64-bit Linux with Python 3.6

## Packages for 64-bit Linux with Python 3.7

## Packages for 64-bit Linux with Python 3.8

## Packages for 64-bit Linux on IBM Power CPUs with Python 3.6

## Packages for 64-bit Linux on IBM Power CPUs with Python 3.7

## Packages for 64-bit Linux on IBM Power CPUs with Python 3.8

## R language packages for Anaconda

- *R Essentials bundle*
- *More resources*
- *List of R packages for Anaconda*

The R language packages are available to install with conda at <http://repo.anaconda.com/pkg/r/>. You can install any of these R language packages into your current environment with the conda command `conda install -c r package-name`.

**Note:** Replace package-name with the name of the package. For example, you can install the package “r-acepack” with the command `conda install -c r r-acepack`.

Many Comprehensive R Archive Network (CRAN) packages are available as conda packages. Anaconda does not provide builds of the entire CRAN repository, so there are some packages in CRAN that are not available as conda packages.

**Tip:** You can also search for any R package if you know the name, such as `conda search -f r-EXACTNAME`. Replace EXACTNAME with the desired CRAN or MRAN R package name. For example, for rbokeh, you would use `conda search -f r-rbokeh`.

## R Essentials bundle

Rather than install each R language package individually, you can get the R Essentials bundle. It includes approximately 80 of the most popular scientific packages for the R programming language.

You can install the R Essentials bundle with this command:

```
conda install -c r r-essentials
```

## More resources

- *Using R language with Anaconda*

- Latest index of R packages built by Anaconda, Inc. on [repo.anaconda.com](https://repo.anaconda.com)
- Latest index of R packages built by Anaconda, Inc. on [Anaconda Cloud](#)

## List of R packages for Anaconda

Number of supported packages: 6993

*A B C D E F G H I J K L M N O P Q R S T U V W X Y Z*

Table 33: Misc

Name	Version	Summary/License	Platforms
<a href="#">_r-mutex</a>	1.0.0	A mutex package to ensure environment exclusivity between Anaconda R and MRO. / BSD	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">_r-xgboost-mutex</a>	2.0	None / None	linux-64, osx-64, win-64

Table 34: A

Name	Version	Summary/License	Platforms
<a href="#">abind</a>	1.4.5	Combine multidimensional arrays into a single array. This is a generalization of 'cbind' and 'rbind'. Works with vectors, matrices, and higher-dimensional arrays. Also provides functions 'adrop', 'asub', and 'afill' for manipulating, extracting and replacing data in arrays. / LGPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">acepack</a>	1.4.1	Two nonparametric methods for multiple regression transform selection are provided. The first, Alternative Conditional Expectations (ACE), is an algorithm to find the fixed point of maximal correlation, i.e. it finds a set of transformed response variables that maximizes $R^2$ using smoothing functions [see Breiman, L., and J.H. Friedman. 1985. Estimating Optimal Transformations for Multiple Regression and Correlation. Journal of the American Statistical Association. 80:580-598. <doi:10.1080/01621459.1985.10478157>]. Also included is the Additivity Variance Stabilization (AVAS) method which works better than ACE when correlation is low [see Tibshirani, R.. 1986. Estimating Transformations for Regression via Additivity and Variance Stabilization. Journal of the American Statistical Association. 83:394-405. <doi:10.1080/01621459.1988.10478610>]. A good introduction to these two methods is in chapter 16 of Frank Harrel's Regression Modeling Strategies in the Springer Series in Statistics. / MIT file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">adgofest</a>	0.3	Anderson-Darling GoF test with p-value calculation based on Marsaglia's 2004 paper Evaluating the Anderson-Darling Distribution / GPL	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">aer</a>	1.2.6	Functions, data sets, examples, demos, and vignettes for the book Christian Kleiber and Achim Zeileis (2008), Applied Econometrics with R, Springer-Verlag, New York. ISBN 978-0-387-77316-2. (See the vignette AER for a package overview.) / GPL-2   GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">afex</a>	0.23.0	Convenience functions for analyzing factorial experiments using ANOVA or mixed models. aov_ez(), aov_car(), and aov_4() allow specification of between, within (i.e., repeated-measures), or mixed (i.e., split-plot) ANOVAs for data in long format (i.e., one observation per row), automatically aggregating multiple observations per individual and cell of the design. mixed() fits mixed models using lme4::lmer() and computes p-values for all fixed effects using either Kenward-Roger or Satterthwaite approximation for degrees of freedom (LMM only), parametric bootstrap (LMMs and GLMMs), or likelihood ratio tests (LMMs and GLMMs). afex_plot() provides a high-level interface for interaction or one-way plots using ggplot2, combining raw data and model es-	linux-32, linux-64, noarch, osx-64, win-32, win-64

Table 35: B

Name	Version	Summary/License	Platforms
<a href="#">backports</a>	1.1.4	Functions introduced or changed since R v3.0.0 are re-implemented in this package. The backports are conditionally exported in order to let R resolve the function name to either the implemented backport, or the respective base version, if available. Package developers can make use of new functions or arguments by selectively importing specific backports to support older installations. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">base64enc</a>	0.1_3	This package provides tools for handling base64 encoding. It is more flexible than the orphaned base64 package. / GPL-2   GPL-3	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">bcp</a>	4.0.3	Provides an implementation of the Barry and Hartigan (1993) product partition model for the normal errors change point problem using Markov Chain Monte Carlo. It also extends the methodology to regression models on a connected graph (Wang and Emerson, 2015); this allows estimation of change point models with multivariate responses. Parallel MCMC, previously available in bcp v.3.0.0, is currently not implemented. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">bdsmatrix</a>	1.3_3	This is a special case of sparse matrices, used by coxme. / LGPL-2	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">bestglm</a>	0.37	Best subset glm using information criteria or cross-validation. Implements PCR and PLS using AIC/BIC. Implements one-standard deviation rule for use with the <i>caret</i> package. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">bh</a>	1.69.0	Boost provides free peer-reviewed portable C source libraries. A large part of Boost is provided as C template code which is resolved entirely at compile-time without linking. This package aims to provide the most useful subset of Boost libraries for template use among CRAN package. By placing these libraries in this package, we offer a more efficient distribution system for CRAN as replication of this code in the sources of other packages is avoided. As of release 1.69.0-1, the following Boost libraries are included: ‘algorithm’ ‘align’	linux-32, linux-64, noarch, osx-64,

Table 36: C

Name	Version	Summary/License	Platforms
<a href="#">cairo</a>	1.5_10	R graphics device using cairographics library that can be used to create high-quality vector (PDF, PostScript and SVG) and bitmap output (PNG,JPEG,TIFF), and high-quality rendering in displays (X11 and Win32). Since it uses the same back-end for all output, copying across formats is WYSIWYG. Files are created without the dependence on X11 or other external programs. This device supports alpha channel (semi-transparent drawing) and resulting images can contain transparent and semi-transparent regions. It is ideal for use in server environments (file output) and as a replacement for other devices that don't have Cairo's capabilities such as alpha support or anti-aliasing. Backends are modular such that any subset of backends is supported. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">callr</a>	3.2.0	It is sometimes useful to perform a computation in a separate R process, without affecting the current R process at all. This packages does exactly that. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">car</a>	3.0_2	Functions to Accompany J. Fox and S. Weisberg, An R Companion to Applied Regression, Third Edition, Sage, in press. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">cardata</a>	3.0_2	Datasets to Accompany J. Fox and S. Weisberg, An R Companion to Applied Regression, Third Edition, Sage (forthcoming). / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">caret</a>	6.0_83	Misc functions for training and plotting classification and regression models. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<b>4.2. Anaconda Individual Edition</b>			<b>win-64 1575</b>
<a href="#">catools</a>	1.17.1	Contains several basic utility functions including: moving (rolling, running) window statistic functions, read/write for GIF and ENVI binary files, fast calculation of AUC, LogitBoost classifier, base64 encoder/decoder, round-off-	linux-32, linux-

Table 37: D

Name	Version	Summary/License	Platforms
<a href="#">data.table</a>	1.12.2	Fast aggregation of large data (e.g. 100GB in RAM), fast ordered joins, fast add/modify/delete of columns by group using no copies at all, list columns, friendly and fast character-separated-value read/write. Offers a natural and flexible syntax, for faster development. / MPL-2.0   file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">dbi</a>	1.0.0	A database interface definition for communication between R and relational database management systems. All classes in this package are virtual and need to be extended by the various R/DBMS implementations. / LGPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">dbplyr</a>	1.4.0	A 'dplyr' back end for databases that allows you to work with remote database tables as if they are in-memory data frames. Basic features works with any database that has a 'DBI' back end; more advanced features require 'SQL' translation to be provided by the package author. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">ddalpha</a>	1.3.9	Contains procedures for depth-based supervised learning, which are entirely non-parametric, in particular the DDalpha-procedure (Lange, Mosler and Mozharovskyi, 2014 <doi:10.1007/s00362-012-0488-4>). The training data sample is transformed by a statistical depth function to a compact low-dimensional space, where the final classification is done. It also offers an extension to functional data and routines for calculating certain notions of statistical depth functions. 50 multivariate and 5 functional classification problems are included. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">debugme</a>	1.1.0	Specify debug messages as special string constants, and control debugging of packages via environment variables. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">deoptimr</a>	1.0_8	Differential Evolution (DE) stochastic algorithms for global optimization of problems with and without constraints. The aim is to curate a collection of its state-of-the-art variants that (1) do not sacrifice simplicity of design, (2) are essentially tuning-free, and (3) can be efficiently implemented directly in	linux-32, linux-64,



Table 38: E

Name	Version	Summary/License	Platforms
<a href="#">e1071</a>	1.7_1	Functions for latent class analysis, short time Fourier transform, fuzzy clustering, support vector machines, shortest path computation, bagged clustering, naive Bayes classifier, ... / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">ellipsis</a>	0.1.0	In S3 generics, it's useful to take ... so that methods can have additional argument. But this flexibility comes at a cost: misspelled arguments will be silently ignored. The ellipsis packages is an experiment that allows a generic to warn if any arguments passed in ... are not used. / GPL-3	linux-64, osx-64, win-32, win-64
<a href="#">emmeans</a>	1.3.4	Obtain estimated marginal means (EMMs) for many linear, generalized linear, and mixed models. Compute contrasts or linear functions of EMMs, trends, and comparisons of slopes. Plots and compact letter displays. Least-squares means are discussed, and the term estimated marginal means is suggested, in Searle, Speed, and Milliken (1980) Population marginal means in the linear model: An alternative to least squares means, The American Statistician 34(4), 216-221 <doi:10.1080/00031305.1980.10483031>. / GPL-2   GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">essentials</a>	3.6.0	Some essential packages for working with R / Various	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">essentials-mrclient</a>	3.4.3	Essential R packages including MS R Client and MS Machine Learning / Various	linux-64, win-64
<a href="#">estimability</a>	1.3	Provides tools for determining estimability of linear functions of regression coefficients, and 'epredict' methods that handle non-estimable cases correctly. Estimability theory is discussed in many linear-models textbooks including Chapter 3 of Monahan, JF (2008), A Primer on Linear Models, Chapman and Hall (ISBN 978-1-4200-6201-4). / GPL (>= 3)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<b>4.2. Anaconda Individual Edition</b>			<b>linux-64 1577</b>
<a href="#">evaluate</a>	0.13	Parsing and evaluation tools that make it easy to recreate the command line behaviour of R. / MIT file LICENSE	linux-32, linux-

Table 39: F

Name	Version	Summary/License	Platforms
<a href="#">fansib</a>	0.4.0	Counterparts to R string manipulation functions that account for the effects of ANSI text formatting control sequences. / GPL ( $\geq 2$ )	linux-64, osx-64, win-32, win-64
<a href="#">fastica</a>	1.2.1	Implementation of FastICA algorithm to perform Independent Component Analysis (ICA) and Projection Pursuit. / GPL-2   GPL-3	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">fbasics</a>	3042.89	Provides a collection of functions to explore and to investigate basic properties of financial returns and related quantities. The covered fields include techniques of explorative data analysis and the investigation of distributional properties, including parameter estimation and hypothesis testing. Even more there are several utility functions for data handling and management. / GPL ( $\geq 2$ )	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">feather</a>	0.3.3	Read and write feather files, a lightweight binary columnar data store designed for maximum speed. / Apache License 2.0	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">fftw</a>	1.0.5	Provides a simple and efficient wrapper around the fastest Fourier transform in the west (FFTW) library < <a href="http://www.fftw.org/">http://www.fftw.org/</a> >. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">fgarch</a>	3042.89	Provides a collection of functions to analyze and model heteroskedastic behavior in financial time series models. / GPL ( $\geq 2$ )	linux-32, linux-64, osx-64, win-32, win-64
1578		Chapter 4. Anaconda Cloud	osx-64, win-32, win-64

Table 40: G

Name	Version	Summary/License	Platforms
<a href="#">gdata</a>	2.18.0	Various R programming tools for data manipulation, including: - medical unit conversions ('ConvertMedUnits', 'MedUnits'), - combining objects ('bindData', 'cbindX', 'combine', 'interleave'), - character vector operations ('centerText', 'startsWith', 'trim'), - factor manipulation ('levels', 'reorder.factor', 'mapLevels'), - obtaining information about R objects ('object.size', 'elem', 'env', 'humanReadable', 'is.what', 'll', 'keep', 'ls.funs', 'Args', 'nPairs', 'nobs'), - manipulating MS-Excel formatted files ('read.xls', 'installXLSX-support', 'sheetCount', 'xlsFormats'), - generating fixed-width format files ('write.fwf'), - extricating components of date & time objects ('getYear', 'getMonth', 'getDay', 'getHour', 'getMin', 'getSec'), - operations on columns of data frames ('matchcols', 'rename.vars'), - matrix operations ('unmatrix', 'upperTriangle', 'lowerTriangle'), - operations on vectors ('case', 'unknown-ToNA', 'duplicated2', 'trimSum'), - operations on data frames ('frameApply', 'wideByFactor'), - value of last evaluated expression ('ans'), and - wrapper for 'sample' that ensures consistent behavior for both scalar and vector arguments ('resample'). / GPL-2	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">generics</a>	0.0.2	In order to reduce potential package dependencies and conflicts, generics provides a number of commonly used S3 generics. / GPL-2	linux-32, linux-64, noarch, osx-64, win-64
<a href="#">geometry</a>	0.4.1	Makes the 'Qhull' library < <a href="http://www.qhull.org">http://www.qhull.org</a> > available in R, in a similar manner as in Octave and MATLAB. Qhull computes convex hulls, Delaunay triangulations, halfspace intersections about a point, Voronoi diagrams, furthest-site Delaunay triangulations, and furthest-site Voronoi diagrams. It runs in 2D, 3D, 4D, and higher dimensions. It implements the Quickhull algorithm for computing the convex hull. Qhull does not support constrained Delaunay triangulations, or mesh generation of non-convex objects, but the package does include some R functions that allow for this. / GPL (>= 3)	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">getopt</a>	1.20.3	Package designed to be used with Rscript to write “#!” shebang scripts that accept short and long flags/options. Many users will prefer using instead the packages optparse or argparse which add extra features like automatically generated help option and usage, support for default values, positional argument support, etc. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">ggplot2</a>	3.1.1	A system for ‘declaratively’ creating graphics, based on The Grammar of Graphics. You provide the data, tell ‘ggplot2’ how to map variables to aesthetics, what graphical primitives to use, and it takes care of the details. / GPL-2   file LICENSE	linux-32, linux-64, noarch, osx-64, win-64
<b>4.2. Anaconda Individual Edition</b>			win-32, win-64

Table 41: H

Name	Version	Summary/License	Platforms
<a href="#">haven</a>	2.1.0	Import foreign statistical formats into R via the embedded 'ReadStat' C library, < <a href="https://github.com/WizardMac/ReadStat">https://github.com/WizardMac/ReadStat</a> >. / MIT file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">hexbin</a>	1.27	Binning and plotting functions for hexagonal bins. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">highcharter</a>	0.7.0	A wrapper for the 'Highcharts' library including shortcut functions to plot R objects. 'Highcharts' < <a href="http://www.highcharts.com/">http://www.highcharts.com/</a> > is a charting library offering numerous chart types with a simple configuration syntax. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">highr</a>	0.8	Provides syntax highlighting for R source code. Currently it supports LaTeX and HTML output. Source code of other languages is supported via Andre Simon's highlight package (< <a href="http://www.andre-simon.de">http://www.andre-simon.de</a> >). / GPL	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">hmisc</a>	4.2_0	Contains many functions useful for data analysis, high-level graphics, utility operations, functions for computing sample size and power, importing and annotating datasets, imputing missing values, advanced table making, variable clustering, character string manipulation, conversion of R objects to LaTeX and html code, and recoding variables. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">hms</a>	0.4.2	Implements an S3 class for storing and formatting time-of-day values, based on the 'difftime' class. / GPL-3	linux-32, linux-64, noarch,

Table 42: I

Name	Version	Summary/License	Platforms
<a href="#">igraph</a>	1.2.4	Routines for simple graphs and network analysis. It can handle large graphs very well and provides functions for generating random and regular graphs, graph visualization, centrality methods and much more. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">implyr</a>	0.2.4	'SQL' back-end to 'dplyr' for Apache Impala, the massively parallel processing query engine for Apache 'Hadoop'. Impala enables low-latency 'SQL' queries on data stored in the 'Hadoop' Distributed File System '(HDFS)', Apache 'HBase', Apache 'Kudu', Amazon Simple Storage Service '(S3)', Microsoft Azure Data Lake Store '(ADLS)', and Dell 'EMC' 'Isilon'. See < <a href="https://impala.apache.org">https://impala.apache.org</a> > for more information about Impala. / Apache License 2.0   file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">influencer</a>	0.1.0	Provides functionality to compute various node centrality measures on networks. Included are functions to compute betweenness centrality (by utilizing Madduri and Bader's SNAP library), implementations of Burt's constraint and effective network size (ENS) metrics, Borgatti's algorithm to identify key players, and Valente's bridging metric. On Unix systems, the betweenness, Key Players, and bridging implementations are parallelized with OpenMP, which may run faster on systems which have OpenMP configured. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">ini</a>	0.3.1	Parse simple '.ini' configuration files to an structured list. Users can manipulate this resulting list with lapply() functions. This same structured list can be used to write back to file after modifications. / GPL-3	noarch
<a href="#">inline</a>	0.3.15	Functionality to dynamically define R functions and S4 methods with 'inlined' C, C or Fortran code supporting the .C and .Call calling conventions. / LGPL	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">ipred</a>	0.9_8	Improved predictive models by indirect classification and bagging for classification, regression and survival problems as well as resampling based estimators of prediction error. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<b>4.2. Anaconda Individual Edition</b>			linux-32, win-64 <b>1581</b>
<a href="#">irdisplay</a>	0.7.0	An interface to the rich display capabilities of 'Jupyter' front-ends (e.g. 'Jupyter Notebook') < <a href="https://jupyter.org">https://jupyter.org</a> >. Designed to be used from a run-	linux-32,

Table 43: J

Name	Version	Summary/License	Platforms
<a href="#">janeaustenr</a>	0.1.5	Full texts for Jane Austen's 6 completed novels, ready for text analysis. These novels are Sense and Sensibility, Pride and Prejudice, Mansfield Park, Emma, Northanger Abbey, and Persuasion. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">jpeg</a>	0.1_8	This package provides an easy and simple way to read, write and display bitmap images stored in the JPEG format. It can read and write both files and in-memory raw vectors. / GPL-2   GPL-3	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">jsonlite</a>	1.6	A fast JSON parser and generator optimized for statistical data and the web. Started out as a fork of 'RJSONIO', but has been completely rewritten in recent versions. The package offers flexible, robust, high performance tools for working with JSON in R and is particularly powerful for building pipelines and interacting with a web API. The implementation is based on the mapping described in the vignette (Ooms, 2014). In addition to converting JSON data from/to R objects, 'jsonlite' contains functions to stream, validate, and prettify JSON data. The unit tests included with the package verify that all edge cases are encoded and decoded consistently for use with dynamic data in systems and applications. / MIT file LICENSE	linux-32, linux-64, osx-64, win-32, win-64

Table 44: K

Name	Version	Summary/License	Platforms
<a href="#">keras</a>	2.2.4	Interface to ‘Keras’ < <a href="https://keras.io">https://keras.io</a> >, a high-level neural networks ‘API’. ‘Keras’ was developed with a focus on enabling fast experimentation, supports both convolution based networks and recurrent networks (as well as combinations of the two), and runs seamlessly on both ‘CPU’ and ‘GPU’ devices. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-64
<a href="#">kernlab</a>	0.9_2	Kernel-based machine learning methods for classification, regression, clustering, novelty detection, quantile regression and dimensionality reduction. Among other methods ‘kernlab’ includes Support Vector Machines, Spectral Clustering, Kernel PCA, Gaussian Processes and a QP solver. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">kernsmooth</a>	2.23_1	Functions for kernel smoothing (and density estimation) corresponding to the book: Wand, M.P. and Jones, M.C. (1995) Kernel Smoothing. / Unlimited	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">knitr</a>	1.22	Provides a general-purpose tool for dynamic report generation in R using Literate Programming techniques. / GPL	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">kohonen</a>	3.0.8	Functions to train self-organising maps (SOMs). Also interrogation of the maps and prediction using trained maps are supported. The name of the package refers to Teuvo Kohonen, the inventor of the SOM. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64

Table 45: L

Name	Version	Summary/License	Platforms
<a href="#">labeling</a>	0.3	Provides a range of axis labeling algorithms / MIT file LICENSE   Unlimited	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">lahman</a>	6.0_0	Provides the tables from the ‘Sean Lahman Baseball Database’ as a set of R data.frames. It uses the data on pitching, hitting and fielding performance and other tables from 1871 through 2015, as recorded in the 2016 version of the database. / GPL	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">lars</a>	1.2	Efficient procedures for fitting an entire lasso sequence with the cost of a single least squares fit. Least angle regression and infinitesimal forward stagewise regression are related to the lasso, as described in the paper below. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">later</a>	0.8.0	Executes arbitrary R or C functions some time after the current time, after the R execution stack has emptied. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">lattice</a>	0.20_38	A powerful and elegant high-level data visualization system inspired by Trellis graphics, with an emphasis on multivariate data. Lattice is sufficient for typical graphics needs, and is also flexible enough to handle most nonstandard requirements. See ?Lattice for an introduction. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">latticeextra</a>	0.6_28	Building on the infrastructure provided by the lattice package, this package provides several new high-level functions and methods, as well as additional utilities such as panel and axis annotation functions. / GPL (>= 2)	linux-32, linux-64, noarch,



Table 46: M

Name	Version	Summary/License	Platforms
<a href="#">magic</a>	1.5_9	A collection of efficient, vectorized algorithms for the creation and investigation of magic squares and hypercubes, including a variety of functions for the manipulation and analysis of arbitrarily dimensioned arrays. The package includes methods for creating normal magic squares of any order greater than 2. The ultimate intention is for the package to be a computerized embodiment all magic square knowledge, including direct numerical verification of properties of magic squares (such as recent results on the determinant of odd-ordered semimagic squares). Some antimagic functionality is included. The package also serves as a rebuttal to the often-heard comment I thought R was just for statistics. / GPL-2	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">magrittr</a>	1.5	Provides a mechanism for chaining commands with a new forward-pipe operator, <code>%&gt;%</code> . This operator will forward a value, or the result of an expression, into the next function call/expression. There is flexible support for the type of right-hand side expressions. For more information, see package vignette. To quote Rene Magritte, Ceci n'est pas un pipe. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">manipulate</a>	1.0.1	Interactive plotting functions for use within RStudio. The manipulate function accepts a plotting expression and a set of controls (e.g. slider, picker, checkbox, or button) which are used to dynamically change values within the expression. When a value is changed using its corresponding control the expression is automatically re-executed and the plot is redrawn. / GPL-2	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">manipulatewidget</a>	0.10.0	Like package 'manipulate' does for static graphics, this package helps to easily add controls like sliders, pickers, checkboxes, etc. that can be used to modify the input data or the parameters of an interactive chart created with package 'htmlwidgets'. / GPL (>= 2)   file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64

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Table 46 – continued from previous page

Name	Version	Summary/License	Platforms
<code>mapproj</code>	1.2.6	Converts latitude/longitude into projected coordinates. / Lucent Public License	linux-32, linux-64, osx-64, win-32, win-64
<code>maps</code>	3.3.0	Display of maps. Projection code and larger maps are in separate packages ('mapproj' and 'mapdata'). / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
<code>maptools</code>	0.9_5	Set of tools for manipulating geographic data. It includes binary access to 'GSHHG' shoreline files. The package also provides interface wrappers for exchanging spatial objects with packages such as 'PBSmapping', 'spatstat', 'maps', 'RArcInfo', and others. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<code>markdown</code>	0.9	Provides R bindings to the 'Sundown' 'Markdown' rendering library (< <a href="https://github.com/vmg/sundown">https://github.com/vmg/sundown</a> >). 'Markdown' is a plain-text formatting syntax that can be converted to 'XHTML' or other formats. See < <a href="http://en.wikipedia.org/wiki/Markdown">http://en.wikipedia.org/wiki/Markdown</a> > for more information about 'Markdown'. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
<code>mass</code>	7.3_5	Functions and datasets to support Venables and Ripley, Modern Applied Statistics with S (4th edition, 2002). / GPL-2   GPL-3	linux-32, linux-64, osx-64, win-32, win-64

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Table 46 – continued from previous page

Name	Version	Summary/License	Platforms
<a href="#">matrix</a>	1.2_1	A rich hierarchy of matrix classes, including triangular, symmetric, and diagonal matrices, both dense and sparse and with pattern, logical and numeric entries. Numerous methods for and operations on these matrices, using ‘LAPACK’ and ‘SuiteSparse’ libraries. / GPL (>= 2)   file LICENCE	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">matrixcalc</a>	1.0_3	A collection of functions to support matrix calculations for probability, econometric and numerical analysis. There are additional functions that are comparable to APL functions which are useful for actuarial models such as pension mathematics. This package is used for teaching and research purposes at the Department of Finance and Risk Engineering, New York University, Polytechnic Institute, Brooklyn, NY 11201. / GPL (>= 2)	linux-64, win-64
<a href="#">matrixmodels</a>	0.4_1	Modelling with sparse and dense ‘Matrix’ matrices, using modular prediction and response module classes. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">matrixstats</a>	0.54.0	High-performing functions operating on rows and columns of matrices, e.g. col / rowMedians(), col / rowRanks(), and col / rowSds(). Functions optimized per data type and for subsetting calculations such that both memory usage and processing time is minimized. There are also optimized vector-based methods, e.g. binMeans(), madDiff() and weightedMedian(). / Artistic-2.0	linux-64, osx-64, win-32, win-64
<a href="#">maxlik</a>	1.3_4	Functions for Maximum Likelihood (ML) estimation and non-linear optimization, and related tools. It includes a unified way to call different optimizers, and classes and methods to handle the results from the ML viewpoint. It also includes a number of convenience tools for testing and developing your own models. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64

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Table 46 – continued from previous page

Name	Version	Summary/License	Platforms
<code>memoise</code>	1.1.0	Cache the results of a function so that when you call it again with the same arguments it returns the pre-computed value. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<code>mgcv</code>	1.8_28	Generalized additive (mixed) models, some of their extensions and other generalized ridge regression with multiple smoothing parameter estimation by (Restricted) Marginal Likelihood, Generalized Cross Validation and similar, or using iterated nested Laplace approximation for fully Bayesian inference. See Wood (2017) <doi:10.1201/9781315370279> for an overview. Includes a <code>gam()</code> function, a wide variety of smoothers, ‘JAGS’ support and distributions beyond the exponential family. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<code>microbenchmark</code>	1.4_6	Provides infrastructure to accurately measure and compare the execution time of R expressions. / BSD_2_clause file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<code>microsoftr</code>	3.5.0.108	Umbrella package with licenses and notices for all Microsoft R packages / file LICENSE	linux-64, osx-64, win-64
<code>mime</code>	0.6	Guesses the MIME type from a filename extension using the data derived from <code>/etc/mime.types</code> in UNIX-type systems. / GPL	linux-32, linux-64, osx-64, win-32, win-64

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Table 46 – continued from previous page

Name	Version	Summary/License	Platforms
<a href="#">miniui</a>	0.1.1	Provides UI widget and layout functions for writing Shiny apps that work well on small screens. / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">minqa</a>	1.2.4	Derivative-free optimization by quadratic approximation based on an interface to Fortran implementations by M. J. D. Powell. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">misctools</a>	0.6.2	Miscellaneous small tools and utilities. Many of them facilitate the work with matrices, e.g. inserting rows or columns, creating symmetric matrices, or checking for semidefiniteness. Other tools facilitate the work with regression models, e.g. extracting the standard errors, obtaining the number of (estimated) parameters, or calculating R-squared values. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">mkl_fft</a>	1.0.14	NumPy-based implementation of Fast Fourier Transform using Intel (R) Math Kernel Library. / BSD 3-Clause	linux-64, osx-64, win-32, win-64
<a href="#">mkl_random</a>	1.0.4	Intel (R) MKL-powered package for sampling from common probability distributions into NumPy arrays. / BSD 3-Clause	linux-64, osx-64, win-32, win-64

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Table 46 – continued from previous page

Name	Version	Summary/License	Platforms
<a href="#">mlmrev</a>	1.0_7	Data and examples from a multilevel modelling software review as well as other well-known data sets from the multilevel modelling literature. / GPL ( $\geq 2$ )	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">mnormt</a>	1.5_5	Functions are provided for computing the density and the distribution function of multivariate normal and t random variables, and for generating random vectors sampled from these distributions. Probabilities are computed via non-Monte Carlo methods; different routines are used in the case $d=1$ , $d=2$ , $d>2$ , if $d$ denotes the number of dimensions. / GPL-2   GPL-3	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">modelmetrics</a>	1.2.2	Collection of metrics for evaluating models written in C using 'Rcpp'. Popular metrics include area under the curve, log loss, root mean square error, etc. / GPL ( $\geq 2$ )	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">modelr</a>	0.1.4	Functions for modelling that help you seamlessly integrate modelling into a pipeline of data manipulation and visualisation. / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64

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Table 46 – continued from previous page

Name	Version	Summary/License	Platforms
<code>modeltools</code>	0.2.2	A collection of tools to deal with statistical models. The functionality is experimental and the user interface is likely to change in the future. The documentation is rather terse, but packages ‘coin’ and ‘party’ have some working examples. However, if you find the implemented ideas interesting we would be very interested in a discussion of this proposal. Contributions are more than welcome! / GPL-2	linux-32, linux-64, noarch, osx-64, win-32, win-64
<code>mongolite</code>	2.0.1	High-performance MongoDB client based on ‘mongo-c-driver’ and ‘jsonlite’. Includes support for aggregation, indexing, map-reduce, streaming, encryption, enterprise authentication, and GridFS. The online user manual provides an overview of the available methods in the package: < <a href="https://jeroen.github.io/mongolite/">https://jeroen.github.io/mongolite/</a> >. / Apache License 2.0	linux-32, linux-64, osx-64, win-32, win-64
<code>mrclient</code>	3.4.3	A free, community-supported, data science tool for high performance analytics / Proprietary	linux-64, win-64
<code>mrclient-mlm</code>	3.4.3	Pre-trained machine learning models for sentiment analysis and image detection / Proprietary	noarch
<code>mrclient-mml</code>	3.4.3	Provides state-of-the-art fast, scalable machine learning algorithms and transforms for R / Proprietary	linux-64, win-64
<code>mro</code>	0.1.1	Computes multiple correlation coefficient when the data matrix is given and tests its significance. / GPL-2	linux-64, win-64
<code>mro-base</code>	3.5.1	R is a free software environment for statistical computing and graphics. / GPL-2   GPL-3	linux-64, osx-64, win-64
<code>mro-base_impl</code>	3.5.1	R is a free software environment for statistical computing and graphics. / GPL-2   GPL-3	linux-64, win-64
<code>mro-basics</code>	3.5.1	None / None	linux-64, osx-64, win-64

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Table 46 – continued from previous page

Name	Version	Summary/License	Platforms
<a href="#">multcomp</a>	1.4_1	Simultaneous tests and confidence intervals for general linear hypotheses in parametric models, including linear, generalized linear, linear mixed effects, and survival models. The package includes demos reproducing analyzes presented in the book <i>Multiple Comparisons Using R</i> (Bretz, Hothorn, Westfall, 2010, CRC Press). / GPL-2	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">munsell</a>	0.5.0	Provides easy access to, and manipulation of, the Munsell colours. Provides a mapping between Munsell's original notation (e.g. 5R 5/10) and hexadecimal strings suitable for use directly in R graphics. Also provides utilities to explore slices through the Munsell colour tree, to transform Munsell colours and display colour palettes. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">mvtnorm</a>	1.0_1	Computes multivariate normal and t probabilities, quantiles, random deviates and densities. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64



Table 47: N

Name	Version	Summary/License	Platforms
<a href="#">networkd3</a>	0.4	Creates 'D3' 'JavaScript' network, tree, dendrogram, and Sankey graphs from 'R'. / GPL (>= 3)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">nlme</a>	3.1_1	Fit and compare Gaussian linear and nonlinear mixed-effects models. / GPL (>= 2)   file LICENCE	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">nlopt-static</a>	2.4.2	nonlinear optimization library / GNU Lesser General Public License (LGPL)	linux-32, linux-64, osx-64
<a href="#">nloptr</a>	1.2.1	Solve optimization problems using an R interface to NLOpt. NLOpt is a free/open-source library for nonlinear optimization, providing a common interface for a number of different free optimization routines available online as well as original implementations of various other algorithms. See <a href="http://ab-initio.mit.edu/wiki/index.php/NLOpt_Introduction">http://ab-initio.mit.edu/wiki/index.php/NLOpt_Introduction</a> for more information on the available algorithms. During installation of nloptr on Unix-based systems, the installer checks whether the NLOpt library is installed on the system. If the NLOpt library cannot be found, the code is compiled using the NLOpt source included in the nloptr package. / LGPL-3	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">nlp</a>	0.2_0	Basic classes and methods for Natural Language Processing. / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">nmf</a>	0.21.0	Provides a framework to perform Non-negative Matrix Factorization (NMF). The package implements a set of already published algorithms and seeding methods, and provides a framework to test, develop and plug new/custom algorithms. Most of the built-in algorithms have been optimized in C, and the main interface function provides an easy way of performing parallel computations on multicore machines. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<b>4.2. Anaconda Individual Edition</b>			<b>1593</b> linux-32, win-64

Table 48: O

Name	Version	Summary/License	Platforms
<a href="#">oce</a>	1.0.1	Supports the analysis of Oceanographic data, including ‘ADCP’ measurements, measurements made with ‘argo’ floats, ‘CTD’ measurements, sectional data, sea-level time series, coastline and topographic data, etc. Provides specialized functions for calculating seawater properties such as potential temperature in either the ‘UNESCO’ or ‘TEOS-10’ equation of state. Produces graphical displays that conform to the conventions of the Oceanographic literature. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">odbc</a>	1.1.6	A DBI-compatible interface to ODBC databases. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">openssl</a>	1.3	Bindings to OpenSSL libssl and libcrypto, plus custom SSH key parsers. Supports RSA, DSA and EC curves P-256, P-384 and P-521. Cryptographic signatures can either be created and verified manually or via x509 certificates. AES can be used in cbc, ctr or gcm mode for symmetric encryption; RSA for asymmetric (public key) encryption or EC for Diffie Hellman. High-level envelope functions combine RSA and AES for encrypting arbitrary sized data. Other utilities include key generators, hash functions (md5, sha1, sha256, etc), base64 encoder, a secure random number generator, and ‘bignum’ math methods for manually performing crypto calculations on large multibyte integers. / MIT file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">openxlsx</a>	4.1.0	Simplifies the creation of Excel .xlsx files by providing a high level interface to writing, styling and editing worksheets. Through the use of ‘Rcpp’, read/write times are comparable to the ‘xlsx’ and ‘XLConnect’ packages with the added benefit of removing the dependency on Java. / MIT file LICENSE	linux-32, linux-64, osx-64, win-32, win-64

Table 49: P

Name	Version	Summary/License	Platforms
<a href="#">packrat</a>	0.5.0	Manage the R packages your project depends on in an isolated, portable, and reproducible way. / GPL-2	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">pbdzmq</a>	0.3_3	'ZeroMQ' is a well-known library for high-performance asynchronous messaging in scalable, distributed applications. This package provides high level R wrapper functions to easily utilize 'ZeroMQ'. We mainly focus on interactive client/server programming frameworks. For convenience, a minimal 'ZeroMQ' library (4.2.2) is shipped with 'pbdZMQ', which can be used if no system installation of 'ZeroMQ' is available. A few wrapper functions compatible with 'rzmq' are also provided. / GPL-3	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">pbivnorm</a>	0.6.0	Provides a vectorized R function for calculating probabilities from a standard bivariate normal CDF. / GPL (>= 2)	linux-64, osx-64, win-32, win-64
<a href="#">pbkrtest</a>	0.4_7	Test in mixed effects models. Attention is on mixed effects models as implemented in the 'lme4' package. This package implements a parametric bootstrap test and a Kenward Roger modification of F-tests for linear mixed effects models and a parametric bootstrap test for generalized linear mixed models. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">pcapp</a>	1.9_7	Provides functions for robust PCA by projection pursuit. The methods are described in Croux et al. (2006) <doi:10.2139/ssrn.968376>, Croux et al. (2013) <doi:10.1080/00401706.2012.727746>, Todorov and Filzmoser (2013) <doi:10.1007/978-3-642-33042-1_31>. / GPL (>= 3)	linux-32, linux-64, osx-64, win-32, win-64

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Table 49 – continued from previous page

Name	Version	Summary/License	Platforms
<a href="#">pdftools</a>	2.2	Utilities based on ‘libpoppler’ for extracting text, fonts, attachments and meta-data from a PDF file. Also supports high quality rendering of PDF documents into PNG, JPEG, TIFF format, or into raw bitmap vectors for further processing in R. / MIT file LICENSE	linux-64, osx-64, win-32, win-64
<a href="#">perm</a>	1.0_0	Perform Exact or Asymptotic permutation tests / GPL	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">pillar</a>	1.3.1	Provides a ‘pillar’ generic designed for formatting columns of data using the full range of colours provided by modern terminals. / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">pkgbuild</a>	1.0.3	Provides functions used to build R packages. Locates compilers needed to build R packages on various platforms and ensures the PATH is configured appropriately so R can use them. / GPL-3	linux-64, noarch, osx-64, win-32, win-64
<a href="#">pkgconfig</a>	2.0.2	Set configuration options on a per-package basis. Options set by a given package only apply to that package, other packages are unaffected. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64

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Table 49 – continued from previous page

Name	Version	Summary/License	Platforms
<a href="#">pkgload</a>	1.0.2	Simulates the process of installing a package and then attaching it. This is a key part of the ‘devtools’ package as it allows you to rapidly iterate while developing a package. / GPL-3	linux-64, osx-64, win-32, win-64
<a href="#">pkgmaker</a>	0.27	Provides some low-level utilities to use for package development. It currently provides managers for multiple package specific options and registries, vignette, unit test and bibtext related utilities. It serves as a base package for packages like NMF, RcppOctave, doRNG, and as an incubator package for other general purposes utilities, that will eventually be packaged separately. It is still under heavy development and changes in the interface(s) are more than likely to happen. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">pki</a>	0.1_5	PKI functions such as verifying certificates, RSA encryption and signing which can be used to build PKI infrastructure and perform cryptographic tasks. / GPL-2   GPL-3   file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">plm</a>	1.7_0	A set of estimators and tests for panel data econometrics. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">plogr</a>	0.2.0	A simple header-only logging library for C. Add ‘LinkingTo: plogr’ to ‘DESCRIPTION’, and ‘#include <plogr.h>’ in your C modules to use it. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64

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Table 49 – continued from previous page

Name	Version	Summary/License	Platforms
<a href="#">plotly</a>	4.9.0	Create interactive web graphics from ‘ggplot2’ graphs and/or a custom interface to the (MIT-licensed) JavaScript library ‘plotly.js’ inspired by the grammar of graphics. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">pls</a>	2.7_1	Multivariate regression methods Partial Least Squares Regression (PLSR), Principal Component Regression (PCR) and Canonical Powered Partial Least Squares (CPPLS). / GPL-2	linux-64, noarch, osx-64, win-32, win-64
<a href="#">plumber</a>	0.4.6	Gives the ability to automatically generate and serve an HTTP API from R functions using the annotations in the R documentation around your functions. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">plyr</a>	1.8.4	A set of tools that solves a common set of problems: you need to break a big problem down into manageable pieces, operate on each piece and then put all the pieces back together. For example, you might want to fit a model to each spatial location or time point in your study, summarise data by panels or collapse high-dimensional arrays to simpler summary statistics. The development of ‘plyr’ has been generously supported by ‘Becton Dickinson’. / MIT file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">png</a>	0.1_7	This package provides an easy and simple way to read, write and display bitmap images stored in the PNG format. It can read and write both files and in-memory raw vectors. / GPL-2   GPL-3	linux-32, linux-64, osx-64, win-32, win-64

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Table 49 – continued from previous page

Name	Version	Summary/License	Platforms
<a href="#">polspline</a>	1.1.14	Routines for the polynomial spline fitting routines hazard regression, hazard estimation with flexible tails, logspline, lspec, polyclass, and polymars, by C. Kooperberg and co-authors. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">pool</a>	0.1.4	Enables the creation of object pools, which make it less computationally expensive to fetch a new object. Currently the only supported pooled objects are 'DBI' connections. / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">praise</a>	1.0.0	Build friendly R packages that praise their users if they have done something good, or they just need it to feel better. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">prettyunits</a>	1.0.2	Pretty, human readable formatting of quantities. Time intervals: 1337000 -> 15d 11h 23m 20s. Vague time intervals: 2674000 -> about a month ago. Bytes: 1337 -> 1.34 kB. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64

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Table 49 – continued from previous page

Name	Version	Summary/License	Platforms
<code>proc</code>	1.14.0	Tools for visualizing, smoothing and comparing receiver operating characteristic (ROC curves). (Partial) area under the curve (AUC) can be compared with statistical tests based on U-statistics or bootstrap. Confidence intervals can be computed for (p)AUC or ROC curves. / GPL (>= 3)	linux-32, linux-64, osx-64, win-32, win-64
<code>processx</code>	3.3.0	Tools to run system processes in the background. It can check if a background process is running; wait on a background process to finish; get the exit status of finished processes; kill background processes. It can read the standard output and error of the processes, using non-blocking connections. 'processx' can poll a process for standard output or error, with a timeout. It can also poll several processes at once. / MIT file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<code>prodlim</code>	2018.04.18	Fast and user friendly implementation of nonparametric estimators for censored event history (survival) analysis. Kaplan-Meier and Aalen-Johansen method. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<code>profilemodel</code>	0.6.0	Provides tools that can be used to calculate, evaluate, plot and use for inference the profiles of <i>arbitrary</i> inference functions for <i>arbitrary</i> 'glm'-like fitted models with linear predictors. More information on the methods that are implemented can be found in Kosmidis (2008) < <a href="https://www.r-project.org/doc/Rnews/Rnews_2008-2.pdf">https://www.r-project.org/doc/Rnews/Rnews_2008-2.pdf</a> >. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<code>profvis</code>	0.3.5	Interactive visualizations for profiling R code. / GPL-3   file LICENSE	linux-32, linux-64, osx-64, win-32, win-64

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Table 49 – continued from previous page

Name	Version	Summary/License	Platforms
<a href="#">progress</a>	1.2.0	Configurable Progress bars, they may include percentage, elapsed time, and/or the estimated completion time. They work in terminals, in ‘Emacs’ ‘ESS’, ‘RStudio’, ‘Windows’ ‘Rgui’ and the ‘macOS’ ‘R.app’. The package also provides a ‘C’ ‘API’, that works with or without ‘Rcpp’. / MIT file LICENSE	noarch
<a href="#">promises</a>	1.0.1	Provides fundamental abstractions for doing asynchronous programming in R using promises. Asynchronous programming is useful for allowing a single R process to orchestrate multiple tasks in the background while also attending to something else. Semantics are similar to ‘JavaScript’ promises, but with a syntax that is idiomatic R. / MIT file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">proto</a>	1.0.0	An object oriented system using object-based, also called prototype-based, rather than class-based object oriented ideas. / GPL-2	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">pryr</a>	0.1.4	Useful tools to pry back the covers of R and understand the language at a deeper level. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">ps</a>	1.3.0	List, query and manipulate all system processes, on ‘Windows’, ‘Linux’ and ‘macOS’. / BSD_3_clause file LICENSE	linux-64, osx-64, win-32, win-64

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Table 49 – continued from previous page

Name	Version	Summary/License	Platforms
<a href="#">pspline</a>	1.0_1	Smoothing splines with penalties on order m derivatives. / Unlimited	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">psych</a>	1.8.12	A general purpose toolbox for personality, psychometric theory and experimental psychology. Functions are primarily for multivariate analysis and scale construction using factor analysis, principal component analysis, cluster analysis and reliability analysis, although others provide basic descriptive statistics. Item Response Theory is done using factor analysis of tetrachoric and polychoric correlations. Functions for analyzing data at multiple levels include within and between group statistics, including correlations and factor analysis. Functions for simulating and testing particular item and test structures are included. Several functions serve as a useful front end for structural equation modeling. Graphical displays of path diagrams, factor analysis and structural equation models are created using basic graphics. Some of the functions are written to support a book on psychometric theory as well as publications in personality research. For more information, see the <a href="https://personality-project.org/r">https://personality-project.org/r</a> web page. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">purrr</a>	0.3.2	A complete and consistent functional programming toolkit for R. / GPL-3   file LICENSE	linux-32, linux-64, osx-64, win-32, win-64

Table 50: Q

Name	Version	Summary/License	Platforms
qpdf	1.1	Content-preserving transformations of PDF files such as split, combine, and compress. This package interfaces directly to the ‘qpdf’ C API and does not require any command line utilities. Note that ‘qpdf’ does not read actual content from PDF files: to extract text and data you need the ‘pdftools’ package. / Apache License 2.0	linux-64, osx-64, win-32, win-64
qrm	0.4_13	Accompanying package to the book Quantitative Risk Management: Concepts, Techniques and Tools by Alexander J. McNeil, Rüdiger Frey, and Paul Embrechts. / GPL (>= 2)	linux-64, osx-64, win-32, win-64
quadprog	1.5_5	This package contains routines and documentation for solving quadratic programming problems. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
quantmod	0.4_14	Specify, build, trade, and analyse quantitative financial trading strategies. / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
quantreg	5.38	Estimation and inference methods for models of conditional quantiles: Linear and nonlinear parametric and non-parametric (total variation penalized) models for conditional quantiles of a univariate response and several methods for handling censored survival data. Portfolio selection methods based on expected shortfall risk are also included. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
qvcalc	0.9_1	Functions to compute quasi variances and associated measures of approximation error. / GPL-2   GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
<b>4.2. Anaconda Individual Edition</b>			<b>1603</b> linux-64, win-32, win-64

Table 51: R

Name	Version	Summary/License	Platforms
r	3.6.0	R is a free software environment for statistical computing and graphics. / GPL-3.0	linux-32, linux-64, osx-64, win-32, win-64
r-abc.data	1.0	Contains data which are used by functions of the ‘abc’ package. / GPL (>= 3)	noarch
r-abc.rap	0.9.0	It aims to identify candidate genes that are “differentially methylated” between cases and controls. It applies Student’s t-test and delta beta analysis to identify candidate genes containing multiple “CpG sites”. / GPL-3	noarch
r-abcoptim	0.15.0	An implementation of Karaboga (2005) Artificial Bee Colony Optimization algorithm < <a href="http://mf.erciyes.edu.tr/abc/pub/tr06_2005.pdf">http://mf.erciyes.edu.tr/abc/pub/tr06_2005.pdf</a> >. This (working) version is a Work-in-progress, which is why it has been implemented using pure R code. This was developed upon the basic version programmed in C and distributed at the algorithm’s official website. / MIT file LICENSE	linux-64, osx-64, win-64
r-abcp2	1.2	Tests the goodness of fit of a distribution of offspring to the Normal, Poisson, and Gamma distribution and estimates the proportional paternity of the second male (P2) based on the best fit distribution. / GPL-2	noarch
r-abe	3.0.1	Performs augmented backward elimination and checks the stability of the obtained model. Augmented backward elimination combines significance or information based criteria with the change in estimate to either select the optimal model for prediction purposes or to serve as a tool to obtain a practically sound, highly interpretable model. More details can be found in Dunkler et al. (2014) < <a href="https://doi.org/10.1371/journal.pone.0113677">doi:10.1371/journal.pone.0113677</a> >. / GPL (>= 2)	noarch
r-abf2	0.7.1	Loads ABF2 files containing gap-free data from electrophysiological recordings, as created by Axon Instruments/Molecular Devices software such as pClamp 10. / Artistic-2.0	noarch
r-abind	1.4.5	Combine multidimensional arrays into a single array. This is a generalization of ‘cbind’ and ‘rbind’. Works with vectors, matrices, and higher-dimensional arrays. Also provides functions ‘adrop’, ‘asub’, and ‘afill’ for manipulating, extracting and replacing data in arrays. / LGPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64

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Table 51 – continued from previous page

Name	Version	Summary/License	Platforms
r-abnormality	0.1.0	Contains the functions to implement the methodology and considerations laid out by Marks et al. in the manuscript Measuring Abnormality in High Dimensional Spaces: Applications in Biomechanical Gait Analysis. As of 2/27/2018 this paper has been submitted and is under scientific review. Using high-dimensional datasets to measure a subject's overall level of abnormality as compared to a reference population is often needed in outcomes research. Utilizing applications in instrumented gait analysis, that article demonstrates how using data that is inherently non-independent to measure overall abnormality may bias results. A methodology is introduced to address this bias to accurately measure overall abnormality in high dimensional spaces. While this methodology is in line with previous literature, it differs in two major ways. Advantageously, it can be applied to datasets in which the number of observations is less than the number of features/variables, and it can be abstracted to practically any number of domains or dimensions. After applying the proposed methodology to the original data, the researcher is left with a set of uncorrelated variables (i.e. principal components) with which overall abnormality can be measured without bias. Different considerations are discussed in that article in deciding the appropriate number of principal components to keep and the aggregate distance measure to utilize. / MIT file LICENSE	noarch
r-abodoutlier	0.1	Performs angle-based outlier detection on a given dataframe. Three methods are available, a full but slow implementation using all the data that has cubic complexity, a fully randomized one which is way more efficient and another using k-nearest neighbours. These algorithms are specially well suited for high dimensional data outlier detection. / MIT file LICENSE	noarch
r-abps	0.3	An implementation of the Abnormal Blood Profile Score (ABPS, part of the Athlete Biological Passport program of the World Anti-Doping Agency), which combines several blood parameters into a single score in order to detect blood doping (Sottas et al. (2006) <doi:10.2202/1557-4679.1011>). The package also contains functions to calculate other scores used in anti-doping programs, such as the OFF-score (Gore et al. (2003) <http://www.haematologica.org/content/88/3/333>), as well as example data. / GPL (>= 2)	noarch
r-ac3net	1.2.2	Infers directional conservative causal core (gene) networks. It is an advanced version of the algorithm C3NET by providing directional network. Gokmen Altay (2018) <doi:10.1101/271031>, bioRxiv. / GPL (>= 3)	noarch
r-aca	1.1	Offers an interactive function for the detection of breakpoints in series. / GPL	noarch
r-acceptancesampling	1.0_6	Provides functionality for creating and evaluating acceptance sampling plans. Sampling plans can be single, double or multiple. / GPL (>= 3)	noarch
r-acclma	1.0	The main function is plotLMA(sourcefile,header) that takes a data set and plots the appropriate LMA and ACC graphs. If no sourcefile (a string) was passed, a manual data entry window is opened. The header parameter indicates by TRUE/FALSE (false by default) if the source CSV file has a head row or not. The data set should contain only one independent variable (X) and one dependent variable (Y) and can contain a weight for each observation / GPL-2	noarch
r-accrued	1.4.1	Package for visualizing data quality of partially accruing data. / GPL-3	noarch
r-acd	1.5.3	Categorical data analysis with complete or missing responses / GPL (>= 2)	noarch

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Table 51 – continued from previous page

Name	Version	Summary/License	Platforms
<a href="#">r-ace2fastq</a>	0.6.0	The ACE file format is used in genomics to store contigs from sequencing machines. This tools converts it into FASTQ format. Both formats contain the sequence characters and their corresponding quality information. Unlike the FASTQ file, the ace file stores the quality values numerically. The conversion algorithm uses the standard Sanger formula. The package facilitates insertion into pipelines, and content inspection. / GPL-3	noarch
<a href="#">r-acepack</a>	1.4.1	Two nonparametric methods for multiple regression transform selection are provided. The first, Alternative Conditional Expectations (ACE), is an algorithm to find the fixed point of maximal correlation, i.e. it finds a set of transformed response variables that maximizes $R^2$ using smoothing functions [see Breiman, L., and J.H. Friedman. 1985. Estimating Optimal Transformations for Multiple Regression and Correlation. Journal of the American Statistical Association. 80:580-598. <doi:10.1080/01621459.1985.10478157>]. Also included is the Additivity Variance Stabilization (AVAS) method which works better than ACE when correlation is low [see Tibshirani, R.. 1986. Estimating Transformations for Regression via Additivity and Variance Stabilization. Journal of the American Statistical Association. 83:394-405. <doi:10.1080/01621459.1988.10478610>]. A good introduction to these two methods is in chapter 16 of Frank Harrel's Regression Modeling Strategies in the Springer Series in Statistics. / MIT file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-acet</a>	1.8.0	Twin models that are able to estimate the dynamic behaviour of the variance components in the classical twin models with respect to age using B-splines and P-splines. / GPL (>= 2)	linux-64, osx-64, win-64
<a href="#">r-acfperiod</a>	1.0.0	Non-robust and robust computations of the sample autocovariance (ACOVF) and sample autocorrelation functions (ACF) of univariate and multivariate processes. The methodology consists in reversing the diagonalization procedure involving the periodogram or the cross-periodogram and the Fourier transform vectors, and, thus, obtaining the ACOVF or the ACF as discussed in Fuller (1995) <doi:10.1002/9780470316917>. The robust version is obtained by fitting robust M-regressors to obtain the M-periodogram or M-cross-periodogram as discussed in Reisen et al. (2017) <doi:10.1016/j.jspi.2017.02.008>. / GPL (>= 2)	noarch
<a href="#">r-acm4r</a>	1.0	Fragment lengths or molecular weights from pairs of lanes are compared, and a number of matching bands are calculated using the Align-and-Count Method. / GPL	noarch
<a href="#">r-acmer</a>	1.1.0	Implementation of estimator ACME, described in Wolpert (2015), ACME: A Partially Periodic Estimator of Avian & Chiropteran Mortality at Wind Turbines (submitted). Unlike most other models, this estimator supports decreasing-hazard Weibull model for persistence; decreasing search proficiency as carcasses age; variable bleed-through at successive searches; and interval mortality estimates. The package provides, based on search data, functions for estimating the mortality inflation factor in Frequentist and Bayesian settings. / MIT file LICENSE	noarch
<a href="#">r-acnr</a>	1.0.0	Provides SNP array data from different types of copy-number regions. These regions were identified manually by the authors of the package and may be used to generate realistic data sets with known truth. / LGPL (>= 2.1)	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-acopula</a>	0.9.3	Archimax copulas are mixture of Archimedean and EV copulas. The package provides definitions of several parametric families of generator and dependence function, computes CDF and PDF, estimates parameters, tests for goodness of fit, generates random sample and checks copula properties for custom constructs. In 2-dimensional case explicit formulas for density are used, in the contrary to higher dimensions when all derivatives are linearly approximated. Several non-archimax families (normal, FGM, Plackett) are provided as well. / GPL-2	noarch
<a href="#">r-acp</a>	2.1	Analysis of count data exhibiting autoregressive properties, using the Autoregressive Conditional Poisson model (ACP(p,q)) proposed by Heinen (2003). / GPL-2	noarch
<a href="#">r-acrt</a>	1.0.1	Functions for testing affine hypotheses on the regression coefficient vector in regression models with autocorrelated errors. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-acss</a>	2.1.4	Provides a general toolkit for downloading, managing, analyzing, and presenting data from the U.S. Census (< <a href="https://www.census.gov/data/developers/data-sets.html">https://www.census.gov/data/developers/data-sets.html</a> >), including SF1 (Decennial short-form), SF3 (Decennial long-form), and the American Community Survey (ACS). Confidence intervals provided with ACS data are converted to standard errors to be bundled with estimates in complex acs objects. Package provides new methods to conduct standard operations on acs objects and present/plot data in statistically appropriate ways. / GPL-3	noarch
<a href="#">r-acss</a>	0.2.5	Main functionality is to provide the algorithmic complexity for short strings, an approximation of the Kolmogorov Complexity of a short string using the coding theorem method (see ?acss). The database containing the complexity is provided in the data only package acss.data, this package provides functions accessing the data such as prob_random returning the posterior probability that a given string was produced by a random process. In addition, two traditional (but problematic) measures of complexity are also provided: entropy and change complexity. / GPL (>= 2)	noarch
<a href="#">r-acss.data</a>	1.0	Data only package providing the algorithmic complexity of short strings, computed using the coding theorem method. For a given set of symbols in a string, all possible or a large number of random samples of Turing machines (TM) with a given number of states (e.g., 5) and number of symbols corresponding to the number of symbols in the strings were simulated until they reached a halting state or failed to end. This package contains data on 4.5 million strings from length 1 to 12 simulated on TMs with 2, 4, 5, 6, and 9 symbols. The complexity of the string corresponds to the distribution of the halting states of the TMs. / GPL (>= 2)	noarch
<a href="#">r-acswt</a>	1.0	A book designed to meet the requirements of masters students. Tattar, P.N., Suresh, R., and Manjunath, B.G. A Course in Statistics with R, J. Wiley, ISBN 978-1-119-15272-9. / GPL-2	noarch

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Table 51 – continued from previous page

Name	Version	Summary/License	Platforms
r-activedriver	1.0.0	A mutation analysis tool that discovers cancer driver genes with frequent mutations in protein signalling sites such as post-translational modifications (phosphorylation, ubiquitination, etc). The Poisson generalised linear regression model identifies genes where cancer mutations in signalling sites are more frequent than expected from the sequence of the entire gene. Integration of mutations with signalling information helps find new driver genes and propose candidate mechanisms to known drivers. Reference: Systematic analysis of somatic mutations in phosphorylation signaling predicts novel cancer drivers. Juri Reimand and Gary D Bader. Molecular Systems Biology (2013) 9:637 <doi:10.1038/msb.2012.68>. / GPL (>= 2)	noarch
r-activityindex	0.3.6	Read raw accelerometry from 'GT3X' data and plain table data to calculate Activity Index from Bai et al. (2016) <doi:10.1371/journal.pone.0160644>. / GPL-3	noarch
r-activpalprocessing	1.0.2	Performs estimation of physical activity and sedentary behavior variables from activPAL (PAL Technologies, Glasgow, Scotland) events files. See < <a href="http://paltechnologies.com">http://paltechnologies.com</a> > for more information on the activPAL. / GPL-2   GPL-3	noarch
r-ada	2.0.5	Performs discrete, real, and gentle boost under both exponential and logistic loss on a given data set. The package ada provides a straightforward, well-documented, and broad boosting routine for classification, ideally suited for small to moderate-sized data sets. / GPL	noarch
r-adagio	0.7.1	The R package 'adagio' will provide methods and algorithms for discrete optimization, e.g. knapsack and subset sum procedures, derivative-free Nelder-Mead and Hooke-Jeeves minimization, and some (evolutionary) global optimization functions. / GPL (>= 3)	linux-64, osx-64, win-64
r-adaptivesparsity	1.6	Implements Figueiredo EM algorithm for adaptive sparsity (Jeffreys prior) (see Figueiredo, M.A.T.; , Adaptive sparseness for supervised learning, Pattern Analysis and Machine Intelligence, IEEE Transactions on , vol.25, no.9, pp. 1150- 1159, Sept. 2003) and Wong algorithm for adaptively sparse gaussian geometric models (see Wong, Eleanor, Suyash Awate, and P. Thomas Fletcher. Adaptive Sparsity in Gaussian Graphical Models. In Proceedings of the 30th International Conference on Machine Learning (ICML-13), pp. 311-319. 2013.) / LGPL (>= 3.0)	linux-64, osx-64, win-64
r-adaptivetau	2.2.3	Implements adaptive tau leaping to approximate the trajectory of a continuous-time stochastic process as described by Cao et al. (2007) The Journal of Chemical Physics <doi:10.1063/1.2745299> (aka. the Gillespie stochastic simulation algorithm). This package is based upon work supported by NSF DBI-0906041 and NIH K99-GM104158 to Philip Johnson and NIH R01-AI049334 to Rustom Antia. / GPL (>= 3)	linux-64, osx-64, win-64
r-adaptmcmc	1.3	Enables sampling from arbitrary distributions if the log density is known up to a constant; a common situation in the context of Bayesian inference. The implemented sampling algorithm was proposed by Vihola (2012) <DOI:10.1007/s11222-011-9269-5> and achieves often a high efficiency by tuning the proposal distributions to a user defined acceptance rate. / GPL (>= 2)	noarch
r-adaptmt	1.0.0	Implementation of adaptive p-value thresholding (AdaPT), including both a framework that allows the user to specify any algorithm to learn local false discovery rate and a pool of convenient functions that implement specific algorithms. See Lei, Lihua and Fithian, William (2016) <arXiv:1609.06035>. / MIT file LICENSE	noarch

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Name	Version	Summary/License	Platforms
r-adapttest	1.0	The functions defined in this program serve for implementing adaptive two-stage tests. Currently, four tests are included: Bauer and Koehne (1994), Lehmacher and Wassmer (1999), Vandemeulebroecke (2006), and the horizontal conditional error function. User-defined tests can also be implemented. Reference: Vandemeulebroecke, An investigation of two-stage tests, Statistica Sinica 2006. / GPL ( $\geq 2$ )	noarch
r-adct	0.1.0	Existing adaptive design methods in clinical trials. The package includes power, stopping boundaries (sample size) calculation functions for two-group group sequential designs, adaptive design with coprimary endpoints, biomarker-informed adaptive design, etc. / GPL ( $\geq 2$ )	noarch
r-addhaz	0.5	Functions to fit the binomial and multinomial additive hazard models and to estimate the contribution of diseases/conditions to the disability prevalence, as proposed by Nusselder and Looman (2004) and extended by Yokota et al (2017). / GPL-3	noarch
r-additivitytests	1.1_4	Implementation of the Tukey, Mandel, Johnson-Graybill, LBI, Tusell and modified Tukey non-additivity tests. / GPL-3	noarch
r-addt	2.0	Accelerated destructive degradation tests (ADDT) are often used to collect necessary data for assessing the long-term properties of polymeric materials. Based on the collected data, a thermal index (TI) is estimated. The TI can be useful for material rating and comparison. This package implements the traditional method based on the least-squares method, the parametric method based on maximum likelihood estimation, and the semiparametric method based on spline methods, and the corresponding methods for estimating TI for polymeric materials. The traditional approach is a two-step approach that is currently used in industrial standards, while the parametric method is widely used in the statistical literature. The semiparametric method is newly developed. Both the parametric and semiparametric approaches allow one to do statistical inference such as quantifying uncertainties in estimation, hypothesis testing, and predictions. Publicly available datasets are provided illustrations. More details can be found in Jin et al. (2017). / GPL-2	noarch
r-ade4	1.7_13	Tools for multivariate data analysis. Several methods are provided for the analysis (i.e., ordination) of one-table (e.g., principal component analysis, correspondence analysis), two-table (e.g., coinertia analysis, redundancy analysis), three-table (e.g., RLQ analysis) and K-table (e.g., STATIS, multiple coinertia analysis). The philosophy of the package is described in Dray and Dufour (2007) <doi:10.18637/jss.v022.i04>. / GPL ( $\geq 2$ )	linux-64, osx-64, win-64
r-ade4tkgui	0.2_9	A Tcl/Tk GUI for some basic functions in the ‘ade4’ package. / GPL ( $\geq 2$ )	noarch
r-adegraphics	1.0_15	Graphical functionalities for the representation of multivariate data. It is a complete re-implementation of the functions available in the ‘ade4’ package. / GPL ( $\geq 2$ )	noarch
r-adeptdata	1.0.1	Created to host raw accelerometry data sets and their derivatives which are used in the corresponding ‘adept’ package. / GPL-3	noarch
r-adequacymodel	2.0.0	The main application concerns to a new robust optimization package with two major contributions. The first contribution refers to the assessment of the adequacy of probabilistic models through a combination of several statistics, which measure the relative quality of statistical models for a given data set. The second one provides a general purpose optimization method based on meta-heuristics functions for maximizing or minimizing an arbitrary objective function. / GPL ( $\geq 2$ )	noarch

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Table 51 – continued from previous page

Name	Version	Summary/License	Platforms
<a href="#">r-adfexplorer</a>	0.1.4	Amiga Disk Files (ADF) are virtual representations of 3.5 inch floppy disks for the Commodore Amiga. Most disk drives from other systems (including modern drives) are not able to read these disks. To be able to emulate this system, the ADF format was created. This package enables you to read ADF files and import and export files from and to such virtual DOS-formatted disks. / GPL-3	noarch
<a href="#">r-adgofest</a>	0.3	Anderson-Darling GoF test with p-value calculation based on Marsaglia's 2004 paper Evaluating the Anderson-Darling Distribution / GPL	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-adimpro</a>	0.9.0	Implements tools for manipulation of digital images and the Propagation Separation approach by Polzehl and Spokoiny (2006) <DOI:10.1007/s00440-005-0464-1> for smoothing digital images, see Polzehl and Tabelow (2007) <DOI:10.18637/jss.v019.i01>. / GPL (>= 2)	linux-64, osx-64, win-64
<a href="#">r-adjclust</a>	0.5.7	Implements a constrained version of hierarchical agglomerative clustering, in which each observation is associated to a position, and only adjacent clusters can be merged. Typical application fields in bioinformatics include Genome-Wide Association Studies or Hi-C data analysis, where the similarity between items is a decreasing function of their genomic distance. Taking advantage of this feature, the implemented algorithm is time and memory efficient. This algorithm is described in Chapter 4 of Alia Dehman (2015) < <a href="https://hal.archives-ouvertes.fr/tel-01288568v1">https://hal.archives-ouvertes.fr/tel-01288568v1</a> >. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-adklakedata</a>	0.6.1	Package for the access and distribution of Long-term lake datasets from lakes in the Adirondack Park, northern New York state. Includes a wide variety of physical, chemical, and biological parameters from 28 lakes. Data are from multiple collection organizations and have been harmonized in both time and space for ease of reuse. / MIT file LICENSE	noarch
<a href="#">r-admisc</a>	0.3	Contains functions used across packages 'QCA', 'DDIwR', and 'venn'. Interprets and translates DNF - Disjunctive Normal Form expressions, for both binary and multi-value crisp sets, and extracts information (set names, set values) from those expressions. Other functions perform various other checks if possibly numeric (even if all numbers reside in a character vector) and coerce to numeric, or check if the numbers are whole. It also offers, among many others, a highly flexible recoding function. / GPL (>= 2)	noarch
<a href="#">r-admit</a>	2.1.3	Provides functions to perform the fitting of an adaptive mixture of Student-t distributions to a target density through its kernel function as described in Ardia et al. (2009) <doi:10.18637/jss.v029.i03>. The mixture approximation can then be used as the importance density in importance sampling or as the candidate density in the Metropolis-Hastings algorithm to obtain quantities of interest for the target density itself. / GPL (>= 2)	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-admmnet</a>	0.1	Fit linear and cox models regularized with net (L1 and Laplacian), elastic-net (L1 and L2) or lasso (L1) penalty, and their adaptive forms, such as adaptive lasso and net adjusting for signs of linked coefficients. In addition, it treats the number of non-zero coefficients as another tuning parameter and simultaneously selects with the regularization parameter. The package uses one-step coordinate descent algorithm and runs extremely fast by taking into account the sparsity structure of coefficients. / GPL ( $\geq 2$ )	linux-64, osx-64, win-64
<a href="#">r-adoptr</a>	0.2.2	Optimize one or two-arm, two-stage designs for clinical trials with respect to several pre-implemented objective criteria or implement custom objectives. Optimization under uncertainty and conditional (given stage-one outcome) constraints are supported. See Pilz M, Kunzmann K, Herrmann C, Rauch G, Kieser M. A variational approach to optimal two-stage designs. Statistics in Medicine. 2019;13. <doi:10.1002/sim.8291> for details. / MIT file LICENSE	noarch
<a href="#">r-adpf</a>	0.0.1	This function takes a vector or matrix of data and smooths the data with an improved Savitzky Golay transform. The Savitzky-Golay method for data smoothing and differentiation calculates convolution weights using Gram polynomials that exactly reproduce the results of least-squares polynomial regression. Use of the Savitzky-Golay method requires specification of both filter length and polynomial degree to calculate convolution weights. For maximum smoothing of statistical noise in data, polynomials with low degrees are desirable, while a high polynomial degree is necessary for accurate reproduction of peaks in the data. Extension of the least-squares regression formalism with statistical testing of additional terms of polynomial degree to a heuristically chosen minimum for each data window leads to an adaptive-degree polynomial filter (ADPF). Based on noise reduction for data that consist of pure noise and on signal reproduction for data that is purely signal, ADPF performed nearly as well as the optimally chosen fixed-degree Savitzky-Golay filter and outperformed sub-optimally chosen Savitzky-Golay filters. For synthetic data consisting of noise and signal, ADPF outperformed both optimally chosen and sub-optimally chosen fixed-degree Savitzky-Golay filters. See Barak, P. (1995) <doi:10.1021/ac00113a006> for more information. / GPL-3	noarch
<a href="#">r-adpss</a>	0.1.1	Provides the functions for planning and conducting a clinical trial with adaptive sample size determination. Maximal statistical efficiency will be exploited even when dramatic or multiple adaptations are made. Such a trial consists of adaptive determination of sample size at an interim analysis and implementation of frequentist statistical test at the interim and final analysis with a prefixed significance level. The required assumptions for the stage-wise test statistics are independent and stationary increments and normality. Predetermination of adaptation rule is not required. / GPL ( $\geq 2$ )	linux-64, osx-64, win-64
<a href="#">r-advdif4</a>	0.7.18	This software solves an Advection Bi-Flux Diffusive Problem using the Finite Difference Method FDM. Vasconcellos, J.F.V., Marinho, G.M., Zanni, J.H., 2016, Numerical analysis of an anomalous diffusion with a bimodal flux distribution. <doi:10.1016/j.rimni.2016.05.001>. Silva, L.G., Knupp, D.C., Bevilacqua, L., Galeao, A.C.N.R., Silva Neto, A.J., 2014, Formulation and solution of an Inverse Anomalous Diffusion Problem with Stochastic Techniques. <doi:10.5902/2179460X13184>. In this version, it is possible to include a source as a function depending on space and time, that is, $s(x,t)$ . / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-adwordsr</a>	0.3.1	Allows access to selected services that are part of the ‘Google Adwords’ API < <a href="https://developers.google.com/adwords/api/docs/guides/start">https://developers.google.com/adwords/api/docs/guides/start</a> >. ‘Google Adwords’ is an online advertising service by ‘Google’, that delivers Ads to users. This package offers a authentication process using ‘OAUTH2’. Currently, there are two methods of data of accessing the API, depending on the type of request. One method uses ‘SOAP’ requests which require building an ‘XML’ structure and then sent to the API. These are used for the ‘ManagedCustomerService’ and the ‘TargetingIdeaService’. The second method is by building ‘AWQL’ queries for the reporting side of the ‘Google Adwords’ API. / MIT file LICENSE	noarch
<a href="#">r-aer</a>	1.2_6	Functions, data sets, examples, demos, and vignettes for the book Christian Kleiber and Achim Zeileis (2008), Applied Econometrics with R, Springer-Verlag, New York. ISBN 978-0-387-77316-2. (See the vignette AER for a package overview.) / GPL-2   GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-afc</a>	1.4.0	This is an implementation of the Generalized Discrimination Score (also known as Two Alternatives Forced Choice Score, 2AFC) for various representations of forecasts and verifying observations. The Generalized Discrimination Score is a generic forecast verification framework which can be applied to any of the following verification contexts: dichotomous, polychotomous (ordinal and nominal), continuous, probabilistic, and ensemble. A comprehensive description of the Generalized Discrimination Score, including all equations used in this package, is provided by Mason and Weigel (2009) < <a href="https://doi.org/10.1175/MWR-D-10-05069.1">doi:10.1175/MWR-D-10-05069.1</a> >. / GPL-3	noarch
<a href="#">r-afex</a>	0.23_0	Convenience functions for analyzing factorial experiments using ANOVA or mixed models. <code>aov_ez()</code> , <code>aov_car()</code> , and <code>aov_4()</code> allow specification of between, within (i.e., repeated-measures), or mixed (i.e., split-plot) ANOVAs for data in long format (i.e., one observation per row), automatically aggregating multiple observations per individual and cell of the design. <code>mixed()</code> fits mixed models using <code>lme4::lmer()</code> and computes p-values for all fixed effects using either Kenward-Roger or Satterthwaite approximation for degrees of freedom (LMM only), parametric bootstrap (LMMs and GLMMs), or likelihood ratio tests (LMMs and GLMMs). <code>afex_plot()</code> provides a high-level interface for interaction or one-way plots using <code>ggplot2</code> , combining raw data and model estimates. <code>afex</code> uses type 3 sums of squares as default (imitating commercial statistical software). / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-affluenceindex</a>	1.0	Computes the statistical indices of affluence (richness) and constructs bootstrap confidence intervals for these indices. Also computes the Wolfson polarization index. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-afpt</a>	1.0.0	Allows estimation and modelling of flight costs in animal (vertebrate) flight, implementing the aerodynamic power model described in Klein Heerenbrink et al. (2015) <doi:10.1098/rspa.2014.0952>. Taking inspiration from the program 'Flight', developed by Colin Pennycuick (Pennycuick (2008) Modelling the flying bird. Amsterdam: Elsevier. ISBN 0-19-857721-4), flight performance is estimated based on basic morphological measurements such as body mass, wingspan and wing area. 'afpt' can be used to make predictions on how animals should adjust their flight behaviour and wingbeat kinematics to varying flight conditions. / GPL (>= 3)	noarch
<a href="#">r-aggregater</a>	0.0.2	Convenience functions for aggregating data frame. Currently mean, sum and variance are supported. For Date variables, recency and duration are supported. There is also support for dummy variables in predictive contexts. / GPL-2	noarch
<a href="#">r-aggregation</a>	1.0.1	Contains functionality for performing the following methods of p-value aggregation: Fisher's method [Fisher, RA (1932, ISBN: 9780028447308)], the Lancaster method (weighted Fisher's method) [Lancaster, HO (1961, <doi:10.1111/j.1467-842X.1961.tb00058.x>)], and Sidak correction [Sidak, Z (1967, <doi:10.1080/01621459.1967.10482935>)]. Please cite Yi et al., the manuscript corresponding to this package [Yi, L et al., (2017), <doi:10.1101/190199>]. / GPL-3	noarch
<a href="#">r-aghmatrix</a>	1.0.2	Computation of A (pedigree), G (genomic-base), and H (A corrected by G) relationship matrices for diploid and autopolyploid species. Several methods are implemented considering additive and non-additive models. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-agop</a>	0.2.2	Tools supporting multi-criteria and group decision making, including variable number of criteria, by means of aggregation operators, spread measures, fuzzy logic connectives, fusion functions, and preordered sets. Possible applications include, but are not limited to, quality management, scientometrics, software engineering, etc. / LGPL (>= 3)	linux-64, osx-64, win-64
<a href="#">r-agreementinterval</a>	0.1.1	A tool for calculating agreement interval of two measurement methods (Jason Liao (2015) <DOI:10.1515/ijb-2014-0030>) and present results in plots with discordance rate and/or clinically meaningful limit to quantify agreement quality. / MIT file LICENSE	noarch
<a href="#">r-agridat</a>	1.16	Datasets from books, papers, and websites related to agriculture. Example graphics and analyses are included. Data come from small-plot trials, multi-environment trials, uniformity trials, yield monitors, and more. / CC BY-SA 4.0	noarch
<a href="#">r-agrmt</a>	1.40.4	Calculate agreement or consensus in ordered rating scales. The package implements van der Eijk's (2001) <DOI: 10.1023/A:1010374114305> measure of agreement A, which can be used to describe agreement, consensus, or polarization among respondents. It also implements measures of consensus (dispersion) by Leik, Tatsle and Wierman, Blair and Lacy, Kvalseth, Berry and Mielke, and Garcia-Montalvo and Reynal-Querol. Furthermore, an implementation of Galtungs AJUS-system is provided to classify distributions, as well as a function to identify the position of multiple modes. / GPL-3	noarch
<a href="#">r-agsemisc</a>	1.3.1	High-featured panel functions for bwplot and xyplot, some plot management helpers, various convenience functions / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-ahaz</a>	1.14	Computationally efficient procedures for regularized estimation with the semi-parametric additive hazards regression model. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-ahocorasicktrie</a>	0.1.0	Aho-Corasick is an optimal algorithm for finding many keywords in a text. It can locate all matches in a text in $O(NM)$ time; i.e., the time needed scales linearly with the number of keywords (N) and the size of the text (M). Compare this to the naive approach which takes $O(N*M)$ time to loop through each pattern and scan for it in the text. This implementation builds the trie (the generic name of the data structure) and runs the search in a single function call. If you want to search multiple texts with the same trie, the function will take a list or vector of texts and return a list of matches to each text. By default, all 128 ASCII characters are allowed in both the keywords and the text. A more efficient trie is possible if the alphabet size can be reduced. For example, DNA sequences use at most 19 distinct characters and usually only 4; protein sequences use at most 26 distinct characters and usually only 20. UTF-8 (Unicode) matching is not currently supported. / Apache License 2.0	linux-64, osx-64, win-64
<a href="#">r-aidar</a>	1.0.5	Read objects from the AIDA (< <a href="http://aida.freehep.org/">http://aida.freehep.org/</a> >) file and make them available as dataframes in R. / LGPL (>= 2)	noarch
<a href="#">r-aim</a>	1.01	R functions for adaptively constructing index models for continuous, binary and survival outcomes. Implementation requires loading R-pacakge survival / LGPL-2	noarch
<a href="#">r-airgr</a>	1.3.2.1	Hydrological modelling tools developed at Irstea-Antony (HYCAR Research Unit, France). The package includes several conceptual rainfall-runoff models (GR4H, GR4J, GR5J, GR6J, GR2M, GR1A), a snow accumulation and melt model (CemaNeige) and the associated functions for their calibration and evaluation. Use help(airGR) for package description and references. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-airthermo</a>	1.2.1	Deals with many computations related to the thermodynamics of atmospheric processes. It includes many functions designed to consider the density of air with varying degrees of water vapour in it, saturation pressures and mixing ratios, conversion of moisture indices, computation of atmospheric states of parcels subject to dry or pseudoadiabatic vertical evolutions and atmospheric instability indices that are routinely used for operational weather forecasts or meteorological diagnostics. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-ake</a>	1.0	Continuous and discrete (count or categorical) estimation of density, probability mass function (p.m.f.) and regression functions are performed using associated kernels. The cross-validation technique and the local Bayesian procedure are also implemented for bandwidth selection. / GPL (>= 2)	noarch
<a href="#">r-akima</a>	0.6_2	Several cubic spline interpolation methods of H. Akima for irregular and regular gridded data are available through this package, both for the bivariate case (irregular data: ACM 761, regular data: ACM 760) and univariate case (ACM 433 and ACM 697). Linear interpolation of irregular gridded data is also covered by reusing D. J. Renkas triangulation code which is part of Akimas Fortran code. A bilinear interpolator for regular grids was also added for comparison with the bicubic interpolator on regular grids. / ACM   file LICENSE (Restricts use)	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-akmeans	1.1	Adaptive K-means algorithm with various threshold settings. It support two distance metric: Euclidean distance, Cosine distance (1 - cosine similarity) In version 1.1, it contains one more threshold condition. / GPL-2	noarch
r-alabama	2015.3	Augmented Lagrangian Adaptive Barrier Minimization Algorithm for optimizing smooth nonlinear objective functions with constraints. Linear or non-linear equality and inequality constraints are allowed. / GPL (>= 2)	noarch
r-albopictus	0.5	Implements discrete time deterministic and stochastic age-structured population dynamics models described in Erguler and others (2016) <doi:10.1371/journal.pone.0149282> and Erguler and others (2017) <doi:10.1371/journal.pone.0174293>. / GPL (>= 3)	noarch
r-ald	1.2	It provides the density, distribution function, quantile function, random number generator, likelihood function, moments and Maximum Likelihood estimators for a given sample, all this for the three parameter Asymmetric Laplace Distribution defined in Koenker and Machado (1999). This is a special case of the skewed family of distributions available in Galarza et.al. (2017) <doi:10.1002/sta4.140> useful for quantile regression. / GPL (>= 2)	noarch
r-alf	1.2.1	Allows you to connect to an 'Alfresco' content management repository and interact with its contents using simple and intuitive functions. You will be able to establish a connection session to the 'Alfresco' repository, read and upload content and manage folder hierarchies. For more details on the 'Alfresco' content management repository see < <a href="https://www.alfresco.com/ecm-software/document-management">https://www.alfresco.com/ecm-software/document-management</a> >. / GPL-3   file LICENSE	noarch
r-algaeclassify	0.1.0	Functions designed to facilitate the assignment of morpho-functional group (MFG) classifications to phytoplankton species based on a combination of taxonomy (Class,Order) and a suite of 7 binomial functional traits. Classifications can also be made using only a species list and a database of trait-derived classifications included in the package. MFG classifications are derived from Salmaso et al. (2015) <doi:10.1111/fwb.12520> and this reference should be cited when using the package. The 'algaeClassify' package is a product of the GEISHA (Global Evaluation of the Impacts of Storms on freshwater Habitat and Structure of phytoplankton Assemblages), funded by CESAB (Centre for Synthesis and Analysis of Biodiversity) and the USGS John Wesley Powell Center, with data and other support provided by members of GLEON (Global Lake Ecology Observation Network). This software is preliminary or provisional and is subject to revision. It is being provided to meet the need for timely best science. The software has not received final approval by the U.S. Geological Survey (USGS). No warranty, expressed or implied, is made by the USGS or the U.S. Government as to the functionality of the software and related material nor shall the fact of release constitute any such warranty. The software is provided on the condition that neither the USGS nor the U.S. Government shall be held liable for any damages resulting from the authorized or unauthorized use of the software. / GPL (>= 3)	noarch
r-algdesign	1.1_7	Algorithmic experimental designs. Calculates exact and approximate theory experimental designs for D,A, and I criteria. Very large designs may be created. Experimental designs may be blocked or blocked designs created from a candidate list, using several criteria. The blocking can be done when whole and within plot factors interact. / GPL (>= 2)	linux-64, osx-64, win-64
r-algebraichaplopackage	1.2	Two unordered pairs of data of two different snips positions is haplotyped by resolving a small number of closed equations. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-algorithmia</a>	0.2.0	The company, Algorithmia, houses the largest marketplace of online algorithms. This package essentially holds a bunch of REST wrappers that make it very easy to call algorithms in the Algorithmia platform and access files and directories in the Algorithmia data API. To learn more about the services they offer and the algorithms in the platform visit <a href="http://algorithmia.com">http://algorithmia.com</a> . More information for developers can be found at <a href="http://developers.algorithmia.com">http://developers.algorithmia.com</a> . / MIT file LICENSE	noarch
<a href="#">r-aliner</a>	1.1.4	Functions are provided to calculate the ‘ALINE’ Distance between words as per (Kondrak 2000) and (Downey, Hallmark, Cox, Norquest, & Lansing, 2008, <doi:10.1080/09296170802326681>). The score is based on phonetic features represented using the Unicode-compliant International Phonetic Alphabet (IPA). Parameterized features weights are used to determine the optimal alignment and functions are provided to estimate optimum values using a genetic algorithm and supervised learning. See (Downey, Sun, and Norquest 2017, <https://journal.r-project.org/archive/2017/RJ-2017-005/index.html>. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-allan</a>	1.01	Automated fitting of linear regression models and a stepwise routine / GPL-3	noarch
<a href="#">r-allanvar</a>	1.1	A collection of tools for stochastic sensor error characterization using the Allan Variance technique originally developed by D. Allan. / GPL-2	noarch
<a href="#">r-allehap</a>	0.9.9	Tools to simulate alphanumeric alleles, impute genetic missing data and reconstruct non-recombinant haplotypes from pedigree databases in a deterministic way. Allelic simulations can be implemented taking into account many factors (such as number of families, markers, alleles per marker, probability and proportion of missing genotypes, recombination rate, etc). Genotype imputation can be used with simulated datasets or real databases (previously loaded in .ped format). Haplotype reconstruction can be carried out even with missing data, since the program firstly imputes each family genotype (without a reference panel), to later reconstruct the corresponding haplotypes for each family member. All this considering that each individual (due to meiosis) should unequivocally have two alleles per marker (one inherited from each parent) and thus imputation and reconstruction results can be deterministically calculated. / GPL (>= 2)	noarch
<a href="#">r-allelematch</a>	2.5.1	Tools for the identification of unique of multilocus genotypes when both genotyping error and missing data may be present. The package is targeted at those working with large datasets and databases containing multiple samples of each individual, a situation that is common in conservation genetics, and particularly in non-invasive wildlife sampling applications. Functions explicitly incorporate missing data, and can tolerate allele mismatches created by genotyping error. If you use this tool, please cite the package using the journal article in Molecular Ecology Resources (Galpern et al., 2012). Please use citation(‘allelematch’) to call the full citation. For users with access to the associated journal article, tutorial material is also available as supplementary material to the article describing this software, the citation for which can be called using citation(‘allelematch’). / GPL-3	noarch
<a href="#">r-alleleretain</a>	2.0.2	Simulate the effect of management or demography on allele retention and inbreeding accumulation in bottlenecked populations of animals with overlapping generations. / GPL (>= 2)	noarch

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Name	Version	Summary/License	Platforms
r-allelic	0.1	This is the implementation in RC of a new association test described in A fast, unbiased and exact allelic exact test for case-control association studies (Submitted). It appears that in most cases the classical chi-square test used for testing for allelic association on genotype data is biased. Our test is unbiased, exact but fast through careful optimization. / GPL ( $\geq 2$ )	linux-64, osx-64, win-64
r-allpossiblespellings	1.1	Contains functions possSpells.fnc and batch.possSpells.fnc. / GPL-2	noarch
r-alluvial	0.1_2	Creating alluvial diagrams (also known as parallel sets plots) for multivariate and time series-like data. / MIT file LICENSE	noarch
r-alpaca	0.3.1	Provides a routine to concentrate out factors with many levels during the optimization of the log-likelihood function of the corresponding generalized linear model (glm). The package is based on the algorithm proposed by Stammann (2018) <arXiv:1707.01815> and is restricted to glm's that are based on maximum likelihood estimation and non-linear. It also offers an efficient algorithm to recover estimates of the fixed effects in a post-estimation routine and includes robust and multi-way clustered standard errors. Further the package provides an analytical bias-correction for binary choice models (logit and probit) derived by Fernandez-Val and Weidner (2016) <doi:10.1016/j.jeconom.2015.12.014>. / GPL-3	linux-64, osx-64, win-64
r-alphasimr	0.10.0	The successor to the 'AlphaSim' software for breeding program simulation [Faux et al. (2016) <doi:10.3835/plantgenome2016.02.0013>]. Used for stochastic simulations of breeding programs to the level of DNA sequence for every individual. Contained is a wide range of functions for modeling common tasks in a breeding program, such as selection and crossing. These functions allow for constructing simulations of highly complex plant and animal breeding programs via scripting in the R software environment. Such simulations can be used to evaluate overall breeding program performance and conduct research into breeding program design, such as implementation of genomic selection. Included is the 'Markovian Coalescent Simulator' ('MaCS') for fast simulation of biallelic sequences according to a population demographic history [Chen et al. (2009) <doi:10.1101/gr.083634.108>]. / MIT file LICENSE	linux-64, osx-64, win-64
r-alphavantageclient	0.0.1	Download data from the Alpha Vantage API (< <a href="https://www.alphavantage.co/">https://www.alphavantage.co/</a> >). Alpha Vantage is a RESTful API which provides various financial data, including stock prices and technical indicators. There is documentation for the underlying API available here: < <a href="https://www.alphavantage.co/documentation/">https://www.alphavantage.co/documentation/</a> >. To get access to this API, the user needs to first claim an API key: < <a href="https://www.alphavantage.co/support/">https://www.alphavantage.co/support/</a> >. / MIT file LICENSE	noarch
r-alscpc	1.0	Using of the accelerated line search algorithm for simultaneously diagonalize a set of symmetric positive definite matrices. / GPL ( $\geq 2$ )	noarch
r-alterryx	0.5.0	A tool to access each of the 'Alteryx' Gallery 'API' endpoints. Users can queue jobs, poll job status, and retrieve application output as a data frame. You will need an 'Alteryx' Server license and have 'Alteryx' Gallery running to utilize this package. The 'API' is accessed through the 'URL' that you setup for the server running 'Alteryx' Gallery and more information on the endpoints can be found at < <a href="https://gallery.alteryx.com/api-docs/">https://gallery.alteryx.com/api-docs/</a> >. / GPL-2	noarch
r-altmeta	2.2	Provides alternative statistical methods for meta-analysis, including new heterogeneity tests and measures that are robust to outliers. / GPL ( $\geq 2$ )	noarch

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Name	Version	Summary/License	Platforms
r-altopt	0.1.1	Creates the optimal (D, U and I) designs for the accelerated life testing with right censoring or interval censoring. It uses generalized linear model (GLM) approach to derive the asymptotic variance-covariance matrix of regression coefficients. The failure time distribution is assumed to follow Weibull distribution with a known shape parameter and log-linear link functions are used to model the relationship between failure time parameters and stress variables. The acceleration model may have multiple stress factors, although most ALTs involve only two or less stress factors. ALTopt package also provides several plotting functions including contour plot, Fraction of Use Space (FUS) plot and Variance Dispersion graphs of Use Space (VDUS) plot. / GPL-3	noarch
r-amap	0.8.1	Tools for Clustering and Principal Component Analysis (With robust methods, and parallelized functions). / GPL	linux-64, osx-64, win-64
r-amap.seq	1.0	An Approximated Most Average Powerful Test with Optimal FDR Control with Application to RNA-seq Data / GPL (>= 2)	noarch
r-ambient	0.1.0	Generation of natural looking noise has many application within simulation, procedural generation, and art, to name a few. The 'ambient' package provides an interface to the 'FastNoise' C library and allows for efficient generation of perlin, simplex, worley, cubic, value, and white noise with optional perturbation in either 2, 3, or 4 (in case of simplex and white noise) dimensions. / MIT file LICENSE	linux-64, osx-64, win-64
r-amcp	0.0.4	Accompanies Designing experiments and analyzing data: A model comparison perspective (3rd ed.) by Maxwell, Delaney, & Kelley (forthcoming from Routledge). Contains all of the data sets in the book's chapters and end-of-chapter exercises. Information about the book is available at < <a href="http://www.DesigningExperiments.com">http://www.DesigningExperiments.com</a> >. / GPL (>= 3)	noarch
r-amctestmaker	1.0.0	Generate code for use with the Optical Mark Recognition free software Auto Multiple Choice (AMC). More specifically, this package provides functions that use as input the question and answer texts, and output the LaTeX code for AMC. / GPL-3	noarch
r-ameco	0.2.9	Annual macro-economic database provided by the European Commission. / CC0	noarch
r-amelia	1.7.5	A tool that multiply imputes missing data in a single cross-section (such as a survey), from a time series (like variables collected for each year in a country), or from a time-series-cross-sectional data set (such as collected by years for each of several countries). Amelia II implements our bootstrapping-based algorithm that gives essentially the same answers as the standard IP or EMis approaches, is usually considerably faster than existing approaches and can handle many more variables. Unlike Amelia I and other statistically rigorous imputation software, it virtually never crashes (but please let us know if you find to the contrary!). The program also generalizes existing approaches by allowing for trends in time series across observations within a cross-sectional unit, as well as priors that allow experts to incorporate beliefs they have about the values of missing cells in their data. Amelia II also includes useful diagnostics of the fit of multiple imputation models. The program works from the R command line or via a graphical user interface that does not require users to know R. / GPL (>= 2)	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-amelie	0.2.1	Implements anomaly detection as binary classification for cross-sectional data. Uses maximum likelihood estimates and normal probability functions to classify observations as anomalous. The method is presented in the following lecture from the Machine Learning course by Andrew Ng: < <a href="https://www.coursera.org/learn/machine-learning/lecture/C8IJp/algorithm/">https://www.coursera.org/learn/machine-learning/lecture/C8IJp/algorithm/</a> >, and is also described in: Aleksandar Lazarevic, Levent Ertoz, Vipin Kumar, Aysel Ozgur, Jaideep Srivastava (2003) <doi:10.1137/1.9781611972733.3>. / GPL (>= 3)	noarch
r-amen	1.3	Analysis of dyadic network and relational data using additive and multiplicative effects (AME) models. The basic model includes regression terms, the covariance structure of the social relations model (Warner, Kenny and Stoto (1979) <DOI:10.1037/0022-3514.37.10.1742>, Wong (1982) <DOI:10.2307/2287296>), and multiplicative factor models (Hoff(2009) <DOI:10.1007/s10588-008-9040-4>). Four different link functions accommodate different relational data structures, including binary/network data (bin), normal relational data (nrm), ordinal relational data (ord) and data from fixed-rank nomination schemes (frn). Several of these link functions are discussed in Hoff, Fosdick, Volfovsky and Stovel (2013) <DOI:10.1017/nws.2013.17>. Development of this software was supported in part by NIH grant R01HD067509. / GPL-3	noarch
r-americancallopt	0.95	This package includes a set of pricing functions for American call options. The following cases are covered: Pricing of an American call using the standard binomial approximation; Hedge parameters for an American call with a standard binomial tree; Binomial pricing of an American call with continuous payout from the underlying asset; Binomial pricing of an American call with an underlying stock that pays proportional dividends in discrete time; Pricing of an American call on futures using a binomial approximation; Pricing of a currency futures American call using a binomial approximation; Pricing of a perpetual American call. The user should kindly notice that this material is for educational purposes only. The codes are not optimized for computational efficiency as they are meant to represent standard cases of analytical and numerical solution. / GPL-3	noarch
r-amerika	0.1.0	A color palette generator inspired by American politics, with colors ranging from blue on the left to gray in the middle and red on the right. A variety of palettes allow for a range of applications from brief discrete scales (e.g., three colors for Democrats, Independents, and Republicans) to continuous interpolated arrays including dozens of shades graded from blue (left) to red (right). This package greatly benefitted from building on the source code (with permission) from Ram and Wickham (2015). / MIT file LICENSE	noarch
r-amget	1.0	AMGET allows to simply and rapidly creates highly informative diagnostic plots for ADAPT 5 models. Features include data analysis prior any modeling form either NONMEM or ADAPT shaped dataset, goodness-of-fit plots (GOF), posthoc-fits plots (PHF), parameters distribution plots (PRM) and visual predictive check plots (VPC) based on ADAPT output. / GPL (>= 2)	noarch
r-aml	0.1.1	This package implements the adaptive mixed lasso (AML) method proposed by Wang et al.(2011). AML applies adaptive lasso penalty to a large number of predictors, thus producing a sparse model, while accounting for the population structure in the linear mixed model framework. The package here is primarily designed for application to genome wide association studies or genomic prediction in plant breeding populations, though it could be applied to other settings of linear mixed models. / GPL (>= 2)	noarch

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Name	Version	Summary/License	Platforms
r-ammoniaconcentration	0.1	Provides a function to calculate the concentration of un-ionized ammonia in the total ammonia in aqueous solution using the pH and temperature values. / MIT file LICENSE	noarch
r-amore	0.2.1	This package was born to release the TAO robust neural network algorithm to the R users. It has grown and I think it can be of interest for the users wanting to implement their own training algorithms as well as for those others whose needs lie only in the user space. / GPL (>= 2)	linux-64, osx-64, win-64
r-ampd	0.2	A method for automatic detection of peaks in noisy periodic and quasi-periodic signals. This method, called automatic multiscale-based peak detection (AMPD), is based on the calculation and analysis of the local maxima scalogram, a matrix comprising the scale-dependent occurrences of local maxima. For further information see <doi:10.3390/a5040588>. / GPL	noarch
r-anacoda	0.1.3.0	Is a collection of models to analyze genome scale codon data using a Bayesian framework. Provides visualization routines and checkpointing for model fittings. Currently published models to analyze gene data for selection on codon usage based on Ribosome Overhead Cost (ROC) are: ROC (Gilchrist et al. (2015) <doi:10.1093/gbe/evv087>), and ROC with phi (Wallace & Drummond (2013) <doi:10.1093/molbev/mst051>). In addition 'AnaCoDa' contains three currently unpublished models. The FONSE (First order approximation On NonSense Error) model analyzes gene data for selection on codon usage against of nonsense error rates. The PA (PAusing time) and PANSE (PAusing time NonSense Error) models use ribosome footprinting data to analyze estimate ribosome pausing times with and without nonsense error rate from ribosome footprinting data. / GPL (>= 2)	linux-64, osx-64, win-64
r-analogsea	0.7.2	Provides a set of functions for interacting with the 'Digital Ocean' API at < <a href="https://developers.digitalocean.com/documentation/v2">https://developers.digitalocean.com/documentation/v2</a> >, including creating images, destroying them, rebooting, getting details on regions, and available images. / MIT	noarch
r-analyz	1.4	Class with methods to read and execute R commands described as steps in a CSV file. / GPL (>= 2)	noarch
r-anapuce	2.3	Functions for normalisation, differentially analysis of microarray data and local False Discovery Rate. / GPL-2	noarch
r-ande	1.0	AODE achieves highly accurate classification by averaging over all of a small space. / GPL-3	noarch
r-andrews	1.0	Andrews curves for visualization of multidimensional data / GPL (>= 2)	noarch
r-anfis	0.99.1	The package implements ANFIS Type 3 Takagi and Sugeno's fuzzy if-then rule network with the following features: (1) Independent number of membership functions(MF) for each input, and also different MF extensible types. (2) Type 3 Takagi and Sugeno's fuzzy if-then rule (3) Full Rule combinations, e.g. 2 inputs 2 membership functions -> 4 fuzzy rules (4) Hybrid learning, i.e. Descent Gradient for precedents and Least Squares Estimation for consequents (5) Multiple outputs. / GPL (>= 2)	noarch
r-anmc	0.2.1	Computationally efficient method to estimate orthant probabilities of high-dimensional Gaussian vectors. Further implements a function to compute conservative estimates of excursion sets under Gaussian random field priors. / GPL-3	linux-64, osx-64, win-64
r-annotlists	1.2	Annotate multiple lists from a specific annotation file. / GPL	noarch

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Name	Version	Summary/License	Platforms
r-anocva	0.1.1	Provides ANOCVA (ANalysis Of Cluster Variability), a non-parametric statistical test to compare clustering structures with applications in functional magnetic resonance imaging data (fMRI). The ANOCVA allows us to compare the clustering structure of multiple groups simultaneously and also to identify features that contribute to the differential clustering. / GPL ( $\geq 3$ )	noarch
r-anoint	1.4	The tools in this package are intended to help researchers assess multiple treatment-covariate interactions with data from a parallel-group randomized controlled clinical trial. / GPL ( $\geq 2$ )	noarch
r-anomalydetection	1.0	A technique for detecting anomalies in seasonal univariate time series. / Apache License 2.0	linux-32, linux-64, osx-64, win-32, win-64
r-anovareplication	1.1.4	Allows for the computation of a prior predictive p-value to test replication of relevant features of original ANOVA studies. Relevant features are captured in informative hypotheses. The package also allows for the computation of sample sizes for new studies, post-hoc power calculations, and comes with a Shiny application in which all calculations can be conducted as well. The statistical underpinnings are described in Zondervan-Zwijenburg (2019) <doi:10.31234/osf.io/6myqh>. / GPL ( $\geq 3$ )	noarch
r-antareseditobject	0.1.7	Edit an ‘Antares’ simulation before running it : create new areas, links, thermal clusters or binding constraints or edit existing ones. Update ‘Antares’ general & optimization settings. ‘Antares’ is an open source power system generator, more information available here : < <a href="https://antares-simulator.org/">https://antares-simulator.org/</a> >. / GPL ( $\geq 2$ )   file LICENSE	noarch
r-antaresprocessing	0.17.0	Process results generated by ‘Antares’, a powerful open source software developed by RTE (Réseau de Transport d’Électricité) to simulate and study electric power systems (more information about ‘Antares’ here: < <a href="https://github.com/AntaresSimulatorTeam/Antares_Simulator">https://github.com/AntaresSimulatorTeam/Antares_Simulator</a> >). You can see the results of several ANTARES studies here : < <a href="http://bpnumerique.rte-france.com/">http://bpnumerique.rte-france.com/</a> >. This package provides functions to create new columns like net load, load factors, upward and downward margins or to compute aggregated statistics like economic surpluses of consumers, producers and sectors. / GPL ( $\geq 2$ )   file LICENSE	noarch
r-antaresread	2.2.4	Import, manipulate and explore results generated by ‘Antares’, a powerful open source software developed by RTE (Réseau de Transport d’Électricité) to simulate and study electric power systems (more information about ‘Antares’ here : < <a href="https://github.com/AntaresSimulatorTeam/Antares_Simulator">https://github.com/AntaresSimulatorTeam/Antares_Simulator</a> >). You can see the results of several ANTARES studies here : < <a href="http://bpnumerique.rte-france.com/">http://bpnumerique.rte-france.com/</a> >. / GPL ( $\geq 2$ )   file LICENSE	noarch
r-antiword	1.3	Wraps the ‘AntiWord’ utility to extract text from Microsoft Word documents. The utility only supports the old ‘doc’ format, not the new xml based ‘docx’ format. Use the ‘xml2’ package to read the latter. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-anylib	1.0.5	Made to make your life simpler with packages, by installing and loading a list of packages, whether they are on CRAN, Bioconductor or github. For github, if you do not have the full path, with the maintainer name in it (e.g. achateigner/topReviGO), it will be able to load it but not to install it. / CC BY-SA 4.0	noarch
r-anytime	0.3.5	Convert input in any one of character, integer, numeric, factor, or ordered type into ‘POSIXct’ (or ‘Date’) objects, using one of a number of predefined formats, and relying on Boost facilities for date and time parsing. / GPL (>= 2)	linux-64, osx-64, win-64
r-aod	1.3.1	Provides a set of functions to analyse overdispersed counts or proportions. Most of the methods are already available elsewhere but are scattered in different packages. The proposed functions should be considered as complements to more sophisticated methods such as generalized estimating equations (GEE) or generalized linear mixed effect models (GLMM). / GPL (>= 2)	noarch
r-aods3	0.4.1	Provides functions to analyse overdispersed counts or proportions. These functions should be considered as complements to more sophisticated methods such as generalized estimating equations (GEE) or generalized linear mixed effect models (GLMM). aods3 is an S3 re-implementation of the deprecated S4 package aod. / GPL (>= 2)	noarch
r-aos	0.5.0	Another implementation of object-orientation in R. It provides syntactic sugar for the S4 class system and two alternative new implementations. One is an experimental version built around S4 and the other one makes it more convenient to work with lists as objects. / MIT file LICENSE	noarch
r-aoptbdtvc	0.0.2	A collection of functions to construct A-optimal block designs for comparing test treatments with one or more control(s). Mainly A-optimal balanced treatment incomplete block designs, weighted A-optimal balanced treatment incomplete block designs, A-optimal group divisible treatment designs and A-optimal balanced bipartite block designs can be constructed using the package. The designs are constructed using algorithms based on linear integer programming. To the best of our knowledge, these facilities to construct A-optimal block designs for comparing test treatments with one or more controls are not available in the existing R packages. For more details on designs for tests versus control(s) comparisons, please see Hedayat, A. S. and Majumdar, D. (1984) <doi:10.1080/00401706.1984.10487989> A-Optimal Incomplete Block Designs for Control-Test Treatment Comparisons, Technometrics, 26, 363-370 and Mandal, B. N. , Gupta, V. K., Parsad, Rajender. (2017) <doi:10.1080/03610926.2015.1071394> Balanced treatment incomplete block designs through integer programming. Communications in Statistics - Theory and Methods 46(8), 3728-3737. / GPL (>= 2)	noarch
r-apachelogprocessor	0.2.3	Provides capabilities to process Apache HTTPD Log files. The main functionalities are to extract data from access and error log files to data frames. / LGPL-3   file LICENSE	noarch
r-apc	1.3	Functions for age-period-cohort analysis. The data can be organised in matrices indexed by age-cohort, age-period or cohort-period. The data can include dose and response or just doses. The statistical model is a generalized linear model (GLM) allowing for 3,2,1 or 0 of the age-period-cohort factors. The canonical parametrisation of Kuang, Nielsen and Nielsen (2008) <DOI:10.1093/biomet/asn026> is used. Thus, the analysis does not rely on ad hoc identification. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-apcanalysis</a>	1.0	Analysis of data from unreplicated orthogonal experiments / GPL-3	noarch
<a href="#">r-apcf</a>	0.1.3	The adapted pair correlation function transfers the concept of the pair correlation function from point patterns to patterns of objects of finite size and irregular shape (e.g. lakes within a country). This is a reimplementation of the method suggested by Nuske et al. (2009) <doi:10.1016/j.foreco.2009.09.050> using the libraries ‘GEOS’ and ‘GDAL’ directly instead of through ‘PostGIS’. / GPL (>= 3)	win-64
<a href="#">r-apcluster</a>	1.4.7	Implements Affinity Propagation clustering introduced by Frey and Dueck (2007) <DOI:10.1126/science.1136800>. The algorithms are largely analogous to the ‘Matlab’ code published by Frey and Dueck. The package further provides leveraged affinity propagation and an algorithm for exemplar-based agglomerative clustering that can also be used to join clusters obtained from affinity propagation. Various plotting functions are available for analyzing clustering results. / GPL (>= 2)	linux-64, osx-64, win-64
<a href="#">r-apdesign</a>	1.0.0	An implementation of the additive polynomial (AP) design matrix. It constructs and appends an AP design matrix to a data frame for use with longitudinal data subject to seasonality. / GPL-3	noarch
<a href="#">r-ape</a>	5.3	Functions for reading, writing, plotting, and manipulating phylogenetic trees, analyses of comparative data in a phylogenetic framework, ancestral character analyses, analyses of diversification and macroevolution, computing distances from DNA sequences, reading and writing nucleotide sequences as well as importing from BioConductor, and several tools such as Mantel’s test, generalized skyline plots, graphical exploration of phylogenetic data (alex, trex, kronoviz), estimation of absolute evolutionary rates and clock-like trees using mean path lengths and penalized likelihood, dating trees with non-contemporaneous sequences, translating DNA into AA sequences, and assessing sequence alignments. Phylogeny estimation can be done with the NJ, BIONJ, ME, MVR, SDM, and triangle methods, and several methods handling incomplete distance matrices (NJ*, BIONJ*, MVR*, and the corresponding triangle method). Some functions call external applications (PhyML, Clustal, T-Coffee, Muscle) whose results are returned into R. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-apercu</a>	0.2.3	The goal is to print an aperçu, a short view of a vector, a matrix, a data.frame, a list or an array. By default, it prints the first 5 elements of each dimension. By default, the number of columns is equal to the number of lines. If you want to control the selection of the elements, you can pass a list, with each element being a vector giving the selection for each dimension. / CC BY-SA 4.0	noarch
<a href="#">r-apfr</a>	1.0.2	Implements a multiple testing approach to the choice of a threshold gamma on the p-values using the Average Power Function (APF) and Bayes False Discovery Rate (FDR) robust estimation. Function apf_fdr() estimates both quantities from either raw data or p-values. Function apf_plot() produces smooth graphs and tables of the relevant results. Details of the methods can be found in Quatto P, Margaritella N, et al. (2019) <doi:10.1177/0962280219844288>. / GPL-3	noarch
<a href="#">r-aplore3</a>	0.9	An unofficial companion to Applied Logistic Regression by D.W. Hosmer, S. Lemeshow and R.X. Sturdivant (3rd ed., 2013) containing the dataset used in the book. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-aplpack</a>	1.3.3	Some functions for drawing some special plots: The function ‘bagplot’ plots a bagplot, ‘faces’ plots chernoff faces, ‘iconplot’ plots a representation of a frequency table or a data matrix, ‘plothulls’ plots hulls of a bivariate data set, ‘plotsummary’ plots a graphical summary of a data set, ‘puticon’ adds icons to a plot, ‘skyline.hist’ combines several histograms of a one dimensional data set in one plot, ‘slider’ functions supports some interactive graphics, ‘spin3R’ helps an inspection of a 3-dim point cloud, ‘stem.leaf’ plots a stem and leaf plot, ‘stem.leaf.backback’ plots back-to-back versions of stem and leaf plot. / GPL ( $\geq 2$ )	noarch
<a href="#">r-apml0</a>	0.9	Fit linear, logistic and Cox models regularized with L0, lasso (L1), elastic-net (L1 and L2), or net (L1 and Laplacian) penalty, and their adaptive forms, such as adaptive lasso / elastic-net and net adjusting for signs of linked coefficients. It solves L0 penalty problem by simultaneously selecting regularization parameters and the number of non-zero coefficients. This augmented and penalized minimization method provides an approximation solution to the L0 penalty problem, but runs as fast as L1 regularization problem. The package uses one-step coordinate descent algorithm and runs extremely fast by taking into account the sparsity structure of coefficients. It could deal with very high dimensional data and has superior selection performance. / GPL ( $\geq 2$ )	linux-64, osx-64, win-64
<a href="#">r-apng</a>	1.0	Convert several png files into an animated png file. This package exports only a single function ‘apng’. Call the apng function with a vector of file names (which should be png files) to convert them to a single animated png file. / GPL-3   file LICENSE	noarch
<a href="#">r-appestimation</a>	0.1.1	Calculating predictive model performance measures adjusted for predictor distributions using density ratio method (Sugiyama et al., (2012, ISBN:9781139035613)). L1 and L2 error for continuous outcome and C-statistics for binomial outcome are computed. / GPL-2	noarch
<a href="#">r-apple</a>	0.3	Approximate Path for Penalized Likelihood Estimators for Generalized Linear Models penalized by LASSO or MCP / GPL-2	linux-64, osx-64, win-64
<a href="#">r-appliedpredictivemodeling</a>	1.1.7	A few functions and several data set for the Springer book ‘Applied Predictive Modeling’. / GPL-2	noarch
<a href="#">r-appnn</a>	1.0.0	Amyloid propensity prediction neural network (APPNN) is an amyloidogenicity propensity predictor based on a machine learning approach through recursive feature selection and feed-forward neural networks, taking advantage of newly published sequences with experimental, in vitro, evidence of amyloid formation. / GPL-3	noarch
<a href="#">r-approximator</a>	1.2.7	Performs Bayesian prediction of complex computer codes when fast approximations are available. It uses a hierarchical version of the Gaussian process, originally proposed by Kennedy and O’Hagan (2000), Biometrika 87(1):1. / GPL-2	noarch
<a href="#">r-approxmatch</a>	1.0	Tools for constructing a matched design with multiple comparison groups. Further specifications of refined covariate balance restriction and exact match on covariate can be imposed. Matches are approximately optimal in the sense that the cost of the solution is at most twice the optimal cost, Crama and Spieksma (1992) <doi:10.1016/0377-2217(92)90078-N>. / MIT file LICENSE	noarch

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Name	Version	Summary/License	Platforms
r-aprean3	1.0.1	An unofficial companion to the textbook Applied Regression Analysis by N.R. Draper and H. Smith (3rd Ed., 1998) including all the accompanying datasets. / GPL-3	noarch
r-aprof	0.4.1	Assists the evaluation of whether and where to focus code optimization, using Amdahl's law and visual aids based on line profiling. Amdahl's profiler organizes profiling output files (including memory profiling) in a visually appealing way. It is meant to help to balance development vs. execution time by helping to identify the most promising sections of code to optimize and projecting potential gains. The package is an addition to R's standard profiling tools and is not a wrapper for them. / GPL (>= 2)	noarch
r-apsimbatch	0.1.0.2014	APSIM in Batch mode / GPL-3	noarch
r-apsrtable	0.8_8	Formats latex tables from one or more model objects side-by-side with standard errors below, not unlike tables found in such journals as the American Political Science Review. / GPL (>= 2)	noarch
r-aptools	6.8.8	We provide tools to estimate two prediction accuracy metrics, the average positive predictive values (AP) as well as the well-known AUC (the area under the receiver operator characteristic curve) for risk scores. The outcome of interest is either binary or censored event time. Note that for censored event time, our functions' estimates, the AP and the AUC, are time-dependent for pre-specified time interval(s). A function that compares the APs of two risk scores/markers is also included. Optional outputs include positive predictive values and true positive fractions at the specified marker cut-off values, and a plot of the time-dependent AP versus time (available for event time data). / LGPL-3	noarch
r-aqr	0.4	This R extension provides methods to use a standalone ActiveQuant Master Server from within R. Currently available features include fetching and storing historical data, receiving and sending live data. Several utility methods for simple data transformations are included, too. For support requests, please join the mailing list at <a href="https://r-forge.r-project.org/mail/?group_id=1518">https://r-forge.r-project.org/mail/?group_id=1518</a> / GPL (>= 2)	linux-64, osx-64, win-64
r-ar	1.1	In mathematics, 'rejection sampling' is a basic technique used to generate observations from a distribution. It is also commonly called 'the Acceptance-Rejection method' or 'Accept-Reject algorithm' and is a type of Monte Carlo method. 'Acceptance-Rejection method' is based on the observation that to sample a random variable one can perform a uniformly random sampling of the 2D cartesian graph, and keep the samples in the region under the graph of its density function. Package 'AR' is able to generate/simulate random data from a probability density function by Acceptance-Rejection method. Moreover, this package is a useful teaching resource for graphical presentation of Acceptance-Rejection method. From the practical point of view, the user needs to calculate a constant in Acceptance-Rejection method, which package 'AR' is able to compute this constant by optimization tools. Several numerical examples are provided to illustrate the graphical presentation for the Acceptance-Rejection Method. / LGPL-3	noarch
r-arabicstemr	1.2	Allows users to stem Arabic texts for text analysis. / GPL (>= 2)	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-ararredux</a>	1.0	Processes noble gas mass spectrometer data to determine the isotopic composition of argon (comprised of Ar36, Ar37, Ar38, Ar39 and Ar40) released from neutron-irradiated potassium-bearing minerals. Then uses these compositions to calculate precise and accurate geochronological ages for multiple samples as well as the covariances between them. Error propagation is done in matrix form, which jointly treats all samples and all isotopes simultaneously at every step of the data reduction process. Includes methods for regression of the time-resolved mass spectrometer signals to t=0 ('time zero') for both single- and multi-collector instruments, blank correction, mass fractionation correction, detector intercalibration, decay corrections, interference corrections, interpolation of the irradiation parameter between neutron fluence monitors, and (weighted mean) age calculation. All operations are performed on the logs of the ratios between the different argon isotopes so as to properly treat them as 'compositional data', sensu Aitchison [1986, The Statistics of Compositional Data, Chapman and Hall]. / GPL-2	noarch
<a href="#">r-arc</a>	1.2	Implements the Classification-based on Association Rules (CBA) (Bing Liu, Wynne Hsu, Yiming Ma (1999) < <a href="http://dl.acm.org/citation.cfm?id=3000292.3000305">http://dl.acm.org/citation.cfm?id=3000292.3000305</a> >) algorithm for association rule classification (ARC). The package also contains several convenience methods that allow to automatically set CBA parameters (minimum confidence, minimum support) and it also natively handles numeric attributes by integrating a pre-discretization step. The rule generation phase is handled by the 'arules' package. To further decrease the size of the CBA models produced by the 'arc' package, postprocessing by the 'qCBA' package is suggested. / AGPL-3	noarch
<a href="#">r-archdata</a>	1.2	The archdata package provides several types of data that are typically used in archaeological research. It provides all of the data sets used in Quantitative Methods in Archaeology Using R by David L Carlson, one of the Cambridge Manuals in Archaeology. / GPL	noarch
<a href="#">r-arco</a>	0.3_1	Set of functions to analyse and estimate Artificial Counterfactual models from Carvalho, Masini and Medeiros (2016) <DOI:10.2139/ssrn.2823687>. / MIT file LICENSE	noarch
<a href="#">r-ardec</a>	2.0	Package ArDec implements autoregressive-based decomposition of a time series based on the constructive approach in West (1997). Particular cases include the extraction of trend and seasonal components. / GPL (>= 2)	noarch
<a href="#">r-areaplot</a>	1.2_1	Plot stacked areas and confidence bands as filled polygons, or add polygons to existing plots. A variety of input formats are supported, including vectors, matrices, data frames, formulas, etc. / GPL (>= 2)	noarch
<a href="#">r-arf3ds4</a>	2.5_10	Activated Region Fitting (ARF) is an analysis method for fMRI data. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-argo</a>	2.0.0	Augmented Regression with General Online data (ARGO) for accurate estimation of influenza epidemics in United States on both national level and regional level. It replicates the method introduced in paper Yang, S., Santillana, M. and Kou, S.C. (2015) <doi:10.1073/pnas.1515373112> and Ning, S., Yang, S. and Kou, S.C. (2019) <doi:10.1038/s41598-019-41559-6>. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-argon2</a>	0.2.0	Utilities for secure password hashing via the argon2 algorithm. It is a relatively new hashing algorithm and is believed to be very secure. The ‘argon2’ implementation included in the package is the reference implementation. The package also includes some utilities that should be useful for digest authentication, including a wrapper of ‘blake2b’. For similar R packages, see sodium and ‘bcrypt’. See < <a href="https://en.wikipedia.org/wiki/Argon2">https://en.wikipedia.org/wiki/Argon2</a> > or < <a href="https://eprint.iacr.org/2015/430.pdf">https://eprint.iacr.org/2015/430.pdf</a> > for more information. / BSD 2-clause License file LICENSE	linux-64, osx-64, win-64
<a href="#">r-argondash</a>	0.1.0	Create awesome ‘Bootstrap 4’ dashboards powered by ‘Argon’. See more here < <a href="https://rinterface.github.io/argonDash/">https://rinterface.github.io/argonDash/</a> >. / GPL-2	noarch
<a href="#">r-argonr</a>	0.1.0	R wrapper around the argon HTML library. More at < <a href="https://demos.creative-tim.com/argon-design-system/">https://demos.creative-tim.com/argon-design-system/</a> >. / GPL-2	noarch
<a href="#">r-argosfilter</a>	0.63	Functions to filters animal satellite tracking data obtained from Argos. It is especially indicated for telemetry studies of marine animals, where Argos locations are predominantly of low-quality. / GPL (>= 2)	noarch
<a href="#">r-argparse</a>	2.0.1	A command line parser to be used with Rscript to write #! shebang scripts that gracefully accept positional and optional arguments and automatically generate usage. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-argparser</a>	0.4	Cross-platform command-line argument parser written purely in R with no external dependencies. It is useful with the Rscript front-end and facilitates turning an R script into an executable script. / GPL (>= 3)	noarch
<a href="#">r-argumentcheck</a>	0.10.2	The typical process of checking arguments in functions is iterative. In this process, an error may be returned and the user may fix it only to receive another error on a different argument. ‘ArgumentCheck’ facilitates a more helpful way to perform argument checks allowing the programmer to run all of the checks and then return all of the errors and warnings in a single message. / GPL-3	noarch
<a href="#">r-arht</a>	0.1.0	Perform the Adaptable Regularized Hotelling’s T <sup>2</sup> test (ARHT) proposed by Li et al., (2016) <arXiv:1609.08725>. Both one-sample and two-sample mean test are available with various probabilistic alternative prior models. It contains a function to consistently estimate higher order moments of the population covariance spectral distribution using the spectral of the sample covariance matrix (Bai et al. (2010) <doi:10.1111/j.1467-842X.2010.00590.x>). In addition, it contains a function to sample from 3-variate chi-squared random vectors approximately with a given correlation matrix when the degrees of freedom are large. / GPL (>= 2)	noarch
<a href="#">r-aricode</a>	0.1.2	Implements an efficient O(n) algorithm based on bucket-sorting for fast computation of standard clustering comparison measures. Available measures include adjusted Rand index (ARI), normalized information distance (NID), normalized mutual information (NMI), adjusted mutual information (AMI), normalized variation information (NVI) and entropy, as described in Vinh et al (2009) <doi:10.1145/1553374.1553511>. / GPL (>= 3)	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-arm	1.10	Functions to accompany A. Gelman and J. Hill, Data Analysis Using Regression and Multilevel/Hierarchical Models, Cambridge University Press, 2007. / GPL ( $\geq 3$ )	noarch
r-armspp	0.0.2	An efficient ‘Rcpp’ implementation of the Adaptive Rejection Metropolis Sampling (ARMS) algorithm proposed by Gilks, W. R., Best, N. G. and Tan, K. K. C. (1995) <doi:10.2307/2986138>. This allows for sampling from a univariate target probability distribution specified by its (potentially unnormalised) log density. / MIT file LICENSE	linux-64, osx-64, win-64
r-arnie	0.1.2	Arnold Schwarzenegger movie weekend box office records from 1982-2014 / CC BY-SA 4.0	noarch
r-arpobservation	1.2.0	Tools for simulating data generated by direct observation recording. Behavior streams are simulated based on an alternating renewal process, given specified distributions of event durations and interim times. Different procedures for recording data can then be applied to the simulated behavior streams. Functions are provided for the following recording methods: continuous duration recording, event counting, momentary time sampling, partial interval recording, whole interval recording, and augmented interval recording. / GPL-3	noarch
r-arpr	0.1.1	Provides convenience functions for programming with magrittr pipes. Conditional pipes, a string prefixer and a function to pipe the given object into a specific argument given by character name are currently supported. It is named after the dadaist Hans Arp, a friend of Rene Magritte. / GPL ( $\geq 3$ )	noarch
r-arpsdca	1.1.1	Functions for Arps decline-curve analysis on oil and gas data. Includes exponential, hyperbolic, harmonic, and hyperbolic-to-exponential models as well as the preceding with initial curtailment or a period of linear rate buildup. Functions included for computing rate, cumulative production, instantaneous decline, EUR, time to economic limit, and performing least-squares best fits. / LGPL-2.1	noarch
r-arrangements	1.1.5	Fast generators and iterators for permutations, combinations and partitions. The iterators allow users to generate arrangements in a memory efficient manner and the generated arrangements are in lexicographical (dictionary) order. Permutations and combinations can be drawn with/without replacement and support multisets. It has been demonstrated that ‘arrangements’ outperforms most of the existing packages of similar kind. Some benchmarks could be found at < <a href="https://randy3k.github.io/arrangements/articles/benchmark.html">https://randy3k.github.io/arrangements/articles/benchmark.html</a> >. / MIT file LICENSE	linux-64, osx-64, win-64
r-arrapply	2.1	High performance variant of apply() for a fixed set of functions. Considerable speedup is a trade-off for universality, user defined functions cannot be used with this package. However, 21 most currently employed functions are available for usage. They can be divided in three types: reducing functions (like mean(), sum() etc., giving a scalar when applied to a vector), mapping function (like normalise(), cumsum() etc., giving a vector of the same length as the input vector) and finally, vector reducing function (like diff()) which produces result vector of a length different from the length of input vector). Optional or mandatory additional arguments required by some functions (e.g. norm type for norm() or normalise() functions) can be passed as named arguments in ‘...’. / GPL ( $\geq 2$ )	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-arrow	0.14.1	Apache 'Arrow' < <a href="https://arrow.apache.org/">https://arrow.apache.org/</a> > is a cross-language development platform for in-memory data. It specifies a standardized language-independent columnar memory format for flat and hierarchical data, organized for efficient analytic operations on modern hardware. This package provides an interface to the 'Arrow C' library. / Apache License (>= 2.0)	linux-64
r-ars	0.6	Adaptive Rejection Sampling, Original version. / GPL (>= 2)	linux-64, osx-64, win-64
r-arsenal	3.2.0	An Arsenal of 'R' functions for large-scale statistical summaries, which are streamlined to work within the latest reporting tools in 'R' and 'RStudio' and which use formulas and versatile summary statistics for summary tables and models. The primary functions include tableby(), a Table-1-like summary of multiple variable types 'by' the levels of one or more categorical variables; paired(), a Table-1-like summary of multiple variable types paired across two time points; modelsum(), which performs simple model fits on one or more endpoints for many variables (univariate or adjusted for covariates); freqlist(), a powerful frequency table across many categorical variables; comparedf(), a function for comparing data.frames; and write2(), a function to output tables to a document. / GPL (>= 2)	noarch
r-artiva	1.2.3	Reversible Jump MCMC (RJ-MCMC)sampling for approximating the posterior distribution of a time varying regulatory network, under the Auto Regressive Time VAring (ARTIVA) model (for a detailed description of the algorithm, see Lebre et al. BMC Systems Biology, 2010). Starting from time-course gene expression measurements for a gene of interest (referred to as target gene) and a set of genes (referred to as parent genes) which may explain the expression of the target gene, the ARTIVA procedure identifies temporal segments for which a set of interactions occur between the parent genes and the target gene. The time points that delimit the different temporal segments are referred to as changepoints (CP). / GPL (>= 2)	noarch
r-artp	2.0.5	For calculating gene and pathway p-values using the Adaptive Rank Truncated Product test. / GPL-2	linux-64, osx-64, win-64
r-artp2	0.9.45	Pathway and gene level association test using raw data or summary statistics. / GPL-2   GPL-3	linux-64, osx-64, win-64
r-arules	1.6_3	Provides the infrastructure for representing, manipulating and analyzing transaction data and patterns (frequent itemsets and association rules). Also provides C implementations of the association mining algorithms Apriori and Eclat. / GPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-arulescba</a>	1.1.4	Provides a function to build an association rule-based classifier for data frames, and to classify incoming data frames using such a classifier. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-arulesnbminer</a>	0.1_5	NBMiner is an implementation of the model-based mining algorithm for mining NB-frequent itemsets presented in Michael Hahsler. A model-based frequency constraint for mining associations from transaction data. Data Mining and Knowledge Discovery, 13(2):137-166, September 2006. In addition an extension for NB-precise rules is implemented. / GPL-2	noarch
<a href="#">r-arulessequences</a>	0.2_2	Add-on for arules to handle and mine frequent sequences. Provides interfaces to the C implementation of cSPADE by Mohammed J. Zaki. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-arxiv</a>	0.5.19	An interface to the API for ‘arXiv’ (< <a href="https://arxiv.org">https://arxiv.org</a> >), a repository of electronic preprints for computer science, mathematics, physics, quantitative biology, quantitative finance, and statistics. / MIT file LICENSE	noarch
<a href="#">r-asaur</a>	0.50	Data sets are referred to in the text Applied Survival Analysis Using R by Dirk F. Moore, Springer, 2016, ISBN: 978-3-319-31243-9, <DOI:10.1007/978-3-319-31245-3>. / CC0	noarch
<a href="#">r-asciiruler</a>	0.2	An ASCII ruler is for measuring text and is especially useful for sequence analysis. Included in this package are methods to create ASCII rulers and associated GenBank sequence blocks, multi-column text displays that make it easy for viewers to locate nucleotides by position. / GPL-3   file LICENSE	noarch
<a href="#">r-asd</a>	2.2	Package runs simulations for adaptive seamless designs with and without early outcomes for treatment selection and subpopulation type designs. / GPL-3	noarch
<a href="#">r-asdreader</a>	0.1_3	A simple driver that reads binary data created by the ASD Inc. portable spectrometer instruments, such as the FieldSpec (for more information, see < <a href="http://www.asdi.com/products/fieldspec-spectroradiometers">http://www.asdi.com/products/fieldspec-spectroradiometers</a> >). Spectral data can be extracted from the ASD files as raw (DN), white reference, radiance, or reflectance. Additionally, the metadata information contained in the ASD file header can also be accessed. / GPL-3	noarch
<a href="#">r-asgs.foyer</a>	0.2.1	The Australian Statistical Geography Standard (‘ASGS’) is a set of shapefiles by the Australian Bureau of Statistics. This package provides an interface to those shapefiles, as well as methods for converting coordinates to shapefiles. / MPL	noarch
<a href="#">r-ash</a>	1.0_1	David Scott’s ASH routines ported from S-PLUS to R. / GPL (>= 2)	linux-64, osx-64, win-64
<a href="#">r-asioheaders</a>	1.12.1	‘Asio’ is a cross-platform C library for network and low-level I/O programming that provides developers with a consistent asynchronous model using a modern C approach. It is also included in Boost but requires linking when used with Boost. Standalone it can be used header-only (provided a recent compiler). ‘Asio’ is written and maintained by Christopher M. Kohlhoff, and released under the ‘Boost Software License’, Version 1.0. / BSL-1.0	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-askpass</a>	1.0	Cross-platform utilities for prompting the user for credentials or a passphrase, for example to authenticate with a server or read a protected key. Includes native programs for MacOS and Windows, hence no ‘tcltk’ is required. Password entry can be invoked in two different ways: directly from R via the askpass() function, or indirectly as password-entry back-end for ‘ssh-agent’ or ‘git-credential’ via the SSH_ASKPASS and GIT_ASKPASS environment variables. Thereby the user can be prompted for credentials or a passphrase if needed when R calls out to git or ssh. / MIT file LICENSE	linux-64, osx-64, win-32, win-64
<a href="#">r-asnipe</a>	1.1.1	Implements several tools that are used in animal social network analysis. In particular, this package provides the tools to infer groups and generate networks from observation data, perform permutation tests on the data, calculate lagged association rates, and performed multiple regression analysis on social network data. / GPL-2	noarch
<a href="#">r-aspbay</a>	1.2	This package allows to make inference on the properties of causal genetic variants in linkage disequilibrium with genotyped markers. In a first step, we select a subset of variants using a score statistic for affected sib-pairs. In a second step, on the selected subset, we make inference on causal genetic variants in the considered region. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-aspc</a>	0.1.2	The aSPC test is designed to test global association between two groups of variables potentially with moderate to high dimension (e.g. in hundreds). The aSPC is particularly useful when the association signals between two groups of variables are sparse. / GPL-3	noarch
<a href="#">r-aspect</a>	1.0.5	Contains various functions for optimal scaling. One function performs optimal scaling by maximizing an aspect (i.e. a target function such as the sum of eigenvalues, sum of squared correlations, squared multiple correlations, etc.) of the corresponding correlation matrix. Another function performs implements the LINEALS approach for optimal scaling by minimization of an aspect based on pairwise correlations and correlation ratios. The resulting correlation matrix and category scores can be used for further multivariate methods such as structural equation models. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-aspi</a>	0.2.0	Tools for the analysis and visualization of bilateral asymmetry in parasitic infections. / GPL-3	noarch
<a href="#">r-assa</a>	1.0	Functions to model and decompose time series into principal components using singular spectrum analysis (de Carvalho and Rua (2017) <doi:10.1016/j.ijforecast.2015.09.004>; de Carvalho et al (2012) <doi:10.1016/j.econlet.2011.09.007>). / GPL (>= 3)	linux-64, osx-64, win-64
<a href="#">r-assertable</a>	0.2.5	Simple, flexible, assertions on data.frame or data.table objects with verbose output for vetting. While other assertion packages apply towards more general use-cases, assertable is tailored towards tabular data. It includes functions to check variable names and values, whether the dataset contains all combinations of a given set of unique identifiers, and whether it is a certain length. In addition, assertable includes utility functions to check the existence of target files and to efficiently import multiple tabular data files into one data.table. / GPL-3	noarch
<a href="#">r-assertive</a>	0.3.5	Lots of predicates (is_* functions) to check the state of your variables, and assertions (assert_* functions) to throw errors if they aren’t in the right form. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-assertive.base	0.0_7	A minimal set of predicates and assertions used by the assertive package. This is mainly for use by other package developers who want to include run-time testing features in their own packages. End-users will usually want to use assertive directly. / GPL ( $\geq 3$ )	noarch
r-assertive.code	0.0_3	A set of predicates and assertions for checking the properties of code. This is mainly for use by other package developers who want to include run-time testing features in their own packages. End-users will usually want to use assertive directly. / GPL-3	noarch
r-assertive.data	0.0_3	A set of predicates and assertions for checking the properties of (country independent) complex data types. This is mainly for use by other package developers who want to include run-time testing features in their own packages. End-users will usually want to use assertive directly. / GPL-3	noarch
r-assertive.data.uk	0.0_2	A set of predicates and assertions for checking the properties of UK-specific complex data types. This is mainly for use by other package developers who want to include run-time testing features in their own packages. End-users will usually want to use assertive directly. / GPL-3	noarch
r-assertive.data.us	0.0_2	A set of predicates and assertions for checking the properties of US-specific complex data types. This is mainly for use by other package developers who want to include run-time testing features in their own packages. End-users will usually want to use assertive directly. / GPL-3	noarch
r-assertive.dates	0.0_2	A set of predicates and assertions for checking the properties of dates and times. This is mainly for use by other package developers who want to include run-time testing features in their own packages. End-users will usually want to use assertive directly. / GPL-3	noarch
r-assertive.files	0.0_2	A set of predicates and assertions for checking the properties of files and connections. This is mainly for use by other package developers who want to include run-time testing features in their own packages. End-users will usually want to use assertive directly. / GPL ( $\geq 3$ )	noarch
r-assertive.matrices	0.0_2	A set of predicates and assertions for checking the properties of matrices. This is mainly for use by other package developers who want to include run-time testing features in their own packages. End-users will usually want to use assertive directly. / GPL ( $\geq 3$ )	noarch
r-assertive.models	0.0_2	A set of predicates and assertions for checking the properties of models. This is mainly for use by other package developers who want to include run-time testing features in their own packages. End-users will usually want to use assertive directly. / GPL ( $\geq 3$ )	noarch
r-assertive.numbers	0.0_2	A set of predicates and assertions for checking the properties of numbers. This is mainly for use by other package developers who want to include run-time testing features in their own packages. End-users will usually want to use assertive directly. / GPL ( $\geq 3$ )	noarch
r-assertive.properties	0.0_4	A set of predicates and assertions for checking the properties of variables, such as length, names and attributes. This is mainly for use by other package developers who want to include run-time testing features in their own packages. End-users will usually want to use assertive directly. / GPL ( $\geq 3$ )	noarch
r-assertive.reflection	0.0_4	A set of predicates and assertions for checking the state and capabilities of R, the operating system it is running on, and the IDE being used. This is mainly for use by other package developers who want to include run-time testing features in their own packages. End-users will usually want to use assertive directly. / GPL ( $\geq 3$ )	noarch

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Name	Version	Summary/License	Platforms
<code>r-assertive.sets</code>	0.0_3	A set of predicates and assertions for checking the properties of sets. This is mainly for use by other package developers who want to include run-time testing features in their own packages. End-users will usually want to use assertive directly. / GPL ( $\geq 3$ )	noarch
<code>r-assertive.strings</code>	0.0_3	A set of predicates and assertions for checking the properties of strings. This is mainly for use by other package developers who want to include run-time testing features in their own packages. End-users will usually want to use assertive directly. / GPL-3	noarch
<code>r-assertive.types</code>	0.0_3	A set of predicates and assertions for checking the types of variables. This is mainly for use by other package developers who want to include run-time testing features in their own packages. End-users will usually want to use assertive directly. / GPL ( $\geq 3$ )	noarch
<code>r-assertthat</code>	0.2.1	An extension to stopifnot() that makes it easy to declare the pre and post conditions that you code should satisfy, while also producing friendly error messages so that your users know what's gone wrong. / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
<code>r-assist</code>	3.1.5	A comprehensive package for fitting various non-parametric/semi-parametric linear/nonlinear fixed/mixed smoothing spline models. / GPL ( $\geq 2$ )	linux-64, osx-64, win-64
<code>r-assocafc</code>	1.0.2	When doing association analysis one does not always have the genotypes for the control population. In such cases it may be necessary to fall back on frequency based tests using well known sources for the frequencies in the control population, for instance, from the 1000 Genomes Project. The Allele Frequency Comparison ('AssocAFC') package performs multiple rare variant association analyses in both population and family-based GWAS (Genome-Wide Association Study) designs. It includes three score tests that are based on the difference of the sum of allele frequencies between cases and controls. Two of these tests, Wcorrected() and Wqls(), are collapsing-based tests and suffer from having protective and risk variants. The third test, afcSKAT(), is a score test that overcomes the mix of SNP (Single-Nucleotide Polymorphism) effect directions. For more details see Saad M and Wijsman EM (2017) <doi:10.1093/bib/bbx107>. / GPL-3	noarch
<code>r-assocind</code>	1.0.1	Implements several new association indices that can control for various types of errors. Also includes existing association indices and functions for simulating the effects of different rates of error on estimates of association strength between individuals using each method. / GPL-2	noarch
<code>r-assortnet</code>	0.12	Functions to calculate the assortment of vertices in social networks. This can be measured on both weighted and binary networks, with discrete or continuous vertex values. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-assotester</a>	0.1_10	R package with statistical tests and methods for genetic association studies with emphasis on rare variants and binary (dichotomous) traits / GPL ( $\geq 3$ )	linux-64, osx-64, win-64
<a href="#">r-ast</a>	0.1.0	Fits a model to adjust and consider additional variations in three dimensions of age groups, time, and space on residuals excluded from a prediction model that have residual such as: linear regression, mixed model and so on. Details are given in Foreman et al. (2015) <doi:10.1186/1478-7954-10-1>. / GPL-2   GPL-3	noarch
<a href="#">r-aster2</a>	0.3	Aster models are exponential family regression models for life history analysis. They are like generalized linear models except that elements of the response vector can have different families (e. g., some Bernoulli, some Poisson, some zero-truncated Poisson, some normal) and can be dependent, the dependence indicated by a graphical structure. Discrete time survival analysis, zero-inflated Poisson regression, and generalized linear models that are exponential family (e. g., logistic regression and Poisson regression with log link) are special cases. Main use is for data in which there is survival over discrete time periods and there is additional data about what happens conditional on survival (e. g., number of offspring). Uses the exponential family canonical parameterization (aster transform of usual parameterization). Unlike the aster package, this package does dependence groups (nodes of the graph need not be conditionally independent given their predecessor node), including multinomial and two-parameter normal as families. Thus this package also generalizes mark-capture-recapture analysis. / GPL ( $\geq 2$ )	linux-64, osx-64, win-64
<a href="#">r-astrodatr</a>	0.1	A collection of 19 datasets from contemporary astronomical research. They are described the textbook ‘Modern Statistical Methods for Astronomy with R Applications’ by Eric D. Feigelson and G. Jogesh Babu (Cambridge University Press, 2012, Appendix C) or on the website of Penn State’s Center for Astrostatistics ( <a href="http://astrostatistics.psu.edu/datasets">http://astrostatistics.psu.edu/datasets</a> ). These datasets can be used to exercise methodology involving: density estimation; heteroscedastic measurement errors; contingency tables; two-sample hypothesis tests; spatial point processes; nonlinear regression; mixture models; censoring and truncation; multivariate analysis; classification and clustering; inhomogeneous Poisson processes; periodic and stochastic time series analysis. / GPL	noarch
<a href="#">r-astrofns</a>	4.1_0	Miscellaneous astronomy functions, utilities, and data. / GPL ( $\geq 2$ )	noarch
<a href="#">r-astrolibr</a>	0.1	Several dozen low-level utilities and codes from the Interactive Data Language (IDL) Astronomy Users Library ( <a href="http://idlastro.gsfc.nasa.gov">http://idlastro.gsfc.nasa.gov</a> ) are implemented in R. They treat: time, coordinate and proper motion transformations; terrestrial precession and nutation, atmospheric refraction and aberration, barycentric corrections, and related effects; utilities for astrometry, photometry, and spectroscopy; and utilities for planetary, stellar, Galactic, and extragalactic science. / GPL	noarch
<a href="#">r-astsa</a>	1.9	Data sets and scripts to accompany Time Series Analysis and Its Applications: With R Examples (4th ed), by R.H. Shumway and D.S. Stoffer. Springer Texts in Statistics, 2017, <DOI:10.1007/978-3-319-52452-8>, and Time Series: A Data Analysis Approach Using R. Chapman-Hall, 2019, <ISBN: 978-0367221096>. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-asyk	0.1.0	Density estimation by using symmetrical kernels and to calculate mean square error. See Scaillet (2004) <doi:10.1080/10485250310001624819> and Khan and Akbar (2019). / GPL-2	noarch
r-asyml	0.1	Computes asymmetric LD measures (ALD) for multi-allelic genetic data. These measures are identical to the correlation measure (r) for bi-allelic data. / GPL-2	noarch
r-asymp	0.1.4	One and two sample mean and variance tests (differences and ratios) are considered. The test statistics are all expressed in the same form as the Student t-test, which facilitates their presentation in the classroom. This contribution also fills the gap of a robust (to non-normality) alternative to the chi-square single variance test for large samples, since no such procedure is implemented in standard statistical software. / GPL (>= 2)	noarch
r-asymlong	2.0	Estimation of regression models for sparse asynchronous longitudinal observations, where time-dependent response and covariates are mismatched and observed intermittently within subjects. Kernel weighted estimating equations are used for generalized linear models with either time-invariant or time-dependent coefficients. / GPL-2	noarch
r-asympow	2015.625	Set of routines written in the S language that calculate power and related quantities utilizing asymptotic likelihood ratio methods. / ACM   file LICENSE (Restricts use)	noarch
r-ate	0.2.0	Nonparametric estimation and inference for average treatment effects based on covariate balancing. / GPL (>= 2)	noarch
r-atlas	1.0.0	Stanford 'ATLAS' (Advanced Temporal Search Engine) is a powerful tool that allows constructing cohorts of patients extremely quickly and efficiently. This package is designed to interface directly with an instance of 'ATLAS' search engine and facilitates API queries and data dumps. Prerequisite is a good knowledge of the temporal language to be able to efficiently construct a query. More information available at < <a href="https://shahlab.stanford.edu/start">https://shahlab.stanford.edu/start</a> >. / GPL-3	noarch
r-atmcmc	1.0	Uses adaptive diagnostics to tune and run a random walk Metropolis MCMC algorithm, to converge to a specified target distribution and estimate means of functionals. / GPL (>= 2)	noarch
r-atmray	1.31	Calculates acoustic traveltimes and ray paths in 1-D, linear atmospheres. Later versions will support arbitrary 1-D atmospheric models, such as radiosonde measurements and standard reference atmospheres. / GPL	linux-64, osx-64, win-64
r-atsa	3.1.2	Contains some tools for testing, analyzing time series data and fitting popular time series models such as ARIMA, Moving Average and Holt Winters, etc. Most functions also provide nice and clear outputs like SAS does, such as identify, estimate and forecast, which are the same statements in PROC ARIMA in SAS. / GPL-2   GPL-3	noarch
r-atsd	1.2.0	Provides functions for retrieving time-series and related meta-data such as entities, metrics, and tags from the Axibase Time-Series Database (ATSD). ATSD is a non-relational clustered database used for storing performance measurements from IT infrastructure resources: servers, network devices, storage systems, and applications. / Apache License 2.0	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-attachment</a>	0.0.9	Tools to help manage dependencies during package development. This can retrieve all dependencies that are used in R files in the R directory, in Rmd files in vignettes directory and in 'roxygen2' documentation of functions. There is a function to update the Description file of your package and a function to create a file with the R commands to install all dependencies of your package. All functions to retrieve dependencies of R scripts and Rmd files can be used independently of a package development. / GPL-3	noarch
<a href="#">r-attempt</a>	0.3.0	Tools for defensive programming, inspired by 'purrr' mappers and based on 'rlang'. 'attempt' extends and facilitates defensive programming by providing a consistent grammar, and provides a set of easy to use functions for common tests and conditions. 'attempt' only depends on 'rlang', and focuses on speed, so it can be easily integrated in other functions and used in data analysis. / MIT file LICENSE	noarch
<a href="#">r-attrcsum</a>	0.1.0	An implementation of tools for design of attribute variable sampling interval cumulative sum chart. It currently provides information for monitoring of mean increase such as average number of sample to signal, average time to signal, a matrix of transient probabilities, suitable control limits when the data are (zero inflated) Poisson/binomial distribution. Functions in the tools can be easily applied to other count processes. Also, tools might be extended to more complicated cumulative sum control chart. We leave these issues as our perpetual work. / GPL (>= 2)	linux-64, osx-64, win-64
<a href="#">r-atus</a>	0.2	Abridged data from the American Time Use Survey (ATUS) for years 2003-2016. The ATUS is an annual survey conducted on a sample of individuals across the United States studying how individuals spent their time over the course of a day. Individual respondents were interviewed about what activities they did, during what times (rounded to 15 minute increments), at what locations, and in the presence of which individuals. The activities are subsequently encoded based on 3 separate tier codes for classification. This package includes data from the multi-year ATUS Activities, ATUS-CPS, and ATUS Respondents files were included. Columns were selected based on completeness of data as well as presence on the Frequently Used Variables list provided by the ATUS website. All activity codes (other than code '50' for 'Unable to Code') were included. Permission was obtained from the Bureau of Labor Statistics for inclusion in this package. The full data can be obtained from <a href="http://www.bls.gov/tus/">http://www.bls.gov/tus/</a> . / GPL (>= 2)	noarch
<a href="#">r-auc</a>	0.3.0	This package includes functions to compute the area under the curve of selected measures: The area under the sensitivity curve (AUSEC), the area under the specificity curve (AUSPC), the area under the accuracy curve (AUACC), and the area under the receiver operating characteristic curve (AUROC). The curves can also be visualized. Support for partial areas is provided. / GPL (>= 2)	noarch
<a href="#">r-aucrf</a>	1.1	Variable selection using Random Forest based on optimizing the area-under-the ROC curve (AUC) of the Random Forest. / GPL (>= 2)	noarch
<a href="#">r-audio</a>	0.1_6	Interfaces to audio devices (mainly sample-based) from R to allow recording and playback of audio. Built-in devices include Windows MM, Mac OS X AudioUnits and PortAudio (the last one is very experimental). / MIT file LICENSE	linux-64, osx-64, win-64
<a href="#">r-audit</a>	0.1_1	Two Bayesian methods for Accounting Populations / MIT	noarch

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Name	Version	Summary/License	Platforms
r-auth0	0.1.1	Uses Auth0 API (see < <a href="https://auth0.com">https://auth0.com</a> > for more information) to use a simple and secure authentication system. It provides tools to log in and out a shiny application using social networks or a list of e-mails. / MIT file LICENSE	noarch
r-auto.pca	0.3	PCA done by eigenvalue decomposition of a data correlation matrix, here it automatically determines the number of factors by eigenvalue greater than 1 and it gives the uncorrelated variables based on the rotated component scores, Such that in each principal component variable which has the high variance are selected. It will be useful for non-statisticians in selection of variables. For more information, see the < <a href="http://www.ijcem.org/papers032013/ijcem_032013_06.pdf">http://www.ijcem.org/papers032013/ijcem_032013_06.pdf</a> > web page. / GPL-2	noarch
r-autodesk	0.1.3	An interface to the ‘AutoDesk’ ‘API’ Platform including the Authentication ‘API’ for obtaining authentication to the ‘AutoDesk’ Forge Platform, Data Management ‘API’ for managing data across the platform’s cloud services, Design Automation ‘API’ for performing automated tasks on design files in the cloud, Model Derivative ‘API’ for translating design files into different formats, sending them to the viewer app, and extracting design data, and Viewer for rendering 2D and 3D models (see < <a href="https://developer.autodesk.com">https://developer.autodesk.com</a> > for more information). / Apache License   file LICENSE	noarch
r-autoencoder	1.1	Implementation of the sparse autoencoder in R environment, following the notes of Andrew Ng ( <a href="http://www.stanford.edu/class/archive/cs/cs294a/cs294a.1104/sparseAutoencoder.pdf">http://www.stanford.edu/class/archive/cs/cs294a/cs294a.1104/sparseAutoencoder.pdf</a> ). The features learned by the hidden layer of the autoencoder (through unsupervised learning of unlabeled data) can be used in constructing deep belief neural networks. / GPL-2	noarch
r-automl	1.2.8	Fits from simple regression to highly customizable deep neural networks either with gradient descent or metaheuristic, using automatic hyper parameters tuning and custom cost function. A mix inspired by the common tricks on Deep Learning and Particle Swarm Optimization. / GNU General Public License	noarch
r-automultinomial	2.0.0	Fits the autologistic model described in Besag’s famous 1974 paper on auto-models < <a href="http://www.jstor.org/stable/2984812">http://www.jstor.org/stable/2984812</a> >. Fits a multicategory generalization of the autologistic model when there are more than 2 response categories. Provides support for both asymptotic and bootstrap confidence intervals. For full model descriptions and a guide to the use of this package, please see the vignette. / GPL-2	noarch
r-autopls	1.3	Some convenience functions for pls regression, including backward variable selection and validation procedures, image based predictions and plotting. / GPL-2	noarch
r-autoregressionmde	1.0	Consider autoregressive model of order p where the distribution function of innovation is unknown, but innovations are independent and symmetrically distributed. The package contains a function named ARMDE which takes X (vector of n observations) and p (order of the model) as input argument and returns minimum distance estimator of the parameters in the model. / GPL-2	noarch
r-autoshiny	0.0.2	Static code compilation of a ‘shiny’ app given an R function (into ‘ui.R’ and ‘server.R’ files or into a ‘shiny’ app object). See examples at < <a href="https://github.com/alekrutkowski/autoshiny">https://github.com/alekrutkowski/autoshiny</a> >. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-autovarcore	1.0.4	Automatically find the best vector autoregression models and networks for a given time series data set. ‘AutovarCore’ evaluates eight kinds of models: models with and without log transforming the data, lag 1 and lag 2 models, and models with and without weekday dummy variables. For each of these 8 model configurations, ‘AutovarCore’ evaluates all possible combinations for including outlier dummies (at 2.5x the standard deviation of the residuals) and retains the best model. Model evaluation includes the Eigenvalue stability test and a configurable set of residual tests. These eight models are further reduced to four models because ‘AutovarCore’ determines whether adding weekday dummies improves the model fit. / MIT file LICENSE	linux-64, osx-64, win-64
r-av	0.2	Bindings to ‘FFmpeg’ < <a href="http://www.ffmpeg.org/">http://www.ffmpeg.org/</a> > AV library for working with audio and video in R. Generate high quality videos files by capturing images from the R graphics device combined with custom audio stream. This package interfaces directly to the C API and does not require any command line utilities. / MIT file LICENSE	linux-64, osx-64
r-averisk	1.0.3	Average population attributable fractions are calculated for a set of risk factors (either binary or ordinal valued) for both prospective and case- control designs. Confidence intervals are found by Monte Carlo simulation. The method can be applied to either prospective or case control designs, provided an estimate of disease prevalence is provided. In addition to an exact calculation of AF, an approximate calculation, based on randomly sampling permutations has been implemented to ensure the calculation is computationally tractable when the number of risk factors is large. / CC0	noarch
r-aweek	1.0.0	Which day a week starts depends heavily on the either the local or professional context. This package is designed to be a lightweight solution to easily switching between week-based date definitions. / MIT file LICENSE	noarch
r-awr	1.11.1	Installs the compiled Java modules of the Amazon Web Services (‘AWS’) ‘SDK’ to be used in downstream R packages interacting with ‘AWS’. See < <a href="https://aws.amazon.com/sdk-for-java">https://aws.amazon.com/sdk-for-java</a> > for more information on the ‘AWS’ ‘SDK’ for Java. / AGPL-3	noarch
r-awr.athena	2.0.7	‘RJDBC’ based ‘DBI’ driver to Amazon Athena, which is an interactive query service to analyze data in Amazon ‘S3’ using standard ‘SQL’. / AGPL-3	noarch
r-awr.kms	0.1	Encrypt plain text and ‘decrypt’ cipher text using encryption keys hosted at Amazon Web Services (‘AWS’) Key Management Service (‘KMS’), on which see < <a href="https://aws.amazon.com/kms">https://aws.amazon.com/kms</a> > for more information. / AGPL-3	noarch
r-aws	2.2.1	We provide a collection of R-functions implementing adaptive smoothing procedures in 1D, 2D and 3D. This includes the Propagation-Separation Approach to adaptive smoothing as described in J. Polzehl and V. Spokoiny (2006) <DOI:10.1007/s00440-005-0464-1>, J. Polzehl and V. Spokoiny (2004) <DOI:10.20347/WIAS.PREPRINT.998> and J. Polzehl, K. Papafitsoros, K. Tabelow (2018) <DOI:10.20347/WIAS.PREPRINT.2520>, the Intersecting Confidence Intervals (ICI), variational approaches and a non-local means filter. / GPL (>= 2)	linux-64, osx-64, win-64
r-aws.cloudtrail	0.1.5	A simple client package for the Amazon Web Services (‘AWS’) ‘CloudTrail’ ‘API’ < <a href="https://aws.amazon.com/cloudtrail/">https://aws.amazon.com/cloudtrail/</a> >. / GPL-2	noarch
r-aws.comprehend	0.1.2	Client for ‘AWS Comprehend’ < <a href="https://aws.amazon.com/comprehend">https://aws.amazon.com/comprehend</a> >, a cloud natural language processing service that can perform a number of quantitative text analyses, including language detection, sentiment analysis, and feature extraction. / GPL (>= 2)	noarch
r-aws.ec2metadata	0.2.0	Retrieve Amazon EC2 instance metadata from within the running instance. / GPL (>= 2)	noarch

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Name	Version	Summary/License	Platforms
r-aws.iam	0.1.7	A simple client for the Amazon Web Services ('AWS') Identity and Access Management ('IAM') 'API' < <a href="https://aws.amazon.com/iam/">https://aws.amazon.com/iam/</a> >. / GPL (>= 2)	noarch
r-aws.kms	0.1.2	Client package for the 'AWS Key Management Service' < <a href="https://aws.amazon.com/kms/">https://aws.amazon.com/kms/</a> >, a cloud service for managing encryption keys. / GPL (>= 2)	noarch
r-aws.lambda	0.1.6	A simple client package for the Amazon Web Services ('AWS') Lambda 'API' < <a href="https://aws.amazon.com/lambda/">https://aws.amazon.com/lambda/</a> >. / GPL (>= 2)	noarch
r-aws.s3	0.3.12	A simple client package for the Amazon Web Services ('AWS') Simple Storage Service ('S3') 'REST' 'API' < <a href="https://aws.amazon.com/s3/">https://aws.amazon.com/s3/</a> >. / GPL (>= 2)	noarch
r-aws.ses	0.1.4	A simple client package for the Amazon Web Services (AWS) Simple Email Service (SES) < <a href="http://aws.amazon.com/ses/">http://aws.amazon.com/ses/</a> > REST API. / GPL (>= 2)	noarch
r-aws.signature	0.5.2	Generates version 2 and version 4 request signatures for Amazon Web Services ('AWS') < <a href="https://aws.amazon.com/">https://aws.amazon.com/</a> > Application Programming Interfaces ('APIs') and provides a mechanism for retrieving credentials from environment variables, 'AWS' credentials files, and 'EC2' instance metadata. For use on 'EC2' instances, users will need to install the suggested package 'aws.ec2metadata' < <a href="https://cran.r-project.org/package=aws.ec2metadata">https://cran.r-project.org/package=aws.ec2metadata</a> >. / GPL (>= 2)	noarch
r-aws.sns	0.1.7	A simple client package for the Amazon Web Services ('AWS') Simple Notification Service ('SNS') 'API' < <a href="https://aws.amazon.com/sns/">https://aws.amazon.com/sns/</a> >. / GPL (>= 2)	noarch
r-aws.sqs	0.1.10	A simple client package for the Amazon Web Services ('AWS') Simple Queue Service ('SQS') < <a href="https://aws.amazon.com/sqs/">https://aws.amazon.com/sqs/</a> > 'API'. / GPL (>= 2)	noarch
r-aws.transcribe	0.1.2	Client for 'AWS Transcribe' < <a href="https://aws.amazon.com/documentation/transcribe">https://aws.amazon.com/documentation/transcribe</a> >, a cloud transcription service that can convert an audio media file in English and other languages into a text transcript. / GPL (>= 2)	noarch
r-aws.translate	0.1.3	A client for 'AWS Translate' < <a href="https://aws.amazon.com/documentation/translate">https://aws.amazon.com/documentation/translate</a> >, a machine translation service that will convert a text input in one language into a text output in another language. / GPL (>= 2)	noarch
r-awsjavasdk	0.2.0	Provides boilerplate access to all of the classes included in the Amazon Web Services ('AWS') Java Software Development Kit (SDK) via package: 'rJava'. According to Amazon, the 'SDK helps take the complexity out of coding by providing Java APIs for many AWS services including Amazon S3, Amazon EC2, DynamoDB, and more'. You can read more about the included Java code on Amazon's website: < <a href="https://aws.amazon.com/sdk-for-java/">https://aws.amazon.com/sdk-for-java/</a> >. / GPL-2	noarch
r-awsmethods	1.1_1	Defines the method extract and provides 'openMP' support as needed in several packages. / GPL (>= 2)	linux-64, osx-64, win-64
r-azurevmmetadata	1.0.0	A simple interface to the instance metadata for a virtual machine running in Microsoft's 'Azure' cloud. This provides information about the VM's configuration, such as its processors, memory, networking, storage, and so on. Part of the 'AzureR' family of packages. / MIT	noarch
r-b2z	1.4	This package fits the Bayesian two-Zone Models. / GPL-2	noarch
r-b6e6rl	1.1	This package contains b6e6rl algorithm, adaptive differential evolution for global optimization. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-babar</a>	1.0	Babar is designed to use nested sampling (a Bayesian analysis technique) to compare possible models for bacterial growth curves, as well as extracting parameters. It allows model evidence and parameter likelihood values to be extracted, and also contains helper functions for comparing distributions as well as direct access to the underlying nested sampling code. / GPL-2	noarch
<a href="#">r-backpipe</a>	0.2.3	Provides a backward-pipe operator for ‘magrittr’ (%<%) or ‘pipeR’ (%<<%) that allows for a performing operations from right-to-left. This allows writing more legible code where right-to-left ordering is natural. This is common with hierarchies and nested structures such as trees, directories or markup languages (e.g. HTML and XML). The package also includes a R-Studio add-in that can be bound to a keyboard shortcut. / GPL-2   file LICENSE	noarch
<a href="#">r-backports</a>	1.1.4	Implementations of functions which have been introduced in R since version 3.0.0. The backports are conditionally exported which results in R resolving the function names to the version shipped with R (if available) and uses the implemented backports as fallback. This way package developers can make use of the new functions without worrying about the minimum required R version. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-backtest</a>	0.3.4	The backtest package provides facilities for exploring portfolio-based conjectures about financial instruments (stocks, bonds, swaps, options, et cetera). / GPL (>= 2)	noarch
<a href="#">r-bacprior</a>	2.0	The BACprior package provides an approximate sensitivity analysis of the Bayesian Adjustment for Confounding (BAC) algorithm (Wang et al., 2012) with regards to the hyperparameter omega. The package also provides functions to guide the user in their choice of an appropriate omega value. The method is based on Lefebvre, Atherton and Talbot (2014). / GPL (>= 2)	noarch
<a href="#">r-badgecreatr</a>	0.2.0	Tired of copy and pasting almost identical markdown for badges in every new R-package that you create, on Github or other code-sharing sites? This package allows you to easily paste badges. If you want to, it will also search your DESCRIPTION file and extract the package name, license, R-version, and current projectversion and transform that into badges. It will also search for a .travis.yml file and create a Travis badge, if you use Codecov.io to check your code coverage after a Travis build this package will also build a Codecov.io-badge. All the badges can be placed individually or can be placed below the top YAML content of your RMarkdown file (Readme.Rmd) or README.md file. Currently creates badges for Projectstatus (Repostatus.org), license Travis Build Status, Codecov, Minimal R version, CRAN status, CRAN downloads, Github stars and forks, Package rank, rdocumentation, current version of your package and last change of README.Rmd. / GPL-3	noarch
<a href="#">r-baessed</a>	1.0.1	Implements sample size calculations following the approach described in Bayesian Average Error Based Approach to Hypothesis Testing and Sample Size Determination. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-bagrboostR</a>	0.0.2	bagRboostR is a set of ensemble classifiers for multinomial classification. The bagging function is the implementation of Breiman's ensemble as described by Opitz & Maclin (1999). The boosting function is the implementation of Stagewise Additive Modeling using a Multi-class Exponential loss function (SAMME) created by Zhu et al (2006). Both bagging and SAMME implementations use randomForest as the weak classifier and expect a character outcome variable. Each ensemble classifier returns a character vector of predictions for the test set. / MIT file LICENSE	noarch
<a href="#">r-bain</a>	0.2.1	Computes approximated adjusted fractional Bayes factors for equality, inequality, and about equality constrained hypotheses. S3 methods are available for specific types of lm() models, namely ANOVA, ANCOVA, and multiple regression, and for the t_test(). The statistical underpinnings are described in Hoijtink, Mulder, van Lissa, and Gu, (2018) <doi:10.31234/osf.io/v3shc>, Gu, Mulder, and Hoijtink, (2018) <doi:10.1111/bmsp.12110>, Hoijtink, Gu, and Mulder, (2018) <doi:10.1111/bmsp.12145>, and Hoijtink, Gu, Mulder, and Rosseel, (2018) <doi:10.1037/met0000187>. / GPL (>= 3)	linux-64, osx-64, win-64
<a href="#">r-bairt</a>	0.1.2	Bayesian estimation of the two and three parameter models of item response theory (IRT). Also, it is possible to use a web interactive application intended for the making of an MCMC estimation and model-fit of the IRT models. / GPL (>= 2)	noarch
<a href="#">r-balancecheck</a>	0.2	Two practical tests are provided for assessing whether multiple covariates in a treatment group and a matched control group are balanced in observational studies. / GPL (>= 2)	noarch
<a href="#">r-bammtools</a>	2.1.6	Provides functions for analyzing and visualizing complex macroevolutionary dynamics on phylogenetic trees. It is a companion package to the command line program BAMB (Bayesian Analysis of Macroevolutionary Mixtures) and is entirely oriented towards the analysis, interpretation, and visualization of evolutionary rates. Functionality includes visualization of rate shifts on phylogenies, estimating evolutionary rates through time, comparing posterior distributions of evolutionary rates across clades, comparing diversification models using Bayes factors, and more. / GPL (>= 2)	linux-64, osx-64, win-64
<a href="#">r-bamp</a>	2.0.7	Bayesian Age-Period-Cohort Modeling and Prediction using efficient Markov Chain Monte Carlo Methods. This is the R version of the previous BAMP software as described in Volker Schmid and Leonhard Held (2007) <DOI:10.18637/jss.v021.i08> Bayesian Age-Period-Cohort Modeling and Prediction - BAMP, Journal of Statistical Software 21:8. This package includes checks of convergence using Gelman's R. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-bannercommenter</a>	0.1.1	A convenience package for use while drafting code. It facilitates making stand-out comment lines decorated with bands of characters. The input text strings are converted into R comment lines, suitably formatted. These are then displayed in a console window and, if possible, automatically transferred to a clipboard ready for pasting into an R script. Designed to save time when drafting R scripts that will need to be navigated and maintained by other programmers. / GPL (>= 2)	noarch
<a href="#">r-banxicor</a>	0.9.0	Provides functions to scrape IQY calls to Bank of Mexico, downloading and ordering the data conveniently. / CC0	noarch
<a href="#">r-baprestopro</a>	0.1	Bayesian estimation and prediction for stochastic processes based on the Euler approximation. Considered processes are: jump diffusion, (mixed) diffusion models, hidden (mixed) diffusion models, non-homogeneous Poisson processes (NHPP), (mixed) regression models for comparison and a regression model including a NHPP. / GPL (>= 2)	noarch

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Name	Version	Summary/License	Platforms
r-barborgradient	1.0.5	Tool to find where a function has its lowest value(minimum). The functions can be any dimensions. Recommended use is with $\text{eps}=10^{-10}$ , but can be run with $10^{-20}$ , although this depends on the function. Two more methods are in this package, simple gradient method (Gradmod) and Powell method (Powell). These are not recommended for use, their purpose are purely for comparison. / GPL-3	noarch
r-barcode	1.1	This package includes the function <code>code{barcode()}</code> , which produces a histogram-like plot of a distribution that shows granularity in the data. / GPL ( $\geq 2$ )	noarch
r-barcodingr	1.0.2	To perform species identification using DNA barcodes. / GPL-2	noarch
r-barnard	1.8	Barnard's unconditional test for 2x2 contingency tables. / GPL-2	linux-64, osx-64, win-64
r-barsurf	0.3.1	Produces heat maps, contour plots, bar plots (in 3D) and surface plots (also, in 3D). Is designed for plotting functions of two variables, however, can plot relatively arbitrary matrices. Uses HCL color space, extensively. Also, supports triangular plots and nested matrices. / GPL ( $\geq 2$ )	noarch
r-bart	2.5	Bayesian Additive Regression Trees (BART) provide flexible nonparametric modeling of covariates for continuous, binary, categorical and time-to-event outcomes. For more information on BART, see Chipman, George and McCulloch (2010) <doi:10.1214/09-AOAS285> and Sparapani, Logan, McCulloch and Laud (2016) <doi:10.1002/sim.6893>. / GPL ( $\geq 2$ )	linux-64, osx-64, win-64
r-bartmachinejars	1.1	These are bartMachine's Java dependency libraries. Note: this package has no functionality of its own and should not be installed as a standalone package without bartMachine. / GPL-3	noarch
r-barycenter	1.3.1	Computations of entropy regularized Wasserstein Distances, a.k.a. dual-Sinkhorn divergences, and entropy regularized Wasserstein Barycenters. Relevant papers are Marco Cuturi (2013) <arXiv:1306.0895>, Marco Cuturi (2014) <arXiv:1310.4375> and Jason Altschuler et al. <arXiv:1705.09634>. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-bas</a>	1.5.3	Package for Bayesian Variable Selection and Model Averaging in linear models and generalized linear models using stochastic or deterministic sampling without replacement from posterior distributions. Prior distributions on coefficients are from Zellner's g-prior or mixtures of g-priors corresponding to the Zellner-Siow Cauchy Priors or the mixture of g-priors from Liang et al (2008) <DOI:10.1198/016214507000001337> for linear models or mixtures of g-priors in GLMs of Li and Clyde (2018) <arXiv:1503.06913>. Other model selection criteria include AIC, BIC and Empirical Bayes estimates of g. Sampling probabilities may be updated based on the sampled models using Sampling w/out Replacement or an efficient MCMC algorithm samples models using the BAS tree structure as an efficient hash table. Uniform priors over all models or beta-binomial prior distributions on model size are allowed, and for large p truncated priors on the model space may be used. The user may force variables to always be included. Details behind the sampling algorithm are provided in Clyde, Ghosh and Littman (2010) <DOI:10.1198/jcgs.2010.09049>. This material is based upon work supported by the National Science Foundation under Grant DMS-1106891. Any opinions, findings, and conclusions or recommendations expressed in this material are those of the author(s) and do not necessarily reflect the views of the National Science Foundation. / GPL (>= 3)	linux-64, osx-64, win-64
<a href="#">r-base</a>	3.6.1	R is a free software environment for statistical computing and graphics. / GPL-3.0	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-base64</a>	2.0	Compatibility wrapper to replace the orphaned package by Romain Francois. New applications should use the 'openssl' or 'base64enc' package instead. / MIT file LICENSE	noarch
<a href="#">r-base64enc</a>	0.1_3	This package provides tools for handling base64 encoding. It is more flexible than the orphaned base64 package. / GPL-2   GPL-3	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-base64url</a>	1.4	In contrast to RFC3548, the 62nd character () is replaced with -, the 63rd character (/) is replaced with _. Furthermore, the encoder does not fill the string with trailing =. The resulting encoded strings comply to the regular expression pattern <b>[A-Za-z0-9_-]</b> and thus are safe to use in URLs or for file names. The package also comes with a simple base32 encoder/decoder suited for case insensitive file systems. / GPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-baseline	1.2.1	Collection of baseline correction algorithms, along with a framework and a GUI for optimising baseline algorithm parameters. Typical use of the package is for removing background effects from spectra originating from various types of spectroscopy and spectrometry, possibly optimizing this with regard to regression or classification results. Correction methods include polynomial fitting, weighted local smoothers and many more. / GPL-2	noarch
r-basetheme	0.1.1	Functions to create and select graphical themes for the base plotting system. Contains: 1) several custom pre-made themes 2) mechanism for creating new themes by making persistent changes to the graphical parameters of base plots. / GPL-2	noarch
r-basismcmcplots	0.2.2	Provides a function for examining posterior MCMC samples from a single chain using trace plots and density plots, and from multiple chains by comparing posterior medians and credible intervals from each chain. These plotting functions have a variety of options, such as figure sizes, legends, parameters to plot, and saving plots to file. Functions interface with the NIMBLE software package, see de Valpine, Turek, Paciorek, Anderson-Bergman, Temple Lang and Bodik (2017) <doi:10.1080/10618600.2016.1172487>. / GPL-3	noarch
r-basicspace	0.20	Conducts Aldrich-McKelvey and Blackbox Scaling (Poole et al 2016) <doi:10.18637/jss.v069.i07> to recover latent dimensions of judgment. / GPL-2	linux-64, osx-64, win-64
r-basix	1.1	BASIX provides some efficient C/C implementations to speed up calculations in R. / GPL-2	linux-64, osx-64, win-64
r-bass	0.2.2	Bayesian fitting and sensitivity analysis methods for adaptive spline surfaces. Built to handle continuous and categorical inputs as well as functional or scalar output. An extension of the methodology in Denison, Mallick and Smith (1998) <doi:10.1023/A:1008824606259>. / GPL-3	linux-64, osx-64, win-64
r-batch	1.1.5	Functions to allow you to easily pass command-line arguments into R, and functions to aid in submitting your R code in parallel on a cluster and joining the results afterward (e.g. multiple parameter values for simulations running in parallel, splitting up a permutation test in parallel, etc.). See ‘parseCommandArgs(...)’ for the main example of how to use this package. / GPL	noarch
r-batchmeans	1.0.3	Provides consistent batch means estimation of Monte Carlo standard errors. / GPL (>= 2)	noarch
r-batchscr	0.1.0	Handy frameworks, such as error handling and log generation, for batch scripts. Use case: in scripts running in remote servers, set error handling mechanism for downloading and uploading and record operation log. / MIT file LICENSE	noarch

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Name	Version	Summary/License	Platforms
r-batman	0.1.0	Survey systems and other third-party data sources commonly use non-standard representations of logical values when it comes to qualitative data - Yes, No and N/A, say. batman is a package designed to seamlessly convert these into logicals. It is highly localised, and contains equivalents to boolean values in languages including German, French, Spanish, Italian, Turkish, Chinese and Polish. / MIT file LICENSE	linux-64, osx-64, win-64
r-bayesbio	1.0.0	A hodgepodge of hopefully helpful functions. Two of these perform shrinkage estimation: one using a simple weighted method where the user can specify the degree of shrinkage required, and one using James-Stein shrinkage estimation for the case of unequal variances. / GPL-3	noarch
r-bayescombo	1.0	Combine diverse evidence across multiple studies to test a high level scientific theory. The methods can also be used as an alternative to a standard meta-analysis. / GPL-3	noarch
r-bayescomm	0.1_2	Bayesian multivariate binary (probit) regression models for analysis of ecological communities. / GPL (>= 2)	linux-64, osx-64, win-64
r-bayesda	2012.04	Functions for Bayesian Data Analysis, with datasets from the book Bayesian data Analysis (second edition) by Gelman, Carlin, Stern and Rubin. Not all datasets yet, hopefully completed soon. / GPL (>= 2)	noarch
r-bayesdccgarch	2.0	Bayesian estimation of dynamic conditional correlation GARCH model for multivariate time series volatility (Fioruci, J.A., Ehlers, R.S. and Andrade-Filho, M.G., (2014), DOI:10.1080/02664763.2013.839635). / GPL (>= 2)	linux-64, osx-64, win-64
r-bayesdistreg	0.1.0	Implements Bayesian Distribution Regression methods. This package contains functions for three estimators (non-asymptotic, semi-asymptotic and asymptotic) and related routines for Bayesian Distribution Regression in Huang and Tsyawo (2018) <doi:10.2139/ssrn.3048658> which is also the recommended reference to cite for this package. The functions can be grouped into three (3) categories. The first computes the logit likelihood function and posterior densities under uniform and normal priors. The second contains Independence and Random Walk Metropolis-Hastings Markov Chain Monte Carlo (MCMC) algorithms as functions and the third category of functions are useful for semi-asymptotic and asymptotic Bayesian distribution regression inference. / GPL-2	noarch
r-bayesgarch	2.1.3	Provides the bayesGARCH() function which performs the Bayesian estimation of the GARCH(1,1) model with Student's t innovations as described in Ardia (2008) <doi:10.1007/978-3-540-78657-3>. / GPL (>= 2)	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-bayesianetas</a>	1.0.3	The Epidemic Type Aftershock Sequence (ETAS) model is one of the best-performing methods for modeling and forecasting earthquake occurrences. This package implements Bayesian estimation routines to draw samples from the full posterior distribution of the model parameters, given an earthquake catalog. The paper on which this package is based is Gordon J. Ross - Bayesian Estimation of the ETAS Model for Earthquake Occurrences (2016), available from the below URL. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-bayesianpower</a>	0.1.6	A collection of methods to determine the required sample size for the evaluation of inequality constrained hypotheses by means of a Bayes factor. Alternatively, for a given sample size, the unconditional error probabilities or the expected conditional error probabilities can be determined. Additional material on the methods in this package is available in Klaassen, F., Hoijtink, H. & Gu, X. (2019) <doi:10.31219/osf.io/d5kf3>. / LGPL-3	noarch
<a href="#">r-bayesimages</a>	0.6_0	Various algorithms for segmentation of 2D and 3D images, such as computed tomography and satellite remote sensing. This package implements Bayesian image analysis using the hidden Potts model with external field prior of Moores et al. (2015) <doi:10.1016/j.cstda.2014.12.001>. Latent labels are sampled using checkerboard updating or Swendsen-Wang. Algorithms for the smoothing parameter include pseudolikelihood, path sampling, the exchange algorithm, approximate Bayesian computation (ABC-MCMC and ABC-SMC), and the parametric functional approximate Bayesian (PFAB) algorithm. Refer to <doi:10.1007/s11222-014-9525-6> and <doi:10.1214/18-BA1130> for further details. / GPL (>= 2)   file LICENSE	linux-64, osx-64, win-64
<a href="#">r-bayesloglin</a>	1.0.1	The function MC3() searches for log-linear models with the highest posterior probability. The function gibbsSampler() is a blocked Gibbs sampler for sampling from the posterior distribution of the log-linear parameters. The functions findPostMean() and findPostCov() compute the posterior mean and covariance matrix for decomposable models which, for these models, is available in closed form. / GPL (>= 2)	linux-64, osx-64, win-64
<a href="#">r-bayesm</a>	3.1_3	Covers many important models used in marketing and micro-econometrics applications. The package includes: Bayes Regression (univariate or multivariate dep var), Bayes Seemingly Unrelated Regression (SUR), Binary and Ordinal Probit, Multinomial Logit (MNL) and Multinomial Probit (MNP), Multivariate Probit, Negative Binomial (Poisson) Regression, Multivariate Mixtures of Normals (including clustering), Dirichlet Process Prior Density Estimation with normal base, Hierarchical Linear Models with normal prior and covariates, Hierarchical Linear Models with a mixture of normals prior and covariates, Hierarchical Multinomial Logits with a mixture of normals prior and covariates, Hierarchical Multinomial Logits with a Dirichlet Process prior and covariates, Hierarchical Negative Binomial Regression Models, Bayesian analysis of choice-based conjoint data, Bayesian treatment of linear instrumental variables models, Analysis of Multivariate Ordinal survey data with scale usage heterogeneity (as in Rossi et al, JASA (01)), Bayesian Analysis of Aggregate Random Coefficient Logit Models as in BLP (see Jiang, Manchanda, Rossi 2009) For further reference, consult our book, Bayesian Statistics and Marketing by Rossi, Allenby and McCulloch (Wiley 2005) and Bayesian Non- and Semi-Parametric Methods and Applications (Princeton U Press 2014). / GPL (>= 2)	linux-64, osx-64, win-64
<a href="#">r-bayesmams</a>	0.1	Calculating Bayesian sample sizes for multi-arm trials where several experimental treatments are compared to a common control, perhaps even at multiple stages. / GPL (>= 2)	noarch

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Name	Version	Summary/License	Platforms
r-bayesmixsurv	0.9.1	Bayesian Mixture Survival Models using Additive Mixture-of-Weibull Hazards, with Lasso Shrinkage and Stratification. As a Bayesian dynamic survival model, it relaxes the proportional-hazard assumption. Lasso shrinkage controls overfitting, given the increase in the number of free parameters in the model due to presence of two Weibull components in the hazard function. / GPL (>= 2)	noarch
r-bayesni	0.1	A Bayesian testing procedure for noninferiority trials with binary endpoints. The prior is constructed based on Bernstein polynomials with options for both informative and non-informative prior. The critical value of the test statistic (Bayes factor) is determined by minimizing total weighted error (TWE) criteria / GPL-2	noarch
r-bayespiecehazselect	1.1.0	Fits a piecewise exponential hazard to survival data using a Hierarchical Bayesian model with an Intrinsic Conditional Autoregressive formulation for the spatial dependency in the hazard rates for each piece. This function uses Metropolis- Hastings-Green MCMC to allow the number of split points to vary and also uses Stochastic Search Variable Selection to determine what covariates drive the risk of the event. This function outputs trace plots depicting the number of split points in the hazard and the number of variables included in the hazard. The function saves all posterior quantities to the desired path. / GPL-2	noarch
r-bayespiecewiseicarb	0.2.1	Fits a piecewise exponential hazard to survival data using a Hierarchical Bayesian model with an Intrinsic Conditional Autoregressive formulation for the spatial dependency in the hazard rates for each piece. This function uses Metropolis- Hastings-Green MCMC to allow the number of split points to vary. This function outputs graphics that display the histogram of the number of split points and the trace plots of the hierarchical parameters. The function outputs a list that contains the posterior samples for the number of split points, the location of the split points, and the log hazard rates corresponding to these splits. Additionally, this outputs the posterior samples of the two hierarchical parameters, Mu and Sigma^2. / GPL-2	noarch
r-bayesqr	2.3	Bayesian quantile regression using the asymmetric Laplace distribution, both continuous as well as binary dependent variables are supported. The package consists of implementations of the methods of Yu & Moyeed (2001) <doi:10.1016/S0167-7152(01)00124-9>, Benoit & Van den Poel (2012) <doi:10.1002/jae.1216> and Al-Hamzawi, Yu & Benoit (2012) <doi:10.1177/1471082X1101200304>. To speed up the calculations, the Markov Chain Monte Carlo core of all algorithms is programmed in Fortran and called from R. / GPL (>= 2)	linux-64, osx-64, win-64
r-bayess	1.4	bayess contains a collection of functions that allows the reenactment of the R programs used in the book Bayesian Essentials with R (revision of Bayesian Core) without further programming. R code being available as well, they can be modified by the user to conduct one's own simulations. / GPL-2	noarch
r-bayessae	1.0_2	Provides a variety of methods from Rao (2003, ISBN:0-471-41374-7) and some other research articles to deal with several specific small area area- level models in Bayesian framework. Models provided range from the basic Fay-Herriot model to its improvement such as You-Chapman models, unmatched models, spatial models and so on. Different types of priors for specific parameters could be chosen to obtain MCMC posterior draws. The main sampling function is written in C with GSL lib so as to facilitate the computation. Model internal checking and model comparison criteria are also involved. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-bayest</a>	1.0	Provides an Markov-Chain-Monte-Carlo algorithm for Bayesian t-tests on the effect size. The underlying Gibbs sampler is based on a two-component Gaussian mixture and approximates the posterior distributions of the effect size, the difference of means and difference of standard deviations. A posterior analysis of the effect size via the region of practical equivalence is provided, too. For more details about the Gibbs sampler see Kelter (2019) <arXiv:1906.07524>. / GPL-2	noarch
<a href="#">r-bayestree</a>	0.3.1	This is an implementation of BART:Bayesian Additive Regression Trees, by Chipman, George, McCulloch (2010). / GPL (>= 2)	linux-64, osx-64, win-64
<a href="#">r-bayestreeprior</a>	1.0.1	Provides a way to simulate from the prior distribution of Bayesian trees by Chipman et al. (1998) <DOI:10.2307/2669832>. The prior distribution of Bayesian trees is highly dependent on the design matrix X, therefore using the suggested hyperparameters by Chipman et al. (1998) <DOI:10.2307/2669832> is not recommended and could lead to unexpected prior distribution. This work is part of my master thesis (expected 2016). / GPL-3	noarch
<a href="#">r-bayesvalidate</a>	0.0	BayesValidate implements the software validation method described in the paper Validation of Software for Bayesian Models using Posterior Quantiles (Cook, Gelman, and Rubin, 2005). It inputs a function to perform Bayesian inference as well as functions to generate data from the Bayesian model being fit, and repeatedly generates and analyzes data to check that the Bayesian inference program works properly. / GPL (>= 2)	noarch
<a href="#">r-bayesvarsel</a>	1.8.0	Conceived to calculate Bayes factors in linear models and then to provide a formal Bayesian answer to testing and variable selection problems. From a theoretical side, the emphasis in this package is placed on the prior distributions and it allows a wide range of them: Jeffreys (1961); Zellner and Siow(1980)<DOI:10.1007/bf02888369>; Zellner and Siow(1984); Zellner (1986)<DOI:10.2307/2233941>; Fernandez et al. (2001)<DOI:10.1016/s0304-4076(00)00076-2>; Liang et al. (2008)<DOI:10.1198/016214507000001337> and Bayarri et al. (2012)<DOI:10.1214/12-aos1013>. The interaction with the package is through a friendly interface that syntactically mimics the well-known lm() command of R. The resulting objects can be easily explored providing the user very valuable information (like marginal, joint and conditional inclusion probabilities of potential variables; the highest posterior probability model, HPM; the median probability model, MPM) about the structure of the true -data generating- model. Additionally, this package incorporates abilities to handle problems with a large number of potential explanatory variables through parallel and heuristic versions of the main commands, Garcia-Donato and Martinez-Beneito (2013)<DOI:10.1080/01621459.2012.742443>. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-bayesxsrc</a>	3.0.1	BayesX performs Bayesian inference in structured additive regression (STAR) models. The R package BayesXsrc provides the BayesX command line tool for easy installation. A convenient R interface is provided in package R2BayesX. / GPL-2   GPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-bayfoxr	0.0.1	A Bayesian, global planktic foraminifera core top calibration to modern sea-surface temperatures. Includes four calibration models, considering species-specific calibration parameters and seasonality. / GPL (>= 3)	noarch
r-bayhap	1.0.1	The package BayHap performs simultaneous estimation of uncertain haplotype frequencies and association with haplotypes based on generalized linear models for quantitative, binary and survival traits. Bayesian statistics and Markov Chain Monte Carlo techniques are the theoretical framework for the methods of estimation included in this package. Prior values for model parameters can be included by the user. Convergence diagnostics and statistical and graphical analysis of the sampling output can be also carried out. / GPL-2	linux-64, osx-64, win-64
r-bayhaz	0.1_3	A suite of R functions for Bayesian estimation of smooth hazard rates via Compound Poisson Process (CPP) and Bayesian Penalized Spline (BPS) priors. / GPL (>= 2)	noarch
r-bayloredpsych	0.5	Functions and data used for Baylor University Educational Psychology Quantitative Courses / GPL (>= 2)	noarch
r-baystar	0.2_9	The manuscript introduces the BAYSTAR package, which provides the functionality for Bayesian estimation in autoregressive threshold models. / GPL (>= 2)	noarch
r-bb	2014.0	Burilai-Borwein spectral methods for solving nonlinear system of equations, and for optimizing nonlinear objective functions subject to simple constraints. A tutorial style introduction to this package is available in a vignette on the CRAN download page or, when the package is loaded in an R session, with vignette(BB). / GPL-3	noarch
r-bbefkr	4.2	Estimating optimal bandwidths for the regression mean function approximated by the functional Nadaraya-Watson estimator and the error density approximated by a kernel density of residuals simultaneously in a scalar-on-function regression. As a by-product of Markov chain Monte Carlo, the optimal choice of semi-metric is selected based on largest marginal likelihood. / GPL (>= 2)	noarch
r-bbemkr	2.0	Bayesian bandwidth estimation for Nadaraya-Watson type multivariate kernel regression with Gaussian error density / GPL (>= 2)	noarch
r-bbl	0.1.5	Supervised learning using Boltzmann Bayes model inference, which extends naive Bayes model to include interactions. Enables classification of data into multiple response groups based on a large number of discrete predictors that can take factor values of heterogeneous levels. Either pseudo-likelihood and mean field inference can be used with L2 regularization, cross-validation, and prediction on new data. Woo et al. (2016) <doi:10.1186/s12864-016-2871-3>. / GPL-2	linux-64, osx-64, win-64
r-bbmisc	1.11	Miscellaneous helper functions for and from B. Bischl and some other guys, mainly for package development. / BSD_2_clause file LICENSE	linux-64, osx-64, win-64
r-bbmle	1.0.20	Methods and functions for fitting maximum likelihood models in R. This package modifies and extends the 'mle' classes in the 'stats4' package. / GPL	noarch
r-bbmm	3.0	The model provides an empirical estimate of a movement path using discrete location data obtained at relatively short time intervals. / GNU General Public License	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-bbm</a>	2.1	Provides a set of functions to fit general macroevolutionary models for continuous traits evolving in adaptive landscapes of any shape. This package implements the Fokker-Planck-Kolmogorov model (FPK), in which the trait evolves under random diffusion but is also subject to a force that pulls it towards specific values - this force can be of any shape. FPK has a version in which hard reflective bounds exist at the extremes of the trait interval: this second model is called BBM. / GPL-2	noarch
<a href="#">r-bbo</a>	0.2	This package provides an R implementation of Biogeography-Based Optimization (BBO), originally invented by Prof. Dan Simon, Cleveland State University, Ohio. This method is an application of the concept of biogeography, a study of the geographical distribution of biological organisms, to optimization problems. More information about this method can be found here: <a href="http://academic.csuohio.edu/simond/bbo/">http://academic.csuohio.edu/simond/bbo/</a> . / GPL (>= 3)	noarch
<a href="#">r-bcboot</a>	0.2.1	Computation of bootstrap confidence intervals in an almost automatic fashion. / GPL (>= 2)	noarch
<a href="#">r-bcbsf</a>	1.0.1	Fully Bayesian Classification with a subset of high-dimensional features, such as expression levels of genes. The data are modeled with a hierarchical Bayesian models using heavy-tailed t distributions as priors. When a large number of features are available, one may like to select only a subset of features to use, typically those features strongly correlated with the response in training cases. Such a feature selection procedure is however invalid since the relationship between the response and the features has been exaggerated by feature selection. This package provides a way to avoid this bias and yield better-calibrated predictions for future cases when one uses F-statistic to select features. / GPL (>= 2)	linux-64, osx-64, win-64
<a href="#">r-bcc1997</a>	0.1.1	Calculates the prices of European options based on the universal solution provided by Bakshi, Cao and Chen (1997) <doi:10.1111/j.1540-6261.1997.tb02749.x>. This solution considers stochastic volatility, stochastic interest and random jumps. Please cite their work if this package is used. / GPL (>= 2)	noarch
<a href="#">r-bcdating</a>	0.9.8	Tools for Dating Business Cycles using Harding-Pagan (Quarterly Business Review) method and various plotting features. / GPL-2	noarch
<a href="#">r-bcf</a>	1.2.1	Causal inference for a binary treatment and continuous outcome using Bayesian Causal Forests. See Hahn, Murray and Carvalho (2017) <arXiv:1706.09523> for additional information. This implementation relies on code originally accompanying Pratola et. al. (2013) <arXiv:1309.1906>. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-bcgee</a>	0.1	Provides bias-corrected estimates for the regression coefficients of a marginal model estimated with generalized estimating equations. Details about the bias formula used are in Lunardon, N., Scharfstein, D. (2017) <doi:10.1002/sim.7366>. / GPL-2	noarch
<a href="#">r-bclust</a>	1.5	Builds a dendrogram using log posterior as a natural distance defined by the model and meanwhile waits the clustering variables. It is also capable to computing equivalent Bayesian discrimination probabilities. The adopted method suits small sample large dimension setting. The model parameter estimation maybe difficult, depending on data structure and the chosen distribution family. / GPL (>= 2)	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-bcp	4.0.3	Provides an implementation of the Barry and Hartigan (1993) product partition model for the normal errors change point problem using Markov Chain Monte Carlo. It also extends the methodology to regression models on a connected graph (Wang and Emerson, 2015); this allows estimation of change point models with multivariate responses. Parallel MCMC, previously available in bcp v.3.0.0, is currently not implemented. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
r-bcpa	1.1	The Behavioral Change Point Analysis (BCPA) is a method of identifying hidden shifts in the underlying parameters of a time series, developed specifically to be applied to animal movement data which is irregularly sampled. The method is based on: E. Gurarie, R. Andrews and K. Laidre A novel method for identifying behavioural changes in animal movement data (2009) Ecology Letters 12:5 395-408. / Unlimited	linux-64, osx-64, win-64
r-bcpmeta	1.0	A Bayesian approach to detect mean shifts in AR(1) time series while accommodating metadata (if available). In addition, a linear trend component is allowed. / GPL (>= 2)	noarch
r-bcra	2.1	Functions provide risk projections of invasive breast cancer based on Gail model according to National Cancer Institute's Breast Cancer Risk Assessment Tool algorithm for specified race/ethnic groups and age intervals. / GPL (>= 2)	noarch
r-bcrypt	1.1	Bindings to the 'blowfish' password hashing algorithm derived from the 'OpenBSD' implementation. / BSD_2_clause file LICENSE	linux-64, osx-64, win-64
r-bcv	1.0.1	Methods for choosing the rank of an SVD approximation via cross validation. The package provides both Gabriel-style block holdouts and Wold-style speckled holdouts. It also includes an implementation of the SVDImpute algorithm. For more information about Bi-cross-validation, see Owen & Perry's 2009 AoAS article (at <a href="http://arxiv.org/abs/0908.2062">http://arxiv.org/abs/0908.2062</a> ) and Perry's 2009 PhD thesis (at <a href="http://arxiv.org/abs/0909.3052">http://arxiv.org/abs/0909.3052</a> ). / BSD_3_clause file LICENSE	linux-64, osx-64, win-64
r-bda	10.1.9	Functions for density estimation based on grouped data, and next-generation gene expression data. / Unlimited	linux-64, osx-64, win-64
r-bdgraph	2.60	Statistical tools for Bayesian structure learning in undirected graphical models for continuous, discrete, and mixed data. The package is implemented the recent improvements in the Bayesian graphical models literature, including Mohammadi and Wit (2015) <doi:10.1214/14-BA889>, Mohammadi and Wit (2019) <doi:10.18637/jss.v089.i03>. / GPL (>= 2)	linux-64, osx-64, win-64
r-bdots	0.1.19	Analyze differences among time series curves with p-value adjustment for multiple comparisons introduced in Oleson et al (2015) <DOI:10.1177/0962280215607411>. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-bdp2</a>	0.1.3	Tools and workflow to choose design parameters in Bayesian adaptive single-arm phase II trial designs with binary endpoint (response, success) with possible stopping for efficacy and futility at interim analyses. Also contains routines to determine and visualize operating characteristics. See Kopp-Schneider et al. (2018) <doi:10.1002/bimj.201700209>. / GPL-2	noarch
<a href="#">r-bdpv</a>	1.3	Computation of asymptotic confidence intervals for negative and positive predictive values in binary diagnostic tests in case-control studies. Experimental design for hypothesis tests on predictive values. / GPL (>= 2)	noarch
<a href="#">r-bdsmatrix</a>	1.3_3	This is a special case of sparse matrices, used by coxme. / LGPL-2	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-beanplot</a>	1.2	Plots univariate comparison graphs, an alternative to boxplot/stripchart/violin plot. / GPL-2	noarch
<a href="#">r-beast</a>	1.1	Assume that a temporal process is composed of contiguous segments with differing slopes and replicated noise-corrupted time series measurements are observed. The unknown mean of the data generating process is modelled as a piecewise linear function of time with an unknown number of change-points. The package infers the joint posterior distribution of the number and position of change-points as well as the unknown mean parameters per time-series by MCMC sampling. A-priori, the proposed model uses an overfitting number of mean parameters but, conditionally on a set of change-points, only a subset of them influences the likelihood. An exponentially decreasing prior distribution on the number of change-points gives rise to a posterior distribution concentrating on sparse representations of the underlying sequence, but also available is the Poisson distribution. See Papastamoulis et al (2017) <arXiv:1709.06111> for a detailed presentation of the method. / GPL-2	noarch
<a href="#">r-bedmatrix</a>	1.6.1	A matrix-like data structure that allows for efficient, convenient, and scalable subsetting of binary genotype/phenotype files generated by PLINK (< <a href="https://www.cog-genomics.org/plink2">https://www.cog-genomics.org/plink2</a> >), the whole genome association analysis toolset, without loading the entire file into memory. / MIT	linux-64, osx-64, win-64
<a href="#">r-beep</a>	1.3	The main function of this package is beep(), with the purpose to make it easy to play notification sounds on whatever platform you are on. It is intended to be useful, for example, if you are running a long analysis in the background and want to know when it is ready. / GPL-3	noarch
<a href="#">r-beeswarm</a>	0.2.3	The bee swarm plot is a one-dimensional scatter plot like stripchart, but with closely-packed, non-overlapping points. / Artistic-2.0	noarch
<a href="#">r-beginr</a>	0.1.7	Useful functions for R beginners, including hints for the arguments of the 'plot()' function, self-defined functions for error bars, user-customized pair plots and hist plots, enhanced linear regression figures, etc.. This package could be helpful to R experts as well. / MIT	noarch
<a href="#">r-behavr</a>	0.3.2	Implements an S3 class based on 'data.table' to store and process efficiently ethomics (high-throughput behavioural) data. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-belex</a>	0.1.0	Tools for downloading historical financial data from the <a href="http://www.belex.rs">www.belex.rs</a> . / GPL-3	noarch
<a href="#">r-belg</a>	0.2.3	Calculates the Boltzmann entropy of a landscape gradient. This package uses the analytical method created by Gao, P., Zhang, H. and Li, Z., 2018 (<doi:10.1111/tgis.12315>). It also extend the original idea by allowing calculations on data with missing values. / MIT file LICENSE	linux-64, osx-64, win-64
<a href="#">r-benchden</a>	1.0.5	Full implementation of the 28 distributions introduced as benchmarks for non-parametric density estimation by Berlinet and Devroye (1994). Includes densities, cdfs, quantile functions and generators for samples as well as additional information on features of the densities. Also contains the 4 histogram densities used in Rozenholc/Mildenberger/Gather (2010). / GPL (>= 2)	noarch
<a href="#">r-benchr</a>	0.2.3	Provides infrastructure to accurately measure and compare the execution time of R expressions. / GPL (>= 2)	linux-64, osx-64, win-64
<a href="#">r-bender</a>	0.1.1	R client for Bender Hyperparameters optimizer : < <a href="https://bender.dreem.com">https://bender.dreem.com</a> > The R client allows you to communicate with the Bender API and therefore submit some new trials within your R script itself. / MIT file LICENSE	noarch
<a href="#">r-benford.analysis</a>	0.1.5	Provides tools that make it easier to validate data using Benford's Law. / GPL-3	noarch
<a href="#">r-benfordtests</a>	1.2.0	Several specialized statistical tests and support functions for determining if numerical data could conform to Benford's law. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-bentcablear</a>	0.3.0	Included are two main interfaces for fitting and diagnosing bent-cable regressions for autoregressive time-series data or independent data (time series or otherwise): 'bentcable.ar()' and 'bentcable.dev.plot()'. Some components in the package can also be used as stand-alone functions. The bent cable (linear-quadratic-linear) generalizes the broken stick (linear-linear), which is also handled by this package. Version 0.2 corrects a glitch in the computation of confidence intervals for the CTP. References that were updated from Versions 0.2.1 and 0.2.2 appear in Version 0.2.3 and up. Version 0.3.0 improves robustness of the error-message producing mechanism. It is the author's intention to distribute any future updates via GitHub. / GPL (>= 3)	noarch
<a href="#">r-beqi2</a>	2.0_0	Tool for analysing benthos data. It estimates several quality indices like the total abundance of species, species richness, Margalef's d, AZTI Marine Biotic Index (AMBI), and the BEQI-2 index. Furthermore, additional (optional) features are provided that enhance data preprocessing: (1) genus to species conversion, i.e., taxa counts at the taxonomic genus level can optionally be converted to the species level and (2) pooling: small samples are combined to bigger samples with a standardized size to (a) meet the data requirements of the AMBI, (b) generate comparable species richness values and (c) give a higher benthos signal to noise ratio. / GPL (>= 3)	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-ber</a>	4.0	The functions in this package remove batch effects from microarray normalized data. The expression levels of the genes are represented in a matrix where rows correspond to independent samples and columns to genes (variables). The batches are represented by categorical variables (objects of class factor). When further covariates of interest are available they can be used to remove efficiently the batch effects and adjust the data. / GPL-2	noarch
<a href="#">r-berryfunctions</a>	1.18.2	Draw horizontal histograms, color scattered points by 3rd dimension, enhance date- and log-axis plots, zoom in X11 graphics, trace errors and warnings, use the unit hydrograph in a linear storage cascade, convert lists to data.frames and arrays, fit multiple functions. / GPL (>= 2)	noarch
<a href="#">r-bess</a>	1.0.6	An implementation of best subset selection in generalized linear model and Cox proportional hazard model via the primal dual active set algorithm proposed by Wen, C., Zhang, A., Quan, S. and Wang, X. (2017) <arXiv:1709.06254>. The algorithm formulates coefficient parameters and residuals as primal and dual variables and utilizes efficient active set selection strategies based on the complementarity of the primal and dual variables. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-bestglm</a>	0.37	Best subset glm using information criteria or cross-validation. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-bestree</a>	0.5.2	Decision tree algorithm with a major feature added. Allows for users to define an ordering on the partitioning process. Resulting in Branch-Exclusive Splits Trees (BEST). Cedric Beaulac and Jeffrey S. Rosentahl (2019) <arXiv:1804.10168>. / MIT file LICENSE	noarch
<a href="#">r-betabit</a>	1.3	Three games: proton, frequon and regression. Each one is a console-based data-crunching game for younger and older data scientists. Act as a data-hacker and find Slawomir Pietraszko's credentials to the Proton server. In proton you have to solve four data-based puzzles to find the login and password. There are many ways to solve these puzzles. You may use loops, data filtering, ordering, aggregation or other tools. Only basics knowledge of R is required to play the game, yet the more functions you know, the more approaches you can try. In frequon you will help to perform statistical cryptanalytic attack on a corpus of ciphered messages. This time seven sub-tasks are pushing the bar much higher. Do you accept the challenge? In regression you will test your modeling skills in a series of eight sub-tasks. Try only if ANOVA is your close friend. It's a part of Beta and Bit project. You will find more about the Beta and Bit project at < <a href="http://betabit.wiki">http://betabit.wiki</a> >. / GPL-2	noarch
<a href="#">r-betacal</a>	0.1.0	Fit beta calibration models and obtain calibrated probabilities from them. / MIT file LICENSE	noarch
<a href="#">r-betafam</a>	1.0	To detecting rare variants for quantitative traits using nuclear families, the linear combination methods are proposed using the estimated regression coefficients from the multiple regression and regularized regression as the weights. / GPL (>= 2)	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-betalink</a>	2.2.1	Measures of beta-diversity in networks, and easy visualization of why two networks are different. / BSD_2_clause file LICENSE	noarch
<a href="#">r-betategarch</a>	3.3	Simulation, estimation and forecasting of first-order Beta-Skew-t-EGARCH models with leverage (one-component, two-component, skewed versions). / GPL-2	linux-64, osx-64, win-64
<a href="#">r-bethel</a>	0.2	The sample size according to the Bethel's procedure. / GPL (>= 2)	noarch
<a href="#">r-bevimed</a>	5.3	A fast integrative genetic association test for rare diseases based on a model for disease status given allele counts at rare variant sites. Probability of association, mode of inheritance and probability of pathogenicity for individual variants are all inferred in a Bayesian framework - 'A Fast Association Test for Identifying Pathogenic Variants Involved in Rare Diseases', Greene et al 2017 <doi:10.1016/j.ajhg.2017.05.015>. / GPL (>= 2)	linux-64, osx-64, win-64
<a href="#">r-beyondbenford</a>	1.1	Allows to compare the goodness of fit of Benford's and Blondeau Da Silva's digit distributions in a dataset. It is used to check whether the data distribution is consistent with theoretical distributions highlighted by Blondeau Da Silva or not (through the <code>dat.distr()</code> function): this ideal theoretical distribution must be at least approximately followed by the data for the use of Blondeau Da Silva's model to be well-founded. It also enables to plot histograms of digit distributions, both observed in the dataset and given by the two theoretical approaches (with the <code>digit.ditr()</code> function). Finally, it proposes to quantify the goodness of fit via Pearson's chi-squared test (with the <code>chi2()</code> function). / GPL-2	noarch
<a href="#">r-bezier</a>	1.1.2	The bezier package is a toolkit for working with Bezier curves and splines. The package provides functions for point generation, arc length estimation, degree elevation and curve fitting. / GPL (>= 2)	noarch
<a href="#">r-bfa</a>	0.4	Provides model fitting for several Bayesian factor models including Gaussian, ordinal probit, mixed and semiparametric Gaussian copula factor models under a range of priors. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-bfp</a>	0.0_40	Implements the Bayesian paradigm for fractional polynomial models under the assumption of normally distributed error terms, see Sabanes Bove, D. and Held, L. (2011) <doi:10.1007/s11222-010-9170-7>. / GPL (>= 2)	linux-64, osx-64, win-64
<a href="#">r-bfsl</a>	0.1.0	Provides the solution from York (1968) <doi:10.1016/S0012-821X(68)80059-7> for fitting a straight line to bivariate data with errors in both coordinates. It gives unbiased estimates of the intercept, slope and standard errors of the best-fit straight line to independent points with (possibly correlated) normally distributed errors in both x and y. Other commonly used errors-in-variables methods, such as orthogonal distance regression, geometric mean regression or Deming regression are special cases of York's solution. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-bgge</a>	0.6.5	Application of genome prediction for a continuous variable, focused on genotype by environment (GE) genomic selection models (GS). It consists a group of functions that help to create regression kernels for some GE genomic models proposed by Jarquín et al. (2014) <doi:10.1007/s00122-013-2243-1> and Lopez-Cruz et al. (2015) <doi:10.1534/g3.114.016097>. Also, it computes genomic predictions based on Bayesian approaches. The prediction function uses an orthogonal transformation of the data and specific priors present by Cuevas et al. (2014) <doi:10.1534/g3.114.013094>. / GPL-3	noarch
<a href="#">r-bgmfiles</a>	0.0.6	A collection of box-geometry model (BGM) files for the Atlantis ecosystem model. Atlantis is a deterministic, biogeochemical, whole-of-ecosystem model (see < <a href="http://atlantis.cmar.csiro.au/">http://atlantis.cmar.csiro.au/</a> > for more information). / CC0	noarch
<a href="#">r-bgphazard</a>	1.2.3	Computes the hazard rate estimate as described by Nieto-Barajas and Walker (2002) and Nieto-Barajas (2003). / GPL (>= 2)	noarch
<a href="#">r-bgsimd</a>	1.0	Implement an efficient block Gibbs sampler with incomplete data from a multinomial distribution taking values from the k categories 1,2,...,k, where data are assumed to miss at random and each missing datum belongs to one and only one of m distinct non-empty proper subsets A1, A2,..., Am of 1,2,...,k and the k categories are labelled such that only consecutive A's may overlap. / GPL (>= 2)	noarch
<a href="#">r-bh</a>	1.69.0	Boost provides free peer-reviewed portable C source libraries. A large part of Boost is provided as C template code which is resolved entirely at compile-time without linking. This package aims to provide the most useful subset of Boost libraries for template use among CRAN package. By placing these libraries in this package, we offer a more efficient distribution system for CRAN as replication of this code in the sources of other packages is avoided. As of release 1.69.0-1, the following Boost libraries are included: 'algorithm' 'align' 'any' 'atomic' 'bimap' 'bind' 'circular_buffer' 'compute' 'concept' 'config' 'container' 'date_time' 'detail' 'dynamic_bitset' 'exception' 'filesystem' 'flyweight' 'foreach' 'functional' 'fusion' 'geometry' 'graph' 'heap' 'icl' 'integer' 'interprocess' 'intrusive' 'io' 'iostreams' 'iterator' 'math' 'move' 'mpl' 'multiprecision' 'numeric' 'pending' 'phoenix' 'preprocessor' 'property_tree' 'random' 'range' 'scope_exit' 'smart_ptr' 'sort' 'spirit' 'tuple' 'type_traits' 'typeof' 'unordered' 'utility' 'uuid'. / BSL-1.0	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-bhat</a>	0.9_10	Functions for MLE, MCMC, CIs (originally in Fortran) / GPL (>= 2)	noarch
<a href="#">r-bhh2</a>	2016.05.11	Functions and data sets reproducing some examples in Box, Hunter and Hunter II. Useful for statistical design of experiments, especially factorial experiments. / GPL (>= 2)	noarch
<a href="#">r-bhm</a>	1.15	Contains tools to fit both predictive and prognostic biomarker effects using biomarker threshold models. Evaluate the treatment effect, biomarker effect and treatment-biomarker interaction using probability index measurement. Test for treatment-biomarker interaction using residual bootstrap method. / GPL (>= 2)	noarch
<a href="#">r-bhsbvar</a>	1.0.4	Provides a function for estimating the parameters of Structural Bayesian Vector Autoregression models with the method developed by Baumeister and Hamilton (2015) <doi:10.3982/ECTA12356>, Baumeister and Hamilton (2017) <doi:10.3386/w24167>, and Baumeister and Hamilton (2018) <doi:10.1016/j.jmoneco.2018.06.005>. Functions for plotting impulse responses, historical decompositions, and posterior distributions of model parameters are also provided. / GPL (>= 3)	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-biasedurn</a>	1.07	Statistical models of biased sampling in the form of univariate and multivariate noncentral hypergeometric distributions, including Wallenius' noncentral hypergeometric distribution and Fisher's noncentral hypergeometric distribution (also called extended hypergeometric distribution). See vignette(UrnTheory) for explanation of these distributions. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-bibplots</a>	0.0.6	Currently, the package provides four functions for plotting and analyzing bibliometric data (JIF, Journal Impact Factor, and paper percentile values), beam-plots with citations, and two plot function to visualize the result of a reference publication year spectroscopy (RPYS) analysis performed in the free software 'CRExplorer' (see < <a href="http://crexplorer.net">http://crexplorer.net</a> >). Further extension to more plot variants is planned. / EUPL	noarch
<a href="#">r-bibtex</a>	0.4.2	Utility to parse a bibtex file. / GPL (>= 2)	linux-64, osx-64, win-32, win-64
<a href="#">r-biclique</a>	1.0.3	A tool for enumerating maximal complete bipartite graphs. The input should be a edge list file or a binary matrix file. The output are maximal complete bipartite graphs. Algorithms used can be found in this paper Y Zhang et al. BMC Bioinformatics 2014 15:110 <doi:10.1186/1471-2105-15-110>. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-bicorn</a>	0.1.0	Prior transcription factor binding knowledge and target gene expression data are integrated in a Bayesian framework for functional cis-regulatory module inference. Using Gibbs sampling, we iteratively estimate transcription factor associations for each gene, regulation strength for each binding event and the hidden activity for each transcription factor. / GPL-2	noarch
<a href="#">r-bidimregression</a>	2.0.0	Calculates the bidimensional regression between two 2D configurations following the approach by Tobler (1965). / GPL-3	noarch
<a href="#">r-bife</a>	0.6	Estimates fixed effects binary choice models (logit and probit) with potentially many individual fixed effects and computes average partial effects. Incidental parameter bias can be reduced with an asymptotic bias-correction proposed by Fernandez-Val (2009) <doi:10.1016/j.jeconom.2009.02.007>. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-bigalgebra</a>	0.8.4	This package provides arithmetic functions for R matrix and big.matrix objects. / LGPL-3	linux-64, osx-64, win-64
<a href="#">r-biganalytics</a>	1.1.14	Extend the 'bigmemory' package with various analytics. Functions 'big-means' and 'binit' may also be used with native R objects. For 'tapply'-like functions, the bigtabulate package may also be helpful. For linear algebra support, see 'bigalgebra'. For mutex (locking) support for advanced shared-memory usage, see 'synchronicity'. / LGPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-bigintegers</a>	0.1.2	Features the multiple polynomial quadratic sieve algorithm for factoring large integers and a vectorized factoring function that returns the complete factorization of an integer. Utilizes the C library GMP (GNU Multiple Precision Arithmetic) and classes created by Antoine Lucas et al. found in the ‘gmp’ package. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-bigm</a>	0.9_1	Regression for data too large to fit in memory / GPL-3	linux-64, osx-64, win-64
<a href="#">r-biglm</a>	0.9_1	Regression for data too large to fit in memory. This package functions exactly like the ‘biglm’ package, but works with later versions of R. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-bigmap</a>	2.1.0	Unsupervised clustering protocol for large scale structured data, based on a low dimensional representation of the data. Dimensionality reduction is performed using a parallelized implementation of the t-Stochastic Neighboring Embedding algorithm (Garriga J. and Bartumeus F. (2018), <arXiv:1812.09869>). / GPL-3	linux-64, osx-64
<a href="#">r-bigmemory</a>	4.5.33	Create, store, access, and manipulate massive matrices. Matrices are allocated to shared memory and may use memory-mapped files. Packages ‘biganalytics’, ‘bigtabulate’, ‘synchronicity’, and ‘bigalgebra’ provide advanced functionality. / LGPL-3	linux-64, osx-64, win-64
<a href="#">r-bigmemory.sri</a>	0.1.3	This package provides a shared resource interface for the bigmemory and synchronicity packages. / LGPL-3	noarch
<a href="#">r-bigml</a>	0.1.2	The ‘bigml’ package contains bindings for the BigML API. The package includes methods that provide straightforward access to basic API functionality, as well as methods that accommodate idiomatic R data types and concepts. / LGPL-3	noarch
<a href="#">r-bigreadr</a>	0.1.9	Read large text files by splitting them in smaller files. Package bigreadr also provides some convenient wrappers of fread/fwrite. / GPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-bigreg	0.1.2	Allows the user to carry out GLM on very large data sets. Data can be created using the <code>data_frame()</code> function and appended to the object with <code>object\$append(data)</code> ; <code>data_frame</code> and <code>data_matrix</code> objects are available that allow the user to store large data on disk. The data is stored as doubles in binary format and any character columns are transformed to factors and then stored as numeric (binary) data while a look-up table is stored in a separate <code>.meta_data</code> file in the same folder. The data is stored in blocks and GLM regression algorithm is modified and carries out a MapReduce-like algorithm to fit the model. The functions <code>bglm()</code> , and <code>summary()</code> and <code>bglm_predict()</code> are available for creating and post-processing of models. The library requires Armadillo installed on your system. It probably won't function on windows since multi-core processing is done using <code>mclapply()</code> which forks R on Unix/Linux type operating systems. / GPL-2	linux-64, osx-64
r-bigsplines	1.1_1	Fits smoothing spline regression models using scalable algorithms designed for large samples. Seven marginal spline types are supported: linear, cubic, different cubic, cubic periodic, cubic thin-plate, ordinal, and nominal. Random effects and parametric effects are also supported. Response can be Gaussian or non-Gaussian: Binomial, Poisson, Gamma, Inverse Gaussian, or Negative Binomial. / GPL-2	linux-64, osx-64, win-64
r-bigtabulate	1.1.5	Extend the bigmemory package with 'table', 'tapply', and 'split' support for 'big.matrix' objects. The functions may also be used with native R matrices for improving speed and memory-efficiency. / LGPL-3	linux-64, osx-64, win-64
r-bigtcr	1.1	For studying recurrent disease and death with competing risks, comparisons based on the well-known cumulative incidence function can be confounded by different prevalence rates of the competing events. Alternatively, comparisons of the conditional distribution of the survival time given the failure event type are more relevant for investigating the prognosis of different patterns of recurrence disease. This package implements a nonparametric estimator for the conditional cumulative incidence function and a nonparametric conditional bivariate cumulative incidence function for the bivariate gap times proposed in Huang et al. (2016) <doi:10.1111/biom.12494>. / GPL-3	linux-64, osx-64, win-64
r-bigtime	0.1.0	Estimation of large Vector AutoRegressive (VAR), Vector AutoRegressive with Exogenous Variables X (VARX) and Vector AutoRegressive Moving Average (VARMA) Models with Structured Lasso Penalties, see Nicholson, Bien and Matteson (2017) <arXiv:1412.5250v2> and Wilms, Basu, Bien and Matteson (2017) <arXiv:1707.09208>. / GPL-2	linux-64, osx-64, win-64
r-bigvar	1.0.4	Estimates VAR and VARX models with structured Lasso Penalties. / GPL-2	linux-64, osx-64, win-64
r-bikeshare14	0.1.2	Anonymised Bay Area bike share trip data for the year 2014. Also contains additional metadata on stations and weather. / CC0	noarch

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Name	Version	Summary/License	Platforms
r-bild	1.1_5	Performs logistic regression for binary longitudinal data, allowing for serial dependence among observations from a given individual and a random intercept term. Estimation is via maximization of the exact likelihood of a suitably defined model. Missing values and unbalanced data are allowed, with some restrictions. / GPL-2	linux-64, osx-64, win-64
r-bimetallic	1.0	A power calculator for Genome-wide association studies (GWAs) with combined gold (error-free) and silver (erroneous) phenotyping per McDavid A, Crane PK, Newton KM, Crosslin DR, et al. (2011) / GPL-2	noarch
r-bimets	1.4.0	Time series analysis, (dis)aggregation and manipulation, e.g. time series extension, merge, projection, lag, lead, delta, moving and cumulative average and product, selection by index, date and year-period, conversion to daily, monthly, quarterly, (semi)annually. Simultaneous equation models definition, estimation, simulation and forecasting with coefficient restrictions, error autocorrelation, exogenization, add-factors, impact and interim multipliers analysis, conditional equation evaluation, endogenous targeting and model renormalization. / EUPL	noarch
r-bimixt	1.0	Estimates non-Gaussian mixture models of case-control data. The four types of models supported are binormal, two component constrained, two component unconstrained, and four component. The most general model is the four component model, under which both cases and controls are distributed according to a mixture of two unimodal distributions. In the four component model, the two component distributions of the control mixture may be distinct from the two components of the case mixture distribution. In the two component unconstrained model, the components of the control and case mixtures are the same; however the mixture probabilities may differ for cases and controls. In the two component constrained model, all controls are distributed according to one of the two components while cases follow a mixture distribution of the two components. In the binormal model, cases and controls are distributed according to distinct unimodal distributions. These models assume that Box-Cox transformed case and control data with a common lambda parameter are distributed according to Gaussian mixture distributions. Model parameters are estimated using the expectation-maximization (EM) algorithm. Likelihood ratio test comparison of nested models can be performed using the lr.test function. AUC and PAUC values can be computed for the model-based and empirical ROC curves using the auc and pauc functions, respectively. The model-based and empirical ROC curves can be graphed using the roc.plot function. Finally, the model-based density estimates can be visualized by plotting a model object created with the bimixt.model function. / GPL-3	noarch
r-binarize	1.3	Provides methods for the binarization of one-dimensional data and some visualization functions. / Artistic-2.0	linux-64, osx-64, win-64
r-binaryemvs	0.1	Implements variable selection for high dimensional datasets with a binary response variable using the EM algorithm. Both probit and logit models are supported. Also included is a useful function to generate high dimensional data with correlated variables. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-binarylogic</a>	0.3.9	Provides the binary S3 class. The instance of binary is used to convert a decimal number (Base10) to a binary number (Base2). The Class provides some features e.G. shift(), rotate(), summary(). Based on logical vectors. / GPL-3	noarch
<a href="#">r-binb</a>	0.0.4	A collection of ‘LaTeX’ styles using ‘Beamer’ customization for pdf-based presentation slides in ‘RMarkdown’. At present it contains ‘RMarkdown’ adaptations of the LaTeX themes ‘Metropolis’ (formerly ‘mtheme’) theme by Matthias Vogelgesang and others (now included in ‘TeXLive’), the ‘IQSS’ by Ista Zahn (which is included here), and the ‘Monash’ theme by Rob J Hyndman. Additional (free) fonts may be needed: ‘Metropolis’ prefers ‘Fira’, and ‘IQSS’ requires ‘Libertinus’. / GPL-2	noarch
<a href="#">r-binda</a>	1.0.3	The binda package implements functions for multi-class discriminant analysis using binary predictors, for corresponding variable selection, and for dichotomizing continuous data. / GPL-3	noarch
<a href="#">r-bindata</a>	0.9_1	Generation of correlated artificial binary data. / GPL-2	noarch
<a href="#">r-bindr</a>	0.1.1	Provides a simple interface for creating active bindings where the bound function accepts additional arguments. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-bindrcpp</a>	0.2.2	Provides an easy way to fill an environment with active bindings that call a C function. / MIT file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-binford</a>	0.1.0	Binford’s hunter-gatherer data includes more than 200 variables coding aspects of hunter-gatherer subsistence, mobility, and social organization for 339 ethnographically documented groups of hunter-gatherers. / GPL-3	noarch
<a href="#">r-binmto</a>	0.0_7	Asymptotic simultaneous confidence intervals for comparison of many treatments with one control, for the difference of binomial proportions, allows for Dunnett-like-adjustment, Bonferroni or unadjusted intervals. Simulation of power of the above interval methods, approximate calculation of any-pair-power, and sample size iteration based on approximate any-pair power. Exact conditional maximum test for many-to-one comparisons to a control. / GPL-2	noarch
<a href="#">r-binnonnor</a>	1.5.1	Generation of multiple binary and continuous non-normal variables simultaneously given the marginal characteristics and association structure based on the methodology proposed by Demirtas et al. (2012) <DOI:10.1002/sim.5362>. / GPL-2   GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-binnor	2.3.1	Generating multiple binary and normal variables simultaneously given marginal characteristics and association structure based on the methodology proposed by Demirtas and Doganay (2012) <DOI:10.1080/10543406.2010.521874>. / GPL-2	noarch
r-binom	1.1_1	Constructs confidence intervals on the probability of success in a binomial experiment via several parameterizations / GPL-3	linux-64, osx-64, win-64
r-binomialcftp	1.0	Binomial random numbers are generated via the perfect sampling algorithm. At each iteration dual markov chains are generated and coalescence is checked. In case coalescence occurs, the resulting number is outputted. In case not, then the algorithm is restarted from $T(t)=2*T(t)$ until coalescence occurs. / GPL-2	noarch
r-binomlogit	1.2	The R package contains different MCMC schemes to estimate the regression coefficients of a binomial (or binary) logit model within a Bayesian framework: a data-augmented independence MH-sampler, an auxiliary mixture sampler and a hybrid auxiliary mixture (HAM) sampler. All sampling procedures are based on algorithms using data augmentation, where the regression coefficients are estimated by rewriting the logit model as a latent variable model called difference random utility model (dRUM). / GPL-3	noarch
r-binomsamsize	0.1_5	A suite of functions to compute confidence intervals and necessary sample sizes for the parameter p of the Bernoulli B(p) distribution under simple random sampling or under pooled sampling. Such computations are e.g. of interest when investigating the incidence or prevalence in populations. The package contains functions to compute coverage probabilities and coverage coefficients of the provided confidence intervals procedures. Sample size calculations are based on expected length. / GPL-3	linux-64, osx-64, win-64
r-binostics	0.1.2	Calculates graph theoretic scagnostics. Scagnostics describe various measures of interest for pairs of variables, based on their appearance on a scatterplot. They are useful tool for discovering interesting or unusual scatterplots from a scatterplot matrix, without having to look at every individual plot. / GPL-3	linux-64, osx-64, win-64
r-binr	1.1	Implementation of algorithms for cutting numerical values exhibiting a potentially highly skewed distribution into evenly distributed groups (bins). This functionality can be applied for binning discrete values, such as counts, as well as for discretization of continuous values, for example, during generation of features used in machine learning algorithms. / Apache License (== 2.0)	noarch
r-binseqtest	1.0.3	For a series of binary responses, create stopping boundary with exact results after stopping, allowing updating for missing assessments. / GPL-3	noarch
r-binst	0.2.1	Various supervised and unsupervised binning tools including using entropy, recursive partition methods and clustering. / MIT	noarch
r-bio.infer	1.3_3	Imports benthic count data, reformats this data, and computes environmental inferences from this data. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-bio3d</a>	2.3_4	Utilities to process, organize and explore protein structure, sequence and dynamics data. Features include the ability to read and write structure, sequence and dynamic trajectory data, perform sequence and structure database searches, data summaries, atom selection, alignment, superposition, rigid core identification, clustering, torsion analysis, distance matrix analysis, structure and sequence conservation analysis, normal mode analysis, principal component analysis of heterogeneous structure data, and correlation network analysis from normal mode and molecular dynamics data. In addition, various utility functions are provided to enable the statistical and graphical power of the R environment to work with biological sequence and structural data. Please refer to the URLs below for more information. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-biocircos</a>	0.3.4	Implement in 'R' interactive Circos-like visualizations of genomic data, to map information such as genetic variants, genomic fusions and aberrations to a circular genome, as proposed by the 'JavaScript' library 'BioCircos.js', based on the 'jQuery' and 'D3' technologies. The output is by default displayed in stand-alone HTML documents or in the 'RStudio' viewer pane. Moreover it can be integrated in 'R Markdown' documents and 'Shiny' applications. / GPL-2	noarch
<a href="#">r-biocmanager</a>	1.30.4	A convenient tool to install and update Bioconductor packages. / Artistic-2.0	noarch
<a href="#">r-biodem</a>	0.4	The Biodem package provides a number of functions for Biodemographic analysis. / GPL-2	noarch
<a href="#">r-biodry</a>	0.6	Multilevel ecological data series (MEDS) are sequences of observations ordered according to temporal/spatial hierarchies that are defined by sample designs, with sample variability confined to ecological factors. Dendroclimatic MEDS of tree rings and climate are modeled into normalized fluctuations of tree growth and aridity. Modeled fluctuations (model frames) are compared with Mantel correlograms on multiple levels defined by sample design. Package implementation can be understood by running examples in modelFrame(), and muleMan() functions. / GPL-3	noarch
<a href="#">r-bioftf</a>	1.2_0	The main drawback of the most common biodiversity indices is that different measures may lead to different rankings among communities. This instrument overcomes this limit using some functional tools with the diversity profiles. In particular, the derivatives, the curvature, the radius of curvature, the arc length, and the surface area are proposed. The goal of this method is to interpret in detail the diversity profiles and obtain an ordering between different ecological communities on the basis of diversity. In contrast to the typical indices of diversity, the proposed method is able to capture the multidimensional aspect of biodiversity, because it takes into account both the evenness and the richness of the species present in an ecological community. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-biogas	1.10.3	High- and low-level functions for processing biogas data and predicting biogas production. Molar mass and calculated oxygen demand (COD') can be determined from a chemical formula. Measured gas volume can be corrected for water vapor and to (possibly user-defined) standard temperature and pressure. Gas quantity can be converted between volume, mass, and moles. Gas composition, cumulative production, or other variables can be interpolated to a specified time. Cumulative biogas and methane production (and rates) can be calculated using volumetric, manometric, or gravimetric methods for any number of reactors. With cumulative methane production data and data on reactor contents, biochemical methane potential (BMP) can be calculated and summarized, including subtraction of the inoculum contribution and normalization by substrate mass. Cumulative production and production rates can be summarized in several different ways (e.g., omitting normalization) using the same function. Biogas quantity and composition can be predicted from substrate composition and additional, optional data. Lastly, inoculum and substrate mass can be determined for planning BMP experiments. / GPL-2	noarch
r-biom.utils	0.9	Provides utilities to facilitate import, export and computation with the BIOM (Biological Observation Matrix) format ( <a href="http://biom-format.org">http://biom-format.org</a> ). / BSD_2_clause	noarch
r-bionetdata	1.0.1	Data Package that includes several examples of chemical and biological data networks, i.e. data graph structured. / GPL-2	noarch
r-biopn	1.2.0	bioPN is a package suited to perform simulation of deterministic and stochastic systems of biochemical reaction networks. Models are defined using a subset of Petri Nets, in a way that is close at how chemical reactions are defined. For deterministic solutions, bioPN creates the associated system of differential equations on the fly, and solves it with a Runge Kutta Dormand Prince 45 explicit algorithm. For stochastic solutions, bioPN offers variants of Gillespie algorithm, or SSA. For hybrid deterministic/stochastic, it employs the Haseltine and Rawlings algorithm, that partitions the system in fast and slow reactions. bioPN algorithms are developed in C to achieve adequate performance. / GPL-2	linux-64, osx-64, win-64
r-bios2cor	1.2	Utilities for computation and analysis of correlation/co-variation in multiple sequence alignments and in side chain motions during molecular dynamics simulations. Features include the computation of correlation/co-variation scores using a variety of scoring functions between either sequence positions in alignments or side chain dihedral angles in molecular dynamics simulations and to analyze the correlation/co-variation matrix through a variety of tools including network representation and principal components analysis. In addition, several utility functions are based on the R graphical environment to provide friendly tools for help in data interpretation. Examples of sequence co-variation analysis and utility tools are provided in: Pele J, Moreau M, Abdi H, Rodien P, Castel H, Chabbert M. (2014) <doi:10.1002/prot.24570>. This work was supported by the French National Research Agency (Grant number: ANR-11-BSV2-026). / GPL-2	noarch
r-biotic	0.1.2	Calculates a range of UK freshwater invertebrate biotic indices including BMWP, Whalley, WHPT, Habitat-specific BMWP, AWIC, LIFE and PSI. / GPL-3	noarch
r-birk	2.1.2	Collection of tools to make R more convenient. Includes tools to summarize data using statistics not available with base R and manipulate objects for analyses. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-birt</a>	1.0.0	R functions for The Basics of Item Response Theory Using R by Frank B. Baker and Seock-Ho Kim (Springer, 2017, ISBN-13: 978-3-319-54204-1) including iccplot(), icccal(), icc(), iccfit(), groupinv(), tcc(), ability(), tif(), and rasch(). For example, iccplot() plots an item characteristic curve under the two-parameter logistic model. / GPL-2	noarch
<a href="#">r-bisect</a>	0.9.0	An implementation of Bisect, a method for inferring cell type composition of samples based on methylation sequencing data (Whole Genome Bisulfite Sequencing and Reduced Representation Sequencing). The method is specifically tailored for sequencing data, and therefore works better than methods developed for methylation arrays. It contains a supervised mode that requires a reference (the methylation probabilities in the pure cell types), and a semi-supervised mode, that requires cell counts for a subset of the samples, but does not require a reference. / GPL-3	noarch
<a href="#">r-bisectr</a>	0.1.0	Tools to find bad commits with git bisect. See <a href="https://github.com/wch/bisectr">https://github.com/wch/bisectr</a> for examples and test script templates. / GPL-2	noarch
<a href="#">r-bisrma</a>	0.2.2	Bisulfite-treated RNA non-conversion in a set of samples is analysed as follows : each sample's non-conversion distribution is identified to a Poisson distribution. P-values adjusted for multiple testing are calculated in each sample. Combined non-conversion P-values and standard errors are calculated on the intersection of the set of samples. For further details, see C Legrand, F Tuorto, M Hartmann, R Liebers, D Jakob, M Helm and F Lyko (2017) <doi:10.1101/gr.210666.116>. / GPL-2	noarch
<a href="#">r-bit</a>	1.1_1	Bitmapped vectors of booleans (no NAs), coercion from and to logicals, integers and integer subscripts; fast boolean operators and fast summary statistics. With 'bit' vectors you can store true binary booleans {FALSE,TRUE} at the expense of 1 bit only, on a 32 bit architecture this means factor 32 less RAM and ~ factor 32 more speed on boolean operations. Due to overhead of R calls, actual speed gain depends on the size of the vector: expect gains for vectors of size > 10000 elements. Even for one-time boolean operations it can pay-off to convert to bit, the pay-off is obvious, when such components are used more than once. Reading from and writing to bit is approximately as fast as accessing standard logicals - mostly due to R's time for memory allocation. The package allows to work with pre-allocated memory for return values by calling .Call() directly: when evaluating the speed of C-access with pre-allocated vector memory, coping from bit to logical requires only 70% of the time for copying from logical to logical; and copying from logical to bit comes at a performance penalty of 150%. the package now contains further classes for representing logical selections: 'bitwhich' for very skewed selections and 'ri' for selecting ranges of values for chunked processing. All three index classes can be used for subsetting 'ff' objects (ff-2.1-0 and higher). / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-bit64</a>	0.9_7	Package 'bit64' provides serializable S3 atomic 64bit (signed) integers. These are useful for handling database keys and exact counting in $-2^{63}$ . WARNING: do not use them as replacement for 32bit integers, integer64 are not supported for subscripting by R-core and they have different semantics when combined with double, e.g. integer64 double => integer64. Class integer64 can be used in vectors, matrices, arrays and data.frames. Methods are available for coercion from and to logicals, integers, doubles, characters and factors as well as many elementwise and summary functions. Many fast algorithmic operations such as 'match' and 'order' support inter- active data exploration and manipulation and optionally leverage caching. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
r-bitops	1.0.6	Functions for bitwise operations on integer vectors. / GPL ( $\geq 2$ )	linux-32, linux-64, osx-64, win-32, win-64
r-bittrina	1.3	Provides methods for the binarization and trinarization of one-dimensional data and some visualization functions. / Artistic-2.0	linux-64, osx-64, win-64
r-bitrugs	0.1	MCMC methods to estimate transmission dynamics and infection routes in hospitals using genomic sampling data. / GPL-3	linux-64, osx-64, win-64
r-bitsqueezr	0.1.0	Provides a implementation of floating-point quantization algorithms for use in precision-preserving compression, similar to the approach taken in the ‘netCDF operators’ (NCO) software package and described in Zender (2016) <doi:10.5194/gmd-2016-63>. / GPL-3	linux-64, osx-64, win-64
r-bivariate.pareto	1.0.2	Perform competing risks analysis under bivariate Pareto models. See Shih et al. (2018) <doi:10.1080/03610926.2018.1425450> for details. / GPL-2	noarch
r-bivarp	1.0	Parameter estimation of bivariate distribution functions modeled as a Archimedean copula function. The input data may contain values from right censored. Used marginal distributions are two-parameter. Methods for density, distribution, survival, random sample generation. / GPL-3	noarch
r-bivarripower	1.2	Implements sample size calculations for bivariate random intercept regression model that are described in Comulada and Weiss (2010) / GPL-2	noarch
r-bivgeo	2.0.1	Computes the joint probability mass function (pmf), the joint cumulative function (cdf), the joint survival function (sf), the correlation coefficient, the covariance, the cross-factorial moment and generate random deviates for the Basu-Dhar bivariate geometric distribution as well the joint probability mass, cumulative and survival function assuming the presence of a cure fraction given by the standard bivariate mixture cure fraction model. The package also computes the estimators based on the method of moments. / GPL-2	noarch
r-bivgeom	1.0	Implements Roy’s bivariate geometric model (Roy (1993) <doi:10.1006/jmva.1993.1065>): joint probability mass function, distribution function, survival function, random generation, parameter estimation, and more. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-bivrec	1.0.0	Alternating recurrent event data arise frequently in biomedical and social sciences where 2 types of events such as hospital admissions and discharge occur alternatively over time. As such we implement a collection of non-parametric and semiparametric methods to analyze such data. The main functions are <code>biv.rec.fit()</code> and <code>biv.rec.np()</code> . Use <code>biv.rec.fit()</code> for estimation of covariate effects on the two alternating event gap times ( $x_{ij}$ and $y_{ij}$ ) using semiparametric methods. The method options are Lee.et.al and Chang. Use <code>biv.rec.np()</code> for estimation of the joint cumulative distribution function (cdf) for the two alternating events gap times ( $x_{ij}$ and $y_{ij}$ ) as well as the marginal survival function for type I gap times ( $x_{ij}$ ) and the conditional cdf of the type II gap times ( $y_{ij}$ ) given an interval of type I gap times ( $x_{ij}$ ) in a non-parametric fashion. The package also provides options to simulate and visualize the data and results of analysis. / GPL-3	linux-64, osx-64, win-64
r-bizdays	1.0.6	Business days calculations based on a list of holidays and nonworking weekdays. Quite useful for fixed income and derivatives pricing. / MIT	noarch
r-bkpc	1.0.1	Bayesian kernel projection classifier is a nonlinear multiclass classifier which performs the classification of the projections of the data to the principal axes of the feature space. A Gibbs sampler is implemented to find the posterior distributions of the parameters. / GPL-2	linux-64, osx-64, win-64
r-blakerci	1.0_6	Fast and accurate calculation of Blaker's binomial and Poisson confidence limits (and some related stuff). / GPL-3	noarch
r-blandaltmanleh	0.3.1	Bland-Altman Plots using either base graphics or ggplot2, augmented with confidence intervals, with detailed return values and a sunflowerplot option for data with ties. / GPL-3	noarch
r-blattr	1.0.1	A wrapper around the 'Blat' command line SMTP mailer for Windows. 'Blat' is public domain software, but be sure to read the license before use. It can be found at the Blat website <a href="http://www.blatt.net">http://www.blatt.net</a> . / MIT	win-64
r-blendedlink	1.0	A new link function that equals one specified link function up to a cutover then a linear rescaling of another specified link function. For use in <code>glm()</code> or <code>glm2()</code> . The intended use is in binary regression, in which case the first link should be set to log and the second to logit. This ensures that fitted probabilities are between 0 and 1 and that exponentiated coefficients can be interpreted as relative risks for probabilities up to the cutoff. / GPL-2   GPL-3	noarch
r-blendstat	1.0.2	Performs a joint analysis of experiments with mixtures and random effects, taking on a process variable represented by a covariable. / GPL-2	noarch
r-blin	0.0.1	Estimate influence networks from longitudinal bipartite relational data, where the longitudinal relations are continuous. The outputs are estimates of weighted influence networks among each actor type in the data set. The generative model is the Bipartite Longitudinal Influence Network (BLIN) model, a linear autoregressive model for these type of data. The supporting paper is "Inferring Influence Networks from Longitudinal Bipartite Relational Data", which is in preparation by the same authors. The model may be estimated using maximum likelihood methods and Bayesian methods. For more detail on methods, see Marrs et. al. <arXiv:1809.03439>. / MIT	noarch
r-blmm	2013.1	Implements regression models for binary data on the absolute risk scale. These models are applicable to cohort and population-based case-control data. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-blme</a>	1.0.4	Maximum a posteriori estimation for linear and generalized linear mixed-effects models in a Bayesian setting. Extends ‘lme4’ by Douglas Bates, Martin Maechler, Ben Bolker, and Steve Walker. / GPL-2	noarch
<a href="#">r-blmodel</a>	1.0.2	Posterior distribution in the Black-Litterman model is computed from a prior distribution given in the form of a time series of asset returns and a continuous distribution of views provided by the user as an external function. / GNU General Public License version 3	noarch
<a href="#">r-blob</a>	1.1.1	R’s raw vector is useful for storing a single binary object. What if you want to put a vector of them in a data frame? The ‘blob’ package provides the blob object, a list of raw vectors, suitable for use as a column in data frame. / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-blockfest</a>	1.6	An R implementation of an extension of the ‘BayeScan’ software (Foll, 2008) <DOI:10.1534/genetics.108.092221> for codominant markers, adding the option to group individual SNPs into pre-defined blocks. A typical application of this new approach is the identification of genomic regions, genes, or gene sets containing one or more SNPs that evolved under directional selection. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-blockforest</a>	0.2.3	A random forest variant ‘block forest’ (‘BlockForest’) tailored to the prediction of binary, survival and continuous outcomes using block-structured covariate data, for example, clinical covariates plus measurements of a certain omics data type or multi-omics data, that is, data for which measurements of different types of omics data and/or clinical data for each patient exist. Examples of different omics data types include gene expression measurements, mutation data and copy number variation measurements. Block forest are presented in Hornung & Wright (2019). The package includes four other random forest variants for multi-omics data: ‘RandomBlock’, ‘BlockVarSel’, ‘VarProb’, and ‘SplitWeights’. These were also considered in Hornung & Wright (2019), but performed worse than block forest in their comparison study based on 20 real multi-omics data sets. Therefore, we recommend to use block forest (‘BlockForest’) in applications. The other random forest variants can, however, be consulted for academic purposes, for example, in the context of further methodological developments. Reference: Hornung, R. & Wright, M. N. (2019) Block Forests: random forests for blocks of clinical and omics covariate data. BMC Bioinformatics 20:358. <doi:10.1186/s12859-019-2942-y>. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-blockmatrix</a>	1.0	Some elementary matrix algebra tools are implemented to manage block matrices or partitioned matrix, i.e. matrix of matrices ( <a href="http://en.wikipedia.org/wiki/Block_matrix">http://en.wikipedia.org/wiki/Block_matrix</a> ). The block matrix is here defined as a new S3 object. In this package, some methods for matrix object are rewritten for blockmatrix object. New methods are implemented. This package was created to solve equation systems with block matrices for the analysis of environmental vector time series. Bugs/comments/questions/collaboration of any kind are warmly welcomed. / GPL-2	noarch
<a href="#">r-blockmessage</a>	1.0	Creates strings that show a text message in 8 by 8 block letters / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-blockmodeling</a>	0.3.4	This is primarily meant as an implementation of generalized block-modeling for valued networks. In addition, measures of similarity or dissimilarity based on structural equivalence and regular equivalence (REGE algorithms) can be computed and partitioned matrices can be plotted: Žiberna (2007)<doi:10.1016/j.socnet.2006.04.002>, Žiberna (2008)<doi:10.1080/00222500701790207>, Žiberna (2014)<doi:10.1016/j.socnet.2014.04.002>. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-blockmodels</a>	1.1.1	Latent and Stochastic Block Model estimation by a Variational EM algorithm. Various probability distribution are provided (Bernoulli, Poisson...), with or without covariates. / LGPL-2.1	linux-64, osx-64, win-64
<a href="#">r-blockrand</a>	1.3	Create randomizations for block random clinical trials. Can also produce a pdf file of randomization cards. / GPL-2	noarch
<a href="#">r-blocksdesign</a>	3.5	Constructs D-optimal or near D-optimal nested and crossed block designs for unstructured or general factorial treatment designs. The treatment design, if required, is found from a model matrix design formula and can be added sequentially, if required. The block design is found from a defined set of block factors and is conditional on the defined treatment design. The block factors are added in sequence and each added block factor is optimized conditional on all previously added block factors. The block design can have repeated nesting down to any required depth of nesting with either simple nested blocks or a crossed blocks design at each level of nesting. Outputs include a table showing the allocation of treatments to blocks and tables showing the achieved D-efficiency factors for each block and treatment design. / GPL-2	noarch
<a href="#">r-blr</a>	1.5	Bayesian Linear Regression. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-blrpm</a>	1.0	Due to a limited availability of observed high-resolution precipitation records with adequate length, simulations with stochastic precipitation models are used to generate series for subsequent studies [e.g. Khaliq and Cunmae, 1996, <doi:10.1016/0022-1694(95)02894-3>, Vandenberghe et al., 2011, <doi:10.1029/2009WR008388>]. This package contains an R implementation of the original Bartlett-Lewis rectangular pulse model (BLRPM), developed by Rodriguez-Iturbe et al. (1987) <doi:10.1098/rspa.1987.0039>. It contains a function for simulating a precipitation time series based on storms and cells generated by the model with given or estimated model parameters. Additionally BLRPM parameters can be estimated from a given or simulated precipitation time series. The model simulations can be plotted in a three-layer plot including an overview of generated storms and cells by the model (which can also be plotted individually), a continuous step-function and a discrete precipitation time series at a chosen aggregation level. / GPL-2	noarch
<a href="#">r-blsapi</a>	0.2.1	Allows users to request data for one or multiple series through the U.S. Bureau of Labor Statistics API. Users provide parameters as specified in < <a href="https://www.bls.gov/developers/api_signature.htm">https://www.bls.gov/developers/api_signature.htm</a> > and the function returns a JSON string. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-blsm</a>	0.1.0	Provides a Bayesian latent space model for complex networks, either weighted or unweighted. Given an observed input graph, the estimates for the latent coordinates of the nodes are obtained through a Bayesian MCMC algorithm. The overall likelihood of the graph depends on a fundamental probability equation, which is defined so that ties are more likely to exist between nodes whose latent space coordinates are close. The package is mainly based on the model by Hoff, Raftery and Handcock (2002) <doi:10.1198/016214502388618906> and contains some extra features (e.g., removal of the Procrustean step, weights implemented as coefficients of the latent distances, 3D plots). The original code related to the above model was retrieved from < <a href="https://www.stat.washington.edu/people/pdhoff/Code/hoff_raftery_handcock_2002_jasa/">https://www.stat.washington.edu/people/pdhoff/Code/hoff_raftery_handcock_2002_jasa/</a> >. Users can inspect the MCMC simulation, create and customize insightful graphical representations or apply clustering techniques. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-bmamevt</a>	1.0.3	Toolkit for Bayesian estimation of the dependence structure in multivariate extreme value parametric models. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-bmass</a>	1.0.3	Multivariate tool for analyzing genome-wide association study results in the form of univariate summary statistics. The goal of ‘bmass’ is to comprehensively test all possible multivariate models given the phenotypes and datasets provided. Multivariate models are determined by assigning each phenotype to being either Unassociated (U), Directly associated (D) or Indirectly associated (I) with the genetic variant of interest. Test results for each model are presented in the form of Bayes factors, thereby allowing direct comparisons between models. The underlying framework implemented here is based on the modeling developed in A Unified Framework for Association Analysis with Multiple Related Phenotypes, M. Stephens (2013) <doi:10.1371/journal.pone.0065245>. / GPL-3	noarch
<a href="#">r-bmix</a>	0.6	This is a bare-bones implementation of sampling algorithms for a variety of Bayesian stick-breaking (marginally DP) mixture models, including particle learning and Gibbs sampling for static DP mixtures, particle learning for dynamic BAR stick-breaking, and DP mixture regression. The software is designed to be easy to customize to suit different situations and for experimentation with stick-breaking models. Since particles are repeatedly copied, it is not an especially efficient implementation. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-bmixture</a>	1.3	Provides statistical tools for Bayesian estimation for finite mixture of distributions, mainly mixture of Gamma, Normal and t-distributions. The package is implemented the recent improvements in Bayesian literature for the finite mixture of distributions, including Mohammadi and et al. (2013) <doi:10.1007/s00180-012-0323-3> and Mohammadi and Salehi-Rad (2012) <doi:10.1080/03610918.2011.588358>. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-bmk</a>	1.0	MCMC diagnostic package that contains tools to diagnose convergence as well as to evaluate sensitivity studies, Includes summary functions which output mean, median, 95percentCI, Gelman & Rubin diagnostics and the Hellinger distance based diagnostics, Also contains functions to determine when an MCMC chain has converged via Hellinger distance, A function is also provided to compare outputs from identically dimensioned chains for determining sensitivity to prior distribution assumptions / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-bmp</a>	0.3	Reads Windows BMP format images. Currently limited to 8 bit greyscale images and 24,32 bit (A)RGB images. Pure R implementation without external dependencies. / GPL-2	noarch
<a href="#">r-bmrbr</a>	0.2.0	Nuclear magnetic resonance (NMR) is a highly versatile analytical technique for studying molecular configuration, conformation, and dynamics, especially those of biomacromolecules such as proteins. Biological Magnetic Resonance Data Bank ('BMRB') is a repository for Data from NMR Spectroscopy on Proteins, Peptides, Nucleic Acids, and other Biomolecules. Currently, 'BMRB' offers an R package 'RBMBr' to fetch data, however, it doesn't easily offer individual data file downloading and storing in a local directory. When using 'RBMBr', the data will stored as an R object, which fundamentally hinders the NMR researches to access the rich information from raw data, for example, the metadata. Here, 'BMRBr' File Downloader ('BMRBr') offers a more fundamental, low level downloader, which will download original deposited .str format file. This type of file contains information such as entry title, authors, citation, protein sequences, and so on. Many factors affect NMR experiment outputs, such as temperature, resonance sensitivity and etc., approximately 40% of the entries in the 'BMRB' have chemical shift accuracy problems [1,2] Unfortunately, current reference correction methods are heavily dependent on the availability of assigned protein chemical shifts or protein structure. This is my current research project is going to solve, which will be included in the future release of the package. The current version of the package is sufficient and robust enough for downloading individual 'BMRB' data file from the 'BMRB' database < <a href="http://www.bmrbr.wisc.edu">http://www.bmrbr.wisc.edu</a> >. The functionalities of this package includes but not limited: * To simplifies NMR researches by combine data downloading and results analysis together. * To allows NMR data reaches a broader audience that could utilize more than just chemical shifts but also metadata. * To offer reference corrected data for entries without assignment or structure information (future release). Reference: [1] E.L. Ulrich, H. Akutsu, J.F. Doreleijers, Y. Harano, Y.E. Ioannidis, J. Lin, et al., BioMagResBank, Nucl. Acids Res. 36 (2008) D402–8. <doi:10.1093/nar/gkm957>. [2] L. Wang, H.R. Eghbalnia, A. Bahrami, J.L. Markley, Linear analysis of carbon-13 chemical shift differences and its application to the detection and correction of errors in referencing and spin system identifications, J. Biomol. NMR. 32 (2005) 13–22. <doi:10.1007/s10858-005-1717-0>. / GPL-3	noarch
<a href="#">r-bmrbr</a>	1.32	Provides two Bayesian models for detecting the association between rare genetic variants and a trait that can be continuous, ordinal or binary. Bayesian latent variable collapsing model (BLVCM) detects interaction effect and is dedicated to twin design while it can also be applied to independent samples. Hierarchical Bayesian multiple regression model (HBMR) incorporates genotype uncertainty information and can be applied to either independent or family samples. Furthermore, it deals with continuous, binary and ordinal traits. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-bms</a>	0.3.4	Bayesian model averaging for linear models with a wide choice of (customizable) priors. Built-in priors include coefficient priors (fixed, flexible and hyper-priors), 5 kinds of model priors, moreover model sampling by enumeration or various MCMC approaches. Post-processing functions allow for inferring posterior inclusion and model probabilities, various moments, coefficient and predictive densities. Plotting functions available for posterior model size, MCMC convergence, predictive and coefficient densities, best models representation, BMA comparison. / Artistic-2.0	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-bnclassify</a>	0.4.2	State-of-the art algorithms for learning discrete Bayesian network classifiers from data, including a number of those described in Bielza & Larranaga (2014) <doi:10.1145/2576868>, with functions for prediction, model evaluation and inspection. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-bndatagenerator</a>	1.0	Data generator based on Bayesian network model / GPL-2	noarch
<a href="#">r-bnlearn</a>	4.5	Bayesian network structure learning, parameter learning and inference. This package implements constraint-based (PC, GS, IAMB, Inter-IAMB, Fast-IAMB, MMPC, Hiton-PC, HPC), pairwise (ARACNE and Chow-Liu), score-based (Hill-Climbing and Tabu Search) and hybrid (MMHC, RSMAX2, H2PC) structure learning algorithms for discrete, Gaussian and conditional Gaussian networks, along with many score functions and conditional independence tests. The Naive Bayes and the Tree-Augmented Naive Bayes (TAN) classifiers are also implemented. Some utility functions (model comparison and manipulation, random data generation, arc orientation testing, simple and advanced plots) are included, as well as support for parameter estimation (maximum likelihood and Bayesian) and inference, conditional probability queries, cross-validation, bootstrap and model averaging. Development snapshots with the latest bugfixes are available from < <a href="http://www.bnlearn.com">http://www.bnlearn.com</a> >. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-bnn</a>	1.0.2	Perform Bayesian variable selection for high-dimensional nonlinear systems and also can be used to test nonlinearity for a general regression problem. The computation can be accelerated using multiple CPUs. You can refer to <doi:10.1080/01621459.2017.1409122> for more detail. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-bnormnlr</a>	1.0	Implementation of Bayesian estimation in normal heteroscedastic nonlinear regression Models following Cepeda-Cuervo, (2001). / GPL-2	noarch
<a href="#">r-bnppmr</a>	1.2	Implements the Bayesian nonparametric monotonic regression method described in Bornkamp & Ickstadt (2009), Biometrics, 65, 198-205. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-bnpsd</a>	1.1.1	The Pritchard-Stephens-Donnelly (PSD) admixture model has k intermediate subpopulations from which n individuals draw their alleles dictated by their individual-specific admixture proportions. The BN-PSD model additionally imposes the Balding-Nichols (BN) allele frequency model to the intermediate populations, which therefore evolved independently from a common ancestral population T with subpopulation-specific FST (Wright's fixation index) parameters. The BN-PSD model can be used to yield complex population structures. Method described in Ochoa and Storey (2016) <doi:10.1101/083923>. / GPL-3	noarch
<a href="#">r-bnptsclust</a>	2.0	Performs the algorithm for time series clustering described in Nieto-Barajas and Contreras-Cristan (2014). / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-bnsl	0.1.4	From a given data frame, this package learns its Bayesian network structure based on a selected score. / GPL-2	linux-64, osx-64, win-64
r-bnstruct	1.0.6	Bayesian Network Structure Learning from Data with Missing Values. The package implements the Silander-Myllymaki complete search, the Max-Min Parents-and-Children, the Hill-Climbing, the Max-Min Hill-climbing heuristic searches, and the Structural Expectation-Maximization algorithm. Available scoring functions are BDeu, AIC, BIC. The package also implements methods for generating and using bootstrap samples, imputed data, inference. / GPL-2	linux-64, osx-64, win-64
r-bnviewer	0.1.4	Bayesian networks provide an intuitive framework for probabilistic reasoning and its graphical nature can be interpreted quite clearly. Graph based methods of machine learning are becoming more popular because they offer a richer model of knowledge that can be understood by a human in a graphical format. The 'bnviewer' is an R Package that allows the interactive visualization of Bayesian Networks. The aim of this package is to improve the Bayesian Networks visualization over the basic and static views offered by existing packages. / MIT	noarch
r-boa	1.1.8	A menu-driven program and library of functions for carrying out convergence diagnostics and statistical and graphical analysis of Markov chain Monte Carlo sampling output. / GPL-2	noarch
r-boardgames	1.0.0	Tools for constructing board/grid based games, as well as readily available game(s) for your entertainment. / GPL-2	noarch
r-bodenmiller	0.1	This data package contains a subset of the Bodenmiller et al, Nat Biotech 2012 dataset for testing single cell, high dimensional analysis and visualization methods. / CC0	noarch
r-boilerpiper	1.3	Generic Extraction of main text content from HTML files; removal of ads, sidebars and headers using the boilerpipe ( <a href="http://code.google.com/p/boilerpipe/">http://code.google.com/p/boilerpipe/</a> ) Java library. The extraction heuristics from boilerpipe show a robust performance for a wide range of web site templates. / Apache License (== 2.0)	noarch
r-bolstad	0.2_40	A set of R functions and data sets for the book Introduction to Bayesian Statistics, Bolstad, W.M. (2017), John Wiley & Sons ISBN 978-1-118-09156-2. / GPL-2	noarch
r-bolstad2	1.0_28	A set of R functions and data sets for the book Understanding Computational Bayesian Statistics, Bolstad, W.M. (2009), John Wiley & Sons ISBN 978-0470046098 / GPL-2	noarch
r-boltzmm	0.1.4	Provides probability computation, data generation, and model estimation for fully-visible Boltzmann machines. It follows the methods described in Nguyen and Wood (2016a) <doi:10.1162/NECO_a_00813> and Nguyen and Wood (2016b) <doi:10.1109/TNNLS.2015.2425898>. / GPL-3	linux-64, osx-64, win-64
r-bondvaluation	0.1.0	Analysis of large datasets of fixed coupon bonds, allowing for irregular first and last coupon periods and various day count conventions. With this package you can compute the yield to maturity, the modified and MacAulay durations and the convexity of fixed-rate bonds. It provides the function AnnivDates, which can be used to evaluate the quality of the data and return time-invariant properties and temporal structure of a bond. / GPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-bookdown</a>	0.13	Output formats and utilities for authoring books and technical documents with R Markdown. / GPL-3	noarch
<a href="#">r-boolnet</a>	2.1.5	Provides methods to reconstruct and generate synchronous, asynchronous, probabilistic and temporal Boolean networks, and to analyze and visualize attractors in Boolean networks. / Artistic-2.0	linux-64, osx-64, win-64
<a href="#">r-boom</a>	0.9.1	A C library for Bayesian modeling, with an emphasis on Markov chain Monte Carlo. Although boom contains a few R utilities (mainly plotting functions), its primary purpose is to install the BOOM C library on your system so that other packages can link against it. / LGPL-2.1	linux-64, osx-64, win-64
<a href="#">r-boomspikeslab</a>	1.1.1	Spike and slab regression a la McCulloch and George (1997). / LGPL-2.1	linux-64, osx-64, win-64
<a href="#">r-boost</a>	1.0.0	boost provides a modular framework that return the focus of ensemble learning back to 'learning' (instead of programming). / GPL-2	noarch
<a href="#">r-boot</a>	1.3_20	Functions and datasets for bootstrapping from the book Bootstrap Methods and Their Application by A. C. Davison and D. V. Hinkley (1997, CUP), originally written by Angelo Canty for S. / Unlimited	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-bootes</a>	1.2	Calculate robust measures of effect sizes using the bootstrap. / GPL-2	noarch
<a href="#">r-bootlr</a>	1.0.2	Computes appropriate confidence intervals for the likelihood ratio tests commonly used in medicine/epidemiology, using the method of Marill et al. (2015) <doi:10.1177/0962280215592907>. It is particularly useful when the sensitivity or specificity in the sample is 100%. Note that this does not perform the test on nested models—for that, see 'epicalc::lrtest'. / LGPL-2.1	noarch
<a href="#">r-bootmr</a>	0.1	Selection of informative features like genes, transcripts, RNA seq, etc. using Bootstrap Maximum Relevance and Minimum Redundancy technique from a given high dimensional genomic dataset. Informative gene selection involves identification of relevant genes and removal of redundant genes as much as possible from a large gene space. Main applications in high-dimensional expression data analysis (e.g. microarray data, NGS expression data and other genomics and proteomics applications). / GPL-2	noarch
<a href="#">r-bootpr</a>	0.60	Bias-Corrected Forecasting and Bootstrap Prediction Intervals for Autoregressive Time Series / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-bootres	1.2.4	Bootstrapped correlation and response functions are widely used in dendrochronology to calibrate tree-ring proxy data against multiple instrumental time series of climatic variables. With this package, we provide functionality similar to DENDROCLIM2002 (Biondi and Waikul (2004) <10.1016/j.cageo.2003.11.004>). A full description with examples is given in Zang and Biondi (2013) <10.1016/j.dendro.2012.08.001>. / GPL-3	noarch
r-bootruin	1.2_4	We provide a framework for testing the probability of ruin in the classical (compound Poisson) risk process. It also includes some procedures for assessing and comparing the performance between the bootstrap test and the test using asymptotic normality. / AGPL-3	linux-64, osx-64, win-64
r-bootspecdens	3.0	Bootstrap for testing the hypothesis that the spectral densities of a number $m$ , $m \geq 2$ , not necessarily independent time series are equal / GPL-2	noarch
r-bootstepaic	1.2_0	Model selection by bootstrapping the stepAIC() procedure. / GPL-2	noarch
r-bootstrap	2019.6	Software (bootstrap, cross-validation, jackknife) and data for the book An Introduction to the Bootstrap by B. Efron and R. Tibshirani, 1993, Chapman and Hall. This package is primarily provided for projects already based on it, and for support of the book. New projects should preferentially use the recommended package boot. / BSD_3_clause	linux-64, osx-64, win-64
r-boottol	2.0	Used to create bootstrap tolerance levels for the Kolmogorov-Smirnov (KS) statistic, the area under receiver operator characteristic curve (AUROC) statistic, and the Gini coefficient for each score cutoff. Also provides a bootstrap alternative to the Vasicek test. / GPL-2	noarch
r-bor	0.1.0	Transforms focal observations' data, where different types of social interactions can be recorded by multiple observers, into asymmetric data matrices. Each cell in these matrices provides counts on the number of times a specific type of social interaction was initiated by the row subject and directed to the column subject. / GPL-3	noarch
r-borrowr	0.1.0	Estimate population average treatment effects from a primary data source with borrowing from supplemental sources. Causal estimation is done with either a Bayesian linear model or with Bayesian additive regression trees (BART) to adjust for confounding. Borrowing is done with multisource exchangeability models (MEMs). For information on BART, see Chipman, George, & McCulloch (2010) <doi:10.1214/09-AOAS285>. For information on MEMs, see Kaizer, Koopmeiners, & Hobbs (2018) <doi:10.1093/biostatistics/kxx031>. / GPL-3	linux-64, osx-64, win-64
r-boruta	6.0.0	An all relevant feature selection wrapper algorithm. It finds relevant features by comparing original attributes' importance with importance achievable at random, estimated using their permuted copies (shadows). / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-bosonsampling</a>	0.1.1	Classical Boson Sampling using the algorithm of Clifford and Clifford (2017) <arXiv:1706.01260>. Also provides functions for generating random unitary matrices, evaluation of matrix permanents (both real and complex) and evaluation of complex permanent minors. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-boussinesq</a>	1.0.3	This package is a collection of R functions implemented from published and available analytic solutions for the One-Dimensional Boussinesq Equation (ground-water). In particular, the function <code>beq.lin</code> is the analytic solution of the linearized form of Boussinesq Equation between two different head-based boundary (Dirichlet) conditions; <code>beq.song</code> is the non-linear power-series analytic solution of the motion of a wetting front over a dry bedrock (Song at al, 2007, see complete reference on function documentation). Bugs/comments/questions/collaboration of any kind are warmly welcomed. / GPL-2	noarch
<a href="#">r-boxoffice</a>	1.2.2	Download daily box office information (how much each movie earned in theaters) using data from either Box Office Mojo (< <a href="http://www.boxofficemojo.com/">http://www.boxofficemojo.com/</a> >) or The Numbers (< <a href="http://www.the-numbers.com/">http://www.the-numbers.com/</a> >). / GPL-3	noarch
<a href="#">r-boxplotdbl</a>	1.3.0	Correlation chart of two set (x and y) of data. Using Quartiles with boxplot style. Visualize the effect of factor. / MIT (FOSS)	noarch
<a href="#">r-bpa</a>	0.1.1	Run basic pattern analyses on character sets, digits, or combined input containing both characters and numeric digits. Useful for data cleaning and for identifying columns containing multiple or nonstandard formats. / GPL-2	noarch
<a href="#">r-bpbounds</a>	0.1.3	Implementation of the nonparametric bounds for the average causal effect under an instrumental variable model by Balke and Pearl (Bounds on Treatment Effects from Studies with Imperfect Compliance, JASA, 1997, 92, 439, 1171-1176). The package can calculate bounds for a binary outcome, a binary treatment/phenotype, and an instrument with either 2 or 3 categories. The package implements bounds for situations where these 3 variables are measured in the same dataset (trivariate data) or where the outcome and instrument are measured in one study and the treatment/phenotype and instrument are measured in another study (bivariate data). / GPL-3	noarch
<a href="#">r-bpcp</a>	1.3.4	Calculates nonparametric pointwise confidence intervals for the survival distribution for right censored data. Has two-sample tests for dissimilarity (e.g., difference, ratio or odds ratio) in survival at a fixed time. Especially important for small sample sizes or heavily censored data. Includes mid-p options. / GPL-2	noarch
<a href="#">r-bpeaks</a>	1.2	bPeaks is a simple approach to identify transcription factor binding sites from ChIP-seq data. Our general philosophy is to provide an easy-to-use tool, well-adapted for small eukaryotic genomes (< 20 Mb). bPeaks uses a combination of 4 cutoffs (T1, T2, T3 and T4) to mimic good peak properties as described by biologists who visually inspect the ChIP-seq data on a genome browser. For yeast genomes, bPeaks calculates the proportion of peaks that fall in promoter sequences. These peaks are good candidates as transcription factor binding sites. / GPL-3	noarch
<a href="#">r-bpkde</a>	1.0_7	Nonparametric multivariate kernel density estimation using a back-projected kernel. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-bpp	1.0.0	Implements functions to update Bayesian Predictive Power Computations after not stopping a clinical trial at an interim analysis. Such an interim analysis can either be blinded or unblinded. Code is provided for Normally distributed endpoints with known variance, with a prominent example being the hazard ratio. / GPL-2	noarch
r-bqtl	1.0_3	QTL mapping toolkit for inbred crosses and recombinant inbred lines. Includes maximum likelihood and Bayesian tools. / GPL-2	linux-64, osx-64, win-64
r-bracer	1.0.1	Performs brace expansions on strings. Made popular by Unix shells, brace expansion allows users to quickly generate certain character vectors by taking a single string and (recursively) expanding the comma-separated lists and double-period-separated integer and character sequences enclosed within braces in that string. The double-period-separated numeric integer expansion also supports padding the resulting numbers with zeros. / MIT	noarch
r-bradleyterry2	1.0_9	Specify and fit the Bradley-Terry model, including structured versions in which the parameters are related to explanatory variables through a linear predictor and versions with contest-specific effects, such as a home advantage. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-braidrm	0.71	Contains functions for evaluating, analyzing, and fitting combined action dose response surfaces with the Bivariate Response to Additive Interacting Dose (BRAID) model of combined action. / GPL-3	noarch
r-branching	0.9.4	Simulation and parameter estimation of multitype Bienayme - Galton - Watson processes. / GPL-2	linux-64, osx-64, win-64
r-brandwatchr	0.3.0	Interact with the 'Brandwatch' API < <a href="https://developers.brandwatch.com/docs">https://developers.brandwatch.com/docs</a> >. Allows you to authenticate to the API and obtain data for projects, queries, query groups tags and categories. Also allows you to directly obtain mentions and aggregate data for a specified query or query group. / MIT	noarch
r-brant	0.2_0	Tests the parallel regression assumption for ordinal logit models generated with the function polr() from the package 'MASS'. / GPL-2	noarch
r-brea	0.2.0	A function to produce MCMC samples for posterior inference in semiparametric Bayesian discrete time competing risks recurrent events models. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-breakaway</a>	3.0	Species richness estimation is an important problem in biodiversity analysis. This package provides methods for total species richness estimation (observed plus unobserved) and a method for modelling total diversity with covariates. <code>breakaway()</code> estimates total (observed plus unobserved) species richness. Microbial diversity datasets are characterized by a large number of rare species and a small number of highly abundant species. The class of models implemented by <code>breakaway()</code> is flexible enough to model both these features. <code>breakaway_nof1()</code> implements a similar procedure however does not require a singleton count. <code>betta()</code> provides a method for modelling total diversity with covariates in a way that accounts for its estimated nature and thus accounts for unobserved taxa, and <code>betta_random()</code> permits random effects modelling. / GPL-2	noarch
<a href="#">r-breakfast</a>	1.0.0	The breakfast package performs multiple change-point detection in data sequences, or sequence segmentation, using computationally efficient multiscale methods. This version of the package implements the Tail-Greedy Unbalanced Haar, Wild Binary Segmentation and Adaptive Wild Binary Segmentation change-point detection and segmentation methodologies. To start with, see the function <code>segment.mean</code> . / GPL-3	noarch
<a href="#">r-breeze</a>	0.4_3	A collection of functions to analyse, visualize and interpret wind data and to calculate the potential energy production of wind turbines. / MIT	noarch
<a href="#">r-bretigea</a>	1.0.0	Analysis of relative cell type proportions in bulk gene expression data. Provides a well-validated set of brain cell type-specific marker genes derived from multiple types of experiments, as described in McKenzie (2018) <doi:10.1038/s41598-018-27293-5>. For brain tissue data sets, there are marker genes available for astrocytes, endothelial cells, microglia, neurons, oligodendrocytes, and oligodendrocyte precursor cells, derived from each of human, mice, and combination human/mouse data sets. However, if you have access to your own marker genes, the functions can be applied to bulk gene expression data from any tissue. Also implements multiple options for relative cell type proportion estimation using these marker genes, adapting and expanding on approaches from the ‘CellCODE’ R package described in Chikina (2015) <doi:10.1093/bioinformatics/btv015>. The number of cell type marker genes used in a given analysis can be increased or decreased based on your preferences and the data set. Finally, provides functions to use the estimates to adjust for variability in the relative proportion of cell types across samples prior to downstream analyses. / MIT	noarch
<a href="#">r-brew</a>	1.0_6	<code>brew</code> implements a templating framework for mixing text and R code for report generation. <code>brew</code> template syntax is similar to PHP, Ruby’s <code>erb</code> module, Java Server Pages, and Python’s <code>psp</code> module. / GPL-2	linux-32, linux-64, noarch, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-brglm</a>	0.6.2	Fit generalized linear models with binomial responses using either an adjusted-score approach to bias reduction or maximum penalized likelihood where penalization is by Jeffreys invariant prior. These procedures return estimates with improved frequentist properties (bias, mean squared error) that are always finite even in cases where the maximum likelihood estimates are infinite (data separation). Fitting takes place by fitting generalized linear models on iteratively updated pseudo-data. The interface is essentially the same as 'glm'. More flexibility is provided by the fact that custom pseudo-data representations can be specified and used for model fitting. Functions are provided for the construction of confidence intervals for the reduced-bias estimates. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-bridgedist</a>	0.1.0	An implementation of the bridge distribution with logit-link in R. In Wang and Louis (2003) <DOI:10.1093/biomet/90.4.765>, such a univariate bridge distribution was derived as the distribution of the random intercept that 'bridged' a marginal logistic regression and a conditional logistic regression. The conditional and marginal regression coefficients are a scalar multiple of each other. Such is not the case if the random intercept distribution was Gaussian. / GPL-2	noarch
<a href="#">r-brlrmr</a>	0.1.5	Provides two main functions, il() and fil(). The il() function implements the EM algorithm developed by Ibrahim and Lipsitz (1996) <DOI:10.2307/2533068> to estimate the parameters of a logistic regression model with the missing response when the missing data mechanism is nonignorable. The fil() function implements the algorithm proposed by Maity et. al. (2017) <https://github.com/arnabkrmaity/brlrmr> to reduce the bias produced by the method of Ibrahim and Lipsitz (1996) <DOI:10.2307/2533068>. / GPL-3	noarch
<a href="#">r-brm</a>	1.0	Fits novel models for the conditional relative risk, risk difference and odds ratio. / MIT	noarch
<a href="#">r-brnn</a>	0.7	Bayesian regularization for feed-forward neural networks. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-brobdingnag</a>	1.2_6	Handles very large numbers in R. Real numbers are held using their natural logarithms, plus a logical flag indicating sign. The package includes a vignette that gives a step-by-step introduction to using S4 methods. / GPL-3	noarch
<a href="#">r-broom</a>	0.5.2	Summarizes key information about statistical objects in tidy tibbles. This makes it easy to report results, create plots and consistently work with large numbers of models at once. Broom provides three verbs that each provide different types of information about a model. tidy() summarizes information about model components such as coefficients of a regression. glance() reports information about an entire model, such as goodness of fit measures like AIC and BIC. augment() adds information about individual observations to a dataset, such as fitted values or influence measures. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-brotli</a>	1.2	A lossless compressed data format that uses a combination of the LZ77 algorithm and Huffman coding. Brotli is similar in speed to deflate (gzip) but offers more dense compression. / MIT	linux-64, osx-64, win-64
<a href="#">r-browndog</a>	0.2.1	An R interface for the Brown Dog which allows researchers to leverage Brown Dog Services that provides modules to identify the conversion options for a file, to convert file to appropriate format, or to extract data from a file. See <a href="http://browndog.ncsa.illinois.edu/">http://browndog.ncsa.illinois.edu/</a> for more information. / FreeBSD   file LICENSE	noarch
<a href="#">r-brq</a>	2.5	Bayesian estimation and variable selection for quantile regression models. / GPL-2	noarch
<a href="#">r-brunermunzel</a>	1.3.5	Provides the functions for Brunner-Munzel test and permuted Brunner-Munzel test, which enable to use formula, matrix, and table as argument. These functions are based on Brunner and Munzel (2000) <doi:10.1002/(SICI)1521-4036(200001)42:1%3C17::AID-BIMJ17%3E3.0.CO;2-U> and Neubert and Brunner (2007) <doi:10.1016/j.csda.2006.05.024>, and are written with FORTRAN. / GPL-2   GPL-3	linux-64, osx-64, win-64
<a href="#">r-bs4dash</a>	0.4.0	Make ‘Bootstrap 4’ dashboards. Use the full power of ‘AdminLTE3’, a dashboard template built on top of ‘Bootstrap 4’ < <a href="https://github.com/almasaeed2010/AdminLTE/tree/v3-dev">https://github.com/almasaeed2010/AdminLTE/tree/v3-dev</a> >. / GPL-2	noarch
<a href="#">r-bsda</a>	1.2.0	Data sets for book Basic Statistics and Data Analysis by Larry J. Kitchens. / GPL-2	noarch
<a href="#">r-bsearchtools</a>	0.0.61	Exposes the binary search functions of the C standard library (std::lower_bound, std::upper_bound) plus other convenience functions, allowing faster lookups on sorted vectors. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-bsmd</a>	2013.0718	Bayesian screening and model discrimination follow-up designs. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-bspec</a>	1.5	Bayesian inference on the (discrete) power spectrum of time series. / GPL-2	noarch
<a href="#">r-bsplinepsd</a>	0.6.0	Implementation of a Metropolis-within-Gibbs MCMC algorithm to flexibly estimate the spectral density of a stationary time series. The algorithm updates a nonparametric B-spline prior using the Whittle likelihood to produce pseudo-posterior samples and is based on the work presented in Edwards, M.C., Meyer, R. and Christensen, N., Statistics and Computing (2018). <doi.org/10.1007/s11222-017-9796-9>. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-bsplus</a>	0.1.1	The Bootstrap framework lets you add some JavaScript functionality to your web site by adding attributes to your HTML tags - Bootstrap takes care of the JavaScript < <a href="https://getbootstrap.com/javascript">https://getbootstrap.com/javascript</a> >. If you are using R Markdown or Shiny, you can use these functions to create collapsible sections, accordion panels, modals, tooltips, popovers, and an accordion sidebar framework (not described at Bootstrap site). / MIT	noarch
<a href="#">r-bspmma</a>	0.1_2	The main functions carry out Gibbs’ sampler routines for nonparametric and semiparametric Bayesian models for random effects meta-analysis. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-bsts	0.9.1	Time series regression using dynamic linear models fit using MCMC. See Scott and Varian (2014) <DOI:10.1504/IJMMNO.2014.059942>, among many other sources. / LGPL-2.1	linux-64, osx-64, win-64
r-btm	0.2.1	Biterm Topic Models find topics in collections of short texts. It is a word co-occurrence based topic model that learns topics by modeling word-word co-occurrences patterns which are called biterms. This in contrast to traditional topic models like Latent Dirichlet Allocation and Probabilistic Latent Semantic Analysis which are word-document co-occurrence topic models. A biterm consists of two words co-occurring in the same short text window. This context window can for example be a twitter message, a short answer on a survey, a sentence of a text or a document identifier. The techniques are explained in detail in the paper ‘A Biterm Topic Model For Short Text’ by Xiaohui Yan, Jiafeng Guo, Yanyan Lan, Xueqi Cheng (2013) < <a href="https://github.com/xiaohuiyan/xiaohuiyan.github.io/blob/master/paper/BTM-WWW13.pdf">https://github.com/xiaohuiyan/xiaohuiyan.github.io/blob/master/paper/BTM-WWW13.pdf</a> >. / Apache License 2.0	linux-64, osx-64, win-64
r-bucky	1.0.5	Provides functions for various statistical techniques commonly used in the social sciences, including functions to compute clustered robust standard errors, combine results across multiply-imputed data sets, and simplify the addition of robust and clustered robust standard errors. The package was originally developed, in part, to assist porting of replication code from ‘Stata’ and attempts to replicate default options from ‘Stata’ where possible. / GPL-3	noarch
r-bucss	1.1.0	Implements a method of correcting for publication bias and uncertainty when planning sample sizes in a future study from an original study. See Anderson, Kelley, & Maxwell (2017; Psychological Science, 28, 1547-1562). / GPL-3	noarch
r-buddle	1.0	Statistical classification has been popular among various fields and stayed in the limelight of scientists of those fields. Examples of the fields include clinical trials where the statistical classification of patients is indispensable to predict the clinical courses of diseases. Considering the negative impact of diseases on performing daily tasks, correctly classifying patients based on the clinical information is vital in that we need to identify patients of the high-risk group to develop a severe state and arrange medical treatment for them at an opportune moment. Deep learning - a part of artificial intelligence - has gained much attention, and research on it burgeons during past decades. It is a veritable technique which was originally designed for the classification, and hence, the EzDL package can provide sublime solutions to various challenging classification problems encountered in the clinical trials. The EzDL package is based on the back-propagation algorithm which performs a multi-layer feed-forward neural network. This package contains two functions: Buddle_Main() and Buddle_Predict(). Buddle_Main() builds a feed-forward neural network model and trains the model. Buddle_Predict() provokes the trained model which is the output of Buddle_Main(), classifies given data, and make a final prediction for the data. / GPL-2	linux-64, osx-64, win-64
r-buildmer	1.2	Finds the largest possible regression model that will still converge for various types of regression analyses (including mixed models and generalized additive models) and then optionally performs stepwise elimination similar to the forward and backward effect selection methods in SAS, based on the change in log-likelihood or its significance, Akaike’s Information Criterion, or the Bayesian Information Criterion. / FreeBSD	noarch

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Name	Version	Summary/License	Platforms
r-bullwhipgame	0.1.0	The bullwhipgame is an educational game that has as purpose the illustration and exploration of the bullwhip effect,i.e, the increase in demand variability along the supply chain. Marchena Marlene (2010) <arXiv:1009.3977>. / GPL-3	noarch
r-bunchr	1.2.0	View and analyze data where bunching is expected. Estimate counter-factual distributions. For earnings data, estimate the compensated elasticity of earnings w.r.t. the net-of-tax rate. / MIT	noarch
r-bundesbank	0.1.9	Download data from the time-series databases of the Bundesbank, the German central bank. See the overview at the Bundesbank website (< <a href="https://www.bundesbank.de/en/statistics/time-series-databases">https://www.bundesbank.de/en/statistics/time-series-databases</a> >) for available series. The package provides only a single function, getSeries(), which supports both traditional and real-time datasets; it will also download meta data if available. Downloaded data can automatically be arranged in various formats, such as data frames or 'zoo' series. The data may optionally be cached, so as to avoid repeated downloads of the same series. / GPL-3	noarch
r-bundesligr	0.1.0	All final tables of Germany's highest football (soccer!) league, the Bundesliga. Contains data from 1964 to 2016. / GPL-3	noarch
r-burstfin	1.02	A suite of functions for finance, including the estimation of variance matrices via a statistical factor model or Ledoit-Wolf shrinkage. / Unlimited	noarch
r-burstmisc	1.1	Script search, corner, genetic optimization, permutation tests, write expect test. / Unlimited	noarch
r-bursts	1.0.1	An implementation of Jon Kleinberg's burst detection algorithm. Uses an infinite Markov model to detect periods of increased activity in a series of discrete events with known times, and provides a simple visualization of the results. / MIT	noarch
r-busdater	0.2.0	Get a current financial year, start of current month, End of current month, start of financial year and end of it. Allow for offset from the date. / MIT	noarch
r-businessduration	0.2.0	Calculates business duration between two dates. This excluding weekends, public holidays and non-business hours. / AGPL-3	noarch
r-buysetest	1.7	Implementation of the Generalized Pairwise Comparisons (GPC). GPC compare two groups of observations (intervention vs. control group) regarding several prioritized endpoints. The net benefit and win ratio statistics can then be estimated and corresponding confidence intervals and p-values can be estimated using resampling methods or the asymptotic U-statistic theory. The software enables the use of thresholds of minimal importance difference, stratification, and corrections to deal with right-censored endpoints or missing values. / GPL-3	linux-64, osx-64, win-64
r-bvar	0.1.5	Toolkit for the estimation of hierarchical Bayesian vector autoregressions. Implements hierarchical prior selection for conjugate priors in the fashion of Giannone, Lenza & Primiceri (2015) <doi:10.1162/REST_a_00483>. Allows for the computation of impulse responses and forecasts and provides functionality for assessing results. / GPL-3	noarch
r-bvars	1.1	R/C implementation of the model proposed by Primiceri (Time Varying Structural Vector Autoregressions and Monetary Policy, Review of Economic Studies, 2005), with functionality for computing posterior predictive distributions and impulse responses. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-bvartools</a>	0.0.2	Assists in the set-up of algorithms for Bayesian inference of vector autoregressive (VAR) models. Functions for posterior simulation, forecasting, impulse response analysis and forecast error variance decomposition are largely based on the introductory texts of Koop and Korobilis (2010) <doi:10.1561/08000000013> and Luetkepohl (2007, ISBN: 9783540262398). / GPL-2	linux-64, osx-64, win-64
<a href="#">r-bvenn</a>	0.1	This package implements a simple alternative to the traditional Venn diagram. It depicts each overlap as a separate bubble with area proportional to the overlap size. Relation of the bubbles to input sets is shown by their arrangement. / GPL-2	noarch
<a href="#">r-bvls</a>	1.4	An R interface to the Stark-Parker implementation of an algorithm for bounded-variable least squares / GPL-2	linux-64, osx-64, win-64
<a href="#">r-bwd</a>	0.1.0	Implements a backward procedure for single and multiple change point detection proposed by Shin et al. <arXiv:1812.10107>. The backward approach is particularly useful to detect short and sparse signals which is common in copy number variation (CNV) detection. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-bwgr</a>	1.6.5	Whole-genome regression methods on Bayesian framework fitted via EM or Gibbs sampling, univariate and multivariate, with optional kernel term and sampling techniques. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-bwimage</a>	1.0	A computational tool to describe patterns in black and white images from natural structures. 'bwimage' implemented functions for exceptionally broad subject. For instance, 'bwimage' provide examples that range from calculation of canopy openness, description of patterns in vertical vegetation structure, to patterns in bird nest structure. / GPL-2	noarch
<a href="#">r-bwstest</a>	0.2.2	Performs the 'Baumgartner-Weiss-Schindler' two-sample test of equal probability distributions, <doi:10.2307/2533862>. Also performs similar rank-based tests for equal probability distributions due to Neuhauser <doi:10.1080/10485250108832874> and Murakami <doi:10.1080/00949655.2010.551516>. / LGPL-3	linux-64, osx-64, win-64
<a href="#">r-bytescircle</a>	1.1	Shows statistics about bytes contained in a file as a circle graph of deviations from mean in sigma increments. The function can be useful for statistically analyze the content of files in a glimpse: text files are shown as a green centered crown, compressed and encrypted files should be shown as equally distributed variations with a very low CV (sigma/mean), and other types of files can be classified between these two categories depending on their text vs binary content, which can be useful to quickly determine how information is stored inside them (databases, multimedia files, etc). / GPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-bzinb	1.0.3	Provides a maximum likelihood estimation of Bivariate Zero-Inflated Negative Binomial (BZINB) model or the nested model parameters. Also estimates the underlying correlation of the a pair of count data. See Cho, H., Liu, C., Preisser, J., and Wu, D. (In preparation) for details. / GPL-2	linux-64, osx-64, win-64
r-c212	0.95	Methods for detecting safety signals in clinical trials using groupings of adverse events by body-system or system organ class. The package title c212 is in reference to the original Engineering and Physical Sciences Research Council (UK) funded project which was named CASE 2/12. / GPL-2	linux-64, osx-64, win-64
r-c2c	0.1.0	Compare two classifications or clustering solutions that may or may not have the same number of classes, and that might have hard or soft (fuzzy, probabilistic) membership. Calculate various metrics to assess how the clusters compare to each other. The calculations are simple, but provide a handy tool for users unfamiliar with matrix multiplication. This package is not geared towards traditional accuracy assessment for classification/ mapping applications - the motivating use case is for comparing a probabilistic clustering solution to a set of reference or existing class labels that could have any number of classes (that is, without having to degrade the probabilistic clustering to hard classes). / GPL-3	noarch
r-c3net	1.1.1	This package allows inferring gene regulatory networks with direct physical interactions from microarray expression data using C3NET. / GPL-3	noarch
r-ca	0.71	Computation and visualization of simple, multiple and joint correspondence analysis. / GPL-3	noarch
r-cabooters	1.0	Performs correspondence analysis on a two-way contingency table and produces bootstrap-based elliptical confidence regions around the projected coordinates for the category points. Includes routines to plot the results in a variety of styles. Also reports the standard numerical output for correspondence analysis. / GPL-2	noarch
r-cacirt	1.4	Computes classification accuracy and consistency indices under Item Response Theory. Implements the total score IRT-based methods in Lee, Hanson & Brennan (2002) and Lee (2010), the IRT-based methods in Rudner (2001, 2005), and the total score nonparametric methods in Lathrop & Cheng (2014). For dichotomous and polytomous tests. / GPL-2	noarch
r-caic4	0.8	Provides functions for the estimation of the conditional Akaike information in generalized mixed-effect models fitted with (g)lmer() from 'lme4'. / GPL-2	noarch
r-cairo	1.5_1	Cairo graphics device that can be use to create high-quality vector (PDF, PostScript and SVG) and bitmap output (PNG, JPEG, TIFF), and high-quality rendering in displays (X11 and Win32). Since it uses the same back-end for all output, copying across formats is WYSIWYG. Files are created without the dependence on X11 or other external programs. This device supports alpha channel (semi-transparent drawing) and resulting images can contain transparent and semi-transparent regions. It is ideal for use in server environments (file output) and as a replacement for other devices that don't have Cairo's capabilities such as alpha support or anti-aliasing. Backends are modular such that any subset of backends is supported. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-calacs</a>	2.2.2	Implements several string comparison algorithms, including calACS (count all common subsequences), lenACS (calculate the lengths of all common subsequences), and lenLCS (calculate the length of the longest common subsequence). Some algorithms differentiate between the more strict definition of subsequence, where a common subsequence cannot be separated by any other items, from its looser counterpart, where a common subsequence can be interrupted by other items. This difference is shown in the suffix of the algorithm (-Strict vs -Loose). For example, q-w is a common subsequence of q-w-e-r and q-e-w-r on the looser definition, but not on the more strict definition. calACSLoose Algorithm from Wang, H. All common subsequences (2007) IJ-CAI International Joint Conference on Artificial Intelligence, pp. 635-640. / GPL-3	noarch
<a href="#">r-calculator.lf.fns</a>	1.3	Arithmetic operations scalar multiplication, addition, subtraction, multiplication and division of LR fuzzy numbers (which are on the basis of extension principle) have a complicate form for using in fuzzy Statistics, fuzzy Mathematics, machine learning, fuzzy data analysis and etc. Calculator for LR Fuzzy Numbers package relieve and aid applied users to achieve a simple and closed form for some complicated operator based on LR fuzzy numbers and also the user can easily draw the membership function of the obtained result by this package. / LGPL-3	noarch
<a href="#">r-calibrate</a>	1.7.2	Package for drawing calibrated scales with tick marks on (non-orthogonal) variable vectors in scatterplots and biplots. / GPL-2	noarch
<a href="#">r-calibrator</a>	1.2.8	Performs Bayesian calibration of computer models as per Kennedy and O'Hagan 2001. The package includes routines to find the hyperparameters and parameters; see the help page for stage1() for a worked example using the toy dataset. A tutorial is provided in the calex.Rnw vignette; and a suite of especially simple one dimensional examples appears in inst/doc/one.dim/. / GPL-2	noarch
<a href="#">r-callr</a>	3.2.0	It is sometimes useful to perform a computation in a separate R process, without affecting the current R process at all. This packages does exactly that. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-caman</a>	0.74	Tools for the analysis of finite semiparametric mixtures. These are useful when data is heterogeneous, e.g. in pharmacokinetics or meta-analysis. The NPMLE and VEM algorithms (flexible support size) and EM algorithms (fixed support size) are provided for univariate and bivariate data. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-camsrad</a>	0.3.0	Copernicus Atmosphere Monitoring Service (CAMS) radiations service provides time series of global, direct, and diffuse irradiances on horizontal surface, and direct irradiation on normal plane for the actual weather conditions as well as for clear-sky conditions. The geographical coverage is the field-of-view of the Meteosat satellite, roughly speaking Europe, Africa, Atlantic Ocean, Middle East. The time coverage of data is from 2004-02-01 up to 2 days ago. Data are available with a time step ranging from 15 min to 1 month. For license terms and to create an account, please see < <a href="http://www.soda-pro.com/web-services/radiation/cams-radiation-service">http://www.soda-pro.com/web-services/radiation/cams-radiation-service</a> >. / MIT	noarch
<a href="#">r-canprot</a>	0.1.2	Datasets are collected here for differentially (up- and down-) expressed proteins identified in proteomic studies of cancer and in cell culture experiments. Tables of amino acid compositions of proteins are used for calculations of chemical composition, projected into selected basis species. Plotting functions are used to visualize the compositional differences and thermodynamic potentials for proteomic transformations. / GPL-3	noarch
<a href="#">r-canvasxpress</a>	1.24.8	Enables creation of visualizations using the CanvasXpress framework in R. CanvasXpress is a standalone JavaScript library for reproducible research with complete tracking of data and end-user modifications stored in a single PNG image that can be played back. See < <a href="http://canvasxpress.org">http://canvasxpress.org</a> > for more information. / GPL-3	noarch
<a href="#">r-caper</a>	1.0.1	Functions for performing phylogenetic comparative analyses. / GPL-2	noarch
<a href="#">r-capitalr</a>	1.2.0	Provides Capital Budgeting Analysis functionality and the essential Annuity loan functions. Also computes Loan Amortization Schedules including schedules with irregular payments. / GPL-3	noarch
<a href="#">r-capn</a>	1.0.0	Implements approximation methods for natural capital asset prices suggested by Fenichel and Abbott (2014) <doi:10.1086/676034> in Journal of the Associations of Environmental and Resource Economists (JAERE), Fenichel et al. (2016) <doi:10.1073/pnas.1513779113> in Proceedings of the National Academy of Sciences (PNAS), and Yun et al. (2017) in PNAS (accepted), and their extensions: creating Chebyshev polynomial nodes and grids, calculating basis of Chebyshev polynomials, approximation and their simulations for: V-approximation (single and multiple stocks, PNAS), P-approximation (single stock, PNAS), and Pdot-approximation (single stock, JAERE). Development of this package was generously supported by the Knobloch Family Foundation. / GPL-2	noarch
<a href="#">r-captioner</a>	2.2.3	Provides a method for automatically numbering figures, tables, or other objects. Captions can be displayed in full, or as citations. This is especially useful for adding figures and tables to R markdown documents without having to numbering them manually. / MIT	noarch
<a href="#">r-captr</a>	0.3.0	Get text from images of text using Captricity Optical Character Recognition (OCR) API. Captricity allows you to get text from handwritten forms — think surveys — and other structured paper documents. And it can output data in form a delimited file keeping field information intact. For more information, read < <a href="https://shreddr.captricity.com/developer/overview/">https://shreddr.captricity.com/developer/overview/</a> >. / MIT	noarch
<a href="#">r-capushe</a>	1.1.1	Calibration of penalized criteria for model selection. The calibration methods available are based on the slope heuristics. / GPL (>= 2.0)	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-capwire</a>	1.1.4	Fits models from Miller et al. 2005 to estimate population sizes from natural populations. Several models are implemented. Package also includes functions to perform a likelihood ratio test to choose between models, perform parametric bootstrapping to obtain confidence intervals and multiple functions to simulate data. / GPL-2	noarch
<a href="#">r-car</a>	3.0_2	Functions to Accompany J. Fox and S. Weisberg, An R Companion to Applied Regression, Third Edition, Sage, in press. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-cardata</a>	3.0_2	Datasets to Accompany J. Fox and S. Weisberg, An R Companion to Applied Regression, Third Edition, Sage (forthcoming). / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-cardiomodel</a>	1.4	Includes over 100 mixed-effects model structures describing the relationship between drug concentration and QT interval, heart rate/pulse rate or blood pressure. Given an exposure-response dataset, the tool fits each model structure to the observed data. / GPL-3	noarch
<a href="#">r-care</a>	1.1.10	Implements the regression approach of Zuber and Strimmer (2011) High-dimensional regression and variable selection using CAR scores SAGMB 10: 34, <DOI:10.2202/1544-6115.1730>. CAR scores measure the correlation between the response and the Mahalanobis-decorrelated predictors. The squared CAR score is a natural measure of variable importance and provides a canonical ordering of variables. This package provides functions for estimating CAR scores, for variable selection using CAR scores, and for estimating corresponding regression coefficients. Both shrinkage as well as empirical estimators are available. / GPL-3	noarch
<a href="#">r-care1</a>	1.1.0	The R package CARE1, the first part of the program CARE (Capture-Recapture) in <a href="http://chao.stat.nthu.edu.tw/softwareCE.html">http://chao.stat.nthu.edu.tw/softwareCE.html</a> , can be used to analyze epidemiological data via sample coverage approach (Chao et al. 2001a). Based on the input of records from several incomplete lists (or samples) of individuals, the R package CARE1 provides output of population size estimate and related statistics. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-careless</a>	1.1.3	When taking online surveys, participants sometimes respond to items without regard to their content. These types of responses, referred to as careless or insufficient effort responding, constitute significant problems for data quality, leading to distortions in data analysis and hypothesis testing, such as spurious correlations. The 'R' package 'careless' provides solutions designed to detect such careless / insufficient effort responses by allowing easy calculation of indices proposed in the literature. It currently supports the calculation of longstring, even-odd consistency, psychometric synonyms/antonyms, Mahalanobis distance, and intra-individual response variability (also termed inter-item standard deviation). For a review of these methods, see Curran (2016) <doi:10.1016/j.jesp.2015.07.006>. / MIT	noarch
<a href="#">r-caret</a>	6.0_83	Misc functions for training and plotting classification and regression models. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-caribou</a>	1.1	This is a package for estimating the population size of migratory caribou herds based on large scale aggregations monitored by radio telemetry. It implements the methodology found in the article by Rivest et al. (1998) about caribou abundance estimation. It also includes a function based on the Lincoln-Petersen Index as applied to radio telemetry data by White and Garrott (1990). / GPL-2	noarch
<a href="#">r-carletonstats</a>	2.0	Includes commands for bootstrapping and permutation tests, a command for created grouped bar plots, and a demo of the quantile-normal plot for data drawn from different distributions. / GPL-2	noarch
<a href="#">r-carlit</a>	1.0	Functions to calculate and plot ecological quality ratios (EQR) as specified by Ballesteros et al. 2007. / GPL-2	noarch
<a href="#">r-caroline</a>	0.7.6	The caroline R library contains dozens of functions useful for: database migration (dbWriteTable2), database style joins & aggregation (nerge, groupBy & bestBy), data structure conversion (nv, tab2df), legend table making (sstable & leghead), plot annotation (labsegs & mvlabs), data visualization (violins, pies & raPlot), character string manipulation (m & pad), file I/O (write.delim), batch scripting and more. The package's greatest contributions lie in the database style merge, aggregation and interface functions as well as in it's extensive use and propagation of row, column and vector names in most functions. / Artistic-2.0	noarch
<a href="#">r-carrier</a>	0.1.0	Sending functions to remote processes can be wasteful of resources because they carry their environments with them. With the carrier package, it is easy to create functions that are isolated from their environment. These isolated functions, also called crates, print at the console with their total size and can be easily tested locally before being sent to a remote. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-cascadedata</a>	1.2	These experimental expression data (5 leukemic ‘CLL’ B-lymphocyte of aggressive form from ‘GSE39411’, <doi:10.1073/pnas.1211130110>), after B-cell receptor stimulation, are used as examples by packages such as the ‘Cascade’ one, a modeling tool allowing gene selection, reverse engineering, and prediction in cascade networks. Jung, N., Bertrand, F., Bahram, S., Vallat, L., and Maumy-Bertrand, M. (2014) <doi:10.1093/bioinformatics/btt705>. / GPL-2	noarch
<a href="#">r-casematch</a>	1.0.7	Allows users to identify similar cases for qualitative case studies using statistical matching methods. / GPL-2	noarch
<a href="#">r-casmap</a>	0.6.0	A significant pattern mining-based toolbox for region-based genome-wide association studies and higher-order epistasis analyses, implementing the methods described in Llinares-López et al. (2017) <doi:10.1093/bioinformatics/btx071>. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-cat</a>	0.0_6	Analysis of categorical-variable with missing values / file LICENSE	linux-64, osx-64, win-64
<a href="#">r-catchr</a>	0.2.1	R has a unique way of dealing with warnings, errors, messages, and other conditions, but it can often be troublesome to users coming from different programming backgrounds. The purpose of this package is to provide flexible and useful tools for handling R conditions with less hassle. In order to lower the barrier of entry, keep code clean and readable, and reduce the amount of typing required, <i>catchr</i> uses a very simple domain-specific language that simplifies things on the front-end. This package aims to maintain a continuous learning curve that lets new users jump straight in to condition-handling, while simultaneously offering depth and complexity for more advanced users. / MIT	noarch
<a href="#">r-catdap</a>	1.3.4	Categorical data analysis by AIC. The methodology is described in Sakamoto (1992) <ISBN 978-0-7923-1429-5>. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-catdata</a>	1.2.1	This R-package contains examples from the book Regression for Categorical Data, Tutz 2011, Cambridge University Press. The names of the examples refer to the chapter and the data set that is used. / GPL-2	noarch
<a href="#">r-catencoders</a>	0.1.1	Contains some commonly used categorical variable encoders, such as ‘LabelEncoder’ and ‘OneHotEncoder’. Inspired by the encoders implemented in Python ‘sklearn.preprocessing’ package (see < <a href="http://scikit-learn.org/stable/modules/preprocessing.html">http://scikit-learn.org/stable/modules/preprocessing.html</a> >). / GPL-2   GPL-3	noarch
<a href="#">r-cateselection</a>	1.0	A multi-factor dimensionality reduction based forward selection method for genetic association mapping. / GPL-2	noarch
<a href="#">r-catirt</a>	0.5_0	Functions designed to simulate data that conform to basic unidimensional IRT models (for now 3-parameter binary response models and graded response models) along with Post-Hoc CAT simulations of those models with various item selection methods, ability estimation methods, and termination criteria. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-catnet</a>	1.15.5	Structure learning and parameter estimation of discrete Bayesian networks using likelihood-based criteria. Exhaustive search for fixed node orders and stochastic search of optimal orders via simulated annealing algorithm are implemented. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-catools</a>	1.17.1	Contains several basic utility functions including: moving (rolling, running) window statistic functions, read/write for GIF and ENVI binary files, fast calculation of AUC, LogitBoost classifier, base64 encoder/decoder, round-off-error-free sum and cumsum, etc. / GPL-3	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-catr</a>	3.16	Provides routines for the generation of response patterns under unidimensional dichotomous and polytomous computerized adaptive testing (CAT) framework. It holds many standard functions to estimate ability, select the first item(s) to administer and optimally select the next item, as well as several stopping rules. Options to control for item exposure and content balancing are also available (Magis and Barrada (2017) <doi:10.18637/jss.v076.c01>). / GPL-2	noarch
<a href="#">r-catseyes</a>	0.2.3	Provides the tools to produce catseye plots, principally by catseyesplot() function which calls R's standard plot() function internally, or alternatively by the catseyes() function to overlay the catseye plot onto an existing R plot window. Catseye plots illustrate the normal distribution of the mean (picture a normal bell curve reflected over its base and rotated 90 degrees), with a shaded confidence interval; they are an intuitive way of illustrating and comparing normally distributed estimates, and are arguably a superior alternative to standard confidence intervals, since they show the full distribution rather than fixed quantile bounds. The catseyesplot and catseyes functions require pre-calculated means and standard errors (or standard deviations), provided as numeric vectors; this allows the flexibility of obtaining this information from a variety of sources, such as direct calculation or prediction from a model. Catseye plots, as illustrations of the normal distribution of the means, are described in Cumming (2013 & 2014). Cumming, G. (2013). The new statistics: Why and how. Psychological Science, 27, 7-29. <doi:10.1177/0956797613504966> pmid:24220629. / GPL-3	noarch
<a href="#">r-catspec</a>	0.97	'ctab' creates (multiway) percentage tables. 'sqtab' contains a set of functions for estimating models for square tables such as quasi-independence, symmetry, uniform association. Examples show how to use these models in a loglinear model using glm or in a multinomial logistic model using mlogit or clogit / GPL-2	noarch
<a href="#">r-catt</a>	2.0	This function conducts the Cochran-Armitage trend test to a 2 by k contingency table. It will report the test statistic (Z) and p-value. A linear trend in the frequencies will be calculated, because the weights (0,1,2) will be used by default. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<code>r-cattexact</code>	0.1.0	Provides functions for computing the one-sided p-values of the Cochran-Armitage trend test statistic for the asymptotic and the exact conditional test. The computation of the p-value for the exact test is performed using an algorithm following an idea by Mehta, et al. (1992) <doi:10.2307/1390598>. / GPL-2   GPL-3	noarch
<code>r-causalmgm</code>	0.1.1	Allows users to learn undirected and directed (causal) graphs over mixed data types (i.e., continuous and discrete variables). To learn a directed graph over mixed data, it first calculates the undirected graph (Sedgewick et al, 2016) and then it uses local search strategies to prune-and-orient this graph (Sedgewick et al, 2017). AJ Sedgewick, I Shi, RM Donovan, PV Benos (2016) <doi:10.1186/s12859-016-1039-0>. AJ Sedgewick, JD Ramsey, P Spirtes, C Glymour, PV Benos (2017) <arXiv:1704.02621>. / GPL-2	noarch
<code>r-causalsens</code>	0.1.2	The causalsens package provides functions to perform sensitivity analyses and to study how various assumptions about selection bias affects estimates of causal effects. / GPL-2	noarch
<code>r-cbanalysis</code>	0.2.0	A set of functions that helps you to generate descriptive statistics based on the variable types. / GPL-2	noarch
<code>r-cbinom</code>	1.3	Implementation of the d/p/q/r family of functions for a continuous analog to the standard discrete binomial with continuous size parameter and continuous support with x in [0, size 1], following Iliencko (2013) <arXiv:1303.5990>. / GPL-2	linux-64, osx-64, win-64
<code>r-cbird</code>	1.0	The clustering of binary data with reducing the dimensionality (CLUSBIRD) proposed by Yamamoto and Hayashi (2015) <doi:10.1016/j.patcog.2015.05.026>. / GPL-2	linux-64, osx-64, win-64
<code>r-cblasr</code>	1.0.0	Provides the 'cblas.h' header file as C interface to the underlying internal 'BLAS' library in R. 'CBLAS' < <a href="https://www.netlib.org/blas/cblas.h">https://www.netlib.org/blas/cblas.h</a> > is a collection of wrappers originally written by Keita Teranishi and provides a C interface to the FORTRAN 'BLAS' library < <a href="https://www.netlib.org/blas/">https://www.netlib.org/blas/</a> >. Note that as internal 'BLAS' library provided by R < <a href="https://svn.r-project.org/R/trunk/src/include/R_ext/BLAS.h">https://svn.r-project.org/R/trunk/src/include/R_ext/BLAS.h</a> > is used and only the double precision / double complex 'BLAS' routines are supported. / GPL-2	linux-64, osx-64, win-64
<code>r-cbsem</code>	1.0.0	The composites are linear combinations of their indicators in composite based structural equation models. Structural models are considered consisting of two blocks. The indicators of the exogenous composites are named by X, the indicators of the endogenous by Y. Reflective relations are given by arrows pointing from the composite to their indicators. Their values are called loadings. In a reflective-reflective scenario all indicators have loadings. Arrows are pointing to their indicators only from the endogenous composites in the formative-reflective scenario. There are no loadings at all in the formative-formative scenario. The covariance matrices are computed for these three scenarios. They can be used to simulate these models. These models can also be estimated and a segmentation procedure is included as well. / GPL-3	noarch
<code>r-cbsodatar</code>	0.3.4	The data and meta data from Statistics Netherlands (< <a href="https://www.cbs.nl">https://www.cbs.nl</a> >) can be browsed and downloaded. The client uses the open data API of Statistics Netherlands. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-cbt	1.0	The Confidence Bound Target (CBT) algorithm is designed for infinite arms bandit problem. It is shown that CBT algorithm achieves the regret lower bound for general reward distributions. Reference: Hock Peng Chan and Shouri Hu (2018) <arXiv:1805.11793>. / GPL-2	noarch
r-cc	1.0	Tools for creating and visualizing statistical process control charts. Control charts are used for monitoring measurement processes, such as those occurring in manufacturing. The objective is to monitor the history of such processes and flag outlying measurements: out-of-control signals. Montgomery, D. (2009, ISBN:978-0-470-16992-6) contains an extensive discussion of the methodology. / GPL-2	noarch
r-ccagfa	1.0.8	Variational Bayesian algorithms for learning canonical correlation analysis (CCA), inter-battery factor analysis (IBFA), and group factor analysis (GFA). Inference with several random initializations can be run with the functions CCAexperiment() and GFAexperiment(). / GPL-2	noarch
r-ccapp	0.3.2	Canonical correlation analysis and maximum correlation via projection pursuit, as well as fast implementations of correlation estimators, with a focus on robust and non-parametric methods. / GPL-2	linux-64, osx-64, win-64
r-ccchooser	0.2.6	ccChooser can be used to developing and evaluation of core collections for germplasm collections (entire collection). This package used to develop a core collection for biological resources like genbanks. A core collection is defined as a sample of accessions that represent, with the lowest possible level of redundancy, the genetic diversity (the richness of gene or genotype categories) of the entire collection. The establishing a core collection that represents genetic diversity of the entire collection with minimum loss of its original diversity and minimum redundancies is an important problem for gene-banks curators and crop breeders. ccChooser establish core collection base on phenotypic data (agronomic, morphological, phenological). / GPL-2	noarch
r-cccp	0.2.4	Routines for solving convex optimization problems with cone constraints by means of interior-point methods. The implemented algorithms are partially ported from CVXOPT, a Python module for convex optimization (see < <a href="http://cvxopt.org">http://cvxopt.org</a> > for more information). / GPL-3	linux-64, osx-64, win-64
r-cccrm	1.2.1	Estimates the Concordance Correlation Coefficient to assess agreement. The scenarios considered are non-repeated measures, non-longitudinal repeated measures (replicates) and longitudinal repeated measures. The estimation approaches implemented are variance components and U-statistics approaches. / GPL-2	noarch
r-ccda	1.1	This package implements the combined cluster and discriminant analysis method for finding homogeneous groups of data with known origin as described in Kovacs et. al (2014): Classification into homogeneous groups using combined cluster and discriminant analysis (CCDA). Environmental Modelling & Software. DOI: <a href="http://dx.doi.org/10.1016/j.envsoft.2014.01.010">http://dx.doi.org/10.1016/j.envsoft.2014.01.010</a> / GPL-2	noarch
r-cchs	0.4.1	Contains a function, also called ‘cchs’, that calculates Estimator III of Borgan et al (2000), <DOI:10.1023/A:1009661900674>. This estimator is for fitting a Cox proportional hazards model to data from a case-cohort study where the subcohort was selected by stratified simple random sampling. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-cclust	0.6.2	Convex Clustering methods, including K-means algorithm, On-line Update algorithm (Hard Competitive Learning) and Neural Gas algorithm (Soft Competitive Learning), and calculation of several indexes for finding the number of clusters in a data set. / GPL-2	linux-64, osx-64, win-64
r-ccm	1.2	Classification method described in Dancik et al (2011) <doi:10.1158/0008-5472.CAN-11-2427> that classifies a sample according to the class with the maximum mean (or any other function of) correlation between the test and training samples with known classes. / GPL-2	noarch
r-ccmm	1.0	Estimate the direct and indirect (mediation) effects of treatment on the outcome when intermediate variables (mediators) are compositional and high-dimensional. Sohn, M.B. and Li, H. (2017). Compositional Mediation Analysis for Microbiome Studies. (AOAS: In revision). / GPL-2	noarch
r-ccp	1.1	Significance tests for canonical correlation analysis, including asymptotic tests and a Monte Carlo method / GPL-3	noarch
r-ccpop	1.0	Tests of association between SNPs or pairs of SNPs and binary phenotypes, in case-control / case-population / case-control-population studies. / GPL-2	noarch
r-ccremover	1.0.4	Implements a method for identifying and removing the cell-cycle effect from scRNA-Seq data. The description of the method is in Barron M. and Li J. (2016) <doi:10.1038/srep33892>. Identifying and removing the cell-cycle effect from single-cell RNA-Sequencing data. Submitted. Different from previous methods, ccRemover implements a mechanism that formally tests whether a component is cell-cycle related or not, and thus while it often thoroughly removes the cell-cycle effect, it preserves other features/signals of interest in the data. / GPL-3	noarch
r-cdb	0.0.1	A constant database is a data structure created by Daniel J. Bernstein in his cdb package. Its format consists on a sequence of (key,value)-pairs. This R package replicates the basic utilities for reading (cdbget) and writing (cddbump) constant databases. / GPL-2	noarch
r-cde	0.4.1	Facilitates searching, download and plotting of Water Framework Directive (WFD) reporting data for all waterbodies within the UK Environment Agency area. The types of data that can be downloaded are: WFD status classification data, Reasons for Not Achieving Good (RNAG) status, objectives set for waterbodies, measures put in place to improve water quality and details of associated protected areas. The site accessed is < <a href="https://environment.data.gov.uk/catchment-planning/">https://environment.data.gov.uk/catchment-planning/</a> >. The data are made available under the Open Government Licence v3.0 < <a href="https://www.nationalarchives.gov.uk/doc/open-government-licence/version/3/">https://www.nationalarchives.gov.uk/doc/open-government-licence/version/3/</a> >. This package has been peer-reviewed by rOpenSci (v. 0.4.0). / GPL-3	noarch
r-cdft	1.0.1	This package proposes a statistical downscaling method for cumulative distribution functions (CDF), as well as the computation of the Cramér-von Mises statistics U, and the Kolmogorov-Smirnov statistics KS. / GPL-2	noarch
r-cdlasso	1.1	Coordinate Descent Algorithms for Lasso Penalized L1, L2, and Logistic Regression / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-cdltools</a>	0.14	Downloads USDA National Agricultural Statistics Service (NASS) cropscape data for a specified state. Utilities for fips, abbreviation, and name conversion are also provided. Full functionality requires an internet connection, but data sets can be cached for later off-line use. / Unlimited	linux-64, osx-64, win-64
<a href="#">r-cdnmoney</a>	2012.4	Components of Canadian Credit Aggregates and Monetary Aggregates with continuity adjustments. / GPL-2	noarch
<a href="#">r-cdrom</a>	1.1	Classification is based on the recently developed phylogenetic approach by Assis and Bachtrog (2013). The method classifies the evolutionary mechanisms retaining pairs of duplicate genes (conservation, neofunctionalization, subfunctionalization, or specialization) by comparing gene expression profiles of duplicate genes in one species to those of their single-copy ancestral genes in a sister species. / GPL-2	noarch
<a href="#">r-cdvine</a>	1.4	Functions for statistical inference of canonical vine (C-vine) and D-vine copulas. Tools for bivariate exploratory data analysis and for bivariate as well as vine copula selection are provided. Models can be estimated either sequentially or by joint maximum likelihood estimation. Sampling algorithms and plotting methods are also included. Data is assumed to lie in the unit hypercube (so-called copula data). / GPL-2	linux-64, osx-64, win-64
<a href="#">r-cec</a>	0.10.2	CEC divides data into Gaussian type clusters. The implementation allows the simultaneous use of various type Gaussian mixture models, performs the reduction of unnecessary clusters and it's able to discover new groups. Based on Spurek, P. and Tabor, J. (2014) <doi:10.1016/j.patcog.2014.03.006>. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-cec2005benchmark</a>	1.0.4	This package is a wrapper for the C implementation of the 25 benchmark functions for the CEC 2005 Special Session on Real-Parameter Optimization. The original C code by Santosh Tiwari and related documentation are available at <a href="http://www.ntu.edu.sg/home/EPNSugan/index_files/CEC-05/CEC05.htm">http://www.ntu.edu.sg/home/EPNSugan/index_files/CEC-05/CEC05.htm</a> . / GPL-3	linux-64, osx-64, win-64
<a href="#">r-cec2013</a>	0.1.5	This package provides R wrappers for the C implementation of 28 benchmark functions defined for the Special Session and Competition on Real-Parameter Single Objective Optimization at CEC-2013. The focus of this package is to provide an open-source and multi-platform implementation of the CEC2013 benchmark functions, in order to make easier for researchers to test the performance of new optimization algorithms in a reproducible way. The original C code (Windows only) was provided by Jane Jing Liang, while GNU/Linux comments were made by Janez Brest. This package was gently authorised for publication on CRAN by Ponnuthurai Nagaratnam Suganthan. The official documentation is available at <a href="http://www.ntu.edu.sg/home/EPNSugan/index_files/CEC2013/CEC2013.htm">http://www.ntu.edu.sg/home/EPNSugan/index_files/CEC2013/CEC2013.htm</a> . Bugs reports/comments/questions are very welcomed (in English, Spanish or Italian). / GPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-cellranger	1.1.0	Helper functions to work with spreadsheets and the A1:D10 style of cell range specification. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-cengam	0.5.3	Implementation of Tobit type I and type II families for censored regression using the ‘mgcv’ package, based on methods detailed in Woods (2016) <doi:10.1080/01621459.2016.1180986>. / GPL-2	noarch
r-censcov	1.0_0	Implementations of threshold regression approaches for linear regression models with a covariate subject to random censoring, including deletion threshold regression and completion threshold regression. Reverse survival regression, which flip the role of response variable and the covariate, is also considered. / GPL-3	noarch
r-censnid	0_0	Implements AS138, AS139. / GPL-2	linux-64, osx-64, win-64
r-censorcopula	2.0	Implement an interval censor method to break ties when using data with ties to fitting a bivariate copula. / GPL-2	noarch
r-censregmod	1.0	Fits univariate censored linear regression model under Normal or Student-t distribution / GPL (>= 3.0)	noarch
r-census2016	0.2.0	Contains selected variables from the time series profiles for statistical areas level 2 from the 2006, 2011, and 2016 censuses of population and housing, Australia. Also provides methods for viewing the questions asked for convenience during analysis. / CC BY 4.0	noarch
r-censusapi	0.6.0	A wrapper for the U.S. Census Bureau APIs that returns data frames of Census data and metadata. Available datasets include the Decennial Census, American Community Survey, Small Area Health Insurance Estimates, Small Area Income and Poverty Estimates, Population Estimates and Projections, and more. / GPL-3	noarch
r-censys	0.1.0	The ‘Censys’ public search engine enables researchers to quickly ask questions about the hosts and networks that compose the Internet. Details on how ‘Censys’ was designed and how it is operated are available at < <a href="https://www.censys.io/about">https://www.censys.io/about</a> >. Both basic and extended research access queries are made available. More information on the SQL dialect used by the ‘Censys’ engine can be found at < <a href="https://cloud.google.com/bigquery/docs/reference/legacy-sql">https://cloud.google.com/bigquery/docs/reference/legacy-sql</a> >. / AGPL-3	noarch
r-centiserve	1.0.0	Calculates centrality indices additional to the ‘igraph’ package centrality functions. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-cents	0.1_4	Fit censored time series / GPL-2	linux-64, osx-64, win-64
r-cepreader	1.1_3	Read Condensed Cornell Ecology Program ('CEP') and legacy 'CANOCO' files into R data frames. / MIT	linux-64, osx-64
r-ceriolioutlierdetection	1.1.9	Implements the iterated RMCD method of Cerioli (2010) for multivariate outlier detection via robust Mahalanobis distances. Also provides the finite-sample RMCD method discussed in the paper, as well as the methods provided in Hardin and Rocke (2005) <doi:10.1198/106186005X77685> and Green and Martin (2017). / GPL-2	noarch
r-cernaseek	2.1	Provides several functions to identify and analyse miRNA sponge, including popular methods for identifying miRNA sponge interactions, two types of global ceRNA regulation prediction methods and four types of context-specific prediction methods( Li Y et al.(2017) <doi:10.1093/bib/bbx137>), which are based on miRNA-messenger RNA regulation alone, or by integrating heterogeneous data, respectively. In addition, For predictive ceRNA relationship pairs, this package provides several downstream analysis algorithms, including regulatory network analysis and functional annotation analysis, as well as survival prognosis analysis based on expression of ceRNA ternary pair. / GPL-3	noarch
r-cernn	0.1	An implementation of the covariance estimation method proposed in Chi and Lange (2014), Stable estimation of a covariance matrix guided by nuclear norm penalties, Computational Statistics and Data Analysis 80:117-128. / MIT	noarch
r-cetcolor	0.2.0	Collection of perceptually uniform colour maps made by Peter Kovesi (2015) Good Colour Maps: How to Design Them <arXiv:1509.03700> at the Centre for Exploration Targeting (CET). / CC BY-SA 4.0	noarch
r-cfa	0.10	Analysis of configuration frequencies for simple and repeated measures, multiple-samples CFA, hierarchical CFA, bootstrap CFA, functional CFA, Kieser-Victor CFA, and Lindner's test using a conventional and an accelerated algorithm. / GPL-2	linux-64, osx-64, win-64
r-cfc	1.1.2	Numerical integration of cause-specific survival curves to arrive at cause-specific cumulative incidence functions, with three usage modes: 1) Convenient API for parametric survival regression followed by competing-risk analysis, 2) API for CFC, accepting user-specified survival functions in R, and 3) Same as 2, but accepting survival functions in C. / GPL-2	linux-64, osx-64, win-64
r-cfestimatequantiles	1.0	Estimate quantiles using formula (18) from <a href="http://www.jaschke-net.de/papers/CoFi.pdf">http://www.jaschke-net.de/papers/CoFi.pdf</a> (Yaschke; 2001) / GPL-2	noarch
r-cfma	1.0	Performs causal functional mediation analysis (CFMA) for functional treatment, functional mediator, and functional outcome. This package includes two functional mediation model types: (1) a concurrent mediation model and (2) a historical influence mediation model. See Zhao et al. (2018), Functional Mediation Analysis with an Application to Functional Magnetic Resonance Imaging Data, <arXiv:1805.06923> for details. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-cgauc	1.2.1	The cgAUC can calculate the AUC-type measure of Obuchowski(2006) when gold standard is continuous, and find the optimal linear combination of variables with respect to this measure. / GPL-2	linux-64, osx-64, win-64
r-cgdsr	1.3.0	Provides a basic set of R functions for querying the Cancer Genomics Data Server (CGDS), hosted by the Computational Biology Center at Memorial-Sloan-Kettering Cancer Center (MSKCC) at <www.cbioportal.org>. / LGPL-3	noarch
r-cge	0.1.9	Developing general equilibrium models, computing general equilibrium and simulating economic dynamics with structural dynamic models in LI (2019, ISBN: 9787521804225) General Equilibrium and Structural Dynamics: Perspectives of New Structural Economics. Beijing: Economic Science Press. / GPL-2   GPL-3	noarch
r-cggp	1.0.1	Run computer experiments using the adaptive composite grid algorithm with a Gaussian process model. The algorithm works best when running an experiment that can evaluate thousands of points from a deterministic computer simulation. This package is an implementation of a forthcoming paper by Plumlee, Erickson, Ankenman, et al. For a preprint of the paper, contact the maintainer of this package. / GPL-3	linux-64, osx-64, win-64
r-cgh	1.0_7	Functions to analyze microarray comparative genome hybridization data using the Smith-Waterman algorithm / GPL-2	linux-64, osx-64, win-64
r-cglasso	1.1.1	The l1-penalized censored Gaussian graphical model is an extension of the graphical lasso estimator developed to handle datasets with censored observations. An EM-like algorithm is implemented to estimate the parameters of the censored Gaussian graphical models. / GPL-2	linux-64, osx-64, win-64
r-cgp	2.1_1	Fit composite Gaussian process (CGP) models as described in Ba and Joseph (2012) Composite Gaussian Process Models for Emulating Expensive Functions, Annals of Applied Statistics. The CGP model is capable of approximating complex surfaces that are not second-order stationary. Important functions in this package are CGP, print.CGP, summary.CGP, predict.CGP and plotCGP. / LGPL-2.1	noarch
r-cgraph	4.0.3	Allows to create, evaluate, and differentiate computational graphs in R. A computational graph is a graph representation of a multivariate function decomposed by its (elementary) operations. Nodes in the graph represent arrays while edges represent dependencies among the arrays. An advantage of expressing a function as a computational graph is that this enables to differentiate the function by automatic differentiation. The 'cgraph' package supports various operations including basic arithmetic, trigonometry operations, and linear algebra operations. It differentiates computational graphs by reverse automatic differentiation. The flexible architecture of the package makes it applicable to solve a variety of problems including local sensitivity analysis, gradient-based optimization, and machine learning. / Apache License 2.0	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-cgwttools</a>	3.0.1	Functions for performing quick observations or evaluations of data, including a variety of ways to list objects by size, class, etc. In addition, functions which mimic Unix shell commands, including 'head', 'tail', 'pushd', and 'popd'. The functions 'seqle' and 'reverse.seqle' mimic the base 'rle' but can search for linear sequences. The function 'splatnd' allows the user to generate zero-argument commands without the need for 'makeActiveBinding'. / LGPL-3	noarch
<a href="#">r-chandwich</a>	1.1.2	Performs adjustments of a user-supplied independence loglikelihood function using a robust sandwich estimator of the parameter covariance matrix, based on the methodology in Chandler and Bate (2007) <doi:10.1093/biomet/asm015>. This can be used for cluster correlated data when interest lies in the parameters of the marginal distributions or for performing inferences that are robust to certain types of model misspecification. Functions for profiling the adjusted loglikelihoods are also provided, as are functions for calculating and plotting confidence intervals, for single model parameters, and confidence regions, for pairs of model parameters. Nested models can be compared using an adjusted likelihood ratio test. / GPL-2	noarch
<a href="#">r-changepoint</a>	2.2.2	Implements various mainstream and specialised changepoint methods for finding single and multiple changepoints within data. Many popular non-parametric and frequentist methods are included. The <code>cpt.mean()</code> , <code>cpt.var()</code> , <code>cpt.meanvar()</code> functions should be your first point of call. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-changepointshd</a>	0.3.1	This implements the methods developed in, L. Bybee and Y. Atchade. (2018). Contains a series of methods for estimating change-points given user specified black-box models. The methods include binary segmentation for multiple change-point estimation. For estimating each individual change-point the package includes simulated annealing, brute force, and, for Gaussian graphical models, an applications specific rank-one update implementation. Additionally, code for estimating Gaussian graphical models is included. The goal of this package is to allow for the efficient estimation of change-points in complicated models with high dimensional data. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-changepointsvar</a>	0.1.0	Detection of change-points for variance of heteroscedastic Gaussian variables with piecewise constant variance function. Adelfio, G. (2012), Change-point detection for variance piecewise constant models, Communications in Statistics, Simulation and Computation, 41:4, 437-448, <doi:10.1080/03610918.2011.592248>. / GPL-2	noarch
<a href="#">r-changepointtesting</a>	1.0	A multiple testing procedure for clustered alternative hypotheses. It is assumed that the p-values under the null hypotheses follow U(0,1) and that the distributions of p-values from the alternative hypotheses are stochastically smaller than U(0,1). By aggregating information, this method is more sensitive to detecting signals of low magnitude than standard methods. Additionally, sporadic small p-values appearing within a null hypotheses sequence are avoided by averaging on the neighboring p-values. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-channelattribution</a>	1.16	Advertisers use a variety of online marketing channels to reach consumers and they want to know the degree each channel contributes to their marketing success. This is called the online multi-channel attribution problem. This package contains a probabilistic algorithm for the attribution problem. The model uses a k-order Markov representation to identify structural correlations in the customer journey data. The package also contains three heuristic algorithms (first-touch, last-touch and linear-touch approach) for the same problem. The algorithms are implemented in C. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-chaos01</a>	1.2.1	Computes and visualize the results of the 0-1 test for chaos proposed by Gottwald and Melbourne (2004) <DOI:10.1137/080718851>. The algorithm is available in parallel for the independent values of parameter c. Additionally, fast RQA is added to distinguish chaos from noise. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-chargetransport</a>	1.0.2	This package provides functions to compute Marcus, Marcus-Levich-Jortner or Landau-Zener charge transfer rates. These rates can then be used to perform kinetic Monte Carlo simulations to estimate charge carrier mobilities in molecular materials. The preparation of this package was supported by the the Fondazione Cariplo (PLENOS project, ref. 2011-0349). / GPL-3	linux-64, osx-64, win-64
<a href="#">r-chcn</a>	1.5	A compilation of historical through contemporary climate measurements scraped from the Environment Canada Website Including tools for scraping data, creating metadata and forming temperature files. / GPL-2	noarch
<a href="#">r-cheb</a>	0.3	Discrete Linear Chebyshev Approximation / GPL-3	linux-64, osx-64, win-64
<a href="#">r-checkarg</a>	0.1.0	Utility functions that allow checking the basic validity of a function argument or any other value, including generating an error and assigning a default in a single line of code. The main purpose of the package is to provide simple and easily readable argument checking to improve code robustness. / GPL-2	noarch
<a href="#">r-checkdigit</a>	0.1_1	A set of functions to calculate check digits according to various algorithms and to verify whether a string ends in a valid check digit / GPL-3	noarch
<a href="#">r-checkmate</a>	1.9.1	Tests and assertions to perform frequent argument checks. A substantial part of the package was written in C to minimize any worries about execution time overhead. / BSD_3_clause file LICENSE	linux-32, linux-64, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-checkpoint</a>	0.4.6	The goal of checkpoint is to solve the problem of package reproducibility in R. Specifically, checkpoint allows you to install packages as they existed on CRAN on a specific snapshot date as if you had a CRAN time machine. To achieve reproducibility, the checkpoint() function installs the packages required or called by your project and scripts to a local library exactly as they existed at the specified point in time. Only those packages are available to your project, thereby avoiding any package updates that came later and may have altered your results. In this way, anyone using checkpoint's checkpoint() can ensure the reproducibility of your scripts or projects at any time. To create the snapshot archives, once a day (at midnight UTC) Microsoft refreshes the Austria CRAN mirror on the Microsoft R Archived Network server (< <a href="https://mran.microsoft.com/">https://mran.microsoft.com/</a> >). Immediately after completion of the rsync mirror process, the process takes a snapshot, thus creating the archive. Snapshot archives exist starting from 2014-09-17. / GPL-2	linux-64, noarch, osx-64, win-64
<a href="#">r-cheddar</a>	0.1.6	Provides a flexible, extendable representation of an ecological community and a range of functions for analysis and visualisation, focusing on food web, body mass and numerical abundance data. Allows inter-web comparisons such as examining changes in community structure over environmental, temporal or spatial gradients. / BSD_2_clause	linux-64, osx-64, win-64
<a href="#">r-chemical</a>	0.2.1	Simple functions for plotting linear calibration functions and estimating standard errors for measurements according to the Handbook of Chemometrics and Qualimetrics: Part A by Massart et al. There are also functions estimating the limit of detection (LOD) and limit of quantification (LOQ). The functions work on model objects from - optionally weighted - linear regression (lm) or robust linear regression ('rlm' from the 'MASS' package). / GPL-2	noarch
<a href="#">r-chemometricswithr</a>	0.1.13	Functions and scripts used in the book Chemometrics with R - Multivariate Data Analysis in the Natural Sciences and Life Sciences by Ron Wehrens, Springer (2011). Data used in the package are available from github. / GPL-2	noarch
<a href="#">r-chemospec</a>	5.1.48	A collection of functions for top-down exploratory data analysis of spectral data including nuclear magnetic resonance (NMR), infrared (IR), Raman, X-ray fluorescence (XRF) and other similar types of spectroscopy. Includes functions for plotting and inspecting spectra, peak alignment, hierarchical cluster analysis (HCA), principal components analysis (PCA) and model-based clustering. Robust methods appropriate for this type of high-dimensional data are available. ChemoSpec is designed for structured experiments, such as metabolomics investigations, where the samples fall into treatment and control groups. Graphical output is formatted consistently for publication quality plots. ChemoSpec is intended to be very user friendly and to help you get usable results quickly. A vignette covering typical operations is available. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-chemospec2d</a>	0.3.16	A collection of functions for exploratory chemometrics of 2D spectroscopic data sets such as COSY (correlated spectroscopy) and HSQC (heteronuclear single quantum coherence) 2D NMR (nuclear magnetic resonance) spectra. ‘ChemoSpec2D’ deploys methods aimed primarily at classification of samples and the identification of spectral features which are important in distinguishing samples from each other. Each 2D spectrum (a matrix) is treated as the unit of observation, and thus the physical sample in the spectrometer corresponds to the sample from a statistical perspective. In addition to chemometric tools, a few tools are provided for plotting 2D spectra, but these are not intended to replace the functionality typically available on the spectrometer. ‘ChemoSpec2D’ takes many of its cues from ‘ChemoSpec’ and tries to create consistent graphical output and to be very user friendly. / GPL-3	noarch
<a href="#">r-chemospecutils</a>	0.3.39	Functions supporting the common needs of packages ‘ChemoSpec’ and ‘ChemoSpec2D’. / GPL-3	noarch
<a href="#">r-cherry</a>	0.6.1	Provides an alternative approach to multiple testing by calculating a simultaneous upper confidence bounds for the number of true null hypotheses among any subset of the hypotheses of interest, using the methods of Goeman and Solari (2011) <doi:10.1214/11-STS356>. / GPL-2	noarch
<a href="#">r-chff</a>	0.1.0	The software matches the current history to the closest history in a time series to build a forecast. / GPL-3	noarch
<a href="#">r-chi</a>	0.1	Light weight implementation of the standard distribution functions for the chi distribution, wrapping those for the chi-squared distribution in the stats package. / GPL-2	noarch
<a href="#">r-chi2x3way</a>	1.1	Provides two index partitions for three-way contingency tables: partition of the association measure chi-squared and of the predictability index tau under several representative hypotheses about the expected frequencies (hypothesized probabilities). / GPL (> 2)	noarch
<a href="#">r-chillmodels</a>	1.0.0	Calculates the chilling and heat accumulation for studies of the temperate fruit trees. The models in this package are: Utah (Richardson et al., 1974, ISSN:0018-5345), Positive Chill Units - PCU (Linsley-Noaks et al., 1995, ISSN:1017-0316), GDH-A - Growing Degree Hours by Anderson et al.(1986, ISSN:0567-7572), GDH-R - Growing Degree Hours by Richardson et al.(1975, ISSN:0018-5345), North Carolina (Shaltout e Unrath, 1983, ISSN:0003-1062), Landsberg Model (Landsberg, 1974, ISSN:0305-7364), Q10 Model (Bidabe, 1967, ISSN:0031-9368), Jones Model (Jones et al., 2013 <DOI:10.1111/j.1438-8677.2012.00590.x>), Low-Chill Model (Gilreath and Buchanan, 1981, ISSN:0003-1062), Model for Cherry Sweetheart (Guak and Nielsen, 2013 <DOI:10.1007/s13580-013-0140-9>), Model for apple Gala (Guak and Nielsen, 2013 <DOI:10.1007/s13580-013-0140-9>), Taiwan Model (Lu et al., 2012 <DOI:10.17660/ActaHortic.2012.962.35>), Dynamic Model (Fishman et al., 1987, ISSN:0022-5193) adapted from the function Dynamic_Model() of the ‘chillR’ package (Luedeling, 2018), Unified Model (Chuine et al., 2016 <DOI:10.1111/gcb.13383>) and Heat Restriction model. / GPL-3	noarch
<a href="#">r-chiptest</a>	1.0	Nonparametric Tests to identify the differential enrichment region for two conditions or time-course ChIP-seq data. It includes: data preprocessing function, estimation of a small constant used in hypothesis testing, a kernel-based two sample nonparametric test, two assumption-free two sample nonparametric test. / GPL (>= 2.15.1)	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-chnosz	1.3.3	An integrated set of tools for thermodynamic calculations in aqueous geochemistry and geobiochemistry. Functions are provided for writing balanced reactions to form species from user-selected basis species and for calculating the standard molal properties of species and reactions, including the standard Gibbs energy and equilibrium constant. Calculations of the non-equilibrium chemical affinity and equilibrium chemical activity of species can be portrayed on diagrams as a function of temperature, pressure, or activity of basis species; in two dimensions, this gives a maximum affinity or predominance diagram. The diagrams have formatted chemical formulas and axis labels, and water stability limits can be added to Eh-pH, oxygen fugacity- temperature, and other diagrams with a redox variable. The package has been developed to handle common calculations in aqueous geochemistry, such as solubility due to complexation of metal ions, mineral buffers of redox or pH, and changing the basis species across a diagram (mosaic diagrams). CHNOSZ also has unique capabilities for comparing the compositional and thermodynamic properties of different proteins. / GPL-2	linux-64, osx-64, win-64
r-choicedes	0.9.3	Design functions for DCMs and other types of choice studies (including MaxDiff and other tradeoffs). / GPL-2	noarch
r-choicemodelr	1.2	Implements an MCMC algorithm to estimate a hierarchical multinomial logit model with a normal heterogeneity distribution. The algorithm uses a hybrid Gibbs Sampler with a random walk metropolis step for the MNL coefficients for each unit. Dependent variable may be discrete or continuous. Independent variables may be discrete or continuous with optional order constraints. Means of the distribution of heterogeneity can optionally be modeled as a linear function of unit characteristics variables. / GPL-3	noarch
r-cholwishart	1.0.1	Sampling from the Cholesky factorization of a Wishart random variable, sampling from the inverse Wishart distribution, sampling from the Cholesky factorization of an inverse Wishart random variable, sampling from the pseudo Wishart distribution, sampling from the generalized inverse Wishart distribution, computing densities for the Wishart and inverse Wishart distributions, and computing the multivariate gamma and digamma functions. / GPL-3	linux-64, osx-64, win-64
r-choplump	1.0.0	Choplump Tests are Permutation Tests for Comparing Two Groups with Some Positive but Many Zero Responses / GPL-3	noarch
r-chopthin	0.2.2	Resampling is a standard step in particle filtering and in sequential Monte Carlo. This package implements the chopthin resampler, which keeps a bound on the ratio between the largest and the smallest weights after resampling. / GPL-3	linux-64, osx-64, win-64
r-chor	0.0.4	Learning the structure of graphical models from datasets with thousands of variables. More information about the research papers detailing the theory behind Chordalysis is available at < <a href="http://www.francois-petitjean.com/Research">http://www.francois-petitjean.com/Research</a> > (KDD 2016, SDM 2015, ICDM 2014, ICDM 2013). The R package development site is < <a href="https://github.com/HerrmannM/Monash-ChoR">https://github.com/HerrmannM/Monash-ChoR</a> >. / GPL-3	noarch
r-chords	0.95.4	Maximum likelihood estimation in respondent driven samples. / GPL-2	noarch
r-choroplethmaps	1.0.1	Contains 3 maps. 1) US States 2) US Counties 3) Countries of the world. / BSD_3_clause	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-chromomap</a>	0.2	Provides interactive, configurable and elegant graphics visualization of the chromosomes or chromosome regions of any living organism allowing users to map chromosome elements (like genes, SNPs etc.) on the chromosome plot. It introduces a special plot viz. the chromosome heatmap that, in addition to mapping elements, can visualize the data associated with chromosome elements (like gene expression) in the form of heat colors which can be highly advantageous in the scientific interpretations and research work. Because of the large size of the chromosomes, it is impractical to visualize each element on the same plot. However, the plot provides a magnified view for each of chromosome locus to render additional information and visualization specific for that location. You can map thousands of genes and can view all mappings easily. Users can investigate the detailed information about the mappings (like gene names or total genes mapped on a location) or can view the magnified single or double stranded view of the chromosome at a location showing each mapped element in sequential order. The package provide multiple features like visualizing multiple sets, chromosome heat-maps, group annotations, adding hyperlinks, and labelling. The plots can be saved as HTML documents that can be customized and shared easily. In addition, you can include them in R Markdown or in R ‘Shiny’ applications. / GPL-3	noarch
<a href="#">r-chron</a>	2.3_5	Provides chronological objects which can handle dates and times. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-chunkr</a>	1.1.1	Read tables chunk by chunk using a C backend and a simple R interface. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-ciaawconsensus</a>	1.3	Calculation of consensus values for atomic weights, isotope amount ratios, and isotopic abundances with the associated uncertainties using multivariate meta-regression approach for consensus building. / Unlimited	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-ciee</a>	0.1.1	In many studies across different disciplines, detailed measures of the variables of interest are available. If assumptions can be made regarding the direction of effects between the assessed variables, this has to be considered in the analysis. The functions in this package implement the novel approach CIEE (causal inference using estimating equations; Konigorski et al., 2018, <DOI:10.1002/gepi.22107>) for estimating and testing the direct effect of an exposure variable on a primary outcome, while adjusting for indirect effects of the exposure on the primary outcome through a secondary intermediate outcome and potential factors influencing the secondary outcome. The underlying directed acyclic graph (DAG) of this considered model is described in the vignette. CIEE can be applied to studies in many different fields, and it is implemented here for the analysis of a continuous primary outcome and a time-to-event primary outcome subject to censoring. CIEE uses estimating equations to obtain estimates of the direct effect and robust sandwich standard error estimates. Then, a large-sample Wald-type test statistic is computed for testing the absence of the direct effect. Additionally, standard multiple regression, regression of residuals, and the structural equation modeling approach are implemented for comparison. / GPL-2	noarch
<a href="#">r-cifsmry</a>	1.0.1	Estimate of cumulative incidence function in two samples. Provide weighted summary statistics based on various methods and weights. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-cim</a>	1.0.0	Produces statistical indicators of the impact of migration on the socio-demographic composition of an area. Three measures can be used: ratios, percentages and the Duncan index of dissimilarity. The input data files are assumed to be in an origin-destination matrix format, with each cell representing a flow count between an origin and a destination area. Columns are expected to represent origins, and rows are expected to represent destinations. The first row and column are assumed to contain labels for each area. See Rodriguez-Vignoli and Rowe (2018) <doi:10.1080/00324728.2017.1416155> for technical details. / GPL-2	noarch
<a href="#">r-cin</a>	0.1	Many experiments in neuroscience involve randomized and fast stimulation while the continuous outcome measures respond at much slower time scale, for example event-related fMRI. This package provide valid statistical tools with causal interpretation under these challenging settings, without imposing model assumptions. / GPL-2	noarch
<a href="#">r-cinid</a>	1.2	This package provides functions to compute a method for identifying the instar of Curculionid larvae from the observed distribution of the headcapsule size of mature larvae. / GPL (>= 2.0)	noarch
<a href="#">r-cinterpolate</a>	1.0.0	Simple interpolation methods designed to be used from C code. Supports constant, linear and spline interpolation. An R wrapper is included but this package is primarily designed to be used from C code using 'LinkingTo'. The spline calculations are classical cubic interpolation, e.g., Forsythe, Malcolm and Moler (1977) <ISBN: 9780131653320>. / MIT	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-ciplot</a>	1.0	Plot confidence interval from the objects of statistical tests such as <code>t.test()</code> , <code>var.test()</code> , <code>cor.test()</code> , <code>prop.test()</code> and <code>fisher.test()</code> ('htest' class), Tukey test [ <code>TukeyHSD()</code> ], Dunnett test [ <code>glht()</code> in 'multcomp' package], logistic regression [ <code>glm()</code> ], and Tukey or Games-Howell test [ <code>posthocTGH()</code> in 'userfriendlyscience' package]. Users are able to set the styles of lines and points. This package contains the function to calculate odds ratios and their confidence intervals from the result of logistic regression. / GPL-2	noarch
<a href="#">r-cir</a>	2.0.0	Isotonic regression (IR), as well as a great small-sample improvement to IR called CIR, interval estimates for both, and additional utilities. / GPL-2	noarch
<a href="#">r-circmle</a>	0.2.1	A series of wrapper functions to implement the 10 maximum likelihood models of animal orientation described by Schnute and Groot (1992) <DOI:10.1016/S0003-3472(05)80068-5>. The functions also include the ability to use different optimizer methods and calculate various model selection metrics (i.e., AIC, AICc, BIC). / GPL-2	noarch
<a href="#">r-circnntsr</a>	2.2	Includes functions for the analysis of circular data using distributions based on Nonnegative Trigonometric Sums (NNTS). The package includes functions for calculation of densities and distributions, for the estimation of parameters, for plotting and more. / GPL-2	noarch
<a href="#">r-circoutlier</a>	3.2.3	Detection of outliers in circular-circular regression models, modifying its and estimating of models parameters. / GPL-2	noarch
<a href="#">r-circstats</a>	0.2_6	Circular Statistics, from Topics in Circular Statistics (2001) S. Rao Jammalamadaka and A. SenGupta, World Scientific. / GPL-2	noarch
<a href="#">r-circular</a>	0.4_9	Circular Statistics, from Topics in circular Statistics (2001) S. Rao Jammalamadaka and A. SenGupta, World Scientific. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-circularddm</a>	0.1.0	Circular drift-diffusion model for continuous reports. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-cirt</a>	1.3.0	Jointly model the accuracy of cognitive responses and item choices within a bayesian hierarchical framework as described by Culpepper and Balamuta (2015) <doi:10.1007/s11336-015-9484-7>. In addition, the package contains the datasets used within the analysis of the paper. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<code>r-cit</code>	2.2	A likelihood-based hypothesis testing approach is implemented for assessing causal mediation. For example, it could be used to test for mediation of a known causal association between a DNA variant, the ‘instrumental variable’, and a clinical outcome or phenotype by gene expression or DNA methylation, the potential mediator. Another example would be testing mediation of the effect of a drug on a clinical outcome by the molecular target. The hypothesis test generates a p-value or permutation-based FDR value with confidence intervals to quantify uncertainty in the causal inference. The outcome can be represented by either a continuous or binary variable, the potential mediator is continuous, and the instrumental variable can be continuous or binary and is not limited to a single variable but may be a design matrix representing multiple variables. / Artistic-2.0	linux-64, osx-64, win-64
<code>r-citbcmst</code>	1.0.4	This package implements the approach to assign tumor gene expression dataset to the 6 CIT Breast Cancer Molecular Subtypes described in Guedj et al 2012. / GPL-2	noarch
<code>r-citccmst</code>	1.0.2	This package implements the approach to assign tumor gene expression dataset to the 6 CIT Colon Cancer Molecular Subtypes described in Marisa et al 2013. / GPL-2	noarch
<code>r-cityplot</code>	2.0	Input: a csv-file for each database table and a controlfile describing relations between tables. Output: An extended ER diagram / LGPL-3	noarch
<code>r-cklrt</code>	0.2.3	Composite Kernel Machine Regression based on Likelihood Ratio Test (CKLRT): in this package, we develop a kernel machine regression framework to model the overall genetic effect of a SNP-set, considering the possible GE interaction. Specifically, we use a composite kernel to specify the overall genetic effect via a nonparametric function and we model additional covariates parametrically within the regression framework. The composite kernel is constructed as a weighted average of two kernels, one corresponding to the genetic main effect and one corresponding to the GE interaction effect. We propose a likelihood ratio test (LRT) and a restricted likelihood ratio test (RLRT) for statistical significance. We derive a Monte Carlo approach for the finite sample distributions of LRT and RLRT statistics. (N. Zhao, H. Zhang, J. Clark, A. Maity, M. Wu. Composite Kernel Machine Regression based on Likelihood Ratio Test with Application for Combined Genetic and Gene-environment Interaction Effect (Submitted).) / GPL-3	linux-64, osx-64, win-64
<code>r-ckmeans.1d.dp</code>	4.2.2	Fast optimal univariate clustering and segmentation by dynamic programming. Three types of problem including univariate k-means, k-median, and k-segments are solved with guaranteed optimality and reproducibility. The core algorithm minimizes the sum of within-cluster distances using respective metrics. Its advantage over heuristic clustering algorithms in efficiency and accuracy is increasingly pronounced as the number of clusters k increases. Weighted k-means and unweighted k-segments algorithms can also optimally segment time series and perform peak calling. An auxiliary function generates histograms that are adaptive to patterns in data. In contrast to heuristic methods, this package provides a powerful set of tools for univariate data analysis with guaranteed optimality. Use four spaces when indenting paragraphs within the Description. / LGPL-3	linux-64, osx-64, win-64
<code>r-cla</code>	0.95	Implements ‘Markovitz’ Critical Line Algorithm (‘CLA’) for classical mean-variance portfolio optimization, see Markovitz (1952) <doi:10.2307/2975974>. Care has been taken for correctness in light of previous buggy implementations. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-cladorcpp</a>	0.15.1	Various cladogenesis-related calculations that are slow in pure R are implemented in C with Rcpp. These include the calculation of the probability of various scenarios for the inheritance of geographic range at the divergence events on a phylogenetic tree, and other calculations necessary for models which are not continuous-time markov chains (CTMC), but where change instead occurs instantaneously at speciation events. Typically these models must assess the probability of every possible combination of (ancestor state, left descendent state, right descendent state). This means that there are up to $(\# \text{ of states})^3$ combinations to investigate, and in biogeographical models, there can easily be hundreds of states, so calculation time becomes an issue. C implementation plus clever tricks (many combinations can be eliminated a priori) can greatly speed the computation time over naive R implementations. CITATION INFO: This package is the result of my Ph.D. research, please cite the package if you use it! Type: <code>citation(package=cladoRcpp)</code> to get the citation information. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-clam</a>	2.3.2	Performs ‘classical’ age-depth modelling of dated sediment deposits - prior to applying more sophisticated techniques such as Bayesian age-depth modelling. Any radiocarbon dated depths are calibrated. Age-depth models are constructed by sampling repeatedly from the dated levels, each time drawing age-depth curves. Model types include linear interpolation, linear or polynomial regression, and a range of splines. See Blaauw (2010). <doi:10.1016/j.quageo.2010.01.002>. / GPL-2	noarch
<a href="#">r-clamr</a>	2.1.1	Implementation of the Wilkinson and Ivany (2002) approach to paleoclimate analysis, applied to isotope data extracted from clams. / GPL-3	noarch
<a href="#">r-clarifai</a>	0.4.2	Get description of images from Clarifai API. For more information, see < <a href="http://clarifai.com">http://clarifai.com</a> >. Clarifai uses a large deep learning cloud to come up with descriptive labels of the things in an image. It also provides how confident it is about each of the labels. / MIT	noarch
<a href="#">r-class</a>	7.3.1	Various functions for classification, including k-nearest neighbour, Learning Vector Quantization and Self-Organizing Maps. / GPL-2   GPL-3	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-classify</a>	0.4	Given $p$ -dimensional training data containing $d$ groups (the design space), a classification algorithm (classifier) predicts which group new data belongs to. Generally the input to these algorithms is high dimensional, and the boundaries between groups will be high dimensional and perhaps curvilinear or multifaceted. This package implements methods for understanding the division of space between the groups. / MIT	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-classint</a>	0.3_1	Selected commonly used methods for choosing univariate class intervals for mapping or other graphics purposes. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-cld2</a>	1.2	Bindings to Google's C library Compact Language Detector 2 (see < <a href="https://github.com/cld2owners/cld2#readme">https://github.com/cld2owners/cld2#readme</a> > for more information). Probabilistically detects over 80 languages in plain text or HTML. For mixed-language input it returns the top three detected languages and their approximate proportion of the total classified text bytes (e.g. 80% English and 20% French out of 1000 bytes). There is also a 'cld3' package on CRAN which uses a neural network model instead. / Apache License 2.0	linux-64, osx-64, win-64
<a href="#">r-cld3</a>	1.2	Google's Compact Language Detector 3 is a neural network model for language identification and the successor of 'cld2' (available from CRAN). The algorithm is still experimental and takes a novel approach to language detection with different properties and outcomes. It can be useful to combine this with the Bayesian classifier results from 'cld2'. See < <a href="https://github.com/google/cld3#readme">https://github.com/google/cld3#readme</a> > for more information. / Apache License 2.0	linux-64, osx-64, win-64
<a href="#">r-cleancall</a>	0.1.0	Wrapper of .Call() that runs exit handlers to clean up C resources. Helps managing C (non-R) resources while using the R API. / MIT	linux-64, osx-64, win-64
<a href="#">r-cleandata</a>	0.3.0	Functions to work with data frames to prepare data for further analysis. The functions for imputation, encoding, partitioning, and other manipulation can produce log files to keep track of process. / MIT	noarch
<a href="#">r-cleanerr</a>	0.1.1	How to deal with missing data?Based on the concept of almost functional dependencies, a method is proposed to fill missing data, as well as help you see what data is missing. The user can specify a measure of error and how many combinations he wish to test the dependencies against, the closer to the length of the dataset, the more precise. But the higher the number, the more time it will take for the process to finish. If the program cannot predict with the accuracy determined by the user it shall not fill the data, the user then can choose to increase the error or deal with the data another way. / MIT	noarch
<a href="#">r-cleanr</a>	1.2.0	Check your R code for some of the most common layout flaws. Many tried to teach us how to write code less dreadful, be it implicitly as B. W. Kernighan and D. M. Ritchie (1988) <ISBN:0-13-110362-8> in 'The C Programming Language' did, be it explicitly as R.C. Martin (2008) <ISBN:0-13-235088-2> in 'Clean Code: A Handbook of Agile Software Craftsmanship' did. So we should check our code for files too long or wide, functions with too many lines, too wide lines, too many arguments or too many levels of nesting. Note: This is not a static code analyzer like pylint or the like. Checkout < <a href="https://cran.r-project.org/package=lintr">https://cran.r-project.org/package=lintr</a> > instead. / BSD_2_clause	noarch

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Name	Version	Summary/License	Platforms
<code>r-cli</code>	1.1.0	A suite of tools designed to build attractive command line interfaces ('CLIs'). Includes tools for drawing rules, boxes, trees, and 'Unicode' symbols with 'ASCII' alternatives. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<code>r-clickclust</code>	1.1.5	Clustering categorical sequences by means of finite mixtures with Markov model components is the main utility of ClickClust. The package also allows detecting blocks of equivalent states by forward and backward state selection procedures. / GPL-2	linux-64, osx-64, win-64
<code>r-clickclustcont</code>	0.1.7	Provides an expectation maximization (EM) algorithm to fit a mixture of continuous time Markov models for use with clickstream or other sequence type data. Gallagher, M.P.B and McNicholas, P.D. (2018) <arXiv:1802.04849>. / GPL-2	noarch
<code>r-clickcorr</code>	1.0	A profile likelihood based method of estimation and inference on the correlation coefficient of bivariate data with different types of censoring and missingness. / GPL-2	noarch
<code>r-climatestability</code>	0.1.1	Climate stability measures are not formalized in the literature and tools for generating stability metrics from existing data are nascent. This package provides tools for calculating climate stability from raster data encapsulating climate change as a series of time slices. The methods follow Owens and Guralnick. Submitted, Biodiversity Informatics. / GPL-3	noarch
<code>r-clime</code>	0.4.1	A robust constrained L1 minimization method for estimating a large sparse inverse covariance matrix (aka precision matrix), and recovering its support for building graphical models. The computation uses linear programming. / GPL-2	noarch
<code>r-clinfun</code>	1.0.1	Utilities to make your clinical collaborations easier if not fun. It contains functions for designing studies such as Simon 2-stage and group sequential designs and for data analysis such as Jonckheere-Terpstra test and estimating survival quantiles. / GPL-2	linux-64, osx-64, win-64
<code>r-clinicaltrialsummary</code>	1.1.1	Provides estimates of several summary measures for clinical trials including the average hazard ratio, the weighted average hazard ratio, the restricted superiority probability ratio, the restricted mean survival difference and the ratio of restricted mean times lost, based on the short-term and long-term hazard ratio model (Yang, 2005 <doi:10.1093/biomet/92.1.1>) which accommodates various non-proportional hazards scenarios. The inference procedures and the asymptotic results for the summary measures are discussed in Yang (2018, <doi:10.1002/sim.7676>). / GPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-clinpk</a>	0.9.0	Calculates equations commonly used in clinical pharmacokinetics and clinical pharmacology, such as equations for dose individualization, compartmental pharmacokinetics, drug exposure, anthropomorphic calculations, clinical chemistry, and conversion of common clinical parameters. Where possible and relevant, it provides multiple published and peer-reviewed equations within the respective R function. / MIT	noarch
<a href="#">r-clinsig</a>	1.2	Functions for calculating clinical significance. / GPL-2	noarch
<a href="#">r-clinutidna</a>	1.0	This package provides the estimation of an index measuring the clinical utility of DNA testing in the context of gene-environment interactions on a disease. The corresponding gene-environment interaction effect on the additive scale can also be obtained. The estimation is based on case-control or cohort data. The method was developed by Nguyen et al. 2013. / GPL-3	noarch
<a href="#">r-clipr</a>	0.6.0	Simple utility functions to read from and write to the Windows, OS X, and X11 clipboards. / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-clisymbols</a>	1.2.0	A small subset of Unicode symbols, that are useful when building command line applications. They fall back to alternatives on terminals that do not support Unicode. Many symbols were taken from the ‘figures’ ‘npm’ package (see <a href="https://github.com/sindresorhus/figures">https://github.com/sindresorhus/figures</a> ). / MIT file LICENSE	noarch
<a href="#">r-clogitboost</a>	1.1	A set of functions to fit a boosting conditional logit model. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-clogitl1</a>	1.5	Tools for the fitting and cross validation of exact conditional logistic regression models with lasso and elastic net penalties. Uses cyclic coordinate descent and warm starts to compute the entire path efficiently. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-cloneseeker</a>	1.0.7	Defines the classes and functions used to simulate and to analyze data sets describing copy number variants and, optionally, sequencing mutations in order to detect clonal subsets. See Zucker et al. (2019) <doi:10.1093/bioinformatics/btz057>. / Apache License (== 2.0)	noarch
<a href="#">r-cloudml</a>	0.6.1	Interface to the Google Cloud Machine Learning Platform < <a href="https://cloud.google.com/ml-engine">https://cloud.google.com/ml-engine</a> >, which provides cloud tools for training machine learning models. / Apache License 2.0	noarch
<a href="#">r-cloudutil</a>	0.1.12	Provides means of plots for comparing utilization data of compute systems. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-clrdag</a>	0.6.0	Provides MLEdag() for constrained maximum likelihood estimation and likelihood ratio test of a large directed acyclic graph. The algorithms are described in the paper by Li, Shen, and Pan (2019) <doi:10.1080/01621459.2019.1623042>. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-clsocp</a>	1.0	This package provides an implementation of a one step smoothing newton method for the solution of second order cone programming problems, originally described by Xiaoni Chi and Sanyang Liu. / GPL-3	noarch
<a href="#">r-clttools</a>	1.3	Central limit theorem experiments presented by data frames or plots. Functions include generating theoretical sample space, corresponding probability, and simulated results as well. / GPL-2	noarch
<a href="#">r-clubsandwich</a>	0.3.5	Provides several cluster-robust variance estimators (i.e., sandwich estimators) for ordinary and weighted least squares linear regression models, including the bias-reduced linearization estimator introduced by Bell and McCaffrey (2002) < <a href="http://www.statcan.gc.ca/pub/12-001-x/2002002/article/9058-eng.pdf">http://www.statcan.gc.ca/pub/12-001-x/2002002/article/9058-eng.pdf</a> > and developed further by Pustejovsky and Tipton (2017) <DOI:10.1080/07350015.2016.1247004>. The package includes functions for estimating the variance-covariance matrix and for testing single- and multiple-contrast hypotheses based on Wald test statistics. Tests of single regression coefficients use Satterthwaite or saddle-point corrections. Tests of multiple-contrast hypotheses use an approximation to Hotelling's T-squared distribution. Methods are provided for a variety of fitted models, including lm() and mlm objects, glm(), ivreg() (from package 'AER'), plm() (from package 'plm'), gls() and lme() (from 'nlme'), robu() (from 'robustmeta'), and rma.uni() and rma.mv() (from 'metafor'). / GPL-3	noarch
<a href="#">r-clue</a>	0.3.5	CLUster Ensembles. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-cluer</a>	1.4	CLUster Evaluation (CLUE) is a computational method for identifying optimal number of clusters in a given time-course dataset clustered by cmeans or kmeans algorithms and subsequently identify key kinases or pathways from each cluster. Its implementation in R is called ClueR. See README on < <a href="https://github.com/PengyiYang/ClueR">https://github.com/PengyiYang/ClueR</a> > for more details. P Yang et al. (2015) <doi:10.1371/journal.pcbi.1004403>. / GPL-3	noarch
<a href="#">r-clues</a>	0.5.9	We developed the clues R package to provide functions for automatically estimating the number of clusters and getting the final cluster partition without any input parameter except the stopping rule for convergence. The package also provides functions to evaluate and compare the performances of partitions of a data set both numerically and graphically. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-cluscov</a>	1.1.0	Clustered covariate regression enables estimation and inference in both linear and non-linear models with linear predictor functions even when the design matrix is column rank deficient. Routines in this package implement algorithms in Soale and Tsyawo (2019) <doi:10.13140/RG.2.2.32355.81441>. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<code>r-clustrank</code>	0.6_2	Non-parametric tests (Wilcoxon rank sum test and Wilcoxon signed rank test) for clustered data. / GPL-3	linux-64, osx-64, win-64
<code>r-clust.bin.pair</code>	0.1.2	Tests, utilities, and case studies for analyzing significance in clustered binary matched-pair data. The central function <code>clust.bin.pair</code> uses one of several tests to calculate a Chi-square statistic. Implemented are the tests Eliasziw (1991) <doi:10.1002/sim.4780101211>, Obuchowski (1998) <doi:10.1002/(SICI)1097-0258(19980715)17:13%3C1495::AID-SIM863%3E3.0.CO;2-I>, Durkalski (2003) <doi:10.1002/sim.1438>, and Yang (2010) <doi:10.1002/bimj.201000035> with McNemar (1947) <doi:10.1007/BF02295996> included for comparison. The utility functions <code>nested.to.contingency</code> and <code>paired.to.contingency</code> convert data between various useful formats. Thyroids and psychiatry are the canonical datasets from Obuchowski and Petryshen (1989) <doi:10.1016/0165-1781(89)90196-0> respectively. / MIT	noarch
<code>r-cluster</code>	2.0.8	Methods for Cluster analysis. Much extended the original from Peter Rousseeuw, Anja Struyf and Mia Hubert, based on Kaufman and Rousseeuw (1990) Finding Groups in Data. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<code>r-cluster.datasets</code>	1.0_1	A collection of data sets for teaching cluster analysis. / GPL-2	noarch
<code>r-clusterbootstrap</code>	1.0.0	Provides functionality for the analysis of clustered data using the cluster bootstrap. / GPL-3	noarch
<code>r-clustercrit</code>	1.2.8	Compute clustering validation indices. / GPL-2	linux-64, osx-64, win-64
<code>r-clustergeneration</code>	1.3.4	We developed the <code>clusterGeneration</code> package to provide functions for generating random clusters, generating random covariance/correlation matrices, calculating a separation index (data and population version) for pairs of clusters or cluster distributions, and 1-D and 2-D projection plots to visualize clusters. The package also contains a function to generate random clusters based on factorial designs with factors such as degree of separation, number of clusters, number of variables, number of noisy variables. / GPL-2	noarch
<code>r-clustergenomics</code>	1.0	The Partitioning Algorithm based on Recursive Thresholding (PART) is used to recursively uncover clusters and subclusters in the data. Functionality is also available for visualization of the clustering. / Artistic-2.0	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-clusterhap</a>	0.1	One haplotype is a combination of SNP (Single Nucleotide Polymorphisms) within the QTL (Quantitative Trait Loci). clusterhap groups together all individuals of a population with the same haplotype. Each group contains individual with the same allele in each SNP, whether or not missing data. Thus, clusterhap groups individuals, that to be imputed, have a non-zero probability of having the same alleles in the entire sequence of SNP's. Moreover, clusterhap calculates such probability from relative frequencies. / GPL-3	noarch
<a href="#">r-clustering.sc.dp</a>	1.0	A dynamic programming algorithm for optimal clustering multidimensional data with sequential constraint. The algorithm minimizes the sum of squares of within-cluster distances. The sequential constraint allows only subsequent items of the input data to form a cluster. The sequential constraint is typically required in clustering data streams or items with time stamps such as video frames, GPS signals of a vehicle, movement data of a person, e-pen data, etc. The algorithm represents an extension of Ckmeans.1d.dp to multiple dimensional spaces. Similarly to the one-dimensional case, the algorithm guarantees optimality and repeatability of clustering. Method clustering.sc.dp can find the optimal clustering if the number of clusters is known. Otherwise, methods findwithinss.sc.dp and backtracking.sc.dp can be used. / LGPL-3	linux-64, osx-64, win-64
<a href="#">r-clusternomics</a>	0.1.1	Integrative context-dependent clustering for heterogeneous biomedical datasets. Identifies local clustering structures in related datasets, and a global clusters that exist across the datasets. / MIT	noarch
<a href="#">r-clusternor</a>	0.0.3	The clustering 'NUMA' Optimized Routines package or 'clusternor' is a highly optimized package for performing clustering in parallel with accelerations specifically targeting multi-core Non-Uniform Memory Access ('NUMA') hardware architectures. Disa Mhembere, Da Zheng, Carey E. Priebe, Joshua T. Vogelstein, Randal Burns (2019) <arXiv:1902.09527>. / Apache License 2.0	linux-64, osx-64, win-64
<a href="#">r-clusterpower</a>	0.6.1	Calculate power for cluster randomized trials (CRTs) that compare two means, two proportions, or two counts using closed-form solutions. In addition, calculate power for cluster randomized crossover trials using Monte Carlo methods. For more information, see Reich et al. (2012) <doi:10.1371/journal.pone.0035564>. / GPL-2	noarch
<a href="#">r-clusterranktest</a>	1.0	Nonparametric rank based tests (rank-sum tests and signed-rank tests) for clustered data, especially useful for clusters having informative cluster size and intra-cluster group size. / GPL-2   GPL-3	noarch
<a href="#">r-clusterrepro</a>	0.9	This is a function for validating microarray clusters via reproducibility, based on the paper referenced below. / GPL-2	noarch
<a href="#">r-clustertend</a>	1.4	Calculate some statistics aiming to help analyzing the clustering tendency of given data. In the first version, Hopkins' statistic is implemented. / GPL-2	noarch
<a href="#">r-clusteval</a>	0.1	An R package that provides a suite of tools to evaluate clustering algorithms, clusterings, and individual clusters. / MIT	linux-64, osx-64, win-64
<a href="#">r-clustmixtype</a>	0.2.1	Functions to perform k-prototypes partitioning clustering for mixed variable-type data according to Z.Huang (1998): Extensions to the k-Means Algorithm for Clustering Large Data Sets with Categorical Variables, Data Mining and Knowledge Discovery 2, 283-304, <DOI:10.1023/A:1009769707641>. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-clustmmdd</a>	1.0.4	An implementation of a variable selection procedure in clustering by mixture models for discrete data (clustMMDD). Genotype data are examples of such data with two unordered observations (alleles) at each locus for diploid individual. The two-fold problem of variable selection and clustering is seen as a model selection problem where competing models are characterized by the number of clusters K, and the subset S of clustering variables. Competing models are compared by penalized maximum likelihood criteria. We considered asymptotic criteria such as Akaike and Bayesian Information criteria, and a family of penalized criteria with penalty function to be data driven calibrated. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-clustsig</a>	1.1	A complimentary package for use with hclust; simprof tests to see which (if any) clusters are statistically different. The null hypothesis is that there is no a priori group structure. See Clarke, K.R., Somerfield, P.J., and Gorley R.N. 2008. Testing of null hypothesis in exploratory community analyses: similarity profiles and biota-environment linkage. J. Exp. Mar. Biol. Ecol. 366, 56-69. / GPL-2	noarch
<a href="#">r-clustvarlv</a>	2.0.0	Functions for the clustering of variables around Latent Variables, for 2-way or 3-way data. Each cluster of variables, which may be defined as a local or directional cluster, is associated with a latent variable. External variables measured on the same observations or/and additional information on the variables can be taken into account. A noise cluster or sparse latent variables can also be defined. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-clv</a>	0.3_2	Package contains most of the popular internal and external cluster validation methods ready to use for the most of the outputs produced by functions coming from package cluster. Package contains also functions and examples of usage for cluster stability approach that might be applied to algorithms implemented in cluster package as well as user defined clustering algorithms. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-clvalid</a>	0.6_6	Statistical and biological validation of clustering results. / LGPL-3	noarch
<a href="#">r-cmaes</a>	1.0_1	Single objective optimization using a CMA-ES. / GPL-2	noarch
<a href="#">r-cmc</a>	1.0	Calculation and plot of the stepwise Cronbach-Mesbah Curve / GPL-2	noarch
<a href="#">r-cmce</a>	0.1.0	Implements the Bayesian calibration model described in Pratola and Chkrebtii (2018) <DOI:10.5705/ss.202016.0403> for stochastic and deterministic simulators. Additive and multiplicative discrepancy models are currently supported. See < <a href="http://www.matthewpratola.com/software">http://www.matthewpratola.com/software</a> > for more information and examples. / AGPL-3	noarch
<a href="#">r-cmf</a>	1.0	Collective matrix factorization (CMF) finds joint low-rank representations for a collection of matrices with shared row or column entities. This code learns variational Bayesian approximation for CMF, supporting multiple likelihood potentials and missing data, while identifying both factors shared by multiple matrices and factors private for each matrix. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-cmls</a>	1.0_0	Solves multivariate least squares (MLS) problems subject to constraints on the coefficients, e.g., non-negativity, orthogonality, equality, inequality, monotonicity, unimodality, smoothness, etc. Includes flexible functions for solving MLS problems subject to user-specified equality and/or inequality constraints, as well as a wrapper function that implements 24 common constraint options. Also does k-fold or generalized cross-validation to tune constraint options for MLS problems. See ten Berge (1993, ISBN:9789066950832) for an overview of MLS problems, and see Goldfarb and Idnani (1983) <doi:10.1007/BF02591962> for a discussion of the underlying quadratic programming algorithm. / GPL-2	noarch
<a href="#">r-cmm</a>	0.12	Quite extensive package for maximum likelihood estimation and weighted least squares estimation of categorical marginal models (CMMs; e.g., Bergsma and Rudas, 2002, < <a href="http://www.jstor.org/stable/2700006?">http://www.jstor.org/stable/2700006?</a> ; Bergsma, Croon and Hagenaars, 2009, <DOI:10.1007/b12532>. / GPL-2	noarch
<a href="#">r-cmna</a>	1.0.2	Provides the source and examples for James P. Howard, II, Computational Methods for Numerical Analysis with R, < <a href="http://howardjp.github.io/cmna/">http://howardjp.github.io/cmna/</a> >, a book on numerical methods in R. / BSD_2_clause	noarch
<a href="#">r-cmocean</a>	0.2	Perceptually uniform palettes for commonly used variables in oceanography as functions taking an integer and producing character vectors of colours. See Thyng, K.M., Greene, C.A., Hetland, R.D., Zimmerle, H.M. and S.F. DiMarco (2016) <doi:10.5670/oceanog.2016.66> for the guidelines adhered to when creating the palettes. / MIT	noarch
<a href="#">r-cmpcontrol</a>	1.0	The main purpose of this package is to juxtapose the different control limits obtained by modelling a data set through the COM-Poisson distribution vs. the classical Poisson distribution. Accordingly, this package offers the ability to compute the COM-Poisson parameter estimates and plot associated Shewhart control charts for a given data set. / GPL-2   GPL-3	noarch
<a href="#">r-cmplot</a>	3.3.3	Manhattan plot, a type of scatter plot, was widely used to display the association results. However, it is usually time-consuming and laborious for a non-specialist user to write scripts and adjust parameters of an elaborate plot. Moreover, the ever-growing traits measured have necessitated the integration of results from different Genome-wide association study researches. Circle Manhattan Plot is the first open R package that can lay out Genome-wide association study P-value results in both traditional rectangular patterns, QQ-plot and novel circular ones. United in only one bull's eye style plot, association results from multiple traits can be compared interactively, thereby to reveal both similarities and differences between signals. / GPL-2	noarch
<a href="#">r-cmpprocess</a>	1.0	A toolkit for flexible modeling of count processes where data (over- or under-) dispersion exists. Estimations can be obtained under two data constructs where one has: (1) data on number of events in an s-unit time interval, or (2) only wait-time data. This package is supplementary to the work set forth in Zhu et al. (2016) <doi:10.1080/00031305.2016.1234976>. / GPL-3	noarch
<a href="#">r-cmprsk</a>	2.2_8	Estimation, testing and regression modeling of subdistribution functions in competing risks, as described in Gray (1988), A class of K-sample tests for comparing the cumulative incidence of a competing risk, Ann. Stat. 16:1141-1154 <DOI:10.1214/aos/1176350951>, and Fine JP and Gray RJ (1999), A proportional hazards model for the subdistribution of a competing risk, JASA, 94:496-509, <DOI:10.1080/01621459.1999.10474144>. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<code>r-cmprskqr</code>	0.9.1	Estimation, testing and regression modeling of subdistribution functions in competing risks using quantile regressions, as described in Peng and Fine (2009) <DOI:10.1198/jasa.2009.tm08228>. / GPL-2	linux-64, osx-64, win-64
<code>r-cmrutils</code>	1.3.1	A collection of useful helper routines developed by students of the Center for Mathematical Research, Stankin, Moscow. / GPL-3	noarch
<code>r-cmvnorm</code>	1.0.6	Various utilities for the complex multivariate Gaussian distribution. / GPL-2	noarch
<code>r-cna</code>	2.2.0	Provides comprehensive functionalities for causal modeling with Coincidence Analysis (CNA), which is a configurational comparative method of causal data analysis that was first introduced in Baumgartner (2009) <doi:10.1177/0049124109339369>, and generalized in Baumgartner & Ambuehl (2018) <doi:10.1017/psrm.2018.45>. CNA is related to Qualitative Comparative Analysis (QCA), but contrary to the latter, it is custom-built for uncovering causal structures with multiple outcomes and it builds causal models from the bottom up by gradually combining single factors to complex dependency structures until the requested thresholds of model fit are met. The new functionalities provided by this package version include functions for evaluating and benchmarking the correctness of CNA's output, a function determining whether a solution is an INUS model, a function bringing non-INUS expressions into INUS form, and a function for identifying cyclic models. The package vignette has been updated accordingly. / GPL-2	linux-64, osx-64, win-64
<code>r-cnrm</code>	1.2.0	Conventional methods for producing standard scores in psychometrics or biometrics are often plagued with jumps or gaps (i.e., discontinuities) in norm tables and low confidence for assessing extreme scores. The continuous norming method introduced by A. Lenhard et al. (2016), <doi:10.1177/1073191116656437>, generates continuous test norm scores on the basis of the raw data from standardization samples, without requiring assumptions about the distribution of the raw data: Norm scores are directly established from raw data by modeling the latter ones as a function of both percentile scores and an explanatory variable (e.g., age). The method minimizes bias arising from sampling and measurement error, while handling marked deviations from normality, addressing bottom or ceiling effects and capturing almost all of the variance in the original norm data sample. / AGPL-3	noarch
<code>r-cobiclust</code>	0.1.0	Implementation of a probabilistic method for biclustering adapted to overdispersed count data. It is a Gamma-Poisson Latent Block Model. It also implements two selection criteria in order to select the number of biclusters. / GPL-2	noarch
<code>r-cobra</code>	0.99.4	This package performs prediction for regression-oriented problems, aggregating in a nonlinear scheme any basic regression machines suggested by the context and provided by the user. If the user has no valuable knowledge on the data, four defaults machines wrappers are implemented so as to cover a minimal spectrum of prediction methods. If necessary, the computations may be parallelized. The method is described in Biau, Fischer, Guedj and Malley (2013), COBRA: A Nonlinear Aggregation Strategy. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-cobs	1.3_3	Qualitatively Constrained (Regression) Smoothing Splines via Linear Programming and Sparse Matrices. / GPL-2	linux-64, osx-64, win-64
r-coclust	0.3_2	A copula based clustering algorithm that finds clusters according to the complex multivariate dependence structure of the data generating process. The updated version of the algorithm is described in Di Lascio, F.M.L. and Gianerini, S. (2016). Clustering dependent observations with copula functions. Statistical Papers, p.1-17. <doi:10.1007/s00362-016-0822-3>. / GPL-2	noarch
r-coconut	1.0.2	Allows for pooled analysis of microarray data by batch-correcting control samples, and then applying the derived correction parameters to non-control samples to obtain bias-free, inter-dataset corrected data. / GPL-3	noarch
r-cocor	1.1_3	Statistical tests for the comparison between two correlations based on either independent or dependent groups. Dependent correlations can either be overlapping or nonoverlapping. A web interface is available on the website <a href="http://comparingcorrelations.org">http://comparingcorrelations.org</a> . A plugin for the R GUI and IDE RKWard is included. Please install RKWard from <a href="https://rkward.kde.org">https://rkward.kde.org</a> to use this feature. The respective R package 'rkward' cannot be installed directly from a repository, as it is a part of RKWard. / GPL-3	noarch
r-cocron	1.0_1	Statistical tests for the comparison between two or more alpha coefficients based on either dependent or independent groups of individuals. A web interface is available at <a href="http://comparingcronbachalphas.org">http://comparingcronbachalphas.org</a> . A plugin for the R GUI and IDE RKWard is included. Please install RKWard from <a href="https://rkward.kde.org">https://rkward.kde.org</a> to use this feature. The respective R package 'rkward' cannot be installed directly from a repository, as it is a part of RKWard. / GPL-3	noarch
r-coda	0.19_2	Provides functions for summarizing and plotting the output from Markov Chain Monte Carlo (MCMC) simulations, as well as diagnostic tests of convergence to the equilibrium distribution of the Markov chain. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-coda.base	0.2.1	A minimum set of functions to perform compositional data analysis using the log-ratio approach introduced by John Aitchison (1982) < <a href="http://www.jstor.org/stable/2345821">http://www.jstor.org/stable/2345821</a> >. Main functions have been implemented in c for better performance. / GPL-3	linux-64, osx-64, win-64
r-codadiags	1.0	Markov chain Monte Carlo burn-in based on bridge statistics, in the way of coda::heidel.diag, but including non asymptotic tabulated statistics. / GPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-codatags	1.43	Computes genomic breeding values using external information on the markers. The package fits a linear mixed model with heteroscedastic random effects, where the random effect variance is fitted using a linear predictor and a log link. The method is described in Mouresan, Selle and Ronnegard (2019) <doi:10.1101/636746>. / GPL-3	noarch
r-code	1.0.0	Generates all necessary C functions allowing the user to work with the compiled-code interface of ode() and bvptwp(). The implementation supports forcings and events. Also provides functions to symbolically compute Jacobians, sensitivity equations and adjoint sensitivities being the basis for sensitivity analysis. / GPL-2	noarch
r-codep	0.9_1	Computation of Multiscale Codependence Analysis and spatial eigenvector maps, as an additional feature. / GPL-3	linux-64, osx-64, win-64
r-codetools	0.2_1	Code analysis tools for R. / GPL	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-codina	1.1.1	Categorize links and nodes from multiple networks in 3 categories: Common links (alpha) specific links (gamma), and different links (beta). Also categorizes the links into sub-categories and groups. The package includes a visualization tool for the networks. More information about the methodology can be found at: Gysi et. al., 2018 <arXiv:1802.00828>. / GPL-2	noarch
r-coenocliner	0.2_2	Simulate species occurrence and abundances (counts) along gradients. / GPL-2	noarch
r-coenoflex	2.2_0	Simulates the composition of samples of vegetation according to gradient-based vegetation theory. Features a flexible algorithm incorporating competition and complex multi-gradient interaction. / GPL-2	linux-64, osx-64, win-64
r-coexist	1.0	species coexistence modeling under asymmetric dispersal and fluctuating source-sink dynamics;testing the proportion of coexistence scenarios driven by neutral and niche processes / GPL (>= 2.0)	noarch
r-cofad	0.1.0	Contrast analysis for factorial designs is an alternative to the classical ANOVA approach with the advantage of testing focused hypothesis. The method is mainly based on Rosenthal, Rosnow and Rubin (2000, ISBN:978-0521659802) and Sedlmeier and Renkewitz (2018, ISBN:978-3868943214). / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-cofra	0.100	Calculates complete functional regulation analysis and visualize the results in a single heatmap. The provided example data is for biological data but the methodology can be used for large data sets to compare quantitative entities that can be grouped. For example, a store might divide entities into cloth, food, car products etc and want to see how sales changes in the groups after some event. The theoretical background for the calculations are provided in New insights into functional regulation in MS-based drug profiling, Ana Sofia Carvalho, Henrik Molina & Rune Matthiesen, Scientific Reports <doi:10.1038/srep18826>. / GPL-2	noarch
r-coin	1.3_0	Conditional inference procedures for the general independence problem including two-sample, K-sample (non-parametric ANOVA), correlation, censored, ordered and multivariate problems. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
r-coindesk	0.1.0	Extract real-time Bitcoin price details by accessing ‘CoinDesk’ Bitcoin price Index API < <a href="https://www.coindesk.com/api/">https://www.coindesk.com/api/</a> >. / CC0	noarch
r-cointmonitor	0.1.0	We propose a consistent monitoring procedure to detect a structural change from a cointegrating relationship to a spurious relationship. The procedure is based on residuals from modified least squares estimation, using either Fully Modified, Dynamic or Integrated Modified OLS. It is inspired by Chu et al. (1996) <DOI:10.2307/2171955> in that it is based on parameter estimation on a pre-break calibration period only, rather than being based on sequential estimation over the full sample. See the discussion paper <DOI:10.2139/ssrn.2624657> for further information. This package provides the monitoring procedures for both the cointegration and the stationarity case (while the latter is just a special case of the former one) as well as printing and plotting methods for a clear presentation of the results. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-cointreg</a>	0.2.0	Cointegration methods are widely used in empirical macroeconomics and empirical finance. It is well known that in a cointegrating regression the ordinary least squares (OLS) estimator of the parameters is super-consistent, i.e. converges at rate equal to the sample size $T$ . When the regressors are endogenous, the limiting distribution of the OLS estimator is contaminated by so-called second order bias terms, see e.g. Phillips and Hansen (1990) <DOI:10.2307/2297545>. The presence of these bias terms renders inference difficult. Consequently, several modifications to OLS that lead to zero mean Gaussian mixture limiting distributions have been proposed, which in turn make standard asymptotic inference feasible. These methods include the fully modified OLS (FM-OLS) approach of Phillips and Hansen (1990) <DOI:10.2307/2297545>, the dynamic OLS (D-OLS) approach of Phillips and Loretan (1991) <DOI:10.2307/2298004>, Saikkonen (1991) <DOI:10.1017/S0266466600004217> and Stock and Watson (1993) <DOI:10.2307/2951763> and the new estimation approach called integrated modified OLS (IM-OLS) of Vogelsang and Wagner (2014) <DOI:10.1016/j.jeconom.2013.10.015>. The latter is based on an augmented partial sum (integration) transformation of the regression model. IM-OLS is similar in spirit to the FM- and D-OLS approaches, with the key difference that it does not require estimation of long run variance matrices and avoids the need to choose tuning parameters (kernels, bandwidths, lags). However, inference does require that a long run variance be scaled out. This package provides functions for the parameter estimation and inference with all three modified OLS approaches. That includes the automatic bandwidth selection approaches of Andrews (1991) <DOI:10.2307/2938229> and of Newey and West (1994) <DOI:10.2307/2297912> as well as the calculation of the long run variance. / GPL-3	noarch
<a href="#">r-cold</a>	2.0_0	Performs regression analysis for longitudinal count data, allowing for serial dependence among observations from a given individual and two dimensional random effects on the linear predictor. Estimation is via maximization of the exact likelihood of a suitably defined model. Missing values and unbalanced data are allowed; M. Helena Goncalves et al.(2007) <doi:10.1016/j.csda.2007.03.002>. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-collectargs</a>	0.4.0	We often want to take all (or most) of the objects in one environment (such as the parameter values of a function) and pass them to another. This might be calling a second function, or iterating over a list, calling the same function. These functions wrap often repeated code. Current stable version (committed on October 14, 2017). / MIT	noarch
<a href="#">r-collections</a>	0.1.6	Provides high performance container data types such as Queue, Stack, Deque, Dict and OrderedDict. Benchmarks < <a href="https://randy3k.github.io/collections/articles/benchmark.html">https://randy3k.github.io/collections/articles/benchmark.html</a> > have shown that these containers are asymptotically more efficient than those offered by other packages. / MIT	linux-64, osx-64, win-64
<a href="#">r-collesslike</a>	1.0	Computation of Colless-Like, Sackin and cophenetic balance indices of a phylogenetic tree and study of the distribution of these balance indices under the alpha-gamma model. For more details see A. Mir, F. Rossello, L. Rotger (2013) <doi:10.1016/j.mbs.2012.10.005>, M. J. Sackin (1972) <doi:10.1093/sysbio/21.2.225>, D. H. Colless (1982) <doi:10.2307/2413420>. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-collutils	1.0.5	Provides some low level functions for processing PLINK input and output files. / GPL-3	linux-64
r-colmozzie	1.1.1	Weekly notified dengue cases and climate variables in Colombo district Sri Lanka from 2008/ week-52 to 2014/ week-21. / CC0	noarch
r-coloredica	1.0.0	It implements colored Independent Component Analysis (Lee et al., 2011) and spatial colored Independent Component Analysis (Shen et al., 2014). They are two algorithms to perform ICA when sources are assumed to be temporal or spatial stochastic processes, respectively. / GPL-2	noarch
r-colorfulvennplot	2.4	Given 2-,3- or 4-dimensional data, plots a Venn diagram, i.e. ‘crossing circles’. The user can specify values, labels for each circle-group and unique colors for each plotted part. Here is what it would look like for a 3-dimensional plot: <a href="http://elliottnoma.files.wordpress.com/2011/02/venndiagram.png">http://elliottnoma.files.wordpress.com/2011/02/venndiagram.png</a> . To see what the 4-dimensional plot looks like, go to <a href="http://elliottnoma.files.wordpress.com/2013/03/4dplot.png">http://elliottnoma.files.wordpress.com/2013/03/4dplot.png</a> . / GPL-2	noarch
r-colorhclplot	1.3.1	Build dendrograms with sample groups highlighted by different colors. Visualize results of hierarchical clustering analyses as dendrograms whose leaves and labels are colored according to sample grouping. Assess whether data point grouping aligns to naturally occurring clusters. / GPL-2	noarch
r-colorpalette	1.0.1	Different methods to generate a color palette based on a specified base color and a number of colors that should be created. / MIT	noarch
r-colorr	1.0.0	Color palettes for EPL, MLB, NBA, NHL, and NFL teams. / MIT	noarch
r-colorramps	2.3	Builds gradient color maps / GPL-3	noarch
r-colorspace	1.4.1	Carries out mapping between assorted color spaces including RGB, HSV, HLS, CIEXYZ, CIELUV, HCL (polar CIELUV), CIELAB and polar CIELAB. Qualitative, sequential, and diverging color palettes based on HCL colors are provided along with an interactive palette picker (with either a Tcl/Tk or a shiny GUI). / BSD_3_clause file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
r-colortools	0.1.5	R package with handy functions to help users select and play with color schemes in an HSV color model / GPL-3	noarch
r-colourlovers	0.3.5	Provides access to the COLOURlovers < <a href="http://www.colourlovers.com/">http://www.colourlovers.com/</a> > API, which offers color inspiration and color palettes. / GPL-2	noarch
r-colourvalues	0.2.2	Maps one of the viridis colour palettes, or a user-specified palette to values. Viridis colour maps are created by StÃ©fan van der Walt and Nathaniel Smith. They were set as the default palette for the ‘Python’ ‘Matplotlib’ library, introduced at SciPy 2015 conference < <a href="http://scipy2015.scipy.org/ehome/index.php?eventid=115969&amp;">http://scipy2015.scipy.org/ehome/index.php?eventid=115969&amp;</a> >. Other palettes available in this library have been derived from ‘RColorBrewer’ < <a href="https://CRAN.R-project.org/package=RColorBrewer">https://CRAN.R-project.org/package=RColorBrewer</a> > and ‘colorspace’ < <a href="https://CRAN.R-project.org/package=colorspace">https://CRAN.R-project.org/package=colorspace</a> > packages. / GPL-3	linux-64, osx-64, win-64
r-colr	0.1.900	Powerful functions to select and rename columns in dataframes, lists and numeric types by ‘Perl’ regular expression. Regular expression (‘regex’) are a very powerful grammar to match strings, such as column names. / GPL-2	noarch
r-colt	0.1.1	A collection of command-line color styles based on the ‘crayon’ package. ‘Colt’ styles are defined in themes that can easily be switched, to ensure command line output looks nice on dark as well as light consoles. / MIT	noarch

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Table 51 – continued from previous page

Name	Version	Summary/License	Platforms
r-comat	0.3.0	Builds co-occurrence matrices based on spatial raster data. It includes creation of weighted co-occurrence matrices (wecoma) and integrated co-occurrence matrices (incoma; Vadivel et al. (2007) <doi:10.1016/j.patrec.2007.01.004>). / MIT	linux-64, osx-64, win-64
r-combat	0.0.4	Genome-wide association studies (GWAS) have been widely used for identifying common variants associated with complex diseases. Due to the small effect sizes of common variants, the power to detect individual risk variants is generally low. Complementary to SNP-level analysis, a variety of gene-based association tests have been proposed. However, the power of existing gene-based tests is often dependent on the underlying genetic models, and it is not known a priori which test is optimal. Here we proposed COMBined Association Test (COMBAT) to incorporate strengths from multiple existing gene-based tests, including VEGAS, GATES and simpleM. Compared to individual tests, COMBAT shows higher overall performance and robustness across a wide range of genetic models. The algorithm behind this method is described in Wang et al (2017) <doi:10.1534/genetics.117.300257>. / GPL-2	noarch
r-combinat	0.0.8	8 routines for combinatorics / GPL-2	noarch
r-combineportfolio	0.4	Estimation of optimal portfolio weights as combination of simple portfolio strategies, like the tangency, global minimum variance (GMV) or naive (1/N) portfolio. It is based on a utility maximizing 8-fund rule. Popular special cases like the Kan-Zhou(2007) 2-fund and 3-fund rule or the Tu-Zhou(2011) estimator are nested. / GPL-2	noarch
r-combinepvalue	1.0	We offer two statistical tests to combine p-values: selfcontained.test vs competitive.test. The goal is to test whether a vector of pvalues are jointly significant when we combine them together. / GPL-3	noarch
r-combins	1.1.1	Series of partially balanced incomplete block designs (PBIB) based on the combinatory method (S) introduced in (Imane Rezgui et al, 2014) <doi:10.3844/jmssp.2014.45.48>; and it gives their associated U-type design. / GPL-3	noarch
r-combmsc	1.4.2	Functions for computing optimal convex combinations of model selection criteria based on ranks, along with utility functions for constructing model lists, MSCs, and priors on model lists. / GPL-2	noarch
r-comclim	0.9.5	Computes community climate statistics for volume and mismatch using species' climate niches either unscaled or scaled relative to a regional species pool. These statistics can be used to describe biogeographic patterns and infer community assembly processes. Includes a vignette outlining usage. / GPL-3	noarch
r-comf	0.1.9	Functions to calculate various common and less common thermal comfort indices, convert physical variables, and evaluate the performance of thermal comfort indices. / GPL-2	noarch
r-comics	1.0.4	Provided are Computational methods for Immune Cell-type Subsets, including:(1) DCQ (Digital Cell Quantifier) to infer global dynamic changes in immune cell quantities within a complex tissue; and (2) VoCAL (Variation of Cell-type Abundance Loci) a deconvolution-based method that utilizes transcriptome data to infer the quantities of immune-cell types, and then uses these quantitative traits to uncover the underlying DNA loci. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-commandr	1.0.1	An S4 representation of the Command design pattern. The Operation class is a simple implementation using closures and supports forward and reverse (undo) evaluation. The more complicated Protocol framework represents each type of command (or analytical protocol) by a formal S4 class. Commands may be grouped and consecutively executed using the Pipeline class. Example use cases include logging, do/undo, analysis pipelines, GUI actions, parallel processing, etc. / Artistic-2.0	noarch
r-commentr	1.0.4	Functions to produce nicely formatted comments to use in R-scripts (or LaTeX/HTML/markdown etc). A comment with formatting is printed to the console and can then be copied to a script. / GPL-2	noarch
r-commonjavajars	1.0.6	Useful libraries for building a Java based GUI under R are provided. / GPL-2	noarch
r-commonmark	1.7	The CommonMark specification defines a rationalized version of markdown syntax. This package uses the 'cmark' reference implementation for converting markdown text into various formats including html, latex and groff man. In addition it exposes the markdown parse tree in xml format. The latest version of this package also adds support for Github extensions including tables, autolinks and strikethrough text. / BSD_2_clause file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
r-commonsmath	1.2.4	Java JAR files for the Apache Commons Mathematics Library for use by users and other packages. / Apache License 2.0   file LICENSE	noarch
r-commontrend	0.7.1	Directly extract and plot stochastic common trends from a cointegration system using different approaches, currently including Kasa (1992) and Gonzalo and Granger (1995). The approach proposed by Gonzalo and Granger, also known as Permanent-Transitory Decomposition, is widely used in macroeconomics and market microstructure literature. Kasa's approach, on the other hand, has a nice property that it only uses the super consistent estimator: the cointegration vector 'beta'. This package also provides functions calculate P-value from Johansen Statistics according to the approximation method proposed by Doornik (1998). Update: 0.7-1: Fix bugs in calculation alpha. Add formulas and more explanations. 0.6-1: Rewrite the description file. 0.5-1: Add functions to calculate P-value from Johansen statistic, and vice versa. / GPL-2	noarch
r-comorbidity	0.5.0	Computing comorbidity scores such as the weighted Charlson score (Charlson, 1987 <doi:10.1016/0021-9681(87)90171-8>) and the Elixhauser comorbidity score (Elixhauser, 1998 <doi:10.1097/00005650-199801000-00004>) using ICD-9-CM or ICD-10 codes (Quan, 2005 <doi:10.1097/01.mlr.0000182534.19832.83>). / GPL-3	noarch
r-comp2roc	1.1.4	Comparison of two ROC curves through the methodology proposed by Ana C. Braga. / GPL-2	noarch
r-compactr	0.1	Creates empty plots with compact axis notation to which users can add whatever they like (points, lines, text, etc.) The notation is more compact in the sense that the axis-labels and tick-labels are closer to the axis and the tick-marks are shorter. Also, if the plot appears as part of a matrix, the x-axis notation is suppressed unless the plot appears along the bottom row and the y-axis notation is suppress unless the plot appears along the left column. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-compare</a>	0.2.6	Functions to compare a model object to a comparison object. If the objects are not identical, the functions can be instructed to explore various modifications of the objects (e.g., sorting rows, dropping names) to see if the modified versions are identical. / GPL-2	noarch
<a href="#">r-comparec</a>	1.3.1	Proposed by Harrell, the C index or concordance C, is considered an overall measure of discrimination in survival analysis between a survival outcome that is possibly right censored and a predictive-score variable, which can represent a measured biomarker or a composite-score output from an algorithm that combines multiple biomarkers. This package aims to statistically compare two C indices with right-censored survival outcome, which commonly arise from a paired design and thus resulting two correlated C indices. / GPL (>= 2.0)	linux-64, osx-64, win-64
<a href="#">r-compareodm</a>	1.2	Input: 2 ODM files (ODM version 1.3) Output: list of identical, matching, similar and differing data items / GPL-3	noarch
<a href="#">r-comparer</a>	0.2.0	Quickly run experiments to compare the run time and output of code blocks. The function mbc() can make fast comparisons of code, and will calculate statistics comparing the resulting outputs. It can be used to compare model fits to the same data or see which function runs faster. The function ffexp() runs a function using all possible combinations of selected inputs. This is useful for comparing the effect of different parameter values. It can also run in parallel and automatically save intermediate results, which is very useful for long computations. / GPL-3	noarch
<a href="#">r-comparetests</a>	1.2	A standard test is observed on all specimens. We treat the second test (or sampled test) as being conducted on only a stratified sample of specimens. Verification Bias is this situation when the specimens for doing the second (sampled) test is not under investigator control. We treat the total sample as stratified two-phase sampling and use inverse probability weighting. We estimate diagnostic accuracy (category-specific classification probabilities; for binary tests reduces to specificity and sensitivity, and also predictive values) and agreement statistics (percent agreement, percent agreement by category, Kappa (unweighted), Kappa (quadratic weighted) and symmetry tests (reduces to McNemar's test for binary tests)). See: Katki HA, Li Y, Edelstein DW, Castle PE. Estimating the agreement and diagnostic accuracy of two diagnostic tests when one test is conducted on only a subsample of specimens. Stat Med. 2012 Feb 28; 31(5) <doi:10.1002/sim.4422>. / GPL-3	noarch
<a href="#">r-compas</a>	0.1	Manipulate and analyze 3-D structural geometry of Protein Data Bank (PDB) files. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-compboost</a>	0.1.0	C implementation of component-wise boosting implementation of component-wise boosting written in C to obtain high runtime performance and full memory control. The main idea is to provide a modular class system which can be extended without editing the source code. Therefore, it is possible to use R functions as well as C functions for custom base-learners, losses, logging mechanisms or stopping criteria. / MIT	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-compglm	2.0	A function (which uses a similar interface to the ‘glm’ function) for the fitting of a Conway-Maxwell-Poisson GLM. There are also various methods for analysis of the model fit. The package also contains functions for the Conway-Maxwell-Poisson distribution in a similar interface to functions ‘dpois’, ‘ppois’ and ‘rpois’. The functions are generally quick, since the workhorse functions are written in C (thanks to the Rcpp package). / GPL-2	linux-64, osx-64, win-64
r-comphclust	1.0_3	Performs the complementary hierarchical clustering procedure and returns X’ (the expected residual matrix) and a vector of the relative gene importances. / GPL-2	linux-64, osx-64, win-64
r-complexity	1.1.1	Allows for the easy computation of complexity: the proportion of the parameter space in line with the hypothesis by chance. The package comes with a Shiny application in which the calculations can be conducted as well. / GPL-2	noarch
r-complognormal	3.0	Computes the probability density function, cumulative distribution function, quantile function, random numbers of any composite model based on the log-normal distribution. / GPL-2	noarch
r-compoisson	0.3	Provides routines for density and moments of the Conway-Maxwell-Poisson distribution as well as functions for fitting the COM-Poisson model for over/under-dispersed count data. / BSD	noarch
r-compoissonreg	0.6.1	Fit Conway-Maxwell Poisson (COM-Poisson or CMP) regression models to count data (Sellers & Shmueli, 2010) <doi:10.1214/09-AOAS306>. The package provides functions for model estimation, dispersion testing, and diagnostics. Zero-inflated CMP regression (Sellers & Raim, 2016) <doi:10.1016/j.csda.2016.01.007> is also supported. / GPL-2   GPL-3	linux-64, osx-64, win-64
r-compound.cox	3.18	Univariate feature selection and compound covariate methods under the Cox model with high-dimensional features (e.g., gene expressions). Available are survival data for non-small-cell lung cancer patients with gene expressions (Chen et al 2007 New Engl J Med) <DOI:10.1056/NEJMoa060096>, statistical methods in Emura et al (2012 PLoS ONE) <DOI:10.1371/journal.pone.0047627>, Emura & Chen (2016 Stat Methods Med Res) <DOI:10.1177/0962280214533378>, and Emura et al. (2019)<DOI:10.1016/j.cmpb.2018.10.020>. Algorithms for generating correlated gene expressions are also available. / GPL-2	noarch
r-compquadform	1.4.3	Computes the distribution function of quadratic forms in normal variables using Imhof’s method, Davies’s algorithm, Farebrother’s algorithm or Liu et al.’s algorithm. / GPL-2	linux-64, osx-64, win-64
r-compr	1.0	Different tools for describing and analysing paired comparison data are presented. Main methods are estimation of products scores according Bradley Terry Luce model. A segmentation of the individual could be conducted on the basis of a mixture distribution approach. The number of classes can be tested by the use of Monte Carlo simulations. This package deals also with multi-criteria paired comparison data. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-comprehenr</a>	0.6.7	Provides ‘Python’-style list comprehensions. List comprehension expressions use usual loops (for(), while() and repeat()) and usual if() as list producers. In many cases it gives more concise notation than standard <i>*apply</i> filter strategy. / GPL-2	noarch
<a href="#">r-compute.es</a>	0.2.4	This package contains several functions for calculating the most widely used effect sizes (ES), along with their variances, confidence intervals and p-values. The output includes ES’s of d (mean difference), g (unbiased estimate of d), r (correlation coefficient), z’ (Fisher’s z), and OR (odds ratio and log odds ratio). In addition, NNT (number needed to treat), U3, CLES (Common Language Effect Size) and Cliff’s Delta are computed. This package uses recommended formulas as described in The Handbook of Research Synthesis and Meta-Analysis (Cooper, Hedges, & Valentine, 2009). / GPL-2	noarch
<a href="#">r-comtradr</a>	0.2.2	Interface with and extract data from the United Nations Comtrade API < <a href="https://comtrade.un.org/data/">https://comtrade.un.org/data/</a> >. Comtrade provides country level shipping data for a variety of commodities, these functions allow for easy API query and data returned as a tidy data frame. / GPL-3	noarch
<a href="#">r-con2aqi</a>	0.1.0	To calculate the AQI (Air Quality Index) from pollutant concentration data. O3, PM2.5, PM10, CO, SO2, and NO2 are available currently. The method can be referenced at Environmental Protection Agency, United States as follows: EPA (2016) < <a href="https://www3.epa.gov/airnow/aqi-technical-assistance-document-may2016.pdf">https://www3.epa.gov/airnow/aqi-technical-assistance-document-may2016.pdf</a> >. / GPL-3	noarch
<a href="#">r-conake</a>	1.0	Continuous smoothing of probability density function on a compact or semi-infinite support is performed using four continuous associated kernels: extended beta, gamma, lognormal and reciprocal inverse Gaussian. The cross-validation technique is also implemented for bandwidth selection. / GPL-2	noarch
<a href="#">r-concatenate</a>	1.0.0	Simple functions for joining strings. Construct human-friendly messages whose elements aren’t known in advance, like in stop, warning, or message, from clean code. / GPL (>= 3.2)	noarch
<a href="#">r-conclust</a>	1.1	There are 4 main functions in this package: ckmeans(), lcvqe(), mpckm() and ccls(). They take an unlabeled dataset and two lists of must-link and cannot-link constraints as input and produce a clustering as output. / GPL-3	noarch
<a href="#">r-conconpiwifun</a>	0.4.6	Continuous convex piecewise linear (ccpl) resp. quadratic (ccpq) functions can be implemented with sorted breakpoints and slopes. This includes functions that are ccpl (resp. ccpq) on a convex set (i.e. an interval or a point) and infinite out of the domain. These functions can be very useful for a large class of optimisation problems. Efficient manipulation (such as log(N) insertion) of such data structure is obtained with map standard template library of C (that hides balanced trees). This package is a wrapper on such a class based on Rcpp modules. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-concor</a>	1.0.0	The four functions svdcp (cp for column partitioned), svdbip or svdbip2 (bip for bi-partitioned), and svdbips (s for a simultaneous optimization of one set of r solutions), correspond to a SVD by blocks notion, by supposing each block depending on relative subspaces, rather than on two whole spaces as usual SVD does. The other functions, based on this notion, are relative to two column partitioned data matrices x and y defining two sets of subsets xi and yj of variables and amount to estimate a link between xi and yj for the pair (xi, yj) relatively to the links associated to all the other pairs. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-concordance</a>	1.6	A set of utilities for matching products in different classification codes used in international trade research. It supports concordance between HS (Combined), ISIC Rev. 2,3, and SITC1,2,3,4 product classification codes, as well as BEC, NAICS, and SIC classifications. It also provides code nomenclature / descriptions look-up, Rauch classification look-up (via concordance to SITC2) and trade elasticity look-up (via concordance to SITC2/3 or HS3.ss). / GPL-2	noarch
<a href="#">r-concreg</a>	0.6	Implements concordance regression which can be used to estimate generalized odds of concordance. Can be used for non- and semi-parametric survival analysis with non-proportional hazards, for binary and for continuous outcome data. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-conditionz</a>	0.1.0	Provides ability to control how many times in function calls conditions are thrown (shown to the user). Includes control of warnings and messages. / MIT	noarch
<a href="#">r-condmvnorm</a>	2015.1	Computes conditional multivariate normal probabilities, random deviates and densities. / GPL-2	noarch
<a href="#">r-condreg</a>	0.20	Based on url{ <a href="http://statistics.stanford.edu/~ckirby/techreports/GEN/2012/2012-10.pdf">http://statistics.stanford.edu/~ckirby/techreports/GEN/2012/2012-10.pdf</a> } / GPL-3	noarch
<a href="#">r-condvis</a>	0.5_1	Exploring fitted models by interactively taking 2-D and 3-D sections in data space. / GPL-2	noarch
<a href="#">r-coneproj</a>	1.14	Routines doing cone projection and quadratic programming, as well as doing estimation and inference for constrained parametric regression and shape-restricted regression problems. See Mary C. Meyer (2013)<doi:10.1080/03610918.2012.659820> for more details. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-conf.design</a>	2.0.0	This small library contains a series of simple tools for constructing and manipulating confounded and fractional factorial designs. / GPL-2	noarch
<a href="#">r-config</a>	0.3	Manage configuration values across multiple environments (e.g. development, test, production). Read values using a function that determines the current environment and returns the appropriate value. / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-configparser</a>	1.0.0	Enhances the ‘ini’ package by adding the ability to interpolate variables. The INI configuration file is read into an R6 ConfigParser object (loosely inspired by Python's ConfigParser module) and the keys can be read, where ‘%(...)s’ instances are interpolated by other included options or outside variables. / GPL-3	noarch
<a href="#">r-confinterpret</a>	1.0.0	Produces descriptive interpretations of confidence intervals. Includes (extensible) support for various test types, specified as sets of interpretations dependent on where the lower and upper confidence limits sit. Provides plotting functions for graphical display of interpretations. / AGPL-3	noarch

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Name	Version	Summary/License	Platforms
<code>r-confintvariance</code>	1.0.2	Surrounds the usual sample variance of a univariate numeric sample with a confidence interval for the population variance. This has been done so far only under the assumption that the underlying distribution is normal. Under the hood, this package implements the unique least-variance unbiased estimator of the variance of the sample variance, in a formula that is equivalent to estimating kurtosis and square of the population variance in an unbiased way and combining them according to the classical formula into an estimator of the variance of the sample variance. Both the sample variance and the estimator of its variance are U-statistics. By the theory of U-statistic, the resulting estimator is unique. See Fuchs, Krautenbacher (2016) <doi:10.1080/15598608.2016.1158675> and the references therein for an overview of unbiased estimation of variances of U-statistics. / GPL-3	noarch
<code>r-conflicted</code>	1.0.4	R's default conflict management system gives the most recently loaded package precedence. This can make it hard to detect conflicts, particularly when they arise because a package update creates ambiguity that did not previously exist. 'conflicted' takes a different approach, making every conflict an error and forcing you to choose which function to use. / GPL-3	noarch
<code>r-confreq</code>	1.5.4	Offers several functions for Configural Frequencies Analysis (CFA), which is a useful statistical tool for the analysis of multiway contingency tables. CFA was introduced by G. A. Lienert as 'Konfigurations Frequenz Analyse - KFA'. Lienert, G. A. (1971). Die Konfigurationsfrequenzanalyse: I. Ein neuer Weg zu Typen und Syndromen. Zeitschrift für Klinische Psychologie und Psychotherapie, 19(2), 99–115. / GPL-3	noarch
<code>r-confsam</code>	0.2	For multiple testing. Computes estimates and confidence bounds for the False Discovery Proportion (FDP), the fraction of false positives among all rejected hypotheses. The methods in the package use permutations of the data. Doing so, they take into account the dependence structure in the data. / GPL-3	noarch
<code>r-conics</code>	0.3	plot conics (ellipses, hyperbolas, parabolas) / GPL-2	noarch
<code>r-conjointchecks</code>	0.0.9	Implementation of a procedure (Domingue, 2012; see also Karabatsos, 2001 and Kyngdon, 2011) to test the single and double cancellation axioms of conjoint measure in data that is dichotomously coded and measured with error. / GPL-2	noarch
<code>r-connmatttools</code>	0.3.3	Collects several different methods for analyzing and working with connectivity data in R. Though primarily oriented towards marine larval dispersal, many of the methods are general and useful for terrestrial systems as well. / GPL-2	noarch
<code>r-conover.test</code>	1.1.5	Computes the Conover-Iman test (1979) for stochastic dominance and reports the results among multiple pairwise comparisons after a Kruskal-Wallis test for stochastic dominance among k groups (Kruskal and Wallis, 1952). The interpretation of stochastic dominance requires an assumption that the CDF of one group does not cross the CDF of the other. <code>conover.test</code> makes $k(k-1)/2$ multiple pairwise comparisons based on Conover-Iman t-test-statistic of the rank differences. The null hypothesis for each pairwise comparison is that the probability of observing a randomly selected value from the first group that is larger than a randomly selected value from the second group equals one half; this null hypothesis corresponds to that of the Wilcoxon-Mann-Whitney rank-sum test. Like the rank-sum test, if the data can be assumed to be continuous, and the distributions are assumed identical except for a difference in location, Conover-Iman test may be understood as a test for median difference. <code>conover.test</code> accounts for tied ranks. The Conover-Iman test is strictly valid if and only if the corresponding Kruskal-Wallis null hypothesis is rejected. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-conquestr	0.3.7	Extends ‘ACER ConQuest’ by allowing R users to call ‘ACER ConQuest’ from within R. The user can also access ‘ACER ConQuest’ data objects by reading ‘ACER ConQuest’ System Files (generated by the ‘ACER ConQuest’ command ‘put’). This is of particular use to those who are parsing text file output (e.g., ‘show’ files) as this is not consistent across releases of ‘ACER ConQuest’. Requires ‘ACER ConQuest’ version 4.29.3 or later. A demonstration version can be downloaded from < <a href="https://shop.acer.edu.au/acer-conquest-4">https://shop.acer.edu.au/acer-conquest-4</a> >. / GPL-3	noarch
r-conspline	1.2	Given response y, continuous predictor x, and covariate matrix, the relationship between E(y) and x is estimated with a shape constrained regression spline. Function outputs fits and various types of inference. / GPL-2   GPL-3	noarch
r-constants	0.0.2	CODATA internationally recommended values of the fundamental physical constants, provided as symbols for direct use within the R language. Optionally, the values with errors and/or the values with units are also provided if the ‘errors’ and/or the ‘units’ packages are installed. The Committee on Data for Science and Technology (CODATA) is an interdisciplinary committee of the International Council for Science which periodically provides the internationally accepted set of values of the fundamental physical constants. This package contains the 2014 CODATA version, published on 25 June 2015: Mohr, P. J., Newell, D. B. and Taylor, B. N. (2016) <DOI:10.1103/RevModPhys.88.035009>, <DOI:10.1063/1.4954402>. / MIT	noarch
r-constellation	0.2.0	Examine any number of time series data frames to identify instances in which various criteria are met within specified time frames. In clinical medicine, these types of events are often called constellations of signs and symptoms, because a single condition depends on a series of events occurring within a certain amount of time of each other. This package was written to work with any number of time series data frames and is optimized for speed to work well with data frames with millions of rows. / GPL-2	noarch
r-container	0.3.0	Common container data structures deque, set and dict (resembling ‘Python’s dict type) with typical member functions to insert, delete and access container elements. Provides iterators and reference semantics. / GPL-3	noarch
r-contfrac	1.1_12	Various utilities for evaluating continued fractions. / GPL-2	linux-64, osx-64, win-64
r-conting	1.7	Bayesian analysis of complete and incomplete contingency tables. / GPL-2	noarch
r-contourfunctions	0.1.1	Provides functions for making contour plots. The contour plot can be created from grid data, a function, or a data set. If non-grid data is given, then a Gaussian process is fit to the data and used to create the contour plot. / GPL-3	noarch
r-controltest	1.1.0	Nonparametric two-sample procedure for comparing survival quantiles. / GPL-3	noarch
r-convergenceclubs	1.4.3	Functions for clustering regions that form convergence clubs, according to the definition of Phillips and Sul (2009) <doi:10.1002/jae.1080>. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-convergenceconcepts</a>	1.2.1	This is a pedagogical package, designed to help students understanding convergence of random variables. It provides a way to investigate interactively various modes of convergence (in probability, almost surely, in law and in mean) of a sequence of i.i.d. random variables. Visualisation of simulated sample paths is possible through interactive plots. The approach is illustrated by examples and exercises through the function ‘investigate’, as described in Lafaye de Micheaux and Lique (2009) < <a href="http://dx.doi.org/10.1198/tas.2009.0032">http://dx.doi.org/10.1198/tas.2009.0032</a> >. The user can study his/her own sequences of random variables. / GPL-2	noarch
<a href="#">r-convertgraph</a>	0.1	Converts graphical file formats (SVG, PNG, JPEG, BMP, GIF, PDF, etc) to one another. The exceptions are the SVG file format that can only be converted to other formats and in contrast, PDF format, which can only be created from others graphical formats. The main purpose of the package was to provide a solution for converting SVG file format to PNG which is often needed for exporting graphical files produced by R widgets. / MIT	noarch
<a href="#">r-coop</a>	0.6_2	Fast implementations of the co-operations: covariance, correlation, and cosine similarity. The implementations are fast and memory-efficient and their use is resolved automatically based on the input data, handled by R’s S3 methods. Full descriptions of the algorithms and benchmarks are available in the package vignettes. / BSD_2_clause	linux-64, osx-64, win-64
<a href="#">r-coppecosenzar</a>	0.1.3	The program implements the COPPE-Cosenza Fuzzy Hierarchy Model. The model was based on the evaluation of local alternatives, representing regional potentialities, so as to fulfill demands of economic projects. After defining demand profiles in terms of their technological coefficients, the degree of importance of factors is defined so as to represent the productive activity. The method can detect a surplus of supply without the restriction of the distance of classical algebra, defining a hierarchy of location alternatives. In COPPE-Cosenza Model, the distance between factors is measured in terms of the difference between grades of memberships of the same factors belonging to two or more sets under comparison. The required factors are classified under the following linguistic variables: Critical (CR); Conditioning (C); Little Conditioning (LC); and Irrelevant (I). And the alternatives can assume the following linguistic variables: Excellent (Ex), Good (G), Regular (R), Weak (W), Empty (Em), Zero (Z) and Inexistent (In). The model also provides flexibility, allowing different aggregation rules to be performed and defined by the Decision Maker. Such feature is considered in this package, allowing the user to define other aggregation matrices, since it considers the same linguistic variables mentioned. / GPL-2	noarch
<a href="#">r-copula</a>	0.999	Copulas (S4) of commonly used elliptical, Archimedean, extreme-value and other copula families, as well as their rotations, mixtures and asymmetrizations. Nested Archimedean copulas, related tools and special functions. Methods for density, distribution, random number generation, bivariate dependence measures, Rosenblatt transform, Kendall distribution function, perspective and contour plots. Fitting of copula models with potentially partly fixed parameters, including standard errors. Serial independence tests, copula specification tests (independence, exchangeability, radial symmetry, extreme-value dependence, goodness-of-fit) and model selection based on cross-validation. Empirical copula, smoothed versions, and non-parametric estimators of the Pickands dependence function. / GPL (>= 3)   file LICENCE	linux-32, linux-64, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-copula.markov</a>	2.4	Estimation and statistical process control are performed under copula-based time-series models. Available are statistical methods in Long and Emura (2014 JCSA), Emura et al. (2017 Commun Stat-Simul) <DOI:10.1080/03610918.2015.1073303>, Huang and Emura(2019, in revision) and Huang, Chen and Emura (2019-, in revision). / GPL-2	noarch
<a href="#">r-copula.surv</a>	1.0	Perform association analysis of bivariate survival data based on copula models. Two different ways to estimate the association parameter in copula models are implemented. A goodness-of-fit test for a given copula model is implemented. See Emura, Lin and Wang (2010) <doi.org/10.1016/j.csda.2010.03.013> for details. / GPL-2	noarch
<a href="#">r-copuladata</a>	0.0_1	Data sets used for copula modeling in addition to those in the package ‘copula’. These include a random subsample from the US National Education Longitudinal Study (NELS) of 1988 and nursing home data from Wisconsin. / GPL-3	noarch
<a href="#">r-coranking</a>	0.1.4	Calculates the co-ranking matrix to assess the quality of a dimensionality reduction. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-corbin</a>	0.3.1	We design algorithms with linear time complexity with respect to the dimension for three commonly studied correlation structures, including exchangeable, decaying-product and K-dependent correlation structures, and extend the algorithms to generate binary data of general non-negative correlation matrices with quadratic time complexity. Jiang, W., Song, S., Hou, L. and Zhao, H. CorBin: An efficient R package to generate high-dimensional binary data with correlation structures. Submitted to Journal of Statistical Software. / GPL-3	noarch
<a href="#">r-corclass</a>	0.1.1	Perform a correlational class analysis of the data, resulting in a partition of the data into separate modules. / GPL-2	noarch
<a href="#">r-cord</a>	0.1.1	Partition data points (variables) into communities/clusters, similar to clustering algorithms, such as k-means and hierarchical clustering. This package implements a clustering algorithm based on a new metric CORD, defined for high dimensional parametric or semi-parametric distributions. Read <a href="http://arxiv.org/abs/1508.01939">http://arxiv.org/abs/1508.01939</a> for more details. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-core</a>	3.0	given a collection of intervals with integer start and end positions, find recurrently targeted regions and estimate the significance of finding. Randomization is implemented by parallel methods, either using local host machines, or submitting grid engine jobs. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-corelearn</a>	1.53.0	A suite of machine learning algorithms written in C with the R interface contains several learning techniques for classification and regression. Predictive models include e.g., classification and regression trees with optional constructive induction and models in the leaves, random forests, kNN, naive Bayes, and locally weighted regression. All predictions obtained with these models can be explained and visualized with the ‘ExplainPrediction’ package. This package is especially strong in feature evaluation where it contains several variants of Relief algorithm and many impurity based attribute evaluation functions, e.g., Gini, information gain, MDL, and DKM. These methods can be used for feature selection or discretization of numeric attributes. The OrdEval algorithm and its visualization is used for evaluation of data sets with ordinal features and class, enabling analysis according to the Kano model of customer satisfaction. Several algorithms support parallel multithreaded execution via OpenMP. The top-level documentation is reachable through ?CORElearn. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-corenlp</a>	0.4.2	Provides a minimal interface for applying annotators from the ‘Stanford CoreNLP’ java library. Methods are provided for tasks such as tokenisation, part of speech tagging, lemmatisation, named entity recognition, coreference detection and sentiment analysis. / GPL-2	noarch
<a href="#">r-coretdt</a>	1.0	Use to analysis case-parent trio sequencing studies. Test the compound heterozygous and recessive disease models / GPL-3	noarch
<a href="#">r-corlink</a>	1.0.0	A matrix of agreement patterns and counts for record pairs is the input for the procedure. An EM algorithm is used to impute plausible values for missing record pairs. A second EM algorithm, incorporating possible correlations between per-field agreement, is used to estimate posterior probabilities that each pair is a true match - i.e. constitutes the same individual. / CC0	noarch
<a href="#">r-coroica</a>	1.0.1	Contains an implementation of a confounding robust independent component analysis (ICA) for noisy and grouped data. The main function <code>coroICA()</code> performs a blind source separation, by maximizing an independence across sources and allows to adjust for varying confounding based on user-specified groups. Additionally, the package contains the function <code>uwedge()</code> which can be used to approximately jointly diagonalize a list of matrices. For more details see the project website < <a href="https://sweichwald.de/coroICA/">https://sweichwald.de/coroICA/</a> >. / AGPL-3	noarch
<a href="#">r-corpcor</a>	1.6.9	Implements a James-Stein-type shrinkage estimator for the covariance matrix, with separate shrinkage for variances and correlations. The details of the method are explained in Schafer and Strimmer (2005) <DOI:10.2202/1544-6115.1175> and Opgen-Rhein and Strimmer (2007) <DOI:10.2202/1544-6115.1252>. The approach is both computationally as well as statistically very efficient, it is applicable to small n, large p data, and always returns a positive definite and well-conditioned covariance matrix. In addition to inferring the covariance matrix the package also provides shrinkage estimators for partial correlations and partial variances. The inverse of the covariance and correlation matrix can be efficiently computed, as well as any arbitrary power of the shrinkage correlation matrix. Furthermore, functions are available for fast singular value decomposition, for computing the pseudoinverse, and for checking the rank and positive definiteness of a matrix. / GPL-3	noarch
<a href="#">r-corpora</a>	0.5	Utility functions for the statistical analysis of corpus frequency data. This package is a companion to the open-source course Statistical Inference: A Gentle Introduction for Computational Linguists and Similar Creatures (‘SIGIL’). / GPL-3	noarch
<a href="#">r-corporacoco</a>	1.1.0	A set of functions used to compare co-occurrence between two corpora. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-corpus	0.10.0	Text corpus data analysis, with full support for international text (Unicode). Functions for reading data from newline-delimited ‘JSON’ files, for normalizing and tokenizing text, for searching for term occurrences, and for computing term occurrence frequencies, including n-grams. / Apache License (== 2.0)   file LICENSE	linux-64, osx-64, win-64
r-corrcoverage	1.0.0	Using a computationally efficient method, the package can be used to find the corrected coverage estimate of a credible set of putative causal variants from Bayesian genetic fine-mapping. The package can also be used to obtain a corrected credible set if required; that is, the smallest set of variants required such that the corrected coverage estimate of the resultant credible set is within some user defined accuracy of the desired coverage. Maller et al. (2012) <doi:10.1038/ng.2435>, Wakefield (2009) <doi:10.1002/gepi.20359>, Fortune and Wallace (2018) <doi:10.1093/bioinformatics/bty898>. / MIT	linux-64, osx-64
r-corr dna	1.0.1	Can be useful for finding associations among different positions in a position-wise aligned sequence dataset. The approach adopted for finding associations among positions is based on the latent multivariate normal distribution. / GPL-2	noarch
r-correctedfdr	1.0	There are many estimators of false discovery rate. In this package we compute the Nonlocal False Discovery Rate (NFDR) and the estimators of local false discovery rate: Corrected False discovery Rate (CFDR), Re-ranked False Discovery rate (RFDR) and the blended estimator. Bickel, D. R. (2016) < <a href="http://hdl.handle.net/10393/34277">http://hdl.handle.net/10393/34277</a> >. / LGPL-3	noarch
r-correctoverloadedpeaks	1.2.17	Analyzes and modifies metabolomics raw data (generated using GC-APCI-MS, Gas Chromatography-Atmospheric Pressure Chemical Ionization-Mass Spectrometry) to correct overloaded signals, i.e. ion intensities exceeding detector saturation leading to a cut-off peak. Data in xcmsRaw format are accepted as input and mzXML files can be processed alternatively. Overloaded signals are detected automatically and modified using an Gaussian or Isotopic-Ratio approach, QC plots are generated and corrected data are stored within the original xcmsRaw or mzXML respectively to allow further processing. / GPL-3	noarch
r-correlplot	1.0_2	Correlplot contains diverse routines for the construction of different plots for representing correlation matrices. / GPL-2	noarch
r-corrmixed	0.1_13	In clinical practice and research settings in medicine and the behavioral sciences, it is often of interest to quantify the correlation of a continuous endpoint that was repeatedly measured (e.g., test-retest correlations, ICC, etc.). This package allows for estimating these correlations based on mixed-effects models. Part of this software has been developed using funding provided from the European Union’s 7th Framework Programme for research, technological development and demonstration under Grant Agreement no 602552. / GPL-2	noarch
r-corrplot	0.84	A graphical display of a correlation matrix or general matrix. It also contains some algorithms to do matrix reordering. In addition, corrplot is good at details, including choosing color, text labels, color labels, layout, etc. / GPL-3	noarch
r-corrsieve	1.6_8	Statistical summary of Structure output. / GPL-3	noarch
r-corset	0.1_4	Set of methods to constrain numerical series and time series within arbitrary boundaries. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-cortest</a>	0.9.8	There are 6 novel robust tests for equal correlation. They are all based on logistic regressions. U are proportion to different types of correlation in 6 methods. The ST1() is based on Pearson correlation. ST2() improved ST1() by using median absolute deviation. ST3() utilized type M correlation and ST4() used Spearman correlation. ST5() and ST6() used two different ways to combine ST3() and ST4(). We highly recommend ST5() according to the passage New Statistical Methods for Constructing Robust Differential Correlation Networks to characterize the interactions among microRNAs published in Scientific Reports. / GPL-2	noarch
<a href="#">r-cortools</a>	1.0	Designed for analysis of the results of a Genome Wide Association Study. Includes tools to pull lists of Chromosome number and SNP position below a certain significance threshold, refine gene networks (including data I/O for Cytoscape), and check SNP base pair changes. / Artistic-2.0	noarch
<a href="#">r-cosmofns</a>	1.0.1	Package encapsulates standard expressions for distances, times, luminosities, and other quantities useful in observational cosmology, including molecular line observations. Currently coded for a flat universe only. / GPL-2	noarch
<a href="#">r-cost</a>	0.1.0	Parameter estimation, one-step ahead forecast and new location prediction methods for spatio-temporal data. / GPL-3	noarch
<a href="#">r-costsensitive</a>	0.1.2	Reduction-based techniques for cost-sensitive multi-class classification, in which each observation has a different cost for classifying it into one class, and the goal is to predict the class with the minimum expected cost for each new observation. Implements Weighted All-Pairs (Beygelzimer, A., Langford, J., & Zadrozny, B., 2008, <doi:10.1007/978-0-387-79361-0_1>), Weighted One-Vs-Rest (Beygelzimer, A., Dani, V., Hayes, T., Langford, J., & Zadrozny, B., 2005, <https://dl.acm.org/citation.cfm?id=1102358>) and Regression One-Vs-Rest. Works with arbitrary classifiers taking observation weights, or with regressors. Also implements cost-proportionate rejection sampling for working with classifiers that don't accept observation weights. / BSD_2_clause	linux-64, osx-64, win-64
<a href="#">r-cotrend</a>	1.0.1	Implements cointegration/cotrending rank selection algorithm in Guo and Shintani (2013) Consistant cotrending rank selection when both stochastic and nonlinear deterministic trends are present. The Econometrics Journal 16: 473-483 <doi:10.1111/j.1368-423X.2012.00392.x>. Numbered examples correspond to Feb 2011 preprint <http://www.fas.nus.edu.sg/ecs/events/seminar/seminar-papers/05Apr11.pdf>. / GPL-3	noarch
<a href="#">r-couchdb</a>	1.4.1	Interface to the couchDB document database < <a href="http://couchdb.apache.org">http://couchdb.apache.org</a> >. / AGPL-3	noarch
<a href="#">r-countgmifs</a>	0.0.1	Provides a function for fitting Poisson and negative binomial regression models when the number of parameters exceeds the sample size, using the the generalized monotone incremental forward stagewise method. / GPL-2	noarch
<a href="#">r-counthmm</a>	0.1.0	Provides tools for penalized estimation of flexible hidden Markov models for time series of counts w/o the need to specify a (parametric) family of distributions. These include functions for model fitting, model checking, and state decoding. For details, see Adam, T., Langrock, R., and WeiÃY, C.H. (2019): Penalized Estimation of Flexible Hidden Markov Models for Time Series of Counts. <arXiv:1901.03275>. / GPL-3	noarch
<a href="#">r-countrycode</a>	1.1.0	Standardize country names, convert them into one of eleven coding schemes, convert between coding schemes, and assign region descriptors. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-covafillr</a>	0.4.3	Facilitates local polynomial regression for state dependent covariates in state-space models. The functionality can also be used from ‘C’ based model builder tools such as ‘Rcpp’/‘inline’, ‘TMB’, or ‘JAGS’. / BSD_2_clause	linux-64, osx-64, win-64
<a href="#">r-covbm</a>	0.1.0	Allows Brownian motion, fractional Brownian motion, and integrated Ornstein-Uhlenbeck process components to be added to linear and non-linear mixed effects models using the structures and methods of the ‘nlme’ package. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-covfefe</a>	0.1.0	Converts any word, sentence or speech into Trump’s infamous covfefe format. Reference: < <a href="https://www.nytimes.com/2017/05/31/us/politics/covfefe-trump-twitter.html">https://www.nytimes.com/2017/05/31/us/politics/covfefe-trump-twitter.html</a> >. Inspiration thanks to: < <a href="https://codegolf.stackexchange.com/questions/123685/covfefify-a-string">https://codegolf.stackexchange.com/questions/123685/covfefify-a-string</a> >. / GPL-3	noarch
<a href="#">r-covr</a>	3.3.1	Track and report code coverage for your package and (optionally) upload the results to a coverage service like ‘Codecov’ < <a href="http://codecov.io">http://codecov.io</a> > or ‘Coveralls’ < <a href="http://coveralls.io">http://coveralls.io</a> >. Code coverage is a measure of the amount of code being exercised by a set of tests. It is an indirect measure of test quality and completeness. This package is compatible with any testing methodology or framework and tracks coverage of both R code and compiled C/C/FORTRAN code. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-covreg</a>	1.0	This package fits a simultaneous regression model for the mean vectors and covariance matrices of multivariate response variables, as described in Hoff and Niu (2012). The explanatory variables can be continuous or discrete. The current version of the package provides the Bayesian estimates. / GPL-2	noarch
<a href="#">r-covrobust</a>	1.1_3	The cov.nnve() function implements robust covariance estimation by the nearest neighbor variance estimation (NNVE) method of Wang and Raftery (2002) <DOI:10.1198/016214502388618780>. / GPL-2	noarch
<a href="#">r-covsep</a>	1.1.0	Functions for testing if the covariance structure of 2-dimensional data (e.g. samples of surfaces $X_i = X_i(s,t)$ ) is separable, i.e. if $\text{covariance}(X) = C_1 \times C_2$ . A complete descriptions of the implemented tests can be found in the paper Aston, John A. D.; Pigoli, Davide; Tavakoli, Shahin. Tests for separability in nonparametric covariance operators of random surfaces. Ann. Statist. 45 (2017), no. 4, 1431–1461. <doi:10.1214/16-AOS1495> < <a href="https://projecteuclid.org/euclid.aos/1498636862">https://projecteuclid.org/euclid.aos/1498636862</a> > <arXiv:1505.02023>. / GPL-2	noarch
<a href="#">r-covtestr</a>	0.1.4	Testing functions for Covariance Matrices. These tests include high-dimension homogeneity of covariance matrix testing described by Schott (2007) <doi:10.1016/j.csda.2007.03.004> and high-dimensional one-sample tests of covariance matrix structure described by Fisher, et al. (2010) <doi:10.1016/j.jmva.2010.07.004>. Covariance matrix tests use C to speed performance and allow larger data sets. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-coxboost</a>	1.4	This package provides routines for fitting Cox models by likelihood based boosting for a single endpoint or in presence of competing risks / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-coxme</a>	2.2.14	This package fits Cox proportional hazards models containing both fixed and random effects. The random effects can have a general form, of which familial interactions (a kinship matrix) is a particular special case. Note that the simplest case of a mixed effects Cox model, i.e. a single random per-group intercept, is also called a frailty model. The approach is based on Rippatti and Palgren, Biometrics 2002. / LGPL-2	linux-64, osx-64, win-64
<a href="#">r-coxphf</a>	1.13	Implements Firth's penalized maximum likelihood bias reduction method for Cox regression which has been shown to provide a solution in case of monotone likelihood (nonconvergence of likelihood function). The program fits profile penalized likelihood confidence intervals which were proved to outperform Wald confidence intervals. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-coxphlb</a>	1.2.0	Performs analysis of right-censored length-biased data using Cox model. It contains model fitting and checking, and the stationarity assumption test. The model fitting and checking methods are described in Qin and Shen (2010) <doi:10.1111/j.1541-0420.2009.01287.x> and Lee, Ning, and Shen (2018) <doi:10.1007/s10985-018-9422-y>. / GPL-2	noarch
<a href="#">r-coxphmic</a>	0.1.0	Sparse estimation for Cox PH models is done via Minimum approximated Information Criterion (MIC) by Su, Wijayasinghe, Fan, and Zhang (2016) <DOI:10.1111/biom.12484>. MIC mimics the best subset selection using a penalized likelihood approach yet with no need of a tuning parameter. The problem is further reformulated with a re-parameterization step so that it reduces to one unconstrained non-convex yet smooth programming problem, which can be solved efficiently. Furthermore, the re-parameterization tactic yields an additional advantage in terms of circumventing post-selection inference. / GPL-2	noarch
<a href="#">r-coxphsgd</a>	0.2.1	Estimate coefficients of Cox proportional hazards model using stochastic gradient descent algorithm for batch data. / GPL-2	noarch
<a href="#">r-coxphw</a>	4.0.1	Implements weighted estimation in Cox regression as proposed by Schemper, Wakounig and Heinze (Statistics in Medicine, 2009, <doi:10.1002/sim.3623>) and as described in Dunkler, Ploner, Schemper and Heinze (Journal of Statistical Software, 2018, <doi:10.18637/jss.v084.i02>). Weighted Cox regression provides unbiased average hazard ratio estimates also in case of non-proportional hazards. Approximated generalized concordance probability an effect size measure for clear-cut decisions can be obtained. The package provides options to estimate time-dependent effects conveniently by including interactions of covariates with arbitrary functions of time, with or without making use of the weighting option. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-coxplus</a>	1.1.1	A high performance package estimating Cox Model when an even has more than one causes. It also supports random and fixed effects, tied events, and time-varying variables. / GPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-coxridge	0.9.2	A package for fitting Cox models with penalized ridge-type partial likelihood. The package includes functions for fitting simple Cox models with all covariates controlled by a ridge penalty. The weight of the penalty is optimised by using a REML type-algorithm. Models with time varying effects of the covariates can also be fitted. Some of the covariates may be allowed to be fixed and thus not controlled by the penalty. There are three different penalty functions, ridge, dynamic and weighted dynamic. Time varying effects can be fitted without the need of an expanded dataset. / GPL-2	noarch
r-coxrobust	1.0	Fit robustly proportional hazards regression model / GPL-2	linux-64, osx-64, win-64
r-coxsei	0.1	It fits a CoxSEI (Cox type Self-Exciting Intensity) model to right-censored counting process data. / GPL-2	linux-64, osx-64, win-64
r-cp	1.6	Functions for calculating the conditional power for different models in survival time analysis within randomized clinical trials with two different treatments to be compared and survival as an endpoint. / GPL-3	noarch
r-cpa	1.0	The package includes functions to test and compare causal models. / GPL-2	noarch
r-cpca	0.1.2	This package contains methods to perform Common Principal Component Analysis (CPCA). The stepwise method by Trendafilov is published in the current version. Please see Trendafilov (2010). Stepwise estimation of common principal components. Computational Statistics & Data Analysis, 54(12), 3446-3457. doi:10.1016/j.csda.2010.03.010 / GPL-3	noarch
r-cpcg	1.0	Solves system of linear equations using (preconditioned) conjugate gradient algorithm, with improved efficiency using Armadillo templated 'C' linear algebra library, and flexibility for user-specified preconditioning method. Please check < <a href="https://github.com/styvonn/cPCG">https://github.com/styvonn/cPCG</a> > for latest updates. / GPL-2	linux-64, osx-64, win-64
r-cpgassoc	2.60	Is designed to test for association between methylation at CpG sites across the genome and a phenotype of interest, adjusting for any relevant covariates. The package can perform standard analyses of large datasets very quickly with no need to impute the data. It can also handle mixed effects models with chip or batch entering the model as a random intercept. Also includes tools to apply quality control filters, perform permutation tests, and create QQ plots, manhattan plots, and scatterplots for individual CpG sites. / GPL-2	noarch
r-cpgfilter	1.1	Filter CpGs based on Intra-class Correlation Coefficients (ICCs) when replicates are available. ICCs are calculated by fitting linear mixed effects models to all samples including the un-replicated samples. Including the large number of un-replicated samples improves ICC estimates dramatically. The method accommodates any replicate design. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-cpk	1.3.1	The package cpk provides simplified clinical pharmacokinetic functions for dose regimen design and modification at the point-of-care. Currently, the following functions are available: (1) ttc.fn for target therapeutic concentration, (2) dr.fn for dose rate, (3) di.fn for dosing interval, (4) dm.fn for maintenance dose, (5) bc.ttc.fn for back calculation, (6) ar.fn for accumulation ratio, (7) dpo.fn for orally administered dose, (8) cmax.fn for peak concentration, (9) css.fn for steady-state concentration, (10) cmin.fn for trough, (11) ct.fn for concentration-time predictions, (12) dlcmax.fn for calculating loading dose based on drug's maximum concentration, (13) dlar.fn for calculating loading dose based on drug's accumulation ratio, and (14) R0.fn for calculating drug infusion rate. Reference: Linares O, Linares A. Computational opioid prescribing: A novel application of clinical pharmacokinetics. J Pain Palliat Care Pharmacother 2011;25:125-135. / GPL-2	noarch
r-cplots	0.4.0	Provides functions to produce some circular plots for circular data, in a height- or area-proportional manner. They include barplots, smooth density plots, stacked dot plots, histograms, multi-class stacked smooth density plots, and multi-class stacked histograms. The new methodology for general area-proportional circular visualization is described in an article submitted (after revision) to Journal of Computational and Graphical Statistics. / GPL-2	noarch
r-cpm	2.2	Sequential and batch change detection for univariate data streams, using the change point model framework. Functions are provided to allow nonparametric distribution-free change detection in the mean, variance, or general distribution of a given sequence of observations. Parametric change detection methods are also provided for Gaussian, Bernoulli and Exponential sequences. Both the batch (Phase I) and sequential (Phase II) settings are supported, and the sequences may contain either a single or multiple change points. / GPL-3	linux-64, osx-64, win-64
r-cpmcglm	1.2	We propose to determine the correction of the significance level after multiple coding of an explanatory variable in Generalized Linear Model. The different methods of correction of the p-value are the Single step Bonferroni procedure, and resampling based methods developed by P.H.Westfall in 1993. Resampling methods are based on the permutation and the parametric bootstrap procedure. If some continuous, and dichotomous transformations are performed this package offers an exact correction of the p-value developed by B.Liquet & D.Commenges in 2005. The naive method with no correction is also available. / GPL (> 2)	noarch
r-cpprouting	1.1	Calculation of distances, shortest paths and isochrones on weighted graphs using several variants of Dijkstra algorithm. Proposed algorithms are unidirectional Dijkstra (Dijkstra, E. W. (1959) <doi:10.1007/BF01386390>), bidirectional Dijkstra (Goldberg, Andrew & Fonseca F. Werneck, Renato (2005) <https://pdfs.semanticscholar.org/0761/18dfbe1d5a220f6ac59b4de4ad07b50283a1.pdf>), A* search (P. E. Hart, N. J. Nilsson et B. Raphael (1968) <doi:10.1109/TSSC.1968.300136>), new bidirectional A* (Pijls & Post (2009) <http://repub.eur.nl/pub/16100/ei2009-10.pdf>). / GPL-2	linux-64, osx-64, win-64
r-cpr	0.2.0	Calculate date of birth, age, and gender, and generate anonymous sequence numbers from CPR numbers. < <a href="https://en.wikipedia.org/wiki/Personal_identification_number_(Denmark)">https://en.wikipedia.org/wiki/Personal_identification_number_(Denmark)</a> >. / GPL-3	noarch
r-cpt	1.0.2	Non-parametric test for equality of multivariate distributions. Trains a classifier to classify (multivariate) observations as coming from one of several distributions. If the classifier is able to classify the observations better than would be expected by chance (using permutation inference), then the null hypothesis that the distributions are equal is rejected. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-cptcity	1.0.4	Incorporates colour gradients from the ‘cpt-city’ web archive available at <a href="http://soliton.vm.bytemark.co.uk/pub/cpt-city/">http://soliton.vm.bytemark.co.uk/pub/cpt-city/</a> . / GPL-3	noarch
r-cptec	0.1.0	Allows to retrieve data from the ‘CPTEC/INPE’ weather forecast API. ‘CPTEC’ stands for ‘Centro de Previsão de Tempo e Estudos Climáticos’ and ‘INPE’ for ‘Instituto Nacional de Pesquisas Espaciais’. ‘CPTEC’ is the most advanced numerical weather and climate forecasting center in Latin America, with high-precision short and medium-term weather forecasting since the beginning of 1995. See <a href="http://www.cptec.inpe.br/">http://www.cptec.inpe.br/</a> for more information. / GPL-3	noarch
r-cqrreg	1.2	Estimate quantile regression(QR) and composite quantile regression (cqr) and with adaptive lasso penalty using interior point (IP), majorize and minimize(MM), coordinate descent (CD), and alternating direction method of multipliers algorithms(ADMM). / GPL-2	linux-64, osx-64, win-64
r-cr	1.0	This package contains R-functions to perform power calculation in a group sequential clinical trial with censored survival data and possibly unequal patient allocation between treatment and control groups. The functions can also be used to determine the study duration in a clinical trial with censored survival data as the sum of the accrual duration, which determines the sample size in a traditional sense, and the follow-up duration, which more or less controls the number of events to be observed. This package also contains R functions and methods to display the computed results. / GPL-2	noarch
r-crac	1.0	R functions for cosmological research. The main functions are similar to the python library, cosmology. / GPL-2	noarch
r-cramer	0.9_3	Provides R routine for the so called two-sample Cramer-Test. This nonparametric two-sample-test on equality of the underlying distributions can be applied to multivariate data as well as univariate data. It offers two possibilities to approximate the critical value both of which are included in this package. / GPL-2	noarch
r-crank	1.1_2	Functions for completing and recalculating rankings and sorting. / GPL-2	noarch
r-cranlogs	2.1.1	‘API’ to the database of ‘CRAN’ package downloads from the ‘RStudio’ ‘CRAN mirror’. The database itself is at <a href="http://cranlogs.r-pkg.org">http://cranlogs.r-pkg.org</a> , see <a href="https://github.com/r-hub/cranlogs.app">https://github.com/r-hub/cranlogs.app</a> for the raw ‘API’. / MIT	noarch
r-crantastic	0.1	Various R tools for <a href="http://crantastic.org/">http://crantastic.org/</a> / GPL-2	noarch
r-crayon	1.3.4	Colored terminal output on terminals that support ‘ANSI’ color and highlight codes. It also works in ‘Emacs’ ‘ESS’. ‘ANSI’ color support is automatically detected. Colors and highlighting can be combined and nested. New styles can also be created easily. This package was inspired by the ‘chalk’ ‘JavaScript’ project. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-crblocks	1.0_0	Implements a statistical test for comparing bar plots or histograms of categorical data derived from a randomized block repeated measures layout. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-cream</a>	1.1.1	Provides a new method for identification of clusters of genomic regions within chromosomes. Primarily, it is used for calling clusters of cis-regulatory elements (COREs). ‘CREAM’ uses genome-wide maps of genomic regions in the tissue or cell type of interest, such as those generated from chromatin-based assays including DNaseI, ATAC or ChIP-Seq. ‘CREAM’ considers proximity of the elements within chromosomes of a given sample to identify COREs in the following steps: 1) It identifies window size or the maximum allowed distance between the elements within each CORE, 2) It identifies number of elements which should be clustered as a CORE, 3) It calls COREs, 4) It filters the COREs with lowest order which does not pass the threshold considered in the approach. / GPL-3	noarch
<a href="#">r-credentials</a>	1.1	Setup and retrieve HTTPS and SSH credentials for use with ‘git’ and other services. For HTTPS remotes the package interfaces the ‘git-credential’ utility which ‘git’ uses to store HTTP usernames and passwords. For SSH remotes we provide convenient functions to find or generate appropriate SSH keys. The package both helps the user to setup a local git installation, and also provides a back-end for git/ssh client libraries to authenticate with existing user credentials. / MIT	noarch
<a href="#">r-creditmetrics</a>	0.0_2	A set of functions for computing the CreditMetrics risk model / Unlimited	noarch
<a href="#">r-credsubs</a>	1.0.1	Functions for constructing simultaneous credible bands and identifying subsets via the credible subsets (also called credible subgroups) method. / GPL-3	noarch
<a href="#">r-credule</a>	0.1.3	It provides functions to bootstrap Credit Curves from market quotes (Credit Default Swap - CDS - spreads) and price Credit Default Swaps - CDS. / MIT	linux-64, osx-64, win-64
<a href="#">r-crf</a>	0.4_2	Implements modeling and computational tools for conditional random fields (CRF) model as well as other probabilistic undirected graphical models of discrete data with pairwise and unary potentials. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-crfsuite</a>	0.3	Wraps the ‘CRFsuite’ library < <a href="https://github.com/chokkan/crfsuite">https://github.com/chokkan/crfsuite</a> > allowing users to fit a Conditional Random Field model and to apply it on existing data. The focus of the implementation is in the area of Natural Language Processing where this R package allows you to easily build and apply models for named entity recognition, text chunking, part of speech tagging, intent recognition or classification of any category you have in mind. Next to training, a small web application is included in the package to allow you to easily construct training data. / BSD_3_clause	linux-64, osx-64, win-64
<a href="#">r-crimcv</a>	0.9.6	A finite mixture of Zero-Inflated Poisson (ZIP) models for analyzing criminal trajectories. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-crisp	1.0.0	Implements convex regression with interpretable sharp partitions (CRISP), which considers the problem of predicting an outcome variable on the basis of two covariates, using an interpretable yet non-additive model. CRISP partitions the covariate space into blocks in a data-adaptive way, and fits a mean model within each block. Unlike other partitioning methods, CRISP is fit using a non-greedy approach by solving a convex optimization problem, resulting in low-variance fits. More details are provided in Petersen, A., Simon, N., and Witten, D. (2016). Convex Regression with Interpretable Sharp Partitions. Journal of Machine Learning Research, 17(94): 1-31 < <a href="http://jmlr.org/papers/volume17/15-344/15-344.pdf">http://jmlr.org/papers/volume17/15-344/15-344.pdf</a> >. / GPL-2	noarch
r-crm	1.2.4	Functions for phase I clinical trials using the continual reassessment method. / GPL-2	linux-64, osx-64, win-64
r-crnl	1.1	The crnl package provides the core functions required to download and format data from the Climate Reference Network. Both daily and hourly data are downloaded from the ftp, a consolidated file of all stations is created, station metadata is extracted. In addition functions for selecting individual variables and creating R friendly datasets for them is provided. / GPL-2	noarch
r-crochet	2.2.0	Functions to help implement the extraction / subsetting / indexing function '[' and replacement function '[<-' of custom matrix-like types (based on S3, S4, etc.), modeled as closely to the base matrix class as possible (with tests to prove it). / MIT	noarch
r-crone	0.1.1	Functions to carry out the most important crystallographic calculations for crystal structures made of 1d Gaussian-shaped atoms, especially useful for methods development. Main reference: E. Smith, G. Evans, J. Foadi (2017) <doi:10.1088/1361-6404/aa8188>. / GPL-2	noarch
r-cronr	0.4.0	Create, edit, and remove 'cron' jobs on your unix-alike system. The package provides a set of easy-to-use wrappers to 'crontab'. It also provides an RStudio add-in to easily launch and schedule your scripts. / MIT	noarch
r-crop	0.0_2	A device closing function which is able to crop graphics (e.g., PDF, PNG files) on Unix-like operating systems with the required underlying command-line tools installed. / GPL-2   GPL-3	noarch
r-cropdatape	1.0.0	Provides peruvian agricultural production data from the Agriculture Ministry of Peru (MINAGRI). The first version includes 6 crops: rice, quinoa, potato, sweet potato, tomato and wheat; all of them across 24 departments. Initially, in excel files which has been transformed and assembled using tidy data principles, i.e. each variable is in a column, each observation is a row and each value is in a cell. The variables variables are sowing and harvest area per crop, yield, production and price per plot, every one year, from 2004 to 2014. / MIT	noarch
r-crossdes	1.1_1	Contains functions for the construction of carryover balanced crossover designs. In addition contains functions to check given designs for balance. / GPL-2	noarch
r-crossreg	1.0	This package provides functions to calculate confidence intervals for crossover points of two simple linear regression lines using the non-linear regression, the delta method, the Fieller method, and the bootstrap methods. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-crosstalk</a>	1.0.0	Provides building blocks for allowing HTML widgets to communicate with each other, with Shiny or without (i.e. static .html files). Currently supports linked brushing and filtering. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-crossva</a>	0.9.9	Enables transformation of Verbal Autopsy data collected with the WHO 2016 questionnaire (versions 1.4.1 & 1.5.1) or the WHO 2014 questionnaire for automated coding of Cause of Death using the InSilicoVA (data.type = WHO2016) and InterVA5 algorithms. Previous versions of this package supported user-supplied mappings (via the map_records function), but this functionality has been removed. This package is made available by WHO and the Bloomberg Data for Health Initiative. / GPL-3	noarch
<a href="#">r-crossval</a>	1.0.3	Contains generic functions for performing cross validation and for computing diagnostic errors. / GPL-3	noarch
<a href="#">r-crov</a>	0.1.3	Fits a constrained regression model for an ordinal response with ordinal predictors and possibly others, Espinosa and Hennig (2018) <arXiv:1804.08715>. The parameter estimates associated with an ordinal predictor are constrained to be monotonic. If a monotonicity direction (isotonic or antitonic) is not specified for an ordinal predictor by the user, then the monotonicity direction classification procedure establishes it. A monotonicity test is also available to test the null hypothesis of monotonicity over a set of parameters associated with an ordinal predictor. / GPL-2	noarch
<a href="#">r-crp.csfp</a>	2.0.2	Modelling credit risks based on the concept of CreditRisk, First Boston Financial Products, 1997 and CreditRisk in the Banking Industry, Gundlach & Lehrbass, Springer, 2003. / GPL-2	noarch
<a href="#">r-crrp</a>	1.0	In competing risks regression, the proportional subdistribution hazards(PSH) model is popular for its direct assessment of covariate effects on the cumulative incidence function. This package allows for penalized variable selection for the PSH model. Penalties include LASSO, SCAD, MCP, and their group versions. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-crrsc</a>	1.1	Extension of cmprsk to Stratified and Clustered data. Goodness of fit test for Fine-Gray model. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-crrstep</a>	2015	Performs forward and backwards stepwise regression for the Proportional subdistribution hazards model in competing risks (Fine & Gray 1999). Procedure uses AIC, BIC and BICcr as selection criteria. BICcr has a penalty of $k = \log(n^*)$ , where $n^*$ is the number of primary events. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-crseventstudy</a>	1.2	Based on Dutta et al. (2018) <doi:10.1016/j.jempfin.2018.02.004>, this package provides their standardized test for abnormal returns in long-horizon event studies. The methods used improve the major weaknesses of size, power, and robustness of long-run statistical tests described in Kothari/Warner (2007) <doi:10.1016/B978-0-444-53265-7.50015-9>. Abnormal returns are weighted by their statistical precision (i.e., standard deviation), resulting in abnormal standardized returns. This procedure efficiently captures the heteroskedasticity problem. Clustering techniques following Cameron et al. (2011) <10.1198/jbes.2010.07136> are adopted for computing cross-sectional correlation robust standard errors. The statistical tests in this package therefore accounts for potential biases arising from returns' cross-sectional correlation, autocorrelation, and volatility clustering without power loss. / BSD_3_clause	noarch
<a href="#">r-crskdiag</a>	1.0.1	Provides the implementation of analytical and graphical approaches for checking the assumptions of the Fine and Gray model. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-crsnls</a>	0.2	Functions for nonlinear regression parameters estimation by algorithms based on Controlled Random Search algorithm. Both functions (crs4hc(), crs4hce()) adapt current search strategy by four heuristics competition. In addition, crs4hce() improves adaptability by adaptive stopping condition. / GPL-2	noarch
<a href="#">r-crso</a>	0.1.1	An algorithm for identifying candidate driver combinations in cancer. CRSO is based on a theoretical model of cancer in which a cancer rule is defined to be a collection of two or more events (i.e., alterations) that are minimally sufficient to cause cancer. A cancer rule set is a set of cancer rules that collectively are assumed to account for all of ways to cause cancer in the population. In CRSO every event is designated explicitly as a passenger or driver within each patient. Each event is associated with a patient-specific, event-specific passenger penalty, reflecting how unlikely the event would have happened by chance, i.e., as a passenger. CRSO evaluates each rule set by assigning all samples to a rule in the rule set, or to the null rule, and then calculating the total statistical penalty from all unassigned event. CRSO uses a three phase procedure find the best rule set of fixed size K for a range of Ks. A core rule set is then identified from among the best rule sets of size K as the rule set that best balances rule set size and statistical penalty. Users should consult the 'crso' vignette for an example walk through of a full CRSO run. The full description, of the CRSO algorithm is presented in: Klein MI, Cannataro V, Townsend J, Stern DF and Zhao H. Identifying combinations of cancer driver in individual patients. BioRxiv 674234 [Preprint]. June 19, 2019. <doi:10.1101/674234>. Please cite this article if you use 'crso'. / GPL-2	noarch
<a href="#">r-crtsize</a>	1.0	Sample size estimation in cluster (group) randomized trials. Contains traditional power-based methods, empirical smoothing (Rotondi and Donner, 2009), and updated meta-analysis techniques (Rotondi and Donner, 2012). / GPL-2	noarch
<a href="#">r-crwrn</a>	0.0.1	To re-calculate the coefficients and the standard deviation when changing the reference group. / GPL-3	noarch
<a href="#">r-cseqpat</a>	0.1.2	Mines contiguous sequential patterns in text. / MIT	noarch
<a href="#">r-cshapes</a>	0.6	Package for CShapes, a GIS dataset of country boundaries (1946-today). Includes functions for data extraction and the computation of distance matrices and -lists. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-csn	1.1.3	Provides functions for computing the density and the log-likelihood function of closed-skew normal variates, and for generating random vectors sampled from this distribution. See Gonzalez-Farias, G., Dominguez-Molina, J., and Gupta, A. (2004). The closed skew normal distribution, Skew-elliptical distributions and their applications: a journey beyond normality, Chapman and Hall/CRC, Boca Raton, FL, pp. 25-42. / GPL-2	noarch
r-csp	0.1.0	Provides the Correlates of State Policy data set for easy use in R. / CC0	noarch
r-csrplus	1.03	Includes two functions to evaluate the hypothesis of complete spatial randomness (csr) in point processes. The function 'mwin' calculates quadrat counts to estimate the intensity of a spatial point process through the moving window approach proposed by Bailey and Gatrell (1995). Event counts are computed within a window of a set size over a fine lattice of points within the region of observation. The function 'pielou' uses the nearest neighbor test statistic and asymptotic distribution proposed by Pielou (1959) to compare the observed point process to one generated under csr. The value can be compared to that given by the more widely used test proposed by Clark and Evans (1954). / GPL-2	noarch
r-cssam	1.2.4	Cell-type specific differential expression of a microarray experiment of heterogeneous tissue samples, using SAM. / LGPL-3	noarch
r-cstar	1.0	Functions that allow a researcher to examine the robustness of the substantive significance of their findings. Implements ideas set out in Esarey and Danne-man (2014). / GPL-2	noarch
r-csv	0.5.3	Reads and writes CSV with selected conventions. Uses the same generic function for reading and writing to promote consistent formats. / GPL-3	noarch
r-csvread	1.2.1	Functions for loading large (10M lines) CSV and other delimited files, similar to read.csv, but typically faster and using less memory than the standard R loader. While not entirely general, it covers many common use cases when the types of columns in the CSV file are known in advance. In addition, the package provides a class 'int64', which represents 64-bit integers exactly when reading from a file. The latter is useful when working with 64-bit integer identifiers exported from databases. The CSV file loader supports common column types including 'integer', 'double', 'string', and 'int64', leaving further type transformations to the user. / Apache License (== 2.0)	linux-64, osx-64, win-64
r-csvy	0.3.0	Support for import from and export to the CSVY file format. CSVY is a file format that combines the simplicity of CSV (comma-separated values) with the metadata of other plain text and binary formats (JSON, XML, Stata, etc.) by placing a YAML header on top of a regular CSV. / GPL-2	noarch
r-cthrasher	1.1.0	Estimation and inference methods for the continuous threshold expectile regression. It can fit the continuous threshold expectile regression and test the existence of change point, for the paper, Feipeng Zhang and Qunhua Li (2016). A continuous threshold expectile regression, submitted. / GPL (>= 2.0)	noarch
r-ctrdata	0.18.2	Provides functions for querying, retrieving and analysing protocol- and results-related information on clinical trials from two public registers, the European Union Clinical Trials Register (EUCTR, < <a href="https://www.clinicaltrialsregister.eu/">https://www.clinicaltrialsregister.eu/</a> >) and ClinicalTrials.gov (CTGOV, < <a href="https://clinicaltrials.gov/">https://clinicaltrials.gov/</a> >). The information is transformed and then stored in a database (mongo). Functions are provided for accessing and analysing the locally stored information on the clinical trials, as well as for identifying duplicate records. The package is motivated by the need for aggregating and trend-analysing the design, conduct and outcomes across clinical trials. / MIT	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-ctrlgene</a>	1.0.1	A simple way to assess the stability of candidate housekeeping genes is implemented in this package. / GPL-2	noarch
<a href="#">r-cts</a>	1.0.2	Functions to fit continuous time autoregressive models with the Kalman filter (Wang (2013) <doi:10.18637/jss.v053.i05>). / GPL-2	linux-64, osx-64, win-64
<a href="#">r-ctt</a>	2.3.3	A collection of common test and item analyses from a classical test theory (CTT) framework. Analyses can be applied to both dichotomous and polytomous data. Functions provide reliability analyses (alpha), item statistics, distractor analyses, disattenuated correlations, scoring routines, and empirical ICCs. / GPL-2	noarch
<a href="#">r-cttinshiny</a>	0.1.0	A Shiny interface developed in close coordination with the CTT package, providing a GUI that guides the user through CTT analyses. / GPL-2	noarch
<a href="#">r-ctv</a>	0.8.5	Infrastructure for task views to CRAN-style repositories: Querying task views and installing the associated packages (client-side tools), generating HTML pages and storing task view information in the repository (server-side tools). / GPL-2   GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-cub</a>	1.1.3	For ordinal rating data, estimate and test models within the family of CUB models and their extensions (where CUB stands for Combination of a discrete Uniform and a shifted Binomial distributions). Simulation routines, plotting facilities and fitting measures are also provided. / GPL-2   GPL-3	noarch
<a href="#">r-cubature</a>	2.0.3	R wrappers around the cubature C library of Steven G. Johnson for adaptive multivariate integration over hypercubes and the Cuba C library of Thomas Hahn for deterministic and Monte Carlo integration. Scalar and vector interfaces for cubature and Cuba routines are provided; the vector interfaces are highly recommended as demonstrated in the package vignette. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-cubeview</a>	0.1.0	Creates a 3D data cube view of a RasterStack/Brick, typically a collection/array of RasterLayers (along z-axis) with the same geographical extent (x and y dimensions) and resolution, provided by package 'raster'. Slices through each dimension (x/y/z), freely adjustable in location, are mapped to the visible sides of the cube. The cube can be freely rotated. Zooming and panning can be used to focus on different areas of the cube. / MIT	noarch
<a href="#">r-cubfits</a>	0.1.3	Estimating mutation and selection coefficients on synonymous codon bias usage based on models of ribosome overhead cost (ROC). Multinomial logistic regression and Markov Chain Monte Carlo are used to estimate and predict protein production rates with/without the presence of expressions and measurement errors. Work flows with examples for simulation, estimation and prediction processes are also provided with parallelization speedup. The whole framework is tested with yeast genome and gene expression data of Yassour, et al. (2009) <doi:10.1073/pnas.0812841106>. / Mozilla Public License 2.0	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-cubist</a>	0.2.2	Regression modeling using rules with added instance-based corrections. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-cump</a>	2.0	Combining Univariate Association Test Results of Multiple Phenotypes for Detecting Pleiotropy. / GPL-2	noarch
<a href="#">r-cumplyr</a>	0.1.1	Extends ddply to allow calculation of cumulative quantities. / MIT	noarch
<a href="#">r-cumseg</a>	1.2	Estimation of number and location of change points in mean-shift (piecewise constant) models. Particularly useful to model genomic sequences of continuous measurements. / GPL-3	noarch
<a href="#">r-cumstats</a>	1.0	Cumulative descriptive statistics for (arithmetic, geometric, harmonic) mean, median, mode, variance, skewness and kurtosis. / GPL-3	noarch
<a href="#">r-curl</a>	3.3	The curl() and curl_download() functions provide highly configurable drop-in replacements for base url() and download.file() with better performance, support for encryption (https, ftps), gzip compression, authentication, and other 'libcurl' goodies. The core of the package implements a framework for performing fully customized requests where data can be processed either in memory, on disk, or streaming via the callback or connection interfaces. Some knowledge of 'libcurl' is recommended; for a more-user-friendly web client see the 'httr' package which builds on this package with http specific tools and logic. / MIT file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-currentsurvival</a>	1.0	The currentSurvival package contains functions for the estimation of the current cumulative incidence (CCI) and the current leukaemia-free survival (CLFS). The CCI is the probability that a patient is alive and in any disease remission (e.g. complete cytogenetic remission in chronic myeloid leukaemia) after initiating his or her therapy (e.g. tyrosine kinase therapy for chronic myeloid leukaemia). The CLFS is the probability that a patient is alive and in any disease remission after achieving the first disease remission. / GPL-2	noarch
<a href="#">r-curry</a>	0.1.1	Partial application is the process of reducing the arity of a function by fixing one or more arguments, thus creating a new function lacking the fixed arguments. The curry package provides three different ways of performing partial function application by fixing arguments from either end of the argument list (currying and tail currying) or by fixing multiple named arguments (partial application). This package provides this functionality through the %<%, %<%<%, and %>>% operators which allows for a programming style comparable to modern functional languages. Compared to other implementations such as purrr::partial() the operators in curry composes functions with named arguments, aiding in autocomplete etc. / GPL-2	noarch
<a href="#">r-curstatci</a>	0.1.1	Computes the maximum likelihood estimator, the smoothed maximum likelihood estimator and pointwise bootstrap confidence intervals for the distribution function under current status data. Groeneboom and Hendrickx (2017) <doi:10.1214/17-EJS1345>. / GPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<code>r-curvecomp</code>	0.1.0	Performs multiple comparison procedures on curve observations among different treatment groups. The methods are applicable in a variety of situations (such as independent groups with equal or unequal sample sizes, or repeated measures) by using parametric bootstrap. References to these procedures can be found at Konietzschke, Gel, and Brunner (2014) <doi:10.1090/conm/622/12431> and Westfall (2011) <doi:10.1080/10543406.2011.607751>. / GPL-2	noarch
<code>r-cusp</code>	2.3.3	Cobb's maximum likelihood method for cusp-catastrophe modeling (Grasman, van der Maas, & Wagenmakers, 2009, JSS, 32:8; Cobb, L, 1981, Behavioral Science, 26:1, 75–78). Includes a cusp() function for model fitting, and several utility functions for plotting, and for comparing the model to linear regression and logistic curve models. / GPL-2	linux-64, osx-64, win-64
<code>r-customerscoringmetrics</code>	1.0.0	Functions for evaluating and visualizing predictive model performance (specifically: binary classifiers) in the field of customer scoring. These metrics include lift, lift index, gain percentage, top-decile lift, F1-score, expected misclassification cost and absolute misclassification cost. See Berry & Linoff (2004, ISBN:0-471-47064-3), Witten and Frank (2005, 0-12-088407-0) and Blattberg, Kim & Neslin (2008, ISBN:978-0-387-72578-9) for details. Visualization functions are included for lift charts and gain percentage charts. All metrics that require class predictions offer the possibility to dynamically determine cutoff values for transforming real-valued probability predictions into class predictions. / GPL-2	noarch
<code>r-cusum</code>	0.4.0	Provides functions for constructing and evaluating CUSUM charts and RA-CUSUM charts with focus on false signal probability. / GPL-2	linux-64, osx-64, win-64
<code>r-cusumdesign</code>	1.1.3	Computation of decision intervals (H) and average run lengths (ARL) for CUSUM charts. / GPL-2	linux-64, osx-64, win-64
<code>r-cutpointsoehr</code>	0.1.2	Use optimal equal-HR method to determine two optimal cutpoints of a continuous predictor that has a U-shaped relationship with survival outcomes based on Cox regression model. The optimal equal-HR method estimates two optimal cut-points that have approximately the same log hazard value based on Cox regression model and divides individuals into different groups according to their HR values. / GPL-3	noarch
<code>r-cuttlefish.model</code>	1.0	This package can be used to standardize abundance indices using the delta-GLM method and to model the English Channel cuttlefish stock using a two-stage biomass model / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-cvauc	1.1.0	This package contains various tools for working with and evaluating cross-validated area under the ROC curve (AUC) estimators. The primary functions of the package are ci.cvAUC and ci.pooled.cvAUC, which report cross-validated AUC and compute confidence intervals for cross-validated AUC estimates based on influence curves for i.i.d. and pooled repeated measures data, respectively. One benefit to using influence curve based confidence intervals is that they require much less computation time than bootstrapping methods. The utility functions, AUC and cvAUC, are simple wrappers for functions from the ROCR package. / Apache License (== 2.0)	noarch
r-cvcalibration	1.0.1	Statistical inferences for estimating the calibration equation with error-in observations / GPL-2	noarch
r-cvd	1.0.2	Methods for color vision deficiencies (CVD), to help understanding and mitigating issues with CVDs and to generate tests for diagnosis and interpretation. / GPL-3	noarch
r-cvequality	0.2.0	Contains functions for testing for significant differences between multiple coefficients of variation. Includes Feltz and Miller's (1996) <DOI:10.1002/(SICI)1097-0258(19960330)15:6%3C647::AID-SIM184%3E3.0.CO;2-P> asymptotic test and Krishnamoorthy and Lee's (2014) <DOI:10.1007/s00180-013-0445-2> modified signed-likelihood ratio test. See the vignette for more, including full details of citations. / MIT	noarch
r-cvgee	0.3.0	Calculates predictions from generalized estimating equations and internally cross-validates them using the logarithmic, quadratic and spherical proper scoring rules; Kung-Yee Liang and Scott L. Zeger (1986) <doi:10.1093/biomet/73.1.13>. / GPL-3	noarch
r-cvmgof	1.0.0	It is devoted to Cramer-von Mises goodness-of-fit tests. It implements three statistical methods based on Cramer-von Mises statistics to estimate and test a regression model. / CeCILL	noarch
r-cvq2	1.2.0	The external prediction capability of quantitative structure-activity relationship (QSAR) models is often quantified using the predictive squared correlation coefficient. This value can be calculated with an external data set or by cross validation. / GPL-3	noarch
r-cvst	0.2.2	The fast cross-validation via sequential testing (CVST) procedure is an improved cross-validation procedure which uses non-parametric testing coupled with sequential analysis to determine the best parameter set on linearly increasing subsets of the data. By eliminating under-performing candidates quickly and keeping promising candidates as long as possible, the method speeds up the computation while preserving the capability of a full cross-validation. Additionally to the CVST the package contains an implementation of the ordinary k-fold cross-validation with a flexible and powerful set of helper objects and methods to handle the overall model selection process. The implementations of the Cochran's Q test with permutations and the sequential testing framework of Wald are generic and can therefore also be used in other contexts. / GPL (>= 2.0)	linux-32, linux-64, noarch, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-cvtools</a>	0.3.2	Tools that allow developers to write functions for cross-validation with minimal programming effort and assist users with model selection. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-cvtuningcov</a>	1.0	This is a package for selecting tuning parameters based on cross-validation (CV) in regularized estimators of large covariance matrices. Four regularized methods are implemented: banding, tapering, hard-thresholding and soft-thresholding. Two types of matrix norms are applied: Frobenius norm and operator norm. Two types of CV are considered: K-fold CV and random CV. Usually K-fold CV use K-1 folds to train a model and the rest one fold to validate the model. The reverse version trains a model with 1 fold and validates with the rest with K-1 folds. Random CV randomly splits the data set to two parts, a training set and a validation set with user-specified sizes. / GPL-2	noarch
<a href="#">r-cvxbiclustr</a>	0.0.1	An iterative algorithm for solving a convex formulation of the biclustering problem. / MIT	linux-64, osx-64, win-64
<a href="#">r-cvxclustr</a>	1.1.1	Alternating Minimization Algorithm (AMA) and Alternating Direction Method of Multipliers (ADMM) splitting methods for convex clustering. / CC BY-NC-SA 4.0	linux-64, osx-64, win-64
<a href="#">r-cwhmisc</a>	6.6	Miscellaneous useful or interesting functions. / GPL-2	noarch
<a href="#">r-cxhull</a>	0.2.0	Computes the convex hull in arbitrary dimension, based on the Qhull library ( <a href="http://www.qhull.org">http://www.qhull.org</a> ). The package provides a complete description of the convex hull: edges, ridges, facets, adjacencies. Triangulation is optional. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-cxxfunplus</a>	1.0	extend cxxfunction by saving the dynamic shared objects for reusing across R sessions / GPL-3	noarch
<a href="#">r-cyclertools</a>	1.1.1	A suite of functions for analysing cycling data. / MIT	linux-64, osx-64, win-64
<a href="#">r-cyclocomp</a>	1.1.0	Cyclomatic complexity is a software metric (measurement), used to indicate the complexity of a program. It is a quantitative measure of the number of linearly independent paths through a program's source code. It was developed by Thomas J. McCabe, Sr. in 1976. / MIT	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-cycloids</a>	1.0	Tools for calculating coordinate representations of hypocycloids, epicycloids, hypotrochoids, and epitrochoids (altogether called ‘cycloids’ here) with different scaling and positioning options. The cycloids can be visualised with any appropriate graphics function in R. / GPL-3	noarch
<a href="#">r-cytobankapi</a>	1.3.0	Tools to interface with Cytobank’s API via R, organized by various endpoints that represent various areas of Cytobank functionality. Learn more about Cytobank at < <a href="https://www.cytobank.org">https://www.cytobank.org</a> >. / Artistic-2.0	noarch
<a href="#">r-cytobankbridger</a>	1.0.0	A collection of tools that leverage the CytobankAPI R package < <a href="https://cran.r-project.org/web/packages/CytobankAPI/vignettes/cytobank-quickstart.html">https://cran.r-project.org/web/packages/CytobankAPI/vignettes/cytobank-quickstart.html</a> > to complete more complex workflows, and add/extend various Cytobank features. / Artistic-2.0	noarch
<a href="#">r-d3network</a>	0.5.2	This packages is intended to make it easy to create D3 JavaScript network, tree, dendrogram, and Sankey graphs from R using data frames. !!! NOTE: Active development has moved to the networkD3 package. !!! / GPL-3	noarch
<a href="#">r-d3plus</a>	0.1.0	Provides functions that offer seamless ‘D3Plus’ integration. The examples provided here are taken from the official ‘D3Plus’ website < <a href="http://d3plus.org">http://d3plus.org</a> >. / MIT	noarch
<a href="#">r-daag</a>	1.22	Various data sets used in examples and exercises in the book Maindonald, J.H. and Braun, W.J. (2003, 2007, 2010) Data Analysis and Graphics Using R. / GPL-3	noarch
<a href="#">r-daagxtras</a>	0.8_4	various data sets used in additional exercises for the book Maindonald, J.H. and Braun, W.J. (3rd edn 2010) Data Analysis and Graphics Using R, and for a ‘Data Mining’ course. Note that a number of datasets that were in earlier versions of this package have been transferred to the DAAG package. / Un-limited	noarch
<a href="#">r-daarem</a>	0.3	Implements the DAAREM method for accelerating the convergence of slow, monotone sequences from smooth, fixed-point iterations such as the EM algorithm. For further details about the DAAREM method. see Henderson, N.C. and Varadhan, R. (2018) <arXiv:1803.06673>. / GPL-2	noarch
<a href="#">r-dacf</a>	1.0.0	An implementation of data analytic methods in R for analyses for data with ceiling/floor effects. The package currently includes functions for mean/variance estimation and mean comparison tests. Implemented methods are from Aitkin (1964) <doi:10.1007/BF02289723> and Liu & Wang (in prep). / GPL-2	noarch
<a href="#">r-dagr</a>	1.1.3	Functions to draw, manipulate, evaluate directed acyclic graphs and simulate corresponding data. / GPL-2	noarch
<a href="#">r-daime</a>	1.1	Reverse and model the effects of changing deposition rates on geological data and rates. Based on Hohmann (2018) <doi:10.13140/RG.2.2.23372.51841> . / CC BY 4.0	noarch
<a href="#">r-dalex2</a>	0.9	Machine Learning models are widely used and have various applications in classification or regression tasks. Due to increasing computational power, availability of new data sources and new methods, ML models are more and more complex. Models created with techniques like boosting, bagging of neural networks are true black boxes. It is hard to trace the link between input variables and model outcomes. They are used because of high performance, but lack of interpretability is one of their weakest sides. In many applications we need to know, understand or prove how input variables are used in the model and what impact do they have on final model prediction. DALEX2 is a collection of tools that help to understand how complex predictive models are working. DALEX2 is a part of DrWhy universe for tools for Explanation, Exploration and Visualisation for Predictive Models. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-daly	1.5.0	The DALY Calculator is a free, open-source Graphical User Interface (GUI) for stochastic disability-adjusted life year (DALY) calculation. / GPL-2	linux-64, osx-64, win-64
r-dam	0.0.1	A collection of functions which aim to assist common computational workflow for analysis of matabolomic data.. / CC0	noarch
r-dams	0.2	The single largest source of dams in the United States is the National Inventory of Dams (NID) < <a href="http://nid.usace.army.mil">http://nid.usace.army.mil</a> > from the US Army Corps of Engineers. Entire data from the NID cannot be obtained all at once and NID's website limits extraction of more than a couple of thousand records at a time. Moreover, selected data from the NID's user interface cannot not be saved to a file. In order to make the analysis of this data easier, all the data from NID was extracted manually. Subsequently, the raw data was checked for potential errors and cleaned. This package provides sample cleaned data from the NID and provides functionality to access the entire cleaned NID data. / GPL-2	noarch
r-dang	0.0.10	A collection of utility functions. / GPL-2	noarch
r-dap	1.0	An implementation of Discriminant Analysis via Projections (DAP) method for high-dimensional binary classification in the case of unequal covariance matrices. See Irina Gaynanova and Tianying Wang (2018) < <a href="https://arxiv.org/abs/1711.04817v2">arXiv:1711.04817v2</a> >. / GPL-2	linux-64, osx-64, win-64
r-dapr	0.0.3	An easy-to-use, dependency-free set of functions for iterating over elements of various input objects. Functions are wrappers around base apply()/lapply()/vapply() functions but designed to have similar functionality to the mapping functions in the 'purrr' package < <a href="https://purrr.tidyverse.org/">https://purrr.tidyverse.org/</a> >. Specifically, function names more explicitly communicate the expected class of the output and functions also allow for the convenient shortcut of '~ .x' instead of the more verbose 'function(.x) .x'. / GPL-3	noarch
r-dark	0.9.8	The recovery of visual sensitivity in a dark environment is known as dark adaptation. In a clinical or research setting the recovery is typically measured after a dazzling flash of light and can be described by the Mahroo, Lamb and Pugh (MLP) model of dark adaptation. The functions in this package take dark adaptation data and use nonlinear regression to find the parameters of the model that 'best' describe the data. They do this by firstly, generating rapid initial objective estimates of data adaptation parameters, then a multi-start algorithm is used to reduce the possibility of a local minimum. There is also a bootstrap method to calculate parameter confidence intervals. The functions rely upon a 'dark' list or object. This object is created as the first step in the workflow and parts of the object are updated as it is processed. / GPL-3	noarch
r-darts	1.0	Are you aiming at the right spot in darts? Maybe not! Use this package to find your optimal aiming location. For a better explanation, go to <a href="http://www-stat.stanford.edu/~ryantibs/darts/">http://www-stat.stanford.edu/~ryantibs/darts/</a> or see the paper A Statistician Plays Darts. / GPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-dashboad	0.1.0	The dashboard package allows users to create web pages which display interactive data visualizations working in a standard modern browser. It displays them locally using the Rook server. No knowledge about web technologies nor Internet connection are required. D3.js is a JavaScript library for manipulating documents based on data. D3 helps the dashboard package bring data to life using HTML, SVG and CSS. / GPL-2	noarch
r-dasst	0.3.3	Provides methods for reading, displaying, processing and writing files originally arranged for the 'DSSAT-CSM' fixed width format. The 'DSSAT-CSM' cropping system model is described at J.W. Jones, G. Hoogenboom, C.H. Porter, K.J. Boote, W.D. Batchelor, L.A. Hunt, P.W. Wilkens, U. Singh, A.J. Gijssman, J.T. Ritchie (2003) <doi:10.1016/S1161-0301(02)00107-7>. / GPL-2	noarch
r-data.table	1.12.2	Fast aggregation of large data (e.g. 100GB in RAM), fast ordered joins, fast add/modify/delete of columns by group using no copies at all, list columns, a fast friendly file reader and parallel file writer. Offers a natural and flexible syntax, for faster development. / MPL-2.0   file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
r-databaseconnectorjars	1.1.0	Provides external JAR dependencies for the 'DatabaseConnector' package. / Apache License	noarch
r-dataclean	1.0	Includes functions that researchers or practitioners may use to clean raw data, transferring html, xlsx, txt data file into other formats. And it also can be used to manipulate text variables, extract numeric variables from text variables and other variable cleaning processes. It is originated from a author's project which focuses on creative performance in online education environment. The resulting paper of that study will be published soon. / GPL-3	noarch
r-dataframes2xls	0.4.7	Writes data frames to xls files. It supports multiple sheets and basic formatting. / BSD_3_clause	noarch
r-datagraph	1.0.1	Functions to save either '.dtable' or '.dtbin' files that can be read by DataGraph, a graphing and analysis application for macOS. Can save a data frame, collection of data frames and sequences of data frames and individual vectors. For more information see < <a href="https://www.visualdatatools.com/DataGraph/Help/DataFiles/R/index.html">https://www.visualdatatools.com/DataGraph/Help/DataFiles/R/index.html</a> >. / GPL-2	linux-64, osx-64, win-64
r-datamap	0.1_1	datamap utilizes variable bindings and objects of class UserDefinedDatabase to provide a simple mapping system to foreign objects. Maps can be used as environments or attached to the search path, and changes to either are persistent. Mapped foreign objects are fetched in real-time and are never cached by the mapping system. / GPL-2	linux-64, osx-64, win-64
r-datamaps	0.0.3	Easily create interactive choropleth maps then add bubbles and arcs by coordinates or region name. These maps can be used directly from the console, from 'RStudio', in 'Shiny' apps and 'R Markdown' documents. 'Shiny' proxies allow to interactively add arcs and bubbles, change choropleth values, or change labels. / MIT	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-dataquality</a>	1.0	The package performs variable level data quality checks including missing values, unique values, frequency tables, and generates summary statistics / MIT	noarch
<a href="#">r-datarium</a>	0.1.0	Contains data organized by topics: categorical data, regression model, means comparisons, independent and repeated measures ANOVA, mixed ANOVA and ANCOVA. / GPL-2	noarch
<a href="#">r-datarobot</a>	2.14.2	For working with the ‘DataRobot’ predictive modeling platform’s API < <a href="https://www.datarobot.com/">https://www.datarobot.com/</a> >. / MIT	noarch
<a href="#">r-datasaurus</a>	0.1.4	The Datasaurus Dozen is a set of datasets with the same summary statistics. They retain the same summary statistics despite having radically different distributions. The datasets represent a larger and quirkier object lesson that is typically taught via Anscombe’s Quartet (available in the ‘datasets’ package). Anscombe’s Quartet contains four very different distributions with the same summary statistics and as such highlights the value of visualisation in understanding data, over and above summary statistics. As well as being an engaging variant on the Quartet, the data is generated in a novel way. The simulated annealing process used to derive datasets from the original Datasaurus is detailed in Same Stats, Different Graphs: Generating Datasets with Varied Appearance and Identical Statistics through Simulated Annealing <doi:10.1145/3025453.3025912>. / MIT	noarch
<a href="#">r-dataseries</a>	0.2.0	Download and import time series from < <a href="http://www.dataseries.org">http://www.dataseries.org</a> >, a comprehensive and up-to-date collection of open data from Switzerland. / GPL-3	noarch
<a href="#">r-datassim</a>	1.0	For estimation of a variable of interest using Kalman filter by incorporating results from previous assessments, i.e. through development weighted estimates where weights are assigned inversely proportional to the variance of existing and new estimates. For reference see Ehlers et al. (2017) <doi:10.20944/preprints201710.0098.v1>. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-datastructures</a>	0.2.8	Implementation of advanced data structures such as hashmaps, heaps, or queues. Advanced data structures are essential in many computer science and statistics problems, for example graph algorithms or string analysis. The package uses ‘Boost’ and ‘STL’ data types and extends these to R with ‘Rcpp’ modules. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-datautils</a>	0.1.5	Contains facilities such as getting the current timestamp in decimal seconds, computing interval w.r.t. a reference timestamp, and custom plotting with error bars. / LGPL-3	linux-64, osx-64, win-64
<a href="#">r-dataverse</a>	0.2.0	Provides access to Dataverse version 4 APIs < <a href="https://dataverse.org/">https://dataverse.org/</a> >, enabling data search, retrieval, and deposit. For Dataverse versions <= 4.0, use the deprecated ‘dvn’ package < <a href="https://cran.r-project.org/package=dvn">https://cran.r-project.org/package=dvn</a> >. / GPL-2	noarch
<a href="#">r-date</a>	1.2_38	Functions for handling dates. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-datetime</a>	0.1.4	Provides methods for working with nominal dates, times, and durations. Base R has sophisticated facilities for handling time, but these can give unexpected results if, for example, timezone is not handled properly. This package provides a more casual approach to support cases which do not require rigorous treatment. It systematically deconstructs the concepts origin and timezone, and de-emphasizes the display of seconds. It also converts among nominal durations such as seconds, hours, days, and weeks. See ‘?datetime’ and ‘?duration’ for examples. Adapted from ‘metrumrg’ < <a href="http://r-forge.r-project.org/R/?group_id=1215">http://r-forge.r-project.org/R/?group_id=1215</a> >. / GPL-3	noarch
<a href="#">r-datetimeutils</a>	0.3.0	Utilities for handling dates and times, such as selecting particular days of the week or month, formatting timestamps as required by RSS feeds, or converting timestamp representations of other software (such as ‘MATLAB’ and ‘Excel’) to R. The package is lightweight (no dependencies, pure R implementations) and relies only on R’s standard classes to represent dates and times (‘Date’ and ‘POSIXt’); it aims to provide efficient implementations, through vectorisation and the use of R’s native numeric representations of timestamps where possible. / GPL-3	noarch
<a href="#">r-datr</a>	0.1.0	Interface with the ‘Dat’ p2p network protocol < <a href="https://datproject.org">https://datproject.org</a> >. Clone archives from the network, share your own files, and install packages from the network. / GPL-3	noarch
<a href="#">r-davies</a>	1.1.9	Various utilities for the Davies distribution. / GPL-2	noarch
<a href="#">r-dbemplikegof</a>	1.2.4	Goodness-of-fit and two sample comparison tests using sample entropy / GPL-2	noarch
<a href="#">r-dbemplikenorm</a>	1.0.0	Test for joint assessment of normality / GPL-2	noarch
<a href="#">r-dbest</a>	1.8	A program for analyzing vegetation time series, with two algorithms: 1) change detection algorithm that detects trend changes, determines their type (abrupt or non-abrupt), and estimates their timing, magnitude, number, and direction; 2) generalization algorithm that simplifies the temporal trend into main features. The user can set the number of major breakpoints or magnitude of greatest changes of interest for detection, and can control the generalization process by setting an additional parameter of generalization-percentage. / GPL-2	noarch
<a href="#">r-dbhydror</a>	0.2.7	Client for programmatic access to the South Florida Water Management District’s ‘DBHYDRO’ database at < <a href="https://www.sfwmd.gov/science-data/dbhydro">https://www.sfwmd.gov/science-data/dbhydro</a> >, with functions for accessing hydrologic and water quality data. / GPL-3	noarch
<a href="#">r-dbi</a>	1.0.0	A database interface definition for communication between R and relational database management systems. All classes in this package are virtual and need to be extended by the various R/DBMS implementations. / LGPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-dblcens</a>	1.1.7	Use EM algorithm to compute the NPMLE of CDF and also the two censoring distributions. For doubly censored data (as described in Chang and Yang (1987) Ann. Stat. 1536-47). You can also specify a constraint, it will return the constrained NPMLE and the -2 log empirical likelihood ratio. This can be used to test the hypothesis about the constraint and find confidence intervals for probability or quantile via empirical likelihood ratio theorem. Influence function of hat F may also be calculated (but may be slow). / GPL-2	linux-64, osx-64, win-64
<a href="#">r-dbplyr</a>	1.4.0	A 'dplyr' back end for databases that allows you to work with remote database tables as if they are in-memory data frames. Basic features works with any database that has a 'DBI' back end; more advanced features require 'SQL' translation to be provided by the package author. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-dbscan</a>	1.1_4	A fast reimplementation of several density-based algorithms of the DBSCAN family for spatial data. Includes the DBSCAN (density-based spatial clustering of applications with noise) and OPTICS (ordering points to identify the clustering structure) clustering algorithms HDBSCAN (hierarchical DBSCAN) and the LOF (local outlier factor) algorithm. The implementations use the kd-tree data structure (from library ANN) for faster k-nearest neighbor search. An R interface to fast kNN and fixed-radius NN search is also provided. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-dbstats</a>	1.0.5	Prediction methods where explanatory information is coded as a matrix of distances between individuals. Distances can either be directly input as a distances matrix, a squared distances matrix, an inner-products matrix or computed from observed predictors. / GPL-2	noarch
<a href="#">r-dbx</a>	0.2.5	Provides select, insert, update, upsert, and delete database operations. Supports 'PostgreSQL', 'MySQL', 'SQLite', and more, and plays nicely with the 'DBI' package. / MIT	noarch
<a href="#">r-dcg</a>	0.9.3	Data cloud geometry (DCG) applies random walks in finding community structures for social networks. Fushing, VanderWaal, McCowan, & Koehl (2013) (<doi:10.1371/journal.pone.0056259>). / GPL-2	noarch
<a href="#">r-dchipio</a>	0.1.5	Functions for reading DCP and CDF.bin files generated by the dChip software. / LGPL-2.1	noarch
<a href="#">r-dcl</a>	0.1.0	Statistical modelling and forecasting in claims reserving in non-life insurance under the Double Chain Ladder framework by Martinez-Miranda, Nielsen and Verrall (2012). / GPL-2	noarch
<a href="#">r-dcovts</a>	1.1	Computing and plotting the distance covariance and correlation function of a univariate or a multivariate time series. Both versions of biased and unbiased estimators of distance covariance and correlation are provided. Test statistics for testing pairwise independence are also implemented. Some data sets are also included. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-dcurver</a>	0.9.1	A Davidian curve defines a seminonparametric density, whose shape and flexibility can be tuned by easy to estimate parameters. Since a special case of a Davidian curve is the standard normal density, Davidian curves can be used for relaxing normality assumption in statistical applications (Zhang & Davidian, 2001) <doi:10.1111/j.0006-341X.2001.00795.x>. This package provides the density function, the gradient of the loglikelihood and a random generator for Davidian curves. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-dcv</a>	0.1.1	This package performs several conventional Cross-validation statistical methods for climate-growth model in the climate reconstruction from tree rings, including Sign Test statistic, Reduction of Error statistic, Product Mean Test, Durbin-Watson statistic etc. This package is at its primary stage, the functions have not been tested exhaustively and more functions would be added in the coming days. / GPL-2	noarch
<a href="#">r-ddalpha</a>	1.3.9	Contains procedures for depth-based supervised learning, which are entirely non-parametric, in particular the DDalpha-procedure (Lange, Mosler and Mozharovskiy, 2014 <doi:10.1007/s00362-012-0488-4>). The training data sample is transformed by a statistical depth function to a compact low-dimensional space, where the final classification is done. It also offers an extension to functional data and routines for calculating certain notions of statistical depth functions. 50 multivariate and 5 functional classification problems are included. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-ddm</a>	1.0_0	A set of three two-census methods to the estimate the degree of death registration coverage for a population. Implemented methods include the Generalized Growth Balance method (GGB), the Synthetic Extinct Generation method (SEG), and a hybrid of the two, GGB-SEG. Each method offers automatic estimation, but users may also specify exact parameters or use a graphical interface to guess parameters in the traditional way if desired. / GPL-2	noarch
<a href="#">r-ddrtree</a>	0.1.5	Provides an implementation of the framework of reversed graph embedding (RGE) which projects data into a reduced dimensional space while constructs a principal tree which passes through the middle of the data simultaneously. DDRTree shows superiority to alternatives (Wishbone, DPT) for inferring the ordering as well as the intrinsic structure of the single cell genomics data. In general, it could be used to reconstruct the temporal progression as well as bifurcation structure of any datatype. / Artistic-2.0	linux-64, osx-64, win-64
<a href="#">r-deadband</a>	0.1.0	Statistical deadband algorithms are based on the Send-On-Delta concept as in Miskowicz(2006,<doi:10.3390/s6010049>). A collection of functions compare effectiveness and fidelity of sampled signals using statistical deadband algorithms. / GPL-2	noarch
<a href="#">r-deal</a>	1.2_3	Bayesian networks with continuous and/or discrete variables can be learned and compared from data. The method is described in Boettcher and Dethlefsen (2003), <doi:10.18637/jss.v008.i20>. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-deamer	1.0	deamer provides deconvolution algorithms for the non-parametric estimation of the density $f$ of an error-prone variable $x$ with additive noise $e$ . The model is $y = x + e$ where the noisy variable $y$ is observed, while $x$ is unobserved. Estimation may be performed for i) a known density of the error ii) with an auxiliary sample of pure noise and iii) with an auxiliary sample of replicate (repeated) measurements. Estimation is performed using adaptive model selection and penalized contrasts. / GPL-3	noarch
r-debugme	1.1.0	Specify debug messages as special string constants, and control debugging of packages via environment variables. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-debugr	0.0.1	Tool to print out the value of R objects/expressions while running an R script. Outputs can be made dependent on user-defined conditions/criteria. Debug messages only appear when a global option for debugging is set. This way, 'debugr' code can even remain in the debugged code for later use without any negative effects during normal runtime. / GPL-3	noarch
r-decide	1.2	Calculates various estimates for measures of educational differentials, the relative importance of primary and secondary effects in the creation of such differentials and compares the estimates obtained from two datasets. / GPL-2	noarch
r-decido	0.2.0	Provides constrained triangulation of polygons. Ear cutting (or ear clipping) applies constrained triangulation by successively 'cutting' triangles from a polygon defined by path/s. Holes are supported by introducing a bridge segment between polygon paths. This package wraps the 'header-only' library 'earcut.hpp' < <a href="https://github.com/mapbox/earcut.hpp.git">https://github.com/mapbox/earcut.hpp.git</a> > which includes a reference to the method used by Held, M. (2001) <doi:10.1007/s00453-001-0028-4>. / MIT	linux-64, osx-64, win-64
r-decision	0.1.0	Contains a function called dmur() which accepts four parameters like possible values, probabilities of the values, selling cost and preparation cost. The dmur() function generates various numeric decision parameters like MEMV (Maximum (optimum) expected monetary value), best choice, EPPI (Expected profit with perfect information), EVPI (Expected value of the perfect information), EOL (Expected opportunity loss), which facilitate effective decision-making. / GPL-2	noarch
r-decode	1.2	Integrated differential expression (DE) and differential co-expression (DC) analysis on gene expression data based on DECODE (Differential CO-expression and Differential Expression) algorithm. / GPL-3	noarch
r-decoder	1.1.13	Main function decode is used to decode coded key values to plain text. Function code can be used to code plain text to code if there is a 1:1 relation between the two. The concept relies on 'keyvalue' objects used for translation. There are several 'keyvalue' objects included in the areas of geographical regional codes, administrative health care unit codes, diagnosis codes and more. It is also easy to extend the use by arbitrary code sets. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-decompr</a>	4.5.0	Two global-value-chain decompositions are implemented. Firstly, the Wang-Wei-Zhu (Wang, Wei, and Zhu, 2013) algorithm splits bilateral gross exports into 16 value-added components. Secondly, the Leontief decomposition (default) derives the value added origin of exports by country and industry, which is also based on Wang, Wei, and Zhu (Wang, Z., S.-J. Wei, and K. Zhu. 2013. Quantifying International Production Sharing at the Bilateral and Sector Levels.). / GPL-3	noarch
<a href="#">r-decon</a>	1.2.4	This package contains a collection of functions to deal with nonparametric measurement error problems using deconvolution kernel methods. We focus two measurement error models in the package: (1) an additive measurement error model, where the goal is to estimate the density or distribution function from contaminated data; (2) nonparametric regression model with errors-in-variables. The R functions allow the measurement errors to be either homoscedastic or heteroscedastic. To make the deconvolution estimators computationally more efficient in R, we adapt the Fast Fourier Transform (FFT) algorithm for density estimation with error-free data to the deconvolution kernel estimation. Several methods for the selection of the data-driven smoothing parameter are also provided in the package. See details in: Wang, X.F. and Wang, B. (2011). Deconvolution estimation in measurement error models: The R package decon. Journal of Statistical Software, 39(10), 1-24. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-deconvolver</a>	1.1	Empirical Bayes methods for learning prior distributions from data. An unknown prior distribution (g) has yielded (unobservable) parameters, each of which produces a data point from a parametric exponential family (f). The goal is to estimate the unknown prior (g-modeling) by deconvolution and Empirical Bayes methods. / GPL-2	noarch
<a href="#">r-deepboost</a>	0.1.6	Provides deep boosting models training, evaluation, predicting and hyper parameter optimising using grid search and cross validation. Based on Google's Deep Boosting algorithm, and Google's C implementation. Cortes, C., Mohri, M., & Syed, U. (2014) < <a href="http://machinelearning.wustl.edu/mlpapers/papers/icml2014c2_cortesb14">http://machinelearning.wustl.edu/mlpapers/papers/icml2014c2_cortesb14</a> >. / Apache License (== 2.0)	linux-64, osx-64, win-64
<a href="#">r-deepgmm</a>	0.1.5	Deep Gaussian mixture models as proposed by Viroli and McLachlan (2019) < <a href="https://doi.org/10.1007/s11222-017-9793-z">doi:10.1007/s11222-017-9793-z</a> > provide a generalization of classical Gaussian mixtures to multiple layers. Each layer contains a set of latent variables that follow a mixture of Gaussian distributions. To avoid overparameterized solutions, dimension reduction is applied at each layer by way of factor models. / GPL-3	noarch
<a href="#">r-deepnet</a>	0.2	Implement some deep learning architectures and neural network algorithms, including BP,RBM,DBN,Deep autoencoder and so on. / GPL-3	noarch
<a href="#">r-deepnn</a>	0.3	Implementation of some Deep Learning methods. Includes multilayer perceptron, different activation functions, regularisation strategies, stochastic gradient descent and dropout. Thanks go to the following references for helping to inspire and develop the package: Ian Goodfellow, Yoshua Bengio, Aaron Courville, Francis Bach (2016, ISBN:978-0262035613) Deep Learning. Terrence J. Sejnowski (2018, ISBN:978-0262038034) The Deep Learning Revolution. Grant Sanderson (3brown1blue) < <a href="https://www.youtube.com/playlist?list=PLZHQObOWTQDNU6R1_67000Dx_ZCJB-3pi">https://www.youtube.com/playlist?list=PLZHQObOWTQDNU6R1_67000Dx_ZCJB-3pi</a> > Neural Networks YouTube playlist. Michael A. Nielsen < <a href="http://neuralnetworksanddeeplearning.com/">http://neuralnetworksanddeeplearning.com/</a> > Neural Networks and Deep Learning. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-deepr	0.1	Tests for, and describe differences in event count profiles in groups of reconstructed cophylogenies / GPL-2	noarch
r-default	1.0.0	A simple syntax to change the default values for function arguments, whether they are in packages or defined locally. / MIT	noarch
r-deformula	0.1.1	Numerical quadrature of functions of one variable over a finite or infinite interval with double exponential formulas. / GPL-2	linux-64, osx-64, win-64
r-deisotoper	0.0.7	Provides a low-level interface for a deisotoper container implemented in the ‘Java’ programming language and means of S3 helper functions for plotting and debugging isotopes of mass spectrometric data. The deisotoper algorithm detects and aggregates peaks which belong to the same isotopic cluster of a given mass spectrum. / GPL-3	linux-64
r-delaporte	7.0.2	Provides probability mass, distribution, quantile, random-variate generation, and method-of-moments parameter-estimation functions for the Delaporte distribution. The Delaporte is a discrete probability distribution which can be considered the convolution of a negative binomial distribution with a Poisson distribution. Alternatively, it can be considered a counting distribution with both Poisson and negative binomial components. It has been studied in actuarial science as a frequency distribution which has more variability than the Poisson, but less than the negative binomial. / BSD_2_clause	linux-64, osx-64, win-64
r-deldir	0.1_2	Calculates the Delaunay triangulation and the Dirichlet or Voronoi tessellation (with respect to the entire plane) of a planar point set. Plots triangulations and tessellations in various ways. Clips tessellations to sub-windows. Calculates perimeters of tessellations. Summarises information about the tiles of the tessellation. / GPL-2	linux-64, osx-64, win-64
r-delt	0.8.2	We implement methods for estimating multivariate densities. We include a discretized kernel estimator, an adaptive histogram (a greedy histogram and a CART-histogram), stagewise minimization, and bootstrap aggregation. / GPL-2	linux-64, osx-64, win-64
r-delta	0.2.0.2	Measure of agreement delta was originally by Martın & Femia (2004) <DOI:10.1348/000711004849268>. Since then has been considered as agreement measure for different fields, since their behavior is usually better than the usual kappa index by Cohen (1960) <DOI:10.1177/001316446002000104>. The main issue with delta is that can not be computed by hand contrary to kappa. The current algorithm is based on the Version 5 of the delta windows program that can be found on < <a href="https://www.ugr.es/~bioest/software/delta/cmd.php?seccion=downloads">https://www.ugr.es/~bioest/software/delta/cmd.php?seccion=downloads</a> >. / GPL-3	noarch
r-deltaplotr	1.6	The deltaPlotR package implements Angoff’s Delta Plot method to detect dichotomous DIF. Several detection thresholds are included, either from multivariate normality assumption or by prior determination. Item purification is supported (Magis and Facon (2014) <doi:10.18637/jss.v059.c01>). / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-deldtd</a>	0.1.0	It plots densities by using asymmetrical kernels which belong to life time distributions and calculate its related MSE. For details see Chen (2000), Jin and Kawczak (2003) and Salha et al. (2014) <doi:10.12988/pms.2014.4616>. / GPL-2	noarch
<a href="#">r-demetics</a>	0.8.7	This package allows to calculate the fixation index $G_{st}$ (Nei, 1973) and the differentiation index $D$ (Jost, 2008) pairwise between or averaged over several populations. P-values, stating the significance of differentiation, and 95 percent confidence intervals can be estimated using bootstrap resamplings. In the case that more than two populations are compared pairwise, the p-values are adjusted by bonferroni correction and in several other ways due to the multiple comparison from one data set. / GPL-2	noarch
<a href="#">r-deming</a>	1.4	Generalized Deming regression, Theil-Sen regression and Passing-Bablok regression functions. / LGPL-2	noarch
<a href="#">r-demogr</a>	0.6.0	Construction and analysis of matrix population models in R. / GPL-2	noarch
<a href="#">r-demokde</a>	0.9.4	Demonstration code showing how (univariate) kernel density estimates are computed, at least conceptually, and allowing users to experiment with different kernels, should they so wish. NOTE: the density function in the stats package should be used for computational efficiency. / GPL-2	noarch
<a href="#">r-demova</a>	1.0	Tool for the development of multi-linear QSPR/QSAR models (Quantitative structure-property/activity relationship). These models are used in chemistry, biology and pharmacy to find a relationship between the structure of a molecule and its property (such as activity, toxicology but also physical properties). The various functions of this package allows: selection of descriptors based of variances, intercorrelation and user expertise; selection of the best multi-linear regression in terms of correlation and robustness; methods of internal validation (Leave-One-Out, Leave-Many-Out, Y-scrambling) and external using test sets. / GPL-2	noarch
<a href="#">r-dendroextras</a>	0.2.3	Provides extra functions to manipulate dendrograms that build on the base functions provided by the 'stats' package. The main functionality it is designed to add is the ability to colour all the edges in an object of class 'dendrogram' according to cluster membership i.e. each subtree is coloured, not just the terminal leaves. In addition it provides some utility functions to cut 'dendrogram' and 'hclust' objects and to set/get labels. / GPL-2	noarch
<a href="#">r-dendsort</a>	0.3.3	An implementation of functions to optimize ordering of nodes in a dendrogram, without affecting the meaning of the dendrogram. A dendrogram can be sorted based on the average distance of subtrees, or based on the smallest distance value. These sorting methods improve readability and interpretability of tree structure, especially for tasks such as comparison of different distance measures or linkage types and identification of tight clusters and outliers. As a result, it also introduces more meaningful reordering for a coupled heatmap visualization. / GPL-2   GPL-3	noarch
<a href="#">r-denoiseq</a>	0.1.1	Given count data from two conditions, it determines which transcripts are differentially expressed across the two conditions using Bayesian inference of the parameters of a bottom-up model for PCR amplification. This model is developed in Ndifon Wilfred, Hilah Gal, Eric Shifrut, Rina Aharoni, Nissan Yissachar, Nir Waysbort, Shlomit Reich Zeliger, Ruth Arnon, and Nir Friedman (2012), < <a href="http://www.pnas.org/content/109/39/15865.full">http://www.pnas.org/content/109/39/15865.full</a> >, and results in a distribution for the counts that is a superposition of the binomial and negative binomial distribution. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-denpro</a>	0.9.2	We provide tools to (1) visualize multivariate density functions and density estimates with level set trees, (2) visualize level sets with shape trees, (3) visualize multivariate data with tail trees, (4) visualize scales of multivariate density estimates with mode graphs and branching maps, and (5) visualize anisotropic spread with 2D volume functions and 2D probability content functions. Level set trees visualize mode structure, shape trees visualize shapes of level sets of unimodal densities, and tail trees visualize connected data sets. The kernel estimator is implemented but the package may also be applied for visualizing other density estimates. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-denseflmm</a>	0.1.2	Estimation of functional linear mixed models for densely sampled data based on functional principal component analysis. / GPL-2	noarch
<a href="#">r-densparcorr</a>	1.1	Provide a Dens-based method for estimating functional connection in large scale brain networks using partial correlation. / GPL-2	noarch
<a href="#">r-densratio</a>	0.2.1	Density ratio estimation. The estimated density ratio function can be used in many applications such as anomaly detection, change-point detection, covariate shift adaptation. The implemented methods are uLSIF (Hido et al. (2011) <doi:10.1007/s10115-010-0283-2>), RuLSIF (Yamada et al. (2011) <doi:10.1162/NECO_a_00442>), and KLIEP (Sugiyama et al. (2007) <doi:10.1007/s10463-008-0197-x>). / MIT	noarch
<a href="#">r-denstrip</a>	1.5.4	Graphical methods for compactly illustrating probability distributions, including density strips, density regions, sectioned density plots and varying width strips. / GPL-2	noarch
<a href="#">r-denvax</a>	0.1.1	Provides the mathematical model described by Serostatus Testing & Dengue Vaccine Cost-Benefit Thresholds in <doi:10.1098/rsif.2019.0234>. Using the functions in the package, that analysis can be repeated using sample life histories, either synthesized from local seroprevalence data using other functions in this package (as in the manuscript) or from some other source. The package provides a vignette which walks through the analysis in the publication, as well as a function to generate a project skeleton for such an analysis. / MIT	noarch
<a href="#">r-deoptim</a>	2.2_4	Implements the differential evolution algorithm for global optimization of a real-valued function of a real-valued parameter vector. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-deoptimr</a>	1.0_8	Differential Evolution (DE) stochastic algorithms for global optimization of problems with and without constraints. The aim is to curate a collection of its state-of-the-art variants that (1) do not sacrifice simplicity of design, (2) are essentially tuning-free, and (3) can be efficiently implemented directly in the R language. Currently, it only provides an implementation of the ‘jDE’ algorithm by Brest et al. (2006) <doi:10.1109/TEVC.2006.872133>. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-depend.truncation</a>	3.0	Estimation and testing methods for dependently truncated data. Semi-parametric methods are based on Emura et al. (2011)<Stat Sinica 21:349-67>, Emura & Wang (2012)<doi:10.1016/j.jmva.2012.03.012>, and Emura & Murotani (2015)<doi:10.1007/s11749-015-0432-8>. Parametric approaches are based on Emura & Konno (2012)<doi:10.1007/s00362-014-0626-2> and Emura & Pan (2017)<doi:10.1007/s00362-017-0947-z>. A regression approach is based on Emura & Wang (2016)<doi:10.1007/s10463-015-0526-9>. Quasi-independence tests are based on Emura & Wang (2010)<doi:10.1016/j.jmva.2009.07.006>. Right-truncated data for Japanese male centenarians are given by Emura & Murotani (2015)<doi:10.1007/s11749-015-0432-8>. / GPL-2	noarch
<a href="#">r-deplogo</a>	1.0	Plots dependency logos from a set of input sequences. / GPL-3	noarch
<a href="#">r-deployrrserve</a>	9.0.0	Rserve acts as a socket server (TCP/IP or local sockets) which allows binary requests to be sent to R. Every connection has a separate workspace and working directory. Client-side implementations are available for popular languages such as C/C and Java, allowing any application to use facilities of R without the need of linking to R code. Rserve supports remote connection, user authentication and file transfer. A simple R client is included in this package as well. / GPL version 2	linux-64, win-64
<a href="#">r-depmix</a>	0.9.15	Fits (multigroup) mixtures of latent or hidden Markov models on mixed categorical and continuous (timeseries) data. The Rdonlp2 package can optionally be used for optimization of the log-likelihood and is available from R-forge. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-depth.plot</a>	0.1	Could be used to obtain spatial depths, spatial ranks and outliers of multivariate random variables. Could also be used to visualize DD-plots (a multivariate generalization of QQ-plots). / GPL-2	noarch
<a href="#">r-depthtools</a>	0.4	depthTools is a package that implements different statistical tools for the description and analysis of gene expression data based on the concept of data depth, namely, the scale curves for visualizing the dispersion of one or various groups of samples (e.g. types of tumors), a rank test to decide whether two groups of samples come from a single distribution and two methods of supervised classification techniques, the DS and TAD methods. All these techniques are based on the Modified Band Depth, which is a recent notion of depth with a low computational cost, what renders it very appropriate for high dimensional data such as gene expression data. / GPL-2	noarch
<a href="#">r-dequer</a>	2.0.1	Queues, stacks, and ‘deque’s are list-like, abstract data types. These are meant to be very cheap to grow, or insert new objects into. A typical use case involves storing data in a list in a streaming fashion, when you do not necessarily know how many elements need to be stored. Unlike R’s lists, the new data structures provided here are not necessarily stored contiguously, making insertions and deletions at the front/end of the structure much faster. The underlying implementation is new and uses a head/tail doubly linked list; thus, we do not rely on R’s environments or hashing. To avoid unnecessary data copying, most operations on these data structures are performed via side-effects. / BSD_2_clause	linux-64, osx-64, win-64
<a href="#">r-derezen-de.ferreira</a>	0.1.0	Modeling the zero coupon yield curve using the dynamic De Rezende and Ferreira (2011) <doi:10.1002/for.1256> five factor model with variable or fixed decaying parameters. For explanatory purposes, the package also includes various short datasets of interest rates for the BRICS countries. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-deriv	3.8.5	R-based solution for symbolic differentiation. It admits user-defined function as well as function substitution in arguments of functions to be differentiated. Some symbolic simplification is part of the work. / GPL-3	noarch
r-derivmks	0.2.4	A set of pricing and expository functions that should be useful in teaching a course on financial derivatives. / MIT	noarch
r-des	1.0.0	Discrete event simulation (DES) involves modeling of systems having discrete, i.e. abrupt, state changes. For instance, when a job arrives to a queue, the queue length abruptly increases by 1. This package is an R implementation of the event-oriented approach to DES; see the tutorial in Matloff (2008) < <a href="http://heather.cs.ucdavis.edu/~matloff/156/PLN/DESimIntro.pdf">http://heather.cs.ucdavis.edu/~matloff/156/PLN/DESimIntro.pdf</a> >. / MIT	noarch
r-desc	1.2.0	Tools to read, write, create, and manipulate DESCRIPTION files. It is intended for packages that create or manipulate other packages. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-descomponer	1.5	Decompose a time series into seasonal, trend and irregular components using transformations to amplitude-frequency domain. / GPL-2	noarch
r-desscr	1.1.4	Weighted frequency and contingency tables of categorical variables and of the comparison of the mean value of a numerical variable by the levels of a factor, and methods to produce xtable objects of the tables and to plot them. There are also functions to facilitate the character encoding conversion of objects, to quickly convert fixed width files into csv ones, and to export a data.frame to a text file with the necessary R and SPSS codes to reread the data. / GPL-2	linux-64, osx-64, win-64
r-describer	0.2.0	Allows users to quickly and easily describe data using common descriptive statistics. / MIT	noarch
r-designgg	1.1	The package provides R scripts for designing genetical genomics experiments. / GPL-3	noarch
r-designlmm	0.1.0	Use simulated annealing to find optimal designs for Poisson regression models with blocks. / GPL-3	noarch
r-desir	1.2.1	Functions for (1) ranking, selecting, and prioritising genes, proteins, and metabolites from high dimensional biology experiments, (2) multivariate hit calling in high content screens, and (3) combining data from diverse sources. / GPL-3	noarch
r-desirability	2.1	S3 classes for multivariate optimization using the desirability function by Derriinger and Suich (1980). / GPL-2	noarch
r-desnowball	1.0	This package implements a statistical data mining method to compare whole genome gene expression profiles, with respect to the presence of a recurrent genetic disturbance event, to identify the affected target genes. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-desolve</a>	1.24	Functions that solve initial value problems of a system of first-order ordinary differential equations ('ODE'), of partial differential equations ('PDE'), of differential algebraic equations ('DAE'), and of delay differential equations. The functions provide an interface to the FORTRAN functions 'lsoda', 'lsodar', 'lsode', 'lsodes' of the 'ODEPACK' collection, to the FORTRAN functions 'dvide', 'zvode' and 'daspk' and a C-implementation of solvers of the 'Runge-Kutta' family with fixed or variable time steps. The package contains routines designed for solving 'ODEs' resulting from 1-D, 2-D and 3-D partial differential equations ('PDE') that have been converted to 'ODEs' by numerical differencing. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-det</a>	2.0.1	Builds both ROC (Receiver Operating Characteristic) and DET (Detection Error Tradeoff) curves from a set of predictors, which are the results of a binary classification system. The curves give a general vision of the performance of the classifier, and are useful for comparing performance of different systems. / GPL-2	noarch
<a href="#">r-detector</a>	0.1.0	Allows users to quickly and easily detect data containing Personally Identifiable Information (PII) through convenience functions. / MIT	noarch
<a href="#">r-dettestset</a>	1.1.6	Solvers and test set for stiff and non-stiff differential equations, and differential algebraic equations. 'Mazzia, F., Cash, J.R. and K. Soetaert, 2012. DOI: 10.1016/j.cam.2012.03.014'. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-detmcd</a>	0.0.5	Implementation of DetMCD, a new algorithm for robust and deterministic estimation of location and scatter. The benefits of robust and deterministic estimation are explained in Hubert, Rousseeuw and Verdonck (2012) <doi:10.1080/10618600.2012.672100>. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-detpack</a>	1.1.3	Density estimation for possibly large data sets and conditional/unconditional random number generation or bootstrapping with distribution element trees. The function 'det.construct' translates a dataset into a distribution element tree. To evaluate the probability density based on a previously computed tree at arbitrary query points, the function 'det.query' is available. The functions 'det1' and 'det2' provide density estimation and plotting for one- and two-dimensional datasets. Conditional/unconditional smooth bootstrapping from an available distribution element tree can be performed by 'det.rnd'. For more details on distribution element trees, see: Meyer, D.W. (2016) <arXiv:1610.00345> or Meyer, D.W., Statistics and Computing (2017) <doi:10.1007/s11222-017-9751-9> and Meyer, D.W. (2017) <arXiv:1711.04632> or Meyer, D.W., Journal of Computational and Graphical Statistics (2018) <doi:10.1080/10618600.2018.1482768>. / GPL-2	noarch
<a href="#">r-detr</a>	0.0.5	DetLTS, DetMM (and DetS) Algorithms for Deterministic, Robust Linear Regression. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-detsel	1.0.3	In the new era of population genomics, surveys of genetic polymorphism (genome scans) offer the opportunity to distinguish locus-specific from genome wide effects at many loci. Identifying presumably neutral regions of the genome that are assumed to be influenced by genome-wide effects only, and excluding presumably selected regions, is therefore critical to infer population demography and phylogenetic history reliably. Conversely, detecting locus-specific effects may help identify those genes that have been, or still are, targeted by natural selection. The software package DetSel has been developed to identify markers that show deviation from neutral expectation in pairwise comparisons of diverging populations. / GPL-2	linux-64, osx-64, win-64
r-devemf	3.6_3	Output graphics to EMF/EMF. / GPL-3	linux-64, osx-64, win-64
r-devfunc	0.1	A concise check of the format of one or multiple input arguments (data type, length or value) is provided. Since multiple input arguments can be tested simultaneously, a lengthy list of checks at the beginning of your function can be avoided, hereby enhancing the readability and maintainability of your code. / GPL-3	noarch
r-devoid	0.1.0	Provides a non-drawing graphic device for benchmarking purpose. In order to properly benchmark graphic drawing code it is necessary to factor out the device implementation itself so that results are not related to the specific graphics device used during benchmarking. The 'devoid' package implements a graphic device that accepts all the required calls from R's graphic engine but performs no action. Apart from benchmarking it is unlikely that this device has any practical use. / MIT	linux-64, osx-64, win-64
r-devore7	0.7.6	Data sets and sample analyses from Jay L. Devore (2008), Probability and Statistics for Engineering and the Sciences (7th ed), Thomson. / GPL-2	noarch
r-devrate	0.1.10	A set of functions to quantify the relationship between development rate and temperature and to build phenological models. The package comprises a set of models and estimated parameters borrowed from a literature review in ectotherms. The methods and literature review are described in Rebaudo et al. (2018) <doi:10.1111/2041-210X.12935> and Rebaudo and Rabhi (2018) <doi:10.1111/eea.12693>. An example can be found in Rebaudo et al. (2017) <doi:10.1007/s13355-017-0480-5>. / GPL-2	noarch
r-devtools	2.0.2	Collection of package development tools. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-df2json	0.0.2	It handles numerics, characters, factors, and logicals. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-dfadjust	1.0.0	Computes small-sample degrees of freedom adjustment for heteroskedasticity robust standard errors, and for clustered standard errors in linear regression. See Imbens and Kolesár (1994) <doi:10.1162/REST_a_00552> for a discussion of these adjustments. / MIT	noarch
r-dfcomb	3.0.0	Phase I/II adaptive dose-finding design for combination studies where toxicity rates are supposed to increase with both agents. / GPL-3	linux-64, osx-64, win-64
r-dfcompare	1.0.0	Compares two dataframes with a common key and returns the delta records. The package will return three dataframes that contain the added, changed, and deleted records. / GPL-3	noarch
r-dferm	0.2.2	Provides functions to run the CRM and TITE-CRM in phase I trials and calibration tools for trial planning purposes. / GPL-2	noarch
r-dfmta	1.7.0	Phase I/II adaptive dose-finding design for single-agent Molecularly Targeted Agent (MTA), according to the paper Phase I/II Dose-Finding Design for Molecularly Targeted Agent: Plateau Determination using Adaptive Randomization, Riviere Marie-Karelle et al. (2016) <doi:10.1177/0962280216631763>. / GPL-3	linux-64, osx-64, win-64
r-dfoptim	2018.1	Derivative-Free optimization algorithms. These algorithms do not require gradient information. More importantly, they can be used to solve non-smooth optimization problems. / GPL-2	noarch
r-dfphase1	1.1.1	Statistical methods for retrospectively detecting changes in location and/or dispersion of univariate and multivariate variables. Data values are assumed to be independent, can be individual (one observation at each instant of time) or subgrouped (more than one observation at each instant of time). Control limits are computed, often using a permutation approach, so that a prescribed false alarm probability is guaranteed without making any parametric assumptions on the stable (in-control) distribution. / LGPL-2	linux-64, osx-64, win-64
r-dga	1.2	Performs Bayesian model averaging for capture-recapture. This includes code to stratify records, check the strata for suitable overlap to be used for capture-recapture, and some functions to plot the estimated population size. / GPL-2	noarch
r-dglars	2.1.2	Differential geometric least angle regression method for fitting sparse generalized linear models. In this version of the package, the user can fit models specifying Gaussian, Poisson, Binomial, Gamma and Inverse Gaussian family. Furthermore, several link functions can be used to model the relationship between the conditional expected value of the response variable and the linear predictor. The solution curve can be computed using an efficient predictor-corrector or a cyclic coordinate descent algorithm, as described in the paper linked to via the URL below. / GPL-2	linux-64, osx-64, win-64
r-dgmb	1.2	A set of functions have been implemented to generate random data to perform Monte Carlo simulations on structural models with formative constructs and interaction and nonlinear effects (Two-Step PLS Mode B structural models). The setup of the true model considers a simple structure with three formative exogenous constructs related to one formative endogenous construct. The routines take into account the interaction and nonlinear effects of the exogenous constructs on the endogenous construct. / GPL-2	noarch
r-dgodata	0.0.2	Provides data used by package ‘dgo’ in examples and vignettes. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-dgof	1.2	This package contains a proposed revision to the <code>stats::ks.test()</code> function and the associated <code>ks.test.Rd</code> help page. With one minor exception, it does not change the existing behavior of <code>ks.test()</code> , and it adds features necessary for doing one-sample tests with hypothesized discrete distributions. The package also contains <code>cvm.test()</code> , for doing one-sample Cramer-von Mises goodness-of-fit tests. / GPL (>= 2.0)	linux-64, osx-64, win-64
r-dhh	0.0.1	The density, cumulative distribution, quantiles, and i.i.d random variables of a heavy-headed distribution. For more information, please see the vignette. / GPL-2	noarch
r-dhsic	2.1	Contains an implementation of the d-variable Hilbert Schmidt independence criterion and several hypothesis tests based on it, as described in Pfister et al. (2017) <doi:10.1111/rssb.12235>. / GPL-3	linux-64, osx-64, win-64
r-di	1.1.4	A set of utilities for calculating the Deficit (frailty) Index (DI) in gerontological studies. The deficit index was first proposed by Arnold Mitnitski and Kenneth Rockwood and represents a proxy measure of aging and also can be served as a sensitive predictor of survival. For more information, see (i) Accumulation of Deficits as a Proxy Measure of Aging by Arnold B. Mitnitski et al. (2001), The Scientific World Journal 1, <DOI:10.1100/tsw.2001.58>; (ii) Frailty, fitness and late-life mortality in relation to chronological and biological age by Arnold B Mitnitski et al. (2001), BMC Geriatrics 2002 2(1), <DOI:10.1186/1471-2318-2-1>. / GPL-3	noarch
r-diagonals	0.4.0	Several tools for handling block-matrix diagonals and similar constructs are implemented. Block-diagonal matrices can be extracted or removed using two small functions implemented here. In addition, non-square matrices are supported. Block diagonal matrices occur when two dimensions of a data set are combined along one edge of a matrix. For example, trade-flow data in the 'decompr' and 'gvc' packages have each country-industry combination occur along both edges of the matrix. / GPL-3	noarch
r-diagrammer	1.0.1	Build graph/network structures using functions for stepwise addition and deletion of nodes and edges. Work with data available in tables for bulk addition of nodes, edges, and associated metadata. Use graph selections and traversals to apply changes to specific nodes or edges. A wide selection of graph algorithms allow for the analysis of graphs. Visualize the graphs and take advantage of any aesthetic properties assigned to nodes and edges. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-dialr	0.3.0	Parse, format, and validate international phone numbers using Google's 'libphonenumber' java library, < <a href="https://github.com/googlei18n/libphonenumber">https://github.com/googlei18n/libphonenumber</a> >. / GPL-3	noarch
r-dialrjars	8.10.1	Collects 'libphonenumber' jars required for the 'dialr' package. / GPL-3	noarch
r-diaplt	1.3.0	Visualize one-factor data frame. Beads plot consists of diamonds of each factor of each data series. A diamond indicates average and range. Look over a data frame with many numeric columns and a factor column. / MIT (FOSS)	noarch

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Name	Version	Summary/License	Platforms
<code>r-dice</code>	1.2	This package provides utilities to calculate the probabilities of various dice-rolling events, such as the probability of rolling a four-sided die six times and getting a 4, a 3, and either a 1 or 2 among the six rolls (in any order); the probability of rolling two six-sided dice three times and getting a 10 on the first roll, followed by a 4 on the second roll, followed by anything but a 7 on the third roll; or the probabilities of each possible sum of rolling five six-sided dice, dropping the lowest two rolls, and summing the remaining dice. / GPL-2	noarch
<code>r-dicedesign</code>	1.8_1	Space-Filling Designs and Uniformity Criteria. / GPL-3	linux-64, osx-64, win-64
<code>r-diceeval</code>	1.4	Estimation, validation and prediction of models of different types : linear models, additive models, MARS, PolyMARS and Kriging. / GPL-3	noarch
<code>r-dicekriging</code>	1.5.6	Estimation, validation and prediction of kriging models. Important functions : km, print.km, plot.km, predict.km. / GPL-2   GPL-3	linux-64, osx-64, win-64
<code>r-dichromat</code>	2.0_0	Collapse red-green or green-blue distinctions to simulate the effects of different types of color-blindness. / GPL-2	linux-32, linux-64, noarch, osx-64, win-32, win-64
<code>r-dicionariosibge</code>	1.6	This package contains the dictionaries for reading microdata from IBGE (Brazilian Institute of Geography and Statistics) surveys PNAD, PME and POF. / GPL-2	noarch
<code>r-didacticboost</code>	0.1.1	A basic, clear implementation of tree-based gradient boosting designed to illustrate the core operation of boosting models. Tuning parameters (such as stochastic subsampling, modified learning rate, or regularization) are not implemented. The only adjustable parameter is the number of training rounds. If you are looking for a high performance boosting implementation with tuning parameters, consider the 'xgboost' package. / GPL-3	noarch
<code>r-dielectric</code>	0.2.3	Physical constants. Gold, silver and glass permittivities, together with spline interpolation functions. / GPL-3	noarch
<code>r-diezeit</code>	0.1_0	A wrapper for the ZEIT ONLINE Content API, available at < <a href="http://developer.zeit.de">http://developer.zeit.de</a> >. 'diezeit' gives access to articles and corresponding metadata from the ZEIT archive and from ZEIT ONLINE. A personal API key is required for usage. / MIT	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-difconet</a>	1.0.4	Estimation of DIFFerential COexpressed NETworks using diverse and user metrics. This package is basically used for three functions related to the estimation of differential coexpression. First, to estimate differential coexpression where the coexpression is estimated, by default, by Spearman correlation. For this, a metric to compare two correlation distributions is needed. The package includes 6 metrics. Some of them needs a threshold. A new metric can also be specified as a user function with specific parameters (see difconet.run). The significance is be estimated by permutations. Second, to generate datasets with controlled differential correlation data. This is done by either adding noise, or adding specific correlation structure. Third, to show the results of differential correlation analyses. Please see < <a href="http://bioinformatica.mty.itesm.mx/difconet">http://bioinformatica.mty.itesm.mx/difconet</a> > for further information. / GPL-2	noarch
<a href="#">r-diffec</a>	1.1.0	This is an R implementation of Fast and Scalable Learning of Sparse Changes in High-Dimensional Gaussian Graphical Model Structure (DIFFEE). The DIFFEE algorithm can be used to fast estimate the differential network between two related datasets. For instance, it can identify differential gene network from datasets of case and control. By performing data-driven network inference from two high-dimensional data sets, this tool can help users effectively translate two aggregated data blocks into knowledge of the changes among entities between two Gaussian Graphical Model. Please run demo(diffecDemo) to learn the basic functions provided by this package. For further details, please read the original paper: Beilun Wang, Arshdeep Sekhon, Yanjun Qi (2018) <arXiv:1710.11223>. / GPL-2	noarch
<a href="#">r-diffmeshgp</a>	0.1.0	This R function implements the nonstationary Kriging model proposed by Tuo, Wu and Yu (2014) <DOI:10.1080/00401706.2013.842935> for analyzing multi-fidelity computer outputs. This function computes the maximum likelihood estimates for the model parameters as well as the predictive means and variances of the exact solution (i.e., the conceptually highest fidelity). / GPL-2	noarch
<a href="#">r-diffobj</a>	0.2.3	Generate a colored diff of two R objects for an intuitive visualization of their differences. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-diffpriv</a>	0.4.2	An implementation of major general-purpose mechanisms for privatizing statistics, models, and machine learners, within the framework of differential privacy of Dwork et al. (2006) <doi:10.1007/11681878_14>. Example mechanisms include the Laplace mechanism for releasing numeric aggregates, and the exponential mechanism for releasing set elements. A sensitivity sampler (Rubinstein & Alda, 2017) <arXiv:1706.02562> permits sampling target non-private function sensitivity; combined with the generic mechanisms, it permits turn-key privatization of arbitrary programs. / MIT	noarch
<a href="#">r-diffr</a>	0.1	An R interface to the 'codediff' JavaScript library (a copy of which is included in the package, see < <a href="https://github.com/danvk/codediff.js">https://github.com/danvk/codediff.js</a> > for information). Allows for visualization of the difference between 2 files, usually text files or R scripts, in a browser. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-diffusr	0.1.4	Implementation of network diffusion algorithms such as heat diffusion or Markov random walks. Network diffusion algorithms generally spread information in the form of node weights along the edges of a graph to other nodes. These weights can for example be interpreted as temperature, an initial amount of water, the activation of neurons in the brain, or the location of a random surfer in the internet. The information (node weights) is iteratively propagated to other nodes until a equilibrium state or stop criterion occurs. / GPL-3	linux-64, osx-64, win-64
r-digest	0.6.18	Implementation of a function 'digest()' for the creation of hash digests of arbitrary R objects (using the 'md5', 'sha-1', 'sha-256', 'crc32', 'xxhash' and 'murmurhash' algorithms) permitting easy comparison of R language objects, as well as a function 'hmac()' to create hash-based message authentication code. Please note that this package is not meant to be deployed for cryptographic purposes for which more comprehensive (and widely tested) libraries such as 'OpenSSL' should be used. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
r-digitalpcr	1.1.0	The assay sensitivity is the minimum number of copies that the digital PCR assay can detect. Users provide serial dilution results in the format of counts of positive and total reaction wells. The output is the estimated assay sensitivity and the copy number per well in the initial dilute. / GPL-2	noarch
r-dils	0.8.1	Combine multiple-relationship networks into a single weighted network. The approach is similar to factor analysis in the that contribution from each constituent network varies so as to maximize the information gleaned from the multiple-relationship networks. This implementation uses Principal Component Analysis calculated using 'prcomp' with bootstrap subsampling. Missing links are imputed using the method of Chen et al. (2012). / MIT	linux-64, osx-64, win-64
r-dime	1.2	A robust differential identification method that considers an ensemble of finite mixture models combined with a local false discovery rate (fdr) to analyze ChIP-seq (high-throughput genomic) data comparing two samples allowing for flexible modeling of data. / GPL-2	linux-64, osx-64, win-64
r-dimred	0.2.2	A collection of dimensionality reduction techniques from R packages and provides a common interface for calling the methods. / GPL-3   file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
r-dinamic	1.0	This function implements the DiNAmIC procedure for assessing the statistical significance of recurrent DNA copy number aberrations (Bioinformatics (2011) 27(5) 678 - 685). / GPL-2	noarch
r-dint	2.1.0	S3 classes and methods to create and work with year-quarter, year-month and year-isoweek vectors. Basic arithmetic operations (such as adding and subtracting) are supported, as well as formatting and converting to and from standard R date types. / MIT	noarch

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Name	Version	Summary/License	Platforms
<code>r-diphiseq</code>	0.2.0	Implements the algorithm described in Jun Li and Alicia T. Lamere, DiPhiSeq: Robust comparison of expression levels on RNA-Seq data with large sample sizes (Unpublished). Detects not only genes that show different average expressions (differential expression, DE), but also genes that show different diversities of expressions in different groups (differentially dispersed, DD). DD genes can be important clinical markers. ‘DiPhiSeq’ uses a redescending penalty on the quasi-likelihood function, and thus has superior robustness against outliers and other noise. Updates from version 0.1.0: (1) Added the option of using adaptive initial value for phi. (2) Added a function for estimating the proportion of outliers in the data. (3) Modified the input parameter names for clarity, and modified the output format for the main function. / GPL-3	noarch
<code>r-diptest</code>	0.75	Compute Hartigan’s dip test statistic for unimodality / multimodality and provide a test with simulation based p-values, where the original public code has been corrected. / GPL-2	linux-64, osx-64, win-64
<code>r-direct</code>	1.0.1	A Bayesian clustering method for replicated time series or replicated measurements from multiple experimental conditions, e.g., time-course gene expression data. It estimates the number of clusters directly from the data using a Dirichlet-process prior. See Fu, A. Q., Russell, S., Bray, S. and Tavare, S. (2013) Bayesian clustering of replicated time-course gene expression data with weak signals. The Annals of Applied Statistics. 7(3) 1334-1361. <doi:10.1214/13-AOAS650>. / GPL-2	linux-64, osx-64, win-64
<code>r-directedclustering</code>	0.1.1	Allows the computation of clustering coefficients for directed and weighted networks by using different approaches. It allows to compute clustering coefficients that are not present in ‘igraph’ package. A description of clustering coefficients can be found in Directed clustering in weighted networks: a new perspective, Clemente, G.P., Grassi, R. (2017), <doi:10.1016/j.chaos.2017.12.007>. / GPL-3	noarch
<code>r-directeffects</code>	0.2	A set of functions to estimate the controlled direct effect of treatment fixing a potential mediator to a specific value. Implements the sequential g-estimation estimator described in Vansteelandt (2009) <doi:10.1097/EDE.0b013e3181b6f4c9> and Acharya, Blackwell, and Sen (2016) <doi:10.1017/S0003055416000216>. / GPL-2	noarch
<code>r-directlabels</code>	2018.05.22	Extensible framework for automatically placing direct labels onto multi-color ‘lattice’ or ‘ggplot2’ plots. Label positions are described using Positioning Methods which can be re-used across several different plots. There are heuristics for examining trellis and ggplot objects and inferring an appropriate Positioning Method. / GPL-3	noarch
<code>r-directstandardisation</code>	1.2	Calculate adjusted means and proportions of a variable by groups defined by another variable by direct standardisation, standardised to the structure of the dataset. / GPL-2	noarch
<code>r-dirmult</code>	0.1.3	Estimate parameters in Dirichlet-Multinomial and compute profile log-likelihoods. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-discfrail	0.1	Functions for fitting Cox proportional hazards models for grouped time-to-event data, where the shared group-specific frailties have a discrete nonparametric distribution. The methods proposed in the package is described by Gasperoni, F., Ieva, F., Paganoni, A. M., Jackson, C. H., Sharples, L. (2018) <doi:10.1093/biostatistics/kxy071>. There are also functions for simulating from these models, with a nonparametric or a parametric baseline hazard function. / GPL-3	noarch
r-disclap	1.5	Discrete Laplace exponential family for models such as a generalized linear model / GPL-2	noarch
r-disclapmix	1.7.3	Make inference in a mixture of discrete Laplace distributions using the EM algorithm. This can e.g. be used for modelling the distribution of Y chromosomal haplotypes as described in [1, 2] (refer to the URL section). / GPL-2	linux-64, osx-64, win-64
r-discretefdr	1.3.1	Multiple testing procedures described in the paper Döhler, Durand and Roquain (2018) New FDR bounds for discrete and heterogeneous tests <doi:10.1214/18-EJS1441>. The main procedures of the paper (HSU and HSD), their adaptive counterparts (AHSU and AHSD), and the HBR variant are available and are coded to take as input a set of observed p-values and their discrete support under the null. A function to compute such p-values and supports for Fisher's exact tests is also provided, along with a wrapper allowing to apply discrete procedures directly from contingency tables. / MIT	linux-64, osx-64, win-64
r-discretelaplace	1.1.1	Probability mass function, distribution function, quantile function, random generation and estimation for the skew discrete Laplace distributions. / GPL-3	noarch
r-discretemput	0.1.2	Multiple testing procedures for discrete test statistics, that use the known discrete null distribution of the p-values for simultaneous inference. / GPL-2	noarch
r-discreteurv	1.2.2	Create, manipulate, transform, and simulate from discrete random variables. The syntax is modeled after that which is used in mathematical statistics and probability courses, but with powerful support for more advanced probability calculations. This includes the creation of joint random variables, and the derivation and manipulation of their conditional and marginal distributions. / GPL-3	noarch
r-discretization	1.0.1	This package is a collection of supervised discretization algorithms. It can also be grouped in terms of top-down or bottom-up, implementing the discretization algorithms. / GPL-3	noarch
r-discriminer	0.1.2	Functions for Discriminant Analysis and Classification purposes covering various methods such as descriptive, geometric, linear, quadratic, PLS, as well as qualitative discriminant analyses / GPL-3	noarch
r-discsurv	1.4.0	Provides data transformations, estimation utilities, predictive evaluation measures and simulation functions for discrete time survival analysis. / GPL-3	noarch
r-diseasemapping	1.4.6	Formatting of population and case data, calculation of Standardized Incidence Ratios, and fitting the BYM model using INLA. / GPL-3	noarch
r-dishet	1.0.0	Model cell type heterogeneity of bulk renal cell carcinoma. The observed gene expression in bulk tumor sample is modeled by a log-normal distribution with the location parameter structured as a linear combination of the component-specific gene expressions. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-dismo	1.1_4	Functions for species distribution modeling, that is, predicting entire geographic distributions from occurrences at a number of sites and the environment at these sites. / GPL-3	linux-64, osx-64, win-64
r-disparityfilter	2.2.3	The disparity filter algorithm is a network reduction technique to identify the ‘backbone’ structure of a weighted network without destroying its multi-scale nature. The algorithm is documented in M. Angeles Serrano, Marian Boguna and Alessandro Vespignani in Extracting the multiscale backbone of complex weighted networks, Proceedings of the National Academy of Sciences 106 (16), 2009. This implementation of the algorithm supports both directed and undirected networks. / GPL-2	noarch
r-displayhts	1.0	A package containing R functions for displaying data and results from high-throughput screening experiments. / GPL-2	noarch
r-dispmmod	1.2	Functions for estimating Gaussian dispersion regression models (Aitkin, 1987 <doi:10.2307/2347792>), overdispersed binomial logit models (Williams, 1987 <doi:10.2307/2347977>), and overdispersed Poisson log-linear models (Breslow, 1984 <doi:10.2307/2347661>), using a quasi-likelihood approach. / GPL-2	noarch
r-disposables	1.0.3	Create disposable R packages for testing. You can create, install and load multiple R packages with a single function call, and then unload, uninstall and destroy them with another function call. This is handy when testing how some R code or an R package behaves with respect to other packages. / MIT	noarch
r-dissutils	1.0	This package has extensible C code for computing dissimilarities between vectors. It also has a number of C functions for assembling collections of dissimilarities. In particular, it lets you find a matrix of dissimilarities between the rows of two input matrices. There are also functions for finding the nearest neighbors of each row of a matrix, either within the matrix itself or within another matrix. / GPL-2	linux-64, osx-64, win-64
r-distance.sample.size	0.0	Calculates the study size (either number of detections, or proportion of region that should be covered) to achieve a target precision for the estimated abundance. The calculation allows for the penalty due to unknown detection function, and for overdispersion. The user must specify a guess at the true detection function. / GPL-2   GPL-3	noarch
r-distances	0.1.7	Provides tools for constructing, manipulating and using distance metrics. / GPL-3	linux-64, osx-64, win-64
r-distcomp	1.0_1	Implementing algorithms and fitting models when sites (possibly remote) share computation summaries rather than actual data over HTTP with a master R process (using ‘opencpu’, for example). A stratified Cox model and a singular value decomposition are provided. The former makes direct use of code from the R ‘survival’ package. (That is, the underlying Cox model code is derived from that in the R ‘survival’ package.) Sites may provide data via several means: CSV files, Redcap API, etc. An extensible design allows for new methods to be added in the future. Web applications are provided (via ‘shiny’) for the implemented methods to help in designing and deploying the computations. / LGPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<code>r-distcrete</code>	1.0.3	Creates discretised versions of continuous distribution functions by mapping continuous values to an underlying discrete grid, based on a (uniform) frequency of discretisation, a valid discretisation point, and an integration range. For a review of discretisation methods, see Chakraborty (2015) <doi:10.1186/s40488-015-0028-6>. / MIT	noarch
<code>r-distdrawr</code>	0.1.3	Download data from the FlorKart database of the floristic field mapping in Germany in a convenient way. The database incorporates distribution data for plants in Germany on the basis of quadrants on a topographical map with a resolution of 1 : 25000 (TK 25). The data is owned and provided by the German Federal Agency for Nature Conservation (BfN) and the Network Phytodiversity in Germany (NetPhyD). For further information please visit < <a href="http://www.floraweb.de/pflanzenarten/hintergrundtexte_florkart_organisation.html">http://www.floraweb.de/pflanzenarten/hintergrundtexte_florkart_organisation.html</a> >. The author of this package is in no way associated with the BfN or NetPhyD. / GPL-2	noarch
<code>r-distfree.cr</code>	1.5.1	Constructs confidence regions without the need to know the sampling distribution of bivariate data. The method was proposed by Zhiqiu Hu & Rong-cai Yang (2013) <doi:10.1371/journal.pone.0081179.g001>. / GPL-2	noarch
<code>r-distillery</code>	1.0_6	Some very simple method functions for confidence interval calculation, bootstrap resampling, and to distill pertinent information from a potentially complex object; primarily used in common with packages extRemes and SpatialVx. / GPL-2	noarch
<code>r-distory</code>	1.4.3	Geodesic distance between phylogenetic trees and associated functions. / BSD	linux-64, osx-64, win-64
<code>r-distrib</code>	1.0	A different way for calculating pdf/pmf, cdf, quantile and random data such that the user is able to consider the name of related distribution as an argument and so easily can be changed by a changing argument by user. It must be mentioned that the core and computation base of package ‘DISTRIB’ is package ‘stats’. Although similar functions are introduced previously in package ‘stats’, but the package ‘DISTRIB’ has some special applications in some special computational programs. / LGPL-3	noarch
<code>r-distributions3</code>	0.1.1	Tools to create and manipulate probability distributions using S3. Generics random(), pdf(), cdf() and quantile() provide replacements for base R’s r/d/p/q style functions. Functions and arguments have been named carefully to minimize confusion for students in intro stats courses. The documentation for each distribution contains detailed mathematical notes. / MIT	noarch
<code>r-distributiontest</code>	1.0	Provides new types of omnibus tests which are generally much more powerful than traditional tests (including the Kolmogorov-Smirnov, Cramer-von Mises and Anderson-Darling tests), see Zhang (2002) <doi:10.1111/1467-9868.00337>. / GPL-3	noarch
<code>r-distributionutils</code>	0.6_0	Utilities are provided which are of use in the packages I have developed for dealing with distributions. Currently these packages are GeneralizedHyperbolic, VarianceGamma, and SkewHyperbolic and NormalLaplace. Each of these packages requires DistributionUtils. Functionality includes sample skewness and kurtosis, log-histogram, tail plots, moments by integration, changing the point about which a moment is calculated, functions for testing distributions using inversion tests and the Massart inequality. Also includes an implementation of the incomplete Bessel K function. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-disttools	0.1.7	Provides convenient methods for accessing the data in ‘dist’ objects with minimal memory and computational overhead. ‘disttools’ can be used to extract the distance between any pair or combination of points encoded by a ‘dist’ object using only the indices of those points. This is an improvement over existing functionality, which requires either coercing a ‘dist’ object into a matrix or calculating the one dimensional index corresponding to a pair of observations. Coercion to a matrix is undesirable because doing so doubles the amount of memory required for storage. In contrast, there is no inherent downside to the latter solution. However, in part due to several edge cases, correctly and efficiently implementing such a solution can be challenging. ‘disttools’ abstracts away these challenges and provides a simple interface to access the data in a ‘dist’ object using the latter approach. / MIT	noarch
r-divdyn	0.8.0	Functions to describe sampling and diversity dynamics of fossil occurrence datasets (e.g. from the Paleobiology Database). The package includes methods to calculate range- and occurrence-based metrics of taxonomic richness, extinction and origination rates, along with traditional sampling measures. A powerful subsampling tool is also included that implements frequently used sampling standardization methods in a multiple bin-framework. The plotting of time series and the occurrence data can be simplified by the functions incorporated in the package, as well other calculations, such as environmental affinities and extinction selectivity testing. Details can be found in: Kocsis, A.T.; Reddin, C.J.; Alroy, J. and Kiessling, W. (2019) <doi:10.1101/423780>. / CC BY 4.0	linux-64, osx-64, win-64
r-divmelt	1.0.3	This package has tools for analyzing DNA melting data to generate HRM scores, the DNA diversity measure output of the HRM Diversity Assay. For additional documentation visit <a href="http://code.google.com/p/divmelt/">http://code.google.com/p/divmelt/</a> . / GPL-2	noarch
r-divo	1.0.0	A set of tools for empirical analysis of diversity (a number and frequency of different types in population) and similarity (a number and frequency of shared types in two populations) in biological or ecological systems. / GPL-3	linux-64, osx-64, win-64
r-dixontest	1.0.0	For outlier detection in small and normally distributed samples the ratio test of Dixon (Q-test) can be used. Density, distribution function, quantile function and random generation for Dixon’s ratio statistics are provided as wrapper functions. The core applies McBane’s Fortran functions <doi:10.18637/jss.v016.i03> that use Gaussian quadrature for a numerical solution. / GPL-3	linux-64, osx-64, win-64
r-dkdna	0.1.1	Compute diffusion kernels on DNA polymorphisms, including SNP and bi-allelic genotypes. / GPL-2	linux-64, osx-64, win-64
r-dlasso	2.0.2	An implementation of the differentiable lasso (dlasso) and SCAD (dSCAD) using iterative ridge algorithm. This package allows selecting the tuning parameter by AIC, BIC, GIC and GIC. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-dlib</a>	1.0.3	Interface for ‘Rcpp’ users to ‘dlib’ < <a href="http://dlib.net">http://dlib.net</a> > which is a ‘C’ toolkit containing machine learning algorithms and computer vision tools. It is used in a wide range of domains including robotics, embedded devices, mobile phones, and large high performance computing environments. This package allows R users to use ‘dlib’ through ‘Rcpp’. / BSL-1.0	linux-64, osx-64, win-64
<a href="#">r-dlm</a>	1.1_5	Provides routines for Maximum likelihood, Kalman filtering and smoothing, and Bayesian analysis of Normal linear State Space models, also known as Dynamic Linear Models. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-dma</a>	1.4_0	Dynamic model averaging for binary and continuous outcomes. / GPL-2	noarch
<a href="#">r-dmrnet</a>	0.2.0	Model selection algorithms for regression and classification, where the predictors can be numerical and categorical and the number of regressors exceeds the number of observations. The selected model consists of a subset of numerical regressors and partitions of levels of factors. Aleksandra Maj-Kańska, Piotr Pokarowski and Agnieszka Prochenka (2015) < <a href="https://doi.org/10.1214/15-EJS1050">doi:10.1214/15-EJS1050</a> >. Piotr Pokarowski and Jan Mielniczuk (2015) < <a href="http://www.jmlr.org/papers/volume16/pokarowski15a/pokarowski15a.pdf">http://www.jmlr.org/papers/volume16/pokarowski15a/pokarowski15a.pdf</a> >. / GPL-2	noarch
<a href="#">r-dmt</a>	0.8.20	Probabilistic dependency modeling toolkit. / BSD_2_clause	noarch
<a href="#">r-dmwr</a>	0.4.1	This package includes functions and data accompanying the book Data Mining with R, learning with case studies by Luis Torgo, CRC Press 2010. / GPL-2	noarch
<a href="#">r-dnaseqtest</a>	1.0	Generates DNA sequences based on Markov model techniques for matched sequences. This can be generalized to several sequences. The sequences (taxa) are then arranged in an evolutionary tree (phylogenetic tree) depicting how taxa diverge from their common ancestors. This gives the tests and estimation methods for the parameters of different models. Standard phylogenetic methods assume stationarity, homogeneity and reversibility for the Markov processes, and often impose further restrictions on the parameters. / GPL-2	noarch
<a href="#">r-dne</a>	2.1.0	The DnE package involves functions to analyse the distribution of a set of given data. The basic idea of the analysis is chi-squared test. Functions which have the form as <code>is.xxdistribution</code> are used to analyse whether the data obeys the <code>xxdistribution</code> . If you do not know which distribution to judge, use function <code>is.dt()</code> . / GPL-2	noarch
<a href="#">r-dng</a>	0.2.1	Provides density, distribution function, quantile function and random generation for the split normal and split-t distributions, and computes their mean, variance, skewness and kurtosis for the two distributions (Li, F, Villani, M. and Kohn, R. (2010) < <a href="https://doi.org/10.1016/j.jspi.2010.04.031">doi:10.1016/j.jspi.2010.04.031</a> >). / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-dnmf	1.3	Discriminant Non-Negative Matrix Factorization aims to extend the Non-negative Matrix Factorization algorithm in order to extract features that enforce not only the spatial locality, but also the separability between classes in a discriminant manner. It refers to three article, Zafeiriou, Stefanos, et al. Exploiting discriminant information in nonnegative matrix factorization with application to frontal face verification. Neural Networks, IEEE Transactions on 17.3 (2006): 683-695. Kim, Bo-Kyeong, and Soo-Young Lee. Spectral Feature Extraction Using dNMF for Emotion Recognition in Vowel Sounds. Neural Information Processing. Springer Berlin Heidelberg, 2013. and Lee, Soo-Young, Hyun-Ah Song, and Shun-ichi Amari. A new discriminant NMF algorithm and its application to the extraction of subtle emotional differences in speech. Cognitive neurodynamics 6.6 (2012): 525-535. / GPL-2	noarch
r-do	1.0.0	Flexibly convert data between long and wide format using just two functions: reshape_toLong() and reshape_toWide(). / GPL-3	noarch
r-dobad	1.0.6	Provides Frequentist (EM) and Bayesian (MCMC) Methods for Inference of Birth-Death-Immigration Markov Chains. / GPL-2	noarch
r-dobson	0.4	Example datasets from the book An Introduction to Generalised Linear Models (Year: 2018, ISBN:9781138741515) by Dobson and Barnett. / GPL-2	noarch
r-dockerfiler	0.1.3	Build a Dockerfile straight from your R session. ‘dockerfiler’ allows you to create step by step a Dockerfile, and provide convenient tools to wrap R code inside this Dockerfile. / MIT	noarch
r-docopt	0.6.1	Define a command-line interface by just giving it a description in the specific format. / MIT	noarch
r-docopulae	0.4.0	A direct approach to optimal designs for copula models based on the Fisher information. Provides flexible functions for building joint PDFs, evaluating the Fisher information and finding optimal designs. It includes an extensible solution to summation and integration called ‘nint’, functions for transforming, plotting and comparing designs, as well as a set of tools for common low-level tasks. / MIT	linux-64, osx-64, win-64
r-docstring	1.0.0	Provides the ability to display something analogous to Python’s docstrings within R. By allowing the user to document their functions as comments at the beginning of their function without requiring putting the function into a package we allow more users to easily provide documentation for their functions. The documentation can be viewed just like any other help files for functions provided by packages as well. / GPL-2	noarch
r-documair	0.6_0	Production of R packages from tagged comments introduced within the code and a minimum of additional documentation files. / GPL (>= 2.15)	linux-64, osx-64, win-64
r-document	3.1.0	Have you ever been tempted to create ‘roxygen2’-style documentation comments for one of your functions that was not part of one of your packages (yet)? This is exactly what this package is about: running ‘roxygen2’ on (chunks of) a single code file. / BSD_2_clause	noarch
r-docusignr	0.0.3	Connect to the ‘DocuSign’ Rest API < <a href="https://www.docusign.com/p/RESTAPIGuide/RESTAPIGuide.htm">https://www.docusign.com/p/RESTAPIGuide/RESTAPIGuide.htm</a> >, which supports embedded signing, and sending of documents. / GPL-3	noarch
r-dodge	0.9_2	A variety of sampling plans are able to be compared using evaluations of their operating characteristics (OC), average outgoing quality (OQ), average total inspection (ATI) etc. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-doe</a> <a href="#">strare</a>	0.2	Rare variant association test integrating variant position information. It aims to identify the presence of clusters of disease-risk variants in specific gene regions. For more details, please read the publication from Persyn et al. (2017) <doi:10.1371/journal.pone.0179364>. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-doex</a>	1.1	Contains several one-way heteroscedastic ANOVA tests such as Alexander-Govern test by Alexandern and Govern (1994) <doi:10.2307/1165140>, Alvandi et al. Generalized F test by Alvandi et al. (2012) <doi:10.1080/03610926.2011.573160>, Approximate F test by Asiribo and Gurland (1990) <doi:10.1080/03610929008830427>, Box F test by Box (1954) <doi:10.1214/aoms/1177728786>, Brown-Forsythe test by Brown and Forsythe (1974) <doi:10.2307/1267501>, B2 test by Ozdemir and Kurt (2006) <http://sjam.selcuk.edu.tr/sjam/article/view/174>, Cochran F test by Cochran (1937) <https://www.jstor.org/stable/pdf/2984123.pdf>, Fiducial Approach test by Li et al. (2011) <doi:10.1016/j.csda.2010.12.009>, Generalized F test by Weerahandi (1995) <doi:10.2307/2532947>, Johansen F test by Johansen (1980) <doi:10.1093/biomet/67.1.85>, Modified Brown-Forsythe test by Mehrotra (1997) <doi:10.1080/03610919708813431>, Modified Welch test by Hartung et al.(2002) <doi:10.1007/s00362-002-0097-8>, One-Stage test by Chen and Chen (1998) <doi:10.1080/03610919808813501>, One-Stage Range test by Chen and Chen (2000) <doi:10.1080/01966324.2000.10737505>, Parametric Bootstrap test by Krishnamoorhty et al.(2007) <doi:10.1016/j.csda.2006.09.039>, Permutation F test by Berry and Mielke (2002) <doi:10.2466/pr0.2002.90.2.495>, Scott-Smith test by Scott and Smith (1971) <doi:10.2307/2346757>, Welch test by Welch(1951) <doi:10.2307/2332579>, and Welch-Aspin test by Aspin (1948) <doi:10.1093/biomet/35.1-2.88>. These tests are used to test the equality of group means under unequal variance. Furthermore, a modified version of Generalized F-test is improved to test the equality of non-normal group means under unequal variances and a revised version of Generalized F-test is given to test the equality of non-normal group means caused by skewness. / GPL-2	noarch
<a href="#">r-domc</a>	1.3.5	Provides a parallel backend for the %dopar% function using the multicore functionality of the parallel package. / GPL-2	linux-32, linux-64, noarch, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-dominanceanalysis</a>	1.0.0	Dominance analysis is a method that allows to compare the relative importance of predictors in multiple regression models: ordinary least squares, generalized linear models and hierarchical linear models. The main principles and methods of dominance analysis are described in Budescu, D. V. (1993) <doi:10.1037/0033-2909.114.3.542> and Azen, R., & Budescu, D. V. (2003) <doi:10.1037/1082-989X.8.2.129> for ordinary least squares regression. Subsequently, the extensions for multivariate regression, logistic regression and hierarchical linear models were described in Azen, R., & Budescu, D. V. (2006) <doi:10.3102/10769986031002157>, Azen, R., & Traxel, N. (2009) <doi:10.3102/1076998609332754> and Luo, W., & Azen, R. (2013) <doi:10.3102/1076998612458319>, respectively. / GPL-2	noarch
<a href="#">r-domino</a>	0.3.1	A wrapper on top of the ‘Domino Command-Line Client’. It lets you run ‘Domino’ commands (e.g., run, upload, download) directly from your R environment. Under the hood, it uses R’s system function to run the ‘Domino’ executable, which must be installed as a prerequisite. ‘Domino’ is a service that makes it easy to run your code on scalable hardware, with integrated version control and collaboration features designed for analytical workflows (see < <a href="http://www.dominodatalab.com">http://www.dominodatalab.com</a> > for more information). / MIT	noarch
<a href="#">r-doparallel</a>	1.0.14	Provides a parallel backend for the <code>%dopar%</code> function using the parallel package. / GPL-2	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-dorng</a>	1.7.1	Provides functions to perform reproducible parallel foreach loops, using independent random streams as generated by L’Ecuyer’s combined multiple-recursive generator [L’Ecuyer (1999), <DOI:10.1287/opre.47.1.159>]. It enables to easily convert standard <code>%dopar%</code> loops into fully reproducible loops, independently of the number of workers, the task scheduling strategy, or the chosen parallel environment and associated foreach backend. / GPL-2	noarch
<a href="#">r-dos</a>	1.0.0	Contains data sets, examples and software from the book Design of Observational Studies by Paul R. Rosenbaum, New York: Springer, <doi:10.1007/978-1-4419-1213-8>, ISBN 978-1-4419-1212-1. / GPL-2	noarch
<a href="#">r-dosearch</a>	1.0.2	Identification of causal effects from arbitrary observational and experimental probability distributions via do-calculus and standard probability manipulations using a search-based algorithm. Allows for the presence of mechanisms related to selection bias (Bareinboim, E. and Tian, J. (2015) < <a href="http://ftp.cs.ucla.edu/pub/stat_ser/r445.pdf">http://ftp.cs.ucla.edu/pub/stat_ser/r445.pdf</a> >), transportability (Bareinboim, E. and Pearl, J. (2014) < <a href="http://ftp.cs.ucla.edu/pub/stat_ser/r443.pdf">http://ftp.cs.ucla.edu/pub/stat_ser/r443.pdf</a> >), missing data (Mohan, K. and Pearl, J. and Tian, J. (2013) < <a href="http://ftp.cs.ucla.edu/pub/stat_ser/r410.pdf">http://ftp.cs.ucla.edu/pub/stat_ser/r410.pdf</a> >) and arbitrary combinations of these. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-dosefinding	0.9.1	The DoseFinding package provides functions for the design and analysis of dose-finding experiments (with focus on pharmaceutical Phase II clinical trials). It provides functions for: multiple contrast tests, fitting non-linear dose-response models (using Bayesian and non-Bayesian estimation), calculating optimal designs and an implementation of the MCPMod methodology. / GPL-3	linux-64, osx-64, win-64
r-dostats	1.3.2	A small package containing helper utilities for creating function for computing statistics. / GPL-3	noarch
r-dotcall64	1.0.0	Provides .C64(), which is an enhanced version of .C() and .Fortran() from the foreign function interface. .C64() supports long vectors, arguments of type 64-bit integer, and provides a mechanism to avoid unnecessary copies of read-only and write-only arguments. This makes it a convenient and fast interface to C/C and Fortran code. / GPL-2	linux-64, osx-64, win-64
r-dotdot	0.1.0	Use ‘.’ on the right hand side of the ‘:=’ operator as a shorthand for the left hand side, so that ‘var := f(.) .’ is equivalent to ‘var <- f(var) var’. This permits the user to be explicit about growing an object or overwriting it using its previous value, avoids repeating a variable name, and saves keystrokes, time, visual space and cognitive load. / GPL-3	noarch
r-dotenv	1.0.2	Load configuration from a ‘.env’ file, that is in the current working directory, into environment variables. / MIT	noarch
r-doubcens	1.1	Contains the discrete nonparametric survivor function estimation algorithm of De Gruttola and Lagakos for doubly interval-censored failure time data and the discrete nonparametric survivor function estimation algorithm of Sun for doubly interval-censored left-truncated failure time data [Victor De Gruttola & Stephen W. Lagakos (1989) <doi:10.2307/2532030>] [Jianguo Sun (1995) <doi:10.2307/2533008>]. / GPL-2	linux-64, osx-64, win-64
r-double.truncation	1.4	Likelihood-based inference methods with doubly-truncated data are developed under various models. Nonparametric models are based on Efron and Petrosian (1999) <doi:10.1080/01621459.1999.10474187> and Emura, Konno, and Michimae (2015) <doi:10.1007/s10985-014-9297-5>. Parametric models from the special exponential family (SEF) are based on Hu and Emura (2015) <doi:10.1007/s00180-015-0564-z> and Emura, Hu and Konno (2017) <doi:10.1007/s00362-015-0730-y>. / GPL-2	noarch
r-doublecone	1.1	Performs hypothesis tests concerning a regression function in a least-squares model, where the null is a parametric function, and the alternative is the union of large-dimensional convex polyhedral cones. See Bodhisattva Sen and Mary C Meyer (2016) <doi:10.1111/rssb.12178> for more details. / GPL-2   GPL-3	noarch
r-doubleexpseq	1.1	Differential exon usage test for RNA-Seq data via an empirical Bayes shrinkage method for the dispersion parameter the utilizes inclusion-exclusion data to analyze the propensity to skip an exon across groups. The input data consists of two matrices where each row represents an exon and the columns represent the biological samples. The first matrix is the count of the number of reads expressing the exon for each sample. The second matrix is the count of the number of reads that either express the exon or explicitly skip the exon across the samples, a.k.a. the total count matrix. Dividing the two matrices yields proportions representing the propensity to express the exon versus skipping the exon for each sample. / GPL-3	noarch
r-dovalidation	1.1.0	Local linear hazard estimator and its multiplicatively bias correction, including three bandwidth selection methods: best one-sided cross-validation, double one-sided cross-validation, and standard cross-validation. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-downloader</a>	0.4	Provides a wrapper for the download.file function, making it possible to download files over HTTPS on Windows, Mac OS X, and other Unix-like platforms. The ‘RCurl’ package provides this functionality (and much more) but can be difficult to install because it must be compiled with external dependencies. This package has no external dependencies, so it is much easier to install. / GPL-2	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-downsize</a>	0.2.2	Toggles the test and production versions of a large workflow. / GPL-3	noarch
<a href="#">r-dparser</a>	0.1.8	A Scannerless GLR parser/parser generator. Note that GLR standing for generalized LR, where L stands for left-to-right and R stands for rightmost (derivation). For more information see < <a href="https://en.wikipedia.org/wiki/GLR_parser">https://en.wikipedia.org/wiki/GLR_parser</a> >. This parser is based on the Tomita (1987) algorithm. (Paper can be found at < <a href="http://acl-arc.comp.nus.edu.sg/archives/acl-arc-090501d3/data/pdf/anthology-PDF/J/J87/J87-1004.pdf">http://acl-arc.comp.nus.edu.sg/archives/acl-arc-090501d3/data/pdf/anthology-PDF/J/J87/J87-1004.pdf</a> >). The original ‘dparser’ package documentation can be found at < <a href="http://dparser.sourceforge.net/">http://dparser.sourceforge.net/</a> >. This allows you to add mini-languages to R (like RxODE’s ODE mini-language Wang, Hallow, and James 2015 <DOI:10.1002/psp4.12052>) or to parse other languages like ‘NONMEM’ to automatically translate them to R code. To use this in your code, add a LinkingTo dparser in your DESCRIPTION file and instead of using #include <dpars.h> use #include <dparser.h>. This also provides a R-based port of the make_dparser < <a href="http://dparser.sourceforge.net/d/make_dparser.cat">http://dparser.sourceforge.net/d/make_dparser.cat</a> > command called mkdparser(). Additionally you can parse an arbitrary grammar within R using the dpars() function, which works on most OSes and is mainly for grammar testing. The fastest parsing, of course, occurs at the C level, and is suggested. / BSD_3_clause	linux-64, osx-64, win-64
<a href="#">r-dpcid</a>	1.0	Differential partial correlation identification with the ridge and the fusion penalties. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-dpglasso</a>	1.0	fits the primal graphical lasso, via one-at-a-time block-coordinate descent. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-dplrcon</a>	1.0	The concordance method is a non-parametric method based on bootstrapping that is used to test the hypothesis that two subsets of time series are similar in terms of mean, variance or both. This method was developed to address a concern within dendroclimatology that young trees may produce a differing climate response to older more established trees. Details of this method are available in Pirie, M. (2013). The Climate of New Zealand reconstructed from kauri tree rings: Enhancement through the use of novel statistical methodology. PhD. Dissertation, School of Environment and Department of Statistics, University of Auckland, New Zealand. This package also produces a figure with 3 panels, each panel is for a different climate variable. An example of this figure is included in On the influence of tree size on the climate - growth relationship of New Zealand kauri ( <i>Agathis australis</i> ): insights from annual, monthly and daily growth patterns. J Wunder, AM Fowler, ER Cook, M Pirie, SPJ McCloskey. <i>Trees</i> 27 (4), 937-948. For further R functions for loading your own dendroclimatology datasets and performing dendrochronology analysis refer to the R package dplr: Dendrochronology Program Library in R. The concordance procedure is intended to add to the standard dendrochronology techniques provided in dplr. / GPL-3	noarch
<a href="#">r-dplyr</a>	0.8.0	A fast, consistent tool for working with data frame like objects, both in memory and out of memory. / MIT file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-dpp</a>	0.1.2	This MCMC method takes a data numeric vector (Y) and assigns the elements of Y to a (potentially infinite) number of normal distributions. The individual normal distributions from a mixture of normals can be inferred. Following the method described in Escobar (1994) <doi:10.2307/2291223> we use a Dirichlet Process Prior (DPP) to describe stochastically our prior assumptions about the dimensionality of the data. / MIT	linux-64, osx-64, win-64
<a href="#">r-dprint</a>	0.0.4	Provides a generalized method for printing tabular data within the R environment in order to make the process of presenting high quality tabular output seamless for the user. Output is directed to the R graphics device so that tables can be exported to any file format supported by the graphics device. Utilizes a formula interface to specify the contents of tables often found in manuscripts or business reports. In addition, formula interface provides inline formatting of the numeric cells of a table and renaming column labels. / GPL-2	noarch
<a href="#">r-dqshiny</a>	0.0.3	Provides highly customizable modules to enhance your shiny apps. Includes layout independent collapsible boxes and value boxes, a very fast autocomplete input, rhandsontable extensions for filtering and paging and much more. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-dr	3.0.10	Functions, methods, and datasets for fitting dimension reduction regression, using slicing (methods SAVE and SIR), Principal Hessian Directions (phd, using residuals and the response), and an iterative IRE. Partial methods, that condition on categorical predictors are also available. A variety of tests, and stepwise deletion of predictors, is also included. Also included is code for computing permutation tests of dimension. Adding additional methods of estimating dimension is straightforward. For documentation, see the vignette in the package. With version 3.0.4, the arguments for dr.step have been modified. / GPL-2	noarch
r-dragonking	0.1.0	Statistical tests and test statistics to identify events in a dataset that are dragon kings (DKs). The statistical methods in this package were reviewed in Wheatley & Sornette (2015) <doi:10.2139/ssrn.2645709>. / GPL-3	noarch
r-dragular	0.3.1	Move elements between containers in ‘Shiny’ without explicitly using ‘JavaScript’. It can be used to build custom inputs or to change the positions of user interface elements like plots or tables. / GPL-2	noarch
r-drat	0.1.5	Creation and use of R Repositories via helper functions to insert packages into a repository, and to add repository information to the current R session. Two primary types of repositories are support: gh-pages at GitHub, as well as local repositories on either the same machine or a local network. Drat is a recursive acronym: Drat R Archive Template. / GPL-2	noarch
r-draw	1.0.0	A set of user-friendly wrapper functions for creating consistent graphics and diagrams with lines, common shapes, text, and page settings. Compatible with and based on the R ‘grid’ package. / MIT	noarch
r-drawr	1.0.1	We present DRaWR, a network-based method for ranking genes or properties related to a given gene set. Such related genes or properties are identified from among the nodes of a large, heterogeneous network of biological information. Our method involves a random walk with restarts, performed on an initial network with multiple node and edge types, preserving more of the original, specific property information than current methods that operate on homogeneous networks. In this first stage of our algorithm, we find the properties that are the most relevant to the given gene set and extract a subnetwork of the original network, comprising only the relevant properties. We then rerank genes by their similarity to the given gene set, based on a second random walk with restarts, performed on the above subnetwork. / GPL-2	noarch
r-driftbursthypothesis	0.1.3	Calculates the T-Statistic for the drift burst hypothesis from the working paper Christensen, Oomen and Reno (2018) <DOI:10.2139/ssrn.2842535>. The authors’ MATLAB code is available upon request, see: <https://papers.ssrn.com/sol3/papers.cfm?abstract_id=2842535>. / GPL-3	linux-64, osx-64, win-64
r-drillr	0.1	Provides a R driver for Apache Drill<https://drill.apache.org>, which could connect to the Apache Drill cluster<https://drill.apache.org/docs/installing-drill-on-the-cluster> or drillbit<https://drill.apache.org/docs/embedded-mode-prerequisites> and get result(in data frame) from the SQL query and check the current configuration status. This link <https://drill.apache.org/docs> contains more information about Apache Drill. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-drimpute	1.0	R codes for imputing dropout events. Many statistical methods in cell type identification, visualization and lineage reconstruction do not account for dropout events ('PCAREduce', 'SC3', 'PCA', 't-SNE', 'Monocle', 'TSCAN', etc). 'DrImpute' can improve the performance of such software by imputing dropout events. / GPL-3	linux-64, osx-64, win-64
r-drmde1	1.3.1	Dual empirical likelihood (DEL) inference under semiparametric density ratio models (DRM) in the presence of multiple samples, including population cumulative distribution function estimation, quantile estimation and comparison, density estimation, composite hypothesis testing for DRM parameters which encompasses testing for changes in population distribution functions as a special case, etc. / GPL-3	linux-64, osx-64, win-64
r-dropr	0.1	Drop out analysis for psychologists in a R based web application. Shiny is used to visualize and analyze drop outs tailored to the methods of online survey methodology. Concept and app presented at the SCIP Conference in Long Beach, California. / GPL-2	noarch
r-dropstest	0.1.3	Generates simulated data representing the LOX drop testing process (also known as impact testing). A simulated process allows for accelerated study of test behavior. Functions are provided to simulate trials, test series, and groups of test series. Functions for creating plots specific to this process are also included. Test attributes and criteria can be set arbitrarily. This work is not endorsed by or affiliated with NASA. See ASTM G86-17, Standard Test Method for Determining Ignition Sensitivity of Materials to Mechanical Impact in Ambient Liquid Oxygen and Pressurized Liquid and Gaseous Oxygen Environments <doi:10.1520/G0086-17>. / MIT	noarch
r-drr	0.0.3	An Implementation of Dimensionality Reduction via Regression using Kernel Ridge Regression. / GPL-3   file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-ds	4.0	Performs various analyzes of descriptive statistics, including correlations, graphics and tables. / GPL-2	noarch
r-dsample	0.91.2	Two discretization-based Monte Carlo algorithms, namely the Fu-Wang algorithm and the Wang-Lee algorithm, are provided for random sample generation from a high dimensional distribution of complex structure. The normalizing constant of the target distribution needs not to be known. / GPL-2	noarch
r-dsbayes	1.1	Calculate posterior modes and credible intervals of parameters of the Dixon-Simon model for subgroup analysis (with binary covariates) in clinical trials. / GPL-2	noarch
r-dsl	0.1_6	An abstract DList class helps storing large list-type objects in a distributed manner. Corresponding high-level functions and methods for handling distributed storage (DStorage) and lists allows for processing such DLists on distributed systems efficiently. In doing so it uses a well defined storage backend implemented based on the DStorage class. / GPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-dst	1.4.0	Using the Theory of Belief Functions for evidence calculus. Basic probability assignments, or mass functions, can be defined on the subsets of a set of possible values and combined. A mass function can be extended to a larger frame. Marginalization, i.e. reduction to a smaller frame can also be done. These features can be combined to analyze small belief networks and take into account situations where information cannot be satisfactorily described by probability distributions. / GPL-2	noarch
r-dstat	1.0.4	A d-statistic tests the null hypothesis of no treatment effect in a matched, nonrandomized study of the effects caused by treatments. A d-statistic focuses on subsets of matched pairs that demonstrate insensitivity to unmeasured bias in such an observational study, correcting for double-use of the data by conditional inference. This conditional inference can, in favorable circumstances, substantially increase the power of a sensitivity analysis (Rosenbaum (2010) <doi:10.1007/978-1-4419-1213-8_14>). There are two examples, one concerning unemployment from Lalive et al. (2006) <doi:10.1111/j.1467-937X.2006.00406.x>, the other concerning smoking and periodontal disease from Rosenbaum (2017) <doi:10.1214/17-STS621>. / GPL-2	noarch
r-dt	0.5	Data objects in R can be rendered as HTML tables using the JavaScript library 'DataTables' (typically via R Markdown or Shiny). The 'DataTables' library has been included in this R package. The package name 'DT' is an abbreviation of 'DataTables'. / GPL-3   file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-dtables	0.2.0	Towards automation of descriptive frequencies and statistics tables. / GPL-3	noarch
r-dtangle	0.3.1	Deconvolving cell types from high-throughput gene profiling data. / GPL-3	noarch
r-dtaxg	0.1.0	To calculate the sensitivity and specificity in the absence of gold standard using the Bayesian method. The Bayesian method can be referenced at Haiyan Gu and Qiguang Chen (1999) <doi:10.3969/j.issn.1002-3674.1999.04.004>. / GPL-3	noarch
r-dtd	0.2.1	Provides fast methods to work with Merton's distance to default model introduced in Merton (1974) <doi:10.1111/j.1540-6261.1974.tb03058.x>. The methods includes simulation and estimation of the parameters. / GPL-2	linux-64, osx-64, win-64
r-dtda	2.1.1	This package implements different algorithms for analyzing randomly truncated data, one-sided and two-sided (i.e. doubly) truncated data. Two real data sets are included. / GPL-2	noarch
r-dtda.cif	1.0	Nonparametric estimator of the cumulative incidences of competing risks under double truncation. The estimator generalizes the Efron-Petrosian NPMLE (Non-Parametric Maximum Likelihood Estimator) to the competing risks setting. Efron, B. and Petrosian, V. (1999) <doi:10.2307/2669997>. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-dtda</a>	1.0	Non-iterative estimator for the cumulative distribution of a doubly truncated variable. de Uña-Álvarez J. (2018) <doi:10.1007/978-3-319-73848-2_37>. / GPL-2	noarch
<a href="#">r-dtk</a>	3.5	This package was created to analyze multi-level one-way experimental designs. It is designed to handle vectorized observation and factor data where there are unequal sample sizes and population variance homogeneity can not be assumed. To conduct the Dunnett modified Tukey-Kramer test (a.k.a. the T3 Procedure), create two vectors: one for your observations and one for the factor level of each observation. The function, <code>gl.unequal</code> , provides a means to more conveniently produce a factor vector with unequal sample sizes. Next, use the <code>DTK.test</code> function to conduct the test and save the output as an object to input into the <code>DTK.plot</code> function, which produces a confidence interval plot for each of the pairwise comparisons. Lastly, the function <code>TK.test</code> conducts the original Tukey-Kramer test. / GPL-2	noarch
<a href="#">r-dtmcpack</a>	0.1_2	A series of functions which aid in both simulating and determining the properties of finite, discrete-time, discrete state markov chains. Two functions (DTMC, MultDTMC) produce n iterations of a Markov Chain(s) based on transition probabilities and an initial distribution. The function <code>FPTIME</code> determines the first passage time into each state. The function <code>statdistr</code> determines the stationary distribution of a Markov Chain. / GPL-2	noarch
<a href="#">r-dtp</a>	0.1.0	Compute the dynamic threshold panel model suggested by (Stephanie Kremer, Alexander Bick and Dieter Nautz (2013) <doi:10.1007/s00181-012-0553-9>) in which they extended the (Hansen (1999) <doi: 10.1016/S0304-4076(99)00025-1>) original static panel threshold estimation and the Caner and (Hansen (2004) <doi:10.1017/S0266466604205011>) cross-sectional instrumental variable threshold model, where generalized methods of moments type estimators are used. / GPL-3	noarch
<a href="#">r-dtrlearn2</a>	1.0	We provide a comprehensive software to estimate general K-stage DTRs from SMARTs with Q-learning and a variety of outcome-weighted learning methods. Penalizations are allowed for variable selection and model regularization. With the outcome-weighted learning scheme, different loss functions - SVM hinge loss, SVM ramp loss, binomial deviance loss, and L2 loss - are adopted to solve the weighted classification problem at each stage; augmentation in the outcomes is allowed to improve efficiency. The estimated DTR can be easily applied to a new sample for individualized treatment recommendations or DTR evaluation. / GPL-2	noarch
<a href="#">r-dtrreg</a>	1.4	Dynamic treatment regime estimation and inference via G-estimation, dynamic weighted ordinary least squares (dWOLS) and Q-learning. Inference via bootstrap and (for G-estimation) recursive sandwich estimation. Estimation and inference for survival outcomes via Dynamic Weighted Survival Modeling (DWSurv). / GPL-2	noarch
<a href="#">r-dtsg</a>	0.1.3	Basic time series functionalities such as listing of missing values, application of arbitrary aggregation as well as rolling window functions and automatic detection of periodicity. As it is mainly based on 'data.table', it is fast and - in combination with the 'R6' package - offers reference semantics. In addition to its native R6 interface, it provides an S3 interface inclusive an S3 wrapper method generator for those who prefer the latter. / MIT	noarch
<a href="#">r-dtt</a>	0.1_2	This package provides functions for 1D and 2D Discrete Cosine Transform (DCT), Discrete Sine Transform (DST) and Discrete Hartley Transform (DHT). / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-dub</a>	0.2.0	Provides an operator for assigning nested components of a list to names via a concise pattern matching syntax. This is especially convenient for assigning individual names to the multiple values that a function may return in the form of a list, and for extracting deeply nested list components. / MIT	noarch
<a href="#">r-dummies</a>	1.5.6	Expands factors, characters and other eligible classes into dummy/indicator variables. / GPL-2	noarch
<a href="#">r-dummy</a>	0.1.3	Efficiently create dummies of all factors and character vectors in a data frame. Support is included for learning the categories on one data set (e.g., a training set) and deploying them on another (e.g., a test set). / GPL-2	noarch
<a href="#">r-dunn.test</a>	1.3.5	Computes Dunn's test (1964) for stochastic dominance and reports the results among multiple pairwise comparisons after a Kruskal-Wallis test for stochastic dominance among k groups (Kruskal and Wallis, 1952). The interpretation of stochastic dominance requires an assumption that the CDF of one group does not cross the CDF of the other. 'dunn.test' makes $k(k-1)/2$ multiple pairwise comparisons based on Dunn's z-test-statistic approximations to the actual rank statistics. The null hypothesis for each pairwise comparison is that the probability of observing a randomly selected value from the first group that is larger than a randomly selected value from the second group equals one half; this null hypothesis corresponds to that of the Wilcoxon-Mann-Whitney rank-sum test. Like the rank-sum test, if the data can be assumed to be continuous, and the distributions are assumed identical except for a difference in location, Dunn's test may be understood as a test for median difference. 'dunn.test' accounts for tied ranks. / GPL-2	noarch
<a href="#">r-dunnetttests</a>	2.0	For the implementation of the step-down or step-up Dunnett testing procedures, the package includes R functions to calculate critical constants and R functions to calculate adjusted P-values of the test statistics. In addition, the package also contains functions to evaluate testing powers and hence the necessary sample sizes specially for the classical problem of comparisons of several treatments with a control. / GPL-2	noarch
<a href="#">r-durmod</a>	1.1_2	Estimation of piecewise constant mixed proportional hazard competing risk model with NPMLE. The model is described in S. Gaure et al. (2007) <doi:10.1016/j.jeconom.2007.01.015>, J. Heckman and B. Singer (1984) <doi:10.2307/1911491>, and B.G. Lindsay (1983) <doi:10.1214/aos/1176346059>. / Artistic-2.0	linux-64, osx-64, win-64
<a href="#">r-dwdlarger</a>	0.1_0	Solving large scale distance weighted discrimination. The main algorithm is a symmetric Gauss-Seidel based alternating direction method of multipliers (ADMM) method. See Lam, X.Y., Marron, J.S., Sun, D.F., and Toh, K.C. (2018) <arXiv:1604.05473> for more details. / GPL-2	noarch
<a href="#">r-dwlm</a>	0.1.0	This linear model solution is useful when both predictor and response have associated uncertainty. The doubly weights linear model solution is invariant on which quantity is used as predictor or response. Based on the results by Reed(1989) <doi:10.1119/1.15963> and Ripley & Thompson(1987) <doi:10.1039/AN9871200377>. / GPL-2	noarch
<a href="#">r-dyads</a>	1.1.2	Contains functions for the MCMC simulation of dyadic network models j2 (Zijlstra, 2017, <doi:10.1080/0022250X.2017.1387858>) and p2 (Van Duijn, Snijders & Zijlstra, 2004, <doi: 10.1046/j.0039-0402.2003.00258.x>) as described in Zijlstra, Van Duijn & Snijders (2009) <doi: 10.1348/000711007X255336>. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-dydea	0.1.0	Finds regular and chaotic intervals in the data using the 0-1 test for chaos proposed by Gottwald and Melbourne (2004) <DOI:10.1137/080718851>. / GPL-3	noarch
r-dygraphs	1.1.1.6	An R interface to the ‘dygraphs’ JavaScript charting library (a copy of which is included in the package). Provides rich facilities for charting time-series data in R, including highly configurable series- and axis-display and interactive features like zoom/pan and series/point highlighting. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-dykstra	1.0_0	Solves quadratic programming problems using Richard L. Dykstra’s cyclic projection algorithm. Routine allows for a combination of equality and inequality constraints. See Dykstra (1983) <doi:10.1080/01621459.1983.10477029> for details. / GPL-2	noarch
r-dym	0.2	Add a Did You Mean feature to the R interactive. With this package, error messages for misspelled input of variable names or package names suggest what you really want to do in addition to notification of the mistake. / BSD_3_clause	noarch
r-dyn	0.2_9	Time series regression. The dyn class interfaces ts, irts(), zoo() and zooreg() time series classes to lm(), glm(), loess(), quantreg::rq(), MASS::rlm(), MCMCpack::MCMCregress(), quantreg::rq(), randomForest::randomForest() and other regression functions allowing those functions to be used with time series including specifications that may contain lags, diffs and missing values. / GPL-3	noarch
r-dynamac	0.1.8	While autoregressive distributed lag (ARDL) models allow for extremely flexible dynamics, interpreting substantive significance of complex lag structures remains difficult. This package is designed to assist users in dynamically simulating and plotting the results of various ARDL models. It also contains post-estimation diagnostics, including a test for cointegration when estimating the error-correction variant of the autoregressive distributed lag model (Pesaran, Shin, and Smith 2001 <doi:10.1002/jae.616>). / GPL-2	noarch
r-dynamicdistribution	1.1	The package is aimed at dynamically visualizing probability distributions and their moments and all the commonly used distributions are included. / GPL-2	noarch
r-dynamicchazard	0.6.5	Contains functions that lets you fit dynamic hazard models using state space models. The first implemented model is described in Fahrmeir (1992) <doi:10.1080/01621459.1992.10475232> and Fahrmeir (1994) <doi:10.1093/biomet/81.2.317>. Extensions hereof are available where the Extended Kalman filter is replaced by an unscented Kalman filter and other options including particle filters. The implemented particle filters support more general state space models. / GPL-2	linux-64, win-64
r-dynamictreecut	1.63	Contains methods for detection of clusters in hierarchical clustering dendrograms. / GPL-2	noarch
r-dynatree	1.2_10	Inference by sequential Monte Carlo for dynamic tree regression and classification models with hooks provided for sequential design and optimization, fully online learning with drift, variable selection, and sensitivity analysis of inputs. Illustrative examples from the original dynamic trees paper are facilitated by demos in the package; see demo(package=dynaTree). / LGPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-dynclust	3.13	DynClust is a two-stage procedure for the denoising and clustering of stack of noisy images acquired over time. Clustering only assumes that the data contain an unknown but small number of dynamic features. The method first denoises the signals using local spatial and full temporal information. The clustering step uses the previous output to aggregate voxels based on the knowledge of their spatial neighborhood. Both steps use a single keytool based on the statistical comparison of the difference of two signals with the null signal. No assumption is therefore required on the shape of the signals. The data are assumed to be normally distributed (or at least follow a symmetric distribution) with a known constant variance. Working pixelwise, the method can be time-consuming depending on the size of the data-array but harnesses the power of multicore cpus. / MIT	noarch
r-dyncomp	0.0.2	While there are many well-established measures for identifying critical fluctuations and phase transitions, these measures only work with many points of measurement and thus are unreliable when studying short and coarse-grained time series. This package provides a measure for complexity in a time series that does not rely on long time series (Kaiser (2017), <doi:10.17605/OSF.IO/GWTKX>). / MIT	noarch
r-dynetnlaresistance	0.1.0	An anonymization algorithm to resist neighbor label attack in a dynamic network. / MIT	noarch
r-dynia	0.2	Fit dynamic intervention model using the arima() function. / GPL-2	noarch
r-dynpanel	0.1.0	Computes the first stage GMM estimate of a dynamic linear model with p lags of the dependent variables. / GPL-3	noarch
r-dynpred	0.1.2	The dynpred package contains functions for dynamic prediction in survival analysis. / GPL-2	linux-64, osx-64, win-64
r-dynprog	0.1.0	A domain-specific language for specifying translating recursions into dynamic-programming algorithms. See < <a href="https://en.wikipedia.org/wiki/Dynamic_programming">https://en.wikipedia.org/wiki/Dynamic_programming</a> > for a description of dynamic programming. / GPL-3	noarch
r-dzexpm	2.0	MCMC method to estimate and predict skewed spatial processes. A real data set is included. Reference: Wang, Yang and Majumdar (2018) <doi.org/10.1007/s00180-017-0741-3>. / GPL-2	noarch
r-e1071	1.7.1	Functions for latent class analysis, short time Fourier transform, fuzzy clustering, support vector machines, shortest path computation, bagged clustering, naive Bayes classifier, ... / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
r-eaf	1.8	Plots of the empirical attainment function for two objectives. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-easyahp</a>	0.1.1	Given the scores from decision makers, the analytic hierarchy process can be conducted easily. / GPL-3	noarch
<a href="#">r-easyanova</a>	7.0	Perform analysis of variance and other important complementary analyses. The functions are easy to use. Performs analysis in various designs, with balanced and unbalanced data. / GPL-2	noarch
<a href="#">r-easycsv</a>	1.0.8	Allows users to easily read multiple comma separated tables and create a data frame under the same name. Is able to read multiple comma separated tables from a local directory, a zip file or a zip file on a remote directory. / GPL-2	noarch
<a href="#">r-easynls</a>	5.0	Fit and plot some nonlinear models. / GPL-2	noarch
<a href="#">r-easypubmed</a>	2.13	Query NCBI Entrez and retrieve PubMed records in XML or text format. Process PubMed records by extracting and aggregating data from selected fields. A large number of records can be easily downloaded via this simple-to-use interface to the NCBI PubMed API. / GPL-2	noarch
<a href="#">r-easyreg</a>	3.0	Performs analysis of regression in simple designs with quantitative treatments, including mixed models and non linear models. / GPL-2	noarch
<a href="#">r-easysvg</a>	0.1.0	This SVG elements generator can easily generate SVG elements such as rect, line, circle, ellipse, polygon, polyline, text and group. Also, it can combine and output SVG elements into a SVG file. / MIT	noarch
<a href="#">r-ebal</a>	0.1_6	Package implements entropy balancing, a data preprocessing procedure that allows users to reweight a dataset such that the covariate distributions in the reweighted data satisfy a set of user specified moment conditions. This can be useful to create balanced samples in observational studies with a binary treatment where the control group data can be reweighted to match the covariate moments in the treatment group. Entropy balancing can also be used to reweight a survey sample to known characteristics from a target population. / GPL-2	noarch
<a href="#">r-ebass</a>	0.1	We propose a new sample size calculation method for trial-based cost-effectiveness analyses. Our strategy is based on the value of perfect information that would remain after the completion of the study. / GPL-3	noarch
<a href="#">r-ebdbnet</a>	1.2.5	Infer the adjacency matrix of a network from time course data using an empirical Bayes estimation procedure based on Dynamic Bayesian Networks. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-eben</a>	4.6	Provides the Empirical Bayesian Elastic Net for handling multicollinearity in generalized linear regression models. As a special case of the 'EBglmnet' package (also available on CRAN), this package encourages a grouping effects to select relevant variables and estimate the corresponding non-zero effects. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-ebgenotyping</a>	2.0.1	Genotyping the population using next generation sequencing data is essentially important for the rare variant detection. In order to distinguish the genomic structural variation from sequencing error, we propose a statistical model which involves the genotype effect through a latent variable to depict the distribution of non-reference allele frequency data among different samples and different genome loci, while decomposing the sequencing error into sample effect and positional effect. An ECM algorithm is implemented to estimate the model parameters, and then the genotypes and SNPs are inferred based on the empirical Bayes method. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-ebglmnet</a>	4.1	Provides empirical Bayesian lasso and elastic net algorithms for variable selection and effect estimation. Key features include sparse variable selection and effect estimation via generalized linear regression models, high dimensionality with $p \gg n$ , and significance test for nonzero effects. This package outperforms other popular methods such as lasso and elastic net methods in terms of power of detection, false discovery rate, and power of detecting grouping effects. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-ebprs</a>	1.1.5	EB-PRS is a novel method that leverages information for effect sizes across all the markers to improve the prediction accuracy. No parameter tuning is needed in the method, and no external information is needed. This R-package provides the calculation of polygenic risk scores from the given training summary statistics and testing data. We can use EB-PRS to extract main information, estimate Empirical Bayes parameters, derive polygenic risk scores for each individual in testing data, and evaluate the PRS according to AUC and predictive $r^2$ . / GPL-3	noarch
<a href="#">r-ebrank</a>	1.0.0	Empirical Bayes ranking applicable to parallel-estimation settings where the estimated parameters are asymptotically unbiased and normal, with known standard errors. A mixture normal prior for each parameter is estimated using Empirical Bayes methods, subsequently ranks for each parameter are simulated from the resulting joint posterior over all parameters (The marginal posterior densities for each parameter are assumed independent). Finally, experiments are ordered by expected posterior rank, although computations minimizing other plausible rank-loss functions are also given. / CC0	noarch
<a href="#">r-ebsnp</a>	1.0	Genotyping and SNP calling tool for single-sample next generation sequencing data analysis using an empirical Bayes method. / GPL-2	noarch
<a href="#">r-ecctmc</a>	0.2.5	Draw sample paths for endpoint-conditioned continuous time Markov chains via modified rejection sampling or uniformization. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-ecfsup</a>	0.1_2	Testing the equality of several covariance functions of functional data. Four different methods are implemented: L2-norm with W-S naive, L2-norm with W-S bias-reduced, L2-norm (Zhang 2013) <ISBN:9781439862735>, and sup-norm with resampling (Guo et al. 2017) <arXiv:1609.04232>. / LGPL-3	linux-64, osx-64, win-64
<a href="#">r-echarts2shiny</a>	0.2.13	Embed interactive charts to their Shiny applications. These charts will be generated by ECharts library developed by Baidu (< <a href="http://echarts.baidu.com/">http://echarts.baidu.com/</a> >). Current version supports line chart, bar chart, pie chart, scatter plot, gauge, word cloud, radar chart, tree map, and heat map. / GPL-2	noarch
<a href="#">r-ecipex</a>	1.0	Provides a function that quickly computes the fine structure isotope patterns of a set of chemical formulas to a given degree of accuracy (up to the limit set by errors in floating point arithmetic). A data-set comprising the masses and isotopic abundances of individual elements is also provided. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-eco</a>	4.0.1	Implements the Bayesian and likelihood methods proposed in Imai, Lu, and Strauss (2008 <DOI: 10.1093/pan/mpm017>) and (2011 <DOI:10.18637/jss.v042.i05>) for ecological inference in 2 by 2 tables as well as the method of bounds introduced by Duncan and Davis (1953). The package fits both parametric and nonparametric models using either the Expectation-Maximization algorithms (for likelihood models) or the Markov chain Monte Carlo algorithms (for Bayesian models). For all models, the individual-level data can be directly incorporated into the estimation whenever such data are available. Along with in-sample and out-of-sample predictions, the package also provides a functionality which allows one to quantify the effect of data aggregation on parameter estimation and hypothesis testing under the parametric likelihood models. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-ecodist</a>	2.0.1	Dissimilarity-based analysis functions including ordination and Mantel test functions, intended for use with spatial and community data. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-ecohydmod</a>	1.0.0	Simulates the soil water balance (soil moisture, evapotranspiration, leakage and runoff), rainfall series by using the marked Poisson process and the vegetation growth through the normalized difference vegetation index (NDVI). Please see Souza et al. (2016) <doi:10.1002/hyp.10953>. / GPL-2	noarch
<a href="#">r-econdemand</a>	1.0	Tools for general properties including price, quantity, elasticity, convexity, marginal revenue and manifold of various economics demand systems including Linear, Translog, CES, LES and CREMR. / GNU General Public License version 2	noarch
<a href="#">r-ecoreg</a>	0.2.2	Estimating individual-level covariate-outcome associations using aggregate data (ecological inference) or a combination of aggregate and individual-level data (hierarchical related regression). / GPL-2	noarch
<a href="#">r-ecosimr</a>	0.1.0	Given a site by species interaction matrix, users can make inferences about species interactions by performance hypothesis comparing test statistics against a null distribution. The current package provides algorithms and metrics for niche-overlap, body size ratios and species co-occurrence. Users can also integrate their own algorithms and metrics within these frameworks or completely novel null models. Detailed explanations about the underlying assumptions of null model analysis in ecology can be found at <a href="http://ecosimr.org">http://ecosimr.org</a> . / MIT	noarch
<a href="#">r-ecosolver</a>	0.5.2	R interface to the Embedded Conic Solver (ECOS), an efficient and robust C library for convex problems. Conic and equality constraints can be specified in addition to integer and boolean variable constraints for mixed-integer problems. This R interface is inspired by the python interface and has similar calling conventions. / GPL-3	linux-64, osx-64, win-64

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Table 51 – continued from previous page

Name	Version	Summary/License	Platforms
r-ecotoxicology	1.0.1	Implementation of the EPA's Ecological Exposure Research Division (EERD) tools (discontinued in 1999) for Probit and Trimmed Spearman-Kärber Analysis. Probit and Spearman-Kärber methods from Finney's book Probit analysis a statistical treatment of the sigmoid response curve with options for most accurate results or identical results to the book. Probit and all the tables from Finney's book (code-generated, not copied) with the generating functions included. Control correction: Abbott, Schneider-Orelli, Henderson-Tilton, Sun-Shepard. Toxicity scales: Horsfall-Barratt, Archer, Gauhl-Stover, Fullerton-Olsen, etc. / GPL-3	noarch
r-ecotroph	1.6	EcoTroph is an approach and software for modelling marine and freshwater ecosystems. It is articulated entirely around trophic levels. EcoTroph's key displays are bivariate plots, with trophic levels as the abscissa, and biomass flows or related quantities as ordinates. Thus, trophic ecosystem functioning can be modelled as a continuous flow of biomass surging up the food web, from lower to higher trophic levels, due to predation and ontogenic processes. Such an approach, wherein species as such disappear, may be viewed as the ultimate stage in the use of the trophic level metric for ecosystem modelling, providing a simplified but potentially useful caricature of ecosystem functioning and impacts of fishing. This version contains catch trophic spectrum analysis (CTSA) function and corrected versions of the mf.diagnosis and create.ETmain functions. / GPL-3	noarch
r-ecovirtual	1.1	Computer simulations of classical ecological models as a learning resource. / GPL-2	noarch
r-ecp	3.1.1	Implements various procedures for finding multiple change-points. Two methods make use of dynamic programming and pruning, with no distributional assumptions other than the existence of certain absolute moments in one method. Hierarchical and exact search methods are included. All methods return the set of estimated change-points as well as other summary information. / GPL-2	linux-64, osx-64, win-64
r-ed50	0.1.1	Functions of five estimation method for ED50 (50 percent effective dose) are provided, and they are respectively Dixon-Mood method (1948) <doi:10.2307/2280071>, Choi's original turning point method (1990) <doi:10.2307/2531453> and it's modified version given by us, as well as logistic regression and isotonic regression. Besides, the package also supports comparison between two estimation results. / GPL-3	noarch
r-edci	1.1_3	Detection of edge points in images based on the difference of two asymmetric M-kernel estimators. Linear and circular regression clustering based on redescending M-estimators. Detection of linear edges in images. / GPL-2	linux-64, osx-64, win-64
r-esign	1.0_13	An implementation of maximum entropy sampling for spatial data is provided. An exact branch-and-bound algorithm as well as greedy and dual greedy heuristics are included. / GPL (>= 2.0)	linux-64, osx-64, win-64
r-edf	1.0.0	Import physiologic data stored in the European Data Format (EDF and EDF) into R. Both EDF and EDF files are supported. Discontinuous EDF files are not yet supported. / MIT	noarch

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Name	Version	Summary/License	Platforms
r-edfreader	1.2.1	Reads European Data Format files EDF and EDF, see < <a href="http://www.edfplus.info/">http://www.edfplus.info/</a> >, BioSemi Data Format files BDF, see < <a href="http://www.biosemi.com/faq/file_format.htm">http://www.biosemi.com/faq/file_format.htm</a> >, and BDF files, see < <a href="http://www.teuniz.net/edfbrowser/bdfplus%20format%20description.html">http://www.teuniz.net/edfbrowser/bdfplus%20format%20description.html</a> >. The files are read in two steps: first the header is read and then the signals (using the header object as a parameter). / GPL-3	noarch
r-edfun	0.2.0	Easily creating empirical distribution functions from data: 'dfun', 'pfun', 'qfun' and 'rfun'. / GPL-2   GPL-3	noarch
r-edgarwebr	1.0.0	A set of methods to access and parse live filing information from the U.S. Securities and Exchange Commission (SEC - < <a href="https://sec.gov">https://sec.gov</a> >) including company and fund filings along with all associated metadata. / MIT	noarch
r-edgebundler	0.1.4	Generates interactive circle plots with the nodes around the circumference and linkages between the connected nodes using hierarchical edge bundling via the D3 JavaScript library. See < <a href="http://d3js.org/">http://d3js.org/</a> > for more information on D3. / GPL-3	noarch
r-edgecorr	1.0	Facilitates basic spatial edge correction to point pattern data. / GPL-2	noarch
r-edison	1.1.1	Package EDISON (Estimation of Directed Interactions from Sequences Of Non-homogeneous gene expression) runs an MCMC simulation to reconstruct networks from time series data, using a non-homogeneous, time-varying dynamic Bayesian network. Networks segments and changepoints are inferred concurrently, and information sharing priors provide a reduction of the inference uncertainty. / GPL-2	noarch
r-edma	1.5_3	Perform dynamic model averaging with grid search as in Dengl and Halling (2012) <doi:10.1016/j.jfineco.2012.04.003> using parallel computing. / GPL-2	linux-64, osx-64, win-64
r-eegkitdata	1.0	Contains the example EEG data used in the package eegkit. Also contains code for easily creating larger EEG datasets from the EEG Database on the UCI Machine Learning Repository. / GPL-2	noarch
r-effectsrelbaseline	0.5	Functions to test for changes of a response to a stimulus grouping relative to a background or baseline response. / GPL-3	noarch
r-effectstars	1.9	Notice: The package EffectStars2 provides a more up-to-date implementation of effect stars! EffectStars provides functions to visualize regression models with categorical response as proposed by Tutz and Schaubberger (2013) <doi:10.1080/10618600.2012.701379>. The effects of the variables are plotted with star plots in order to allow for an optical impression of the fitted model. / GPL-2	noarch
r-effectstars2	0.1_2	Provides functions for the method of effect stars as proposed by Tutz and Schaubberger (2013) <doi:10.1080/10618600.2012.701379>. Effect stars can be used to visualize estimates of parameters corresponding to different groups, for example in multinomial logit models. Beside the main function 'effect-stars' there exist methods for special objects, for example for 'vglm' objects from the 'VGAM' package. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-effecttreat</a>	0.4	In personalized medicine, one wants to know, for a given patient and his or her outcome for a predictor (pre-treatment variable), how likely it is that a treatment will be more beneficial than an alternative treatment. This package allows for the quantification of the predictive causal association (i.e., the association between the predictor variable and the individual causal effect of the treatment) and related metrics. Part of this software has been developed using funding provided from the European Union's 7th Framework Programme for research, technological development and demonstration under Grant Agreement no 602552. / GPL-2	noarch
<a href="#">r-efficientmaxeigenpair</a>	0.1.4	An implementation for using efficient initials to compute the maximal eigenpair in R. It provides three algorithms to find the efficient initials under two cases: the tridiagonal matrix case and the general matrix case. Besides, it also provides two algorithms for the next to the maximal eigenpair under these two cases. / MIT	noarch
<a href="#">r-efflog</a>	1.0	Fitting a causal loglinear model and calculating the causal effects for a causal loglinear model with the multiplicative interaction or without the multiplicative interaction, obtaining the natural direct, indirect and the total effect. It calculates also the cell effect, which is a new interaction effect. / GPL-2	noarch
<a href="#">r-effsize</a>	0.7.6	A collection of functions to compute the standardized effect sizes for experiments (Cohen d, Hedges g, Cliff delta, Vargha-Delaney A). The computation algorithms have been optimized to allow efficient computation even with very large data sets. / GPL-2	noarch
<a href="#">r-egst</a>	1.0.0	Genetic predisposition for complex traits is often manifested through multiple tissues of interest at different time points in the development. As an example, the genetic predisposition for obesity could be manifested through inherited variants that control metabolism through regulation of genes expressed in the brain and/or through the control of fat storage in the adipose tissue by dysregulation of genes expressed in adipose tissue. We present a method eGST (eQTL-based genetic subtyper) that integrates tissue-specific eQTLs with GWAS data for a complex trait to probabilistically assign a tissue of interest to the phenotype of each individual in the study. eGST estimates the posterior probability that an individual's phenotype can be assigned to a tissue based on individual-level genotype data of tissue-specific eQTLs and marginal phenotype data in a genome-wide association study (GWAS) cohort. Under a Bayesian framework of mixture model, eGST employs a maximum a posteriori (MAP) expectation-maximization (EM) algorithm to estimate the tissue-specific posterior probability across individuals. Methodology is available from: A Majumdar, C Giambartolomei, N Cai, MK Freund, T Halder, T Schwarz, J Flint, B Pasaniuc (2019) <doi:10.1101/674226>. / GPL-3	noarch
<a href="#">r-eha</a>	2.6.0	Sampling of risk sets in Cox regression, selections in the Lexis diagram, bootstrapping. Parametric proportional hazards fitting with left truncation and right censoring for common families of distributions, piecewise constant hazards, and discrete models. Parametric accelerated failure time models for left truncated and right censored data. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-ehof</a>	1.8	Extended and enhanced hierarchical logistic regression models (called Huisman-Olff-Fresco in biology, see Huisman et al. 1993 JVS <doi:10.1111/jvs.12050>) models. Response curves along one-dimensional gradients including no response, monotone, plateau, unimodal and bimodal models. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-eiadata</a>	0.0.5	An R wrapper to allow the user to query categories and Series IDs, and import data, from the EIA's API < <a href="https://www.eia.gov/opendata/">https://www.eia.gov/opendata/</a> >. / GPL-2	noarch
<a href="#">r-eigeninv</a>	2011.8	Solves the “inverse eigenvalue problem” which is to generate a real-valued matrix that has the specified real eigenvalue spectrum. It can generate infinitely many dense matrices, symmetric or asymmetric, with the given set of eigenvalues. Algorithm can also generate stochastic and doubly stochastic matrices. / GPL-2	noarch
<a href="#">r-eigenmodel</a>	1.11	Estimation of the parameters in a model for symmetric relational data (e.g., the above-diagonal part of a square matrix), using a model-based eigenvalue decomposition and regression. Missing data is accommodated, and a posterior mean for missing data is calculated under the assumption that the data are missing at random. The marginal distribution of the relational data can be arbitrary, and is fit with an ordered probit specification. See Hoff (2007) <arXiv:0711.1146> for details on the model. / GPL-2	noarch
<a href="#">r-eigenprcomp</a>	1.0	Computes confidence intervals for the proportion explained by the first 1,2,k principal components, and computes confidence intervals for each eigenvalue. Both computations are done via nonparametric bootstrap. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<code>r-eikosograms</code>	0.1.1	An eikosogram (ancient Greek for probability picture) divides the unit square into rectangular regions whose areas, sides, and widths, represent various probabilities associated with the values of one or more categorical variates. Rectangle areas are joint probabilities, widths are always marginal (though possibly joint margins, i.e. marginal joint distributions of two or more variates), and heights of rectangles are always conditional probabilities. Eikosograms embed the rules of probability and are useful for introducing elementary probability theory, including axioms, marginal, conditional, and joint probabilities, and their relationships (including Bayes theorem as a completely trivial consequence). They are markedly superior to Venn diagrams for this purpose, especially in distinguishing probabilistic independence, mutually exclusive events, coincident events, and associations. They also are useful for identifying and understanding conditional independence structure. As data analysis tools, eikosograms display categorical data in a manner similar to Mosaic plots, especially when only two variates are involved (the only case in which they are essentially identical, though eikosograms purposely disallow spacing between rectangles). Unlike Mosaic plots, eikosograms do not alternate axes as each new categorical variate (beyond two) is introduced. Instead, only one categorical variate, designated the response, presents on the vertical axis and all others, designated the conditioning variates, appear on the horizontal. In this way, conditional probability appears only as height and marginal probabilities as widths. The eikosogram is therefore much better suited to a response model analysis (e.g. logistic model) than is a Mosaic plot. Mosaic plots are better suited to log-linear style modelling as in discrete multivariate analysis. Of course, eikosograms are also suited to discrete multivariate analysis with each variate in turn appearing as the response. This makes it better suited than Mosaic plots to discrete graphical models based on conditional independence graphs (i.e. Bayesian Networks or BayesNets). The eikosogram and its superiority to Venn diagrams in teaching probability is described in W.H. Cherry and R.W. Oldford (2003) < <a href="https://math.uwaterloo.ca/~rwoldfor/papers/eikosograms/paper.pdf">https://math.uwaterloo.ca/~rwoldfor/papers/eikosograms/paper.pdf</a> >, its value in exploring conditional independence structure and relation to graphical and log-linear models is described in R.W. Oldford (2003) < <a href="https://math.uwaterloo.ca/~rwoldfor/papers/eikosograms/independence/paper.pdf">https://math.uwaterloo.ca/~rwoldfor/papers/eikosograms/independence/paper.pdf</a> >, and a number of problems, puzzles, and paradoxes that are easily explained with eikosograms are given in R.W. Oldford (2003) < <a href="https://math.uwaterloo.ca/~rwoldfor/papers/eikosograms/examples/paper.pdf">https://math.uwaterloo.ca/~rwoldfor/papers/eikosograms/examples/paper.pdf</a> >. / GPL-3	noarch
<code>r-eila</code>	0.1_2	Implementation of Efficient Inference of Local Ancestry using fused quantile regression and k-means classifier / GPL-2	noarch
<code>r-eipartialid</code>	0.1.2	Estimate district-level bounds for 2x2 ecological inference based on the approach described in the forthcoming article Jiang et al. (2019), Ecological Regression with Partial Identification, Political Analysis. Interval data regression is used to bound the nonidentified regression parameter in a linear contextual effects model, from which district-level bounds are derived. The approach here can be useful as a baseline of comparison for future work on ecological inference. / MIT	noarch

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Name	Version	Summary/License	Platforms
r-eive	2.3	Performs a compact genetic algorithm search to reduce errors-in-variables bias in linear regression. The algorithm estimates the regression parameters with lower biases and higher variances but mean-square errors (MSEs) are reduced. / GPL-3	linux-64, osx-64, win-64
r-eiwild	0.6.7	This package allows to use the hybrid Multinomial-Dirichlet-Model of Ecological Inference for estimating inner Cells of RxC-Tables. This was already implemented in the eiPack-package. eiwild-package now has the possibility to use individual level data to support the aggregate level data and using different Hyperprior-Distributions. / GPL-3	linux-64, osx-64, win-64
r-ekmcmc	0.1.0	Functions for estimating catalytic constant and Michaelis-Menten constant for enzyme kinetics model using Metropolis-Hasting algorithm within Gibbs sampler based on the Bayesian framework. Additionally, a function to create plot to identify the goodness-of-fit is included. / GPL-3	noarch
r-el	1.0	Empirical likelihood (EL) inference for two-sample problems. The following statistics are included: the difference of two-sample means, smooth Huber estimators, quantile (qdiff) and cumulative distribution functions (ddiff), probability-probability (P-P) and quantile-quantile (Q-Q) plots as well as receiver operating characteristic (ROC) curves. / GPL-2	linux-64, osx-64
r-el2surv	1.1	Functions for computing critical values and implementing the one-sided/two-sided EL tests. / GPL-2	noarch
r-elasth	0.3.1	O pacote disponibiliza funções para estimar modelos de componentes não observados e determinar intervenções automaticamente. Com especial atenção para a replicação dos modelos utilizados na metodologia de calculo do resultado estrutural da SPE/MF. The package provides simple ways to estimates general unobserved components models and automatically detects interventions. It is specially useful to replicate Brazilian Ministry of Finance methodology to estimate income-output gap elasticities. / GPL-3	noarch
r-elasticnet	1.1.1	Provides functions for fitting the entire solution path of the Elastic-Net and also provides functions for estimating sparse Principal Components. The Lasso solution paths can be computed by the same function. First version: 2005-10. / GPL-2	noarch
r-elec	0.1.2	This is a bizarre collection of functions written to do various sorts of statistical election audits. There are also functions to generate simulated voting data, and simulated truth so as to do simulations to check characteristics of these methods. / GPL-2	noarch
r-elec.strat	0.1.1	An extension of the elec package intended for use on election audits using stratified random samples. Includes functions to obtain conservative and exact p-values, and functions that give sample sizes that may make election audits more efficient. / GPL-2	linux-64, osx-64, win-64
r-elections	1.0	This includes a dataset on the outcomes of the USA presidential elections since 1920, and various predictors, as used in < <a href="http://vanderwalresearch.com/blog/15-elections">http://vanderwalresearch.com/blog/15-elections</a> >. / GPL-2	noarch
r-electivity	1.0.2	Provides all electivity algorithms (including Vanderploeg and Scavia electivity) that were examined in Lechowicz (1982) <doi:10.1007/BF00349007>, plus the example data that were provided for moth resource utilisation. / MIT	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-elemstatlearn</a>	2015.0361	When reading the book above mentioned, in the documentation referred to as ‘the book’. / GPL-2	noarch
<a href="#">r-elexr</a>	1.0	Provides R access to election results data. Wraps <a href="https://github.com/newsdev/elex/">elex (https://github.com/newsdev/elex/)</a> , a Python package and command line tool for fetching and parsing Associated Press election results. / MIT	noarch
<a href="#">r-elhmc</a>	1.1.0	A tool to draw samples from a Empirical Likelihood Bayesian posterior of parameters using Hamiltonian Monte Carlo. / GPL-2	noarch
<a href="#">r-elitism</a>	1.0.4	Recently many new p-value based multiple test procedures have been proposed, and these new methods are more powerful than the widely used Hochberg procedure. These procedures strongly control the familywise error rate (FWER). This is a comprehensive collection of p-value based FWER-control stepwise multiple test procedures, including six procedure families and thirty multiple test procedures. In this collection, the conservative Hochberg procedure, linear time Hommel procedures, asymptotic Rom procedure, Gou-Tamhane-Xi-Rom procedures, and Quick procedures are all developed in recent five years since 2014. The package name elitism is an acronym of equipment for logarithmic and linear time stepwise multiple hypothesis testing. Version 1.0.0 was released on June 26, 2019. See Gou, J., and Zhang, F. (2020). Quick multiple test procedures and p-value adjustments. Technical report. / GPL-3	noarch
<a href="#">r-elliptot</a>	1.2.0	Correlation chart of two set (x and y) of data. Using Quantiles. Visualize the effect of factor. / MIT (FOSS)	noarch
<a href="#">r-ellipse</a>	0.4.1	Contains various routines for drawing ellipses and ellipse-like confidence regions, implementing the plots described in Murdoch and Chow (1996), A graphical display of large correlation matrices, The American Statistician 50, 178-180. There are also routines implementing the profile plots described in Bates and Watts (1988), Nonlinear Regression Analysis and its Applications. / GPL-2	noarch
<a href="#">r-ellipsis</a>	0.1.0	In S3 generics, it’s useful to take ... so that methods can have additional argument. But this flexibility comes at a cost: misspelled arguments will be silently ignored. The ellipsis packages is an experiment that allows a generic to warn if any arguments passed in ... are not used. / GPL-3	linux-64, osx-64, win-32, win-64
<a href="#">r-elliptic</a>	1.4_0	A suite of elliptic and related functions including Weierstrass and Jacobi forms. Also includes various tools for manipulating and visualizing complex functions. / GPL-2	noarch
<a href="#">r-elmr</a>	1.0	Training and prediction functions are provided for the Extreme Learning Machine algorithm (ELM). The ELM use a Single Hidden Layer Feedforward Neural Network (SLFN) with random generated weights and no gradient-based backpropagation. The training time is very short and the online version allows to update the model using small chunk of the training set at each iteration. The only parameter to tune is the hidden layer size and the learning function. / GPL-2   GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-elms</a>	1.0.0	An implementation of the algorithm described in Efficient Large- Scale Internet Media Selection Optimization for Online Display Advertising by Paulson, Luo, and James (Journal of Marketing Research 2018; see URL below for journal text/citation and < <a href="http://www-bcf.usc.edu/~gareth/research/ELMSO.pdf">http://www-bcf.usc.edu/~gareth/research/ELMSO.pdf</a> > for a full-text version of the paper). The algorithm here is designed to allocate budget across a set of online advertising opportunities using a coordinate-descent approach, but it can be used in any resource-allocation problem with a matrix of visitation (in the case of the paper, website page- views) and channels (in the paper, websites). The package contains allocation functions both in the presence of bidding, when allocation is dependent on channel-specific cost curves, and when advertising costs are fixed at each channel. / GPL-3	noarch
<a href="#">r-elo</a>	2.0.0	A flexible framework for calculating Elo ratings and resulting rankings of any two-team-per-matchup system (chess, sports leagues, ‘Go’, etc.). This implementation is capable of evaluating a variety of matchups, Elo rating updates, and win probabilities, all based on the basic Elo rating system. It also includes methods to benchmark performance, including logistic regression and Markov chain models. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-elm</a>	1.2.4	Implements a Markov Chain Monte Carlo algorithm to approximate exact conditional inference for logistic regression models. Exact conditional inference is based on the distribution of the sufficient statistics for the parameters of interest given the sufficient statistics for the remaining nuisance parameters. Using model formula notation, users specify a logistic model and model terms of interest for exact inference. See Zamar et al. (2007) <doi:10.18637/jss.v021.i03> for more details. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-elyp</a>	0.7_5	Empirical likelihood ratio tests for the Yang and Prentice (short/long term hazards ratio) models. Empirical likelihood tests within a Cox model, for parameters defined via both baseline hazard function and regression parameters. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-embc</a>	2.0.2	Unsupervised, multivariate, binary clustering for meaningful annotation of data, taking into account the uncertainty in the data. A specific constructor for trajectory analysis in movement ecology yields behavioural annotation of trajectories based on estimated local measures of velocity and turning angle, eventually with solar position covariate as a daytime indicator, (Expectation-Maximization Binary Clustering for Behavioural Annotation). / GPL-3	linux-64, osx-64, win-64
<a href="#">r-embedsom</a>	1.9.1	Provides a smooth mapping of multidimensional points into low-dimensional space defined by a self-organizing map. Designed to work with ‘Flow-SOM’ and flow-cytometry use-cases. See Kratochvil et al. (2019) <doi:10.1101/496869>. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-emc</a>	1.3	random walk Metropolis, Metropolis Hasting, parallel tempering, evolutionary Monte Carlo, temperature ladder construction and placement / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-emcdf	0.1.2	Computes and visualizes empirical joint distribution of multivariate data with optimized algorithms and multi-thread computation. There is a faster algorithm using dynamic programming to compute the whole empirical joint distribution of a bivariate data. There are optimized algorithms for computing empirical joint CDF function values for other multivariate data. Visualization is focused on bivariate data. Levelplots and wireframes are included. / GPL-3	linux-64, osx-64, win-64
r-emcluster	0.2.1	EM algorithms and several efficient initialization methods for model-based clustering of finite mixture Gaussian distribution with unstructured dispersion in both of unsupervised and semi-supervised learning. / Mozilla Public License 2.0	linux-64, osx-64, win-64
r-emdbook	1.3.1	Auxiliary functions and data sets for Ecological Models and Data, a book presenting maximum likelihood estimation and related topics for ecologists (ISBN 978-0-691-12522-0). / GPL-3	noarch
r-emdist	0.3.1	Package providing calculation of Earth Mover's Distance (EMD). / MIT	linux-64, osx-64, win-64
r-emg	1.0.7	Provides basic distribution functions for a mixture model of a Gaussian and exponential distribution. / GPL-2	noarch
r-emhawkes	0.9.0	Simulate and fitting exponential multivariate Hawkes model. This package simulates a multivariate Hawkes model, introduced by Hawkes (1971) <doi:10.1093/biomet/58.1.83>, with an exponential kernel and fits the parameters from the data. Models with the constant parameters, as well as complex dependent structures, can also be simulated and estimated. The estimation is based on the maximum likelihood method, introduced by introduced by Ozaki (1979) <doi:10.1007/BF02480272>, with 'maxLik' package. / GPL-2	noarch
r-emistatr	1.2.2.0	Provides a fast and parallelised calculator to estimate combined wastewater emissions. It supports the planning and design of urban drainage systems, without the requirement of extensive simulation tools. The 'EmiStatR' package implements modular R methods. This enables to add new functionalities through the R framework. / GPL-3	noarch
r-emme2	0.9	This package includes functions to read and write to an EMME/2 databank / GPL-3	noarch
r-emmeans	1.3.4	Obtain estimated marginal means (EMMs) for many linear, generalized linear, and mixed models. Compute contrasts or linear functions of EMMs, trends, and comparisons of slopes. Plots and compact letter displays. Least-squares means are discussed, and the term estimated marginal means is suggested, in Searle, Speed, and Milliken (1980) Population marginal means in the linear model: An alternative to least squares means, The American Statistician 34(4), 216-221 <doi:10.1080/00031305.1980.10483031>. / GPL-2   GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-emmixmapfa</a>	2.0.7	We provide functions to fit finite mixtures of multivariate normal or t-distributions to data with various factor analytic structures adopted for the covariance/scale matrices. The factor analytic structures available include mixtures of factor analyzers and mixtures of common factor analyzers. The latter approach is so termed because the matrix of factor loadings is common to components before the component-specific rotation of the component factors to make them white noise. Note that the component-factor loadings are not common after this rotation. Maximum likelihood estimators of model parameters are obtained via the Expectation-Maximization algorithm. See descriptions of the algorithms used in McLachlan GJ, Peel D (2000) <doi:10.1002/0471721182.ch8> McLachlan GJ, Peel D (2000) <ISBN:1-55860-707-2> McLachlan GJ, Peel D, Bean RW (2003) <doi:10.1016/S0167-9473(02)00183-4> McLachlan GJ, Bean RW, Ben-Tovim Jones L (2007) <doi:10.1016/j.csda.2006.09.015> Baek J, McLachlan GJ, Flack LK (2010) <doi:10.1109/TPAMI.2009.149> Baek J, McLachlan GJ (2011) <doi:10.1093/bioinformatics/btr112> McLachlan GJ, Baek J, Rathnayake SI (2011) <doi:10.1002/9781119995678.ch9>. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-emmixskew</a>	1.0.3	EM algorithm for Fitting Mixture of Multivariate Skew Normal and Skew t Distributions. An implementation of the algorithm described in Wang, Ng, and McLachlan (2009) <doi:10.1109/DICTA.2009.88>. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-emmli</a>	0.0.3	Fit models of modularity to morphological landmarks. Perform model selection on results. Fit models with a single within-module correlation or with separate within-module correlations fitted to each module. / MIT	noarch
<a href="#">r-emmreml</a>	3.1	The main functions are ‘emmreml’, and ‘emmremlMultiKernel’. ‘emmreml’ solves a mixed model with known covariance structure using the ‘EMMA’ algorithm. ‘emmremlMultiKernel’ is a wrapper for ‘emmreml’ to handle multiple random components with known covariance structures. The function ‘emmremlMultivariate’ solves a multivariate gaussian mixed model with known covariance structure using the ‘ECM’ algorithm. / GPL-2	noarch
<a href="#">r-emoa</a>	0.5.0	Collection of building blocks for the design and analysis of evolutionary multiobjective optimization algorithms. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-emon</a>	1.3.2	Statistical tools for environmental and ecological surveys. Simulation-based power and precision analysis; detection probabilities from different survey designs; visual fast count estimation. / GPL-3	noarch
<a href="#">r-emov</a>	0.1.1	Fixation and saccade detection in eye movement recordings. This package implements a dispersion-based algorithm (I-DT) proposed by Salvucci & Goldberg (2000) which detects fixation duration and position. / GPL-3	noarch
<a href="#">r-emp</a>	2.0.5	Functions for estimating EMP (Expected Maximum Profit Measure) in Credit Risk Scoring and Customer Churn Prediction, according to Verbraken et al (2013, 2014) <DOI:10.1109/TKDE.2012.50>, <DOI:10.1016/j.ejor.2014.04.001>. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-empichar</a>	1.0.0	Evaluates the empirical characteristic function of univariate and multivariate samples. This package uses 'RcppArmadillo' for fast evaluation. It is also possible to export the code to be used in other packages at 'C' level. / MIT	linux-64, osx-64, win-64
<a href="#">r-emplik</a>	1.0_4	Empirical likelihood ratio tests for means/quantiles/hazards from possibly censored and/or truncated data. Now does regression too. This version contains some C code. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-emplik2</a>	1.21	Calculates the p-value for a mean-type hypothesis (or multiple mean-type hypotheses) based on two samples with censored data. / GPL-2	noarch
<a href="#">r-ems</a>	1.2.7	Collection of functions for data analysis and editing of clinical and epidemiological data. Most of them are related to benchmark with prediction models. / GPL-2	noarch
<a href="#">r-emsaov</a>	2.3	Provides the analysis of variance table including the expected mean squares (EMS) for various types of experimental design. When some variables are random effects or we use special experimental design such as nested design, repeated-measures design, or split-plot design, it is not easy to find the appropriate test, especially denominator for F-statistic which depends on EMS. / GPL-2	noarch
<a href="#">r-emsnm</a>	1.0	It provides a method based on EM algorithm to estimate the parameter of a mixture model, Sigmoid-Normal Model, where the samples come from several normal distributions (also call them subgroups) whose mean is determined by co-variable Z and coefficient alpha while the variance are homogeneous. Meanwhile, the subgroup each item belongs to is determined by co-variables X and coefficient eta through Sigmoid link function which is the extension of Logistic Link function. It uses bootstrap to estimate the standard error of parameters. When sample is indeed separable, removing estimation with abnormal sigma, the estimation of alpha is quite well. I used this method to explore the subgroup structure of HIV patients and it can be used in other domains where exists subgroup structure. / GPL-2	noarch
<a href="#">r-emt</a>	1.1	The package provides functions to carry out a Goodness-of-fit test for discrete multivariate data. It is tested if a given observation is likely to have occurred under the assumption of an ab-initio model. A p-value can be calculated using different distance measures between observed and expected frequencies. A Monte Carlo method is provided to make the package capable of solving high-dimensional problems. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-emulator</a>	1.2_20	Allows one to estimate the output of a computer program, as a function of the input parameters, without actually running it. The computer program is assumed to be a Gaussian process, whose parameters are estimated using Bayesian techniques that give a PDF of expected program output. This PDF is conditional on a training set of runs, each consisting of a point in parameter space and the model output at that point. The emphasis is on complex codes that take weeks or months to run, and that have a large number of undetermined input parameters; many climate prediction models fall into this class. The emulator essentially determines Bayesian posterior estimates of the PDF of the output of a model, conditioned on results from previous runs and a user-specified prior linear model. A vignette is provided and the help pages include examples. / GPL-3	noarch
<a href="#">r-emvs</a>	1.0	An efficient expectation-maximization algorithm for fitting Bayesian spike-and-slab regularization paths for linear regression. Rockova and George (2014) <doi:10.1080/01621459.2013.869223>. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-enc</a>	0.2.1	Implements an S3 class for storing ‘UTF-8’ strings, based on regular character vectors. Also contains routines to portably read and write ‘UTF-8’ encoded text files, to convert all strings in an object to ‘UTF-8’, and to create character vectors with various encodings. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-encode</a>	0.3.6	Interconverts between ordered lists and compact string notation. Useful for capturing code lists, and pair-wise codes and decodes, for text storage. Analogous to factor levels and labels. Generics encode() and decode() perform interconversion, while codes() and decodes() extract components of an encoding. The function encoded() checks whether something is interpretable as an encoding. If a vector has an encoded ‘guide’ attribute, as_factor() uses it to coerce to factor. / GPL-3	noarch
<a href="#">r-endogenous</a>	1.0	Likelihood-based approaches to estimate linear regression parameters and treatment effects in the presence of endogeneity. Specifically, this package includes James Heckman’s classical simultaneous equation models-the sample selection model for outcome selection bias and hybrid model with structural shift for endogenous treatment. For more information, see the seminal paper of Heckman (1978) <DOI:10.3386/w0177> in which the details of these models are provided. This package accommodates repeated measures on subjects with a working independence approach. The hybrid model further accommodates treatment effect modification. / GPL-2	noarch
<a href="#">r-endogmnp</a>	0.2_1	endogMNP is an R package that fits a Bayesian multinomial probit model with endogenous selection, which is sometimes called an endogenous switching model. This can be used to model discrete choice data when respondents select themselves into one of several groups. This package is based on the MNP package by Kosuke Imai and David A. van Dyk. This package modifies their code. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-endorse</a>	1.6.1	Fit the hierarchical and non-hierarchical Bayesian measurement models proposed by Bullock, Imai, and Shapiro (2011) <DOI:10.1093/pan/mpr031> to analyze endorsement experiments. Endorsement experiments are a survey methodology for eliciting truthful responses to sensitive questions. This methodology is helpful when measuring support for socially sensitive political actors such as militant groups. The model is fitted with a Markov chain Monte Carlo algorithm and produces the output containing draws from the posterior distribution. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-energy</a>	1.7_6	E-statistics (energy) tests and statistics for multivariate and univariate inference, including distance correlation, one-sample, two-sample, and multi-sample tests for comparing multivariate distributions, are implemented. Measuring and testing multivariate independence based on distance correlation, partial distance correlation, multivariate goodness-of-fit tests, k-groups and hierarchical clustering based on energy distance, testing for multivariate normality, distance components (disco) for non-parametric analysis of structured data, and other energy statistics/methods are implemented. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-energyonlinecpm</a>	1.0	Provides a function for distribution free control chart based on the change point model, for multivariate statistical process control. The main constituent of the chart is the energy test that focuses on the discrepancy between empirical characteristic functions of two random vectors. This new control chart highlights in three aspects. Firstly, it is distribution free, requiring no knowledge of the random processes. Secondly, this control chart can monitor mean and variance simultaneously. Thirdly it is devised for multivariate time series which is more practical in real data application. Fourthly, it is designed for online detection (Phase II), which is central for real time surveillance of stream data. For more information please refer to O. Okhrin and Y.F. Xu (2017) < <a href="https://github.com/YafeiXu/working_paper/raw/master/CPM102.pdf">https://github.com/YafeiXu/working_paper/raw/master/CPM102.pdf</a> >. / GPL-3	noarch
<a href="#">r-english</a>	1.2_3	Allow numbers to be presented in an English language version, one, two, three, ... Ordinals are also available, first, second, third, ... / GPL-2	noarch
<a href="#">r-engrext</a>	0.1_8	Datasets from Nelson, Coffin and Copeland Introductory Statistics for Engineering Experimentation (Elsevier, 2003) with sample code. / GPL-2	noarch
<a href="#">r-enrichr</a>	2.1	Provides an R interface to all ‘Enrichr’ databases. ‘Enrichr’ is a web-based tool for analysing gene sets and returns any enrichment of common annotated biological features. Quoting from their website ‘Enrichment analysis is a computational method for inferring knowledge about an input gene set by comparing it to annotated gene sets representing prior biological knowledge.’ See (< <a href="http://amp.pharm.mssm.edu/Enrichr/">http://amp.pharm.mssm.edu/Enrichr/</a> >) for further details. / GPL-2	noarch
<a href="#">r-enrichvs</a>	0.0.5	These programs are used for calculating enrichment factors, drawing enrichment curves to evaluate virtual screening approaches. / BSD	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-enrichwith</a>	0.2	Provides the <code>enrich</code> method to enrich list-like R objects with new, relevant components. The current version has methods for enriching objects of class ‘family’, ‘link-glm’, ‘lm’, ‘glm’ and ‘betareg’. The resulting objects preserve their class, so all methods associated with them still apply. The package also provides the ‘ <code>enriched_glm</code> ’ function that has the same interface as ‘ <code>glm</code> ’ but results in objects of class ‘ <code>enriched_glm</code> ’. In addition to the usual components in a <i>glm</i> object, ‘ <code>enriched_glm</code> ’ objects carry an object-specific <code>simulate</code> method and functions to compute the scores, the observed and expected information matrix, the first-order bias, as well as model densities, probabilities, and quantiles at arbitrary parameter values. The package can also be used to produce customizable source code templates for the structured implementation of methods to compute new components and enrich arbitrary objects. / GPL-2   GPL-3	noarch
<a href="#">r-ensemblebma</a>	5.1.5	Bayesian Model Averaging to create probabilistic forecasts from ensemble forecasts and weather observations. / GPL-2	noarch
<a href="#">r-ensemblepp</a>	1.0_0	Data sets for the chapter Ensemble Postprocessing with R of the book Stephane Vannitsem, Daniel S. Wilks, and Jakob W. Messner (2018) Statistical Post-processing of Ensemble Forecasts, Elsevier, 362pp. These data sets contain temperature and precipitation ensemble weather forecasts and corresponding observations at Innsbruck/Austria. Additionally, a demo with the full code of the book chapter is provided. / GPL-2   GPL-3	noarch
<a href="#">r-ensurer</a>	1.1	Add simple runtime contracts to R values. These ensure that values fulfil certain conditions and will raise appropriate errors if they do not. / MIT	noarch
<a href="#">r-entropy</a>	1.2.1	This package implements various estimators of entropy, such as the shrinkage estimator by Hausser and Strimmer, the maximum likelihood and the Millow-Madow estimator, various Bayesian estimators, and the Chao-Shen estimator. It also offers an R interface to the NSB estimator. Furthermore, it provides functions for estimating Kullback-Leibler divergence, chi-squared, mutual information, and chi-squared statistic of independence. In addition there are functions for discretizing continuous random variables. / GPL-3	noarch
<a href="#">r-entropyestimation</a>	1.2	Contains methods for the estimation of Shannon’s entropy, variants of Renyi’s entropy, mutual information, Kullback-Leibler divergence, and generalized Simpson’s indices. The estimators used have a bias that decays exponentially fast. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-entropyexplorer</a>	1.1	Rows of two matrices are compared for Shannon entropy, coefficient of variation, and expression. P-values can be requested for all metrics. / GPL-3	noarch
<a href="#">r-envcpt</a>	1.1.1	Tools for automatic model selection and diagnostics for Climate and Environmental data. In particular the <code>envcpt()</code> function does automatic model selection between a variety of trend, changepoint and autocorrelation models. The <code>envcpt()</code> function should be your first port of call. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-envdocument</a>	2.4.1	Prints out information about the R working environment (system, R version, loaded and attached packages and versions) from a single function <code>env_doc()</code> . Optionally adds information on git repository, tags, commits and remotes (if available). / GPL (>= 3.0)	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-envipat</a>	2.4	Fast and very memory-efficient calculation of isotope patterns, subsequent convolution to theoretical envelopes (profiles) plus valley detection and centroidization or intensoid calculation. Batch processing, resolution interpolation, wrapper, adduct calculations and molecular formula parsing. Loos, M., Gerber, C., Corona, F., Hollender, J., Singer, H. (2015) <doi:10.1021/acs.analchem.5b00941>. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-envirostat</a>	0.4.2	Functions and datasets to support the book by Nhu D Le and James V Zidek, Springer (2006). / AGPL-3	linux-64, osx-64, win-64
<a href="#">r-envnames</a>	0.4.0	Set of functions to keep track of user-defined environment names (which cannot be retrieved with the built-in function environmentName()). The package also provides functionality to search for objects in environments, deal with function calling chains, and retrieve an object's memory address. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-epandist</a>	1.1.1	Analyzing censored variables usually requires the use of optimization algorithms. This package provides an alternative algebraic approach to the task of determining the expected value of a random censored variable with a known censoring point. Likewise this approach allows for the determination of the censoring point if the expected value is known. These results are derived under the assumption that the variable follows an Epanechnikov kernel distribution with known mean and range prior to censoring. Statistical functions related to the uncensored Epanechnikov distribution are also provided by this package. / LGPL-3	noarch
<a href="#">r-epanet2toolkit</a>	0.3.2	Enables simulation of water piping networks using 'EPANET'. The package provides functions from the 'EPANET' programmer's toolkit as R functions so that basic or customized simulations can be carried out from R. The package uses 'EPANET' version 2.1 from Open Water Analytics < <a href="https://github.com/OpenWaterAnalytics/EPANET/releases/tag/v2.1">https://github.com/OpenWaterAnalytics/EPANET/releases/tag/v2.1</a> >. / MIT	linux-64, osx-64, win-64
<a href="#">r-epanetreader</a>	0.7.3	Reads water network simulation data in 'Epanet' text-based '.inp' and '.rpt' formats into R. Also reads results from 'Epanet-msx'. Provides basic summary information and plots. The README file has a quick introduction. See < <a href="http://www2.epa.gov/water-research/epanet">http://www2.epa.gov/water-research/epanet</a> > for more information on the Epanet software for modeling hydraulic and water quality behavior of water piping systems. / MIT	noarch
<a href="#">r-epibasix</a>	1.5	Contains elementary tools for analysis of common epidemiological problems, ranging from sample size estimation, through 2x2 contingency table analysis and basic measures of agreement (kappa, sensitivity/specificity). Appropriate print and summary statements are also written to facilitate interpretation wherever possible. Source code is commented throughout to facilitate modification. The target audience includes advanced undergraduate and graduate students in epidemiology or biostatistics courses, and clinical researchers. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-epicontacttrace	0.12.0	Routines for epidemiological contact tracing and visualisation of network of contacts. / EUPL	linux-64, osx-64, win-64
r-epidisplay	3.5.0	Package for data exploration and result presentation. Full ‘epicalc’ package with data management functions is available at ‘< <a href="http://medipe.psu.ac.th/epicalc">http://medipe.psu.ac.th/epicalc</a> >’. / GPL-2	noarch
r-epiilm	1.4.2	Provides tools for simulating from discrete-time individual level models for infectious disease data analysis. This epidemic model class contains spatial and contact-network based models with two disease types: Susceptible-Infectious (SI) and Susceptible-Infectious-Removed (SIR). / GPL-2	linux-64, osx-64, win-64
r-epiilmct	1.1.3	Provides tools for simulating from continuous-time individual level models of disease transmission, and carrying out infectious disease data analyses with the same models. The epidemic models considered are distance-based and/or contact network-based models within Susceptible-Infectious-Removed (SIR) or Susceptible-Infectious-Notified-Removed (SINR) compartmental frameworks. / GPL-2	linux-64, osx-64, win-64
r-epimdr	0.6_4	Functions, data sets and shiny apps for Epidemics: Models and Data in R by Ottar N. Bjornstad (ISBN 978-3-319-97487-3) < <a href="https://www.springer.com/gp/book/9783319974866">https://www.springer.com/gp/book/9783319974866</a> >. The package contains functions to study the S(E)IR model, spatial and age-structured SIR models; time-series SIR and chain-binomial stochastic models; catalytic disease models; coupled map lattice models of spatial transmission and network models for social spread of infection. The package is also an advanced quantitative companion to the coursera Epidemics Massive Online Open Course < <a href="https://www.coursera.org/learn/epidemics">https://www.coursera.org/learn/epidemics</a> >. / GPL-3	noarch
r-epir	1.0_4	Tools for the analysis of epidemiological data. Contains functions for directly and indirectly adjusting measures of disease frequency, quantifying measures of association on the basis of single or multiple strata of count data presented in a contingency table, and computing confidence intervals around incidence risk and incidence rate estimates. Miscellaneous functions for use in meta-analysis, diagnostic test interpretation, and sample size calculations. / GPL-2	noarch
r-episcan	0.0.1	Searching genomic interactions with linear/logistic regression in a high-dimensional dataset is a time-consuming task. This package provides some efficient ways to scan epistasis in genome-wide interaction studies (GWIS). Both case-control status (binary outcome) and quantitative phenotype (continuous outcome) are supported (the main references: 1. Kam-Thong, T., D. Czamara, K. Tsuda, K. Borgwardt, C. M. Lewis, A. Erhardt-Lehmann, B. Hemmer, et al. (2011). <doi:10.1038/ejhg.2010.196>. 2. Kam-Thong, T., B. Pütz, N. Karbalai, B. Müller-Myhsok, and K. Borgwardt. (2011). <doi:10.1093/bioinformatics/btr218>.) / GPL-2	noarch
r-epistemicgametheory	0.1.2	Constructing an epistemic model such that, for every player i and for every choice c(i) which is optimal, there is one type that expresses common belief in rationality. / GPL-3	noarch
r-epitools	0.5_1	Tools for training and practicing epidemiologists including methods for two-way and multi-way contingency tables. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-eplot	1.0	Aim: Adjust the graphical parameters to create nicer longitudinal series plots. The default set of graphical parameters is very general, and can be improved upon when we are interested in plotting data points observed over time. Functions facilitate plotting those kind of series, univariate plots, bivariate plots (with vertical axis on both left and right hand sides), multivariate plots and plots which allow to examine whether a new observation is ‘unusual’ via construction and visualization of prediction intervals around it. / GPL-2	noarch
r-eplot	0.1.2	Evaluate a function over a data frame of expressions. / GPL-3	noarch
r-epsiwal	0.1.0	Implements the conditional estimation procedure of Lee, Sun, Sun and Taylor (2016) <doi:10.1214/15-AOS1371>. This procedure allows hypothesis testing on the mean of a normal random vector subject to linear constraints. / LGPL-3	noarch
r-epxtor	0.3_0	Import data from ‘Epidata’ XML files ‘.epx’ and convert it to R data structures. / GPL-3	noarch
r-eq5d	0.2.0	EQ-5D is a popular health related quality of life instrument used in the clinical and economic evaluation of health care. Developed by the EuroQol group < <a href="https://www.euroqol.org">https://www.euroqol.org</a> >, the instrument consists of two components: health state description and evaluation. For the description component a subject self-rates their health in terms of five dimensions; mobility, self-care, usual activities, pain/discomfort, and anxiety/depression using either a three-level (EQ-5D-3L, < <a href="https://www.euroqol.org/eq-5d-instruments/eq-5d-3l-about">https://www.euroqol.org/eq-5d-instruments/eq-5d-3l-about</a> >) or a five-level (EQ-5D-5L, < <a href="https://www.euroqol.org/eq-5d-instruments/eq-5d-5l-about">https://www.euroqol.org/eq-5d-instruments/eq-5d-5l-about</a> >) scale. Frequently the scores on these five dimensions are converted to a single utility index using country specific value sets, which can be used in the clinical and economic evaluation of health care as well as in population health surveys. The eq5d package provides methods to calculate index scores from a subject’s dimension scores. 19 TTO and 9 VAS EQ-5D-3L value sets including those for countries in Szende et al (2007) <doi:10.1007/1-4020-5511-0> and Szende et al (2014) <doi:10.1007/978-94-007-7596-1>, 15 EQ-5D-5L EQ-VT value sets from the EuroQol website, and the EQ-5D-5L crosswalk value sets developed by van Hout et al. (2012) <doi:10.1016/j.jval.2012.02.008> are included. Additionally, a shiny web tool is included to enable the calculation and visualisation of EQ-5D index values via a web browser using EQ-5D dimension scores stored in CSV or Excel files. / MIT	noarch
r-eqs2lavaan	3.0	Transitioning from EQS to R for structural equation modeling (SEM) is made easier with a set of functions to convert .out files into R code. The EQS output can be converted into lavaan syntax and run in the R environment. Other functions parse descriptive statistics and the covariance matrix from an EQS .out file. A heat map plot of a covariance matrix is also included. / GPL-2	noarch
r-equalcovs	1.0	Tests the equality of two covariance matrices, used in paper Two sample tests for high dimensional covariance matrices. Li and Chen (2012) <arXiv:1206.0917>. / GPL-2	linux-64, osx-64, win-64
r-equalden.hd	1.2	The equality of a large number k of densities is tested by measuring the L2 distance between the corresponding kernel density estimators and the one based on the pooled sample. The test even works for sample sizes as small as 2. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-equaltestmi</a>	0.1.0	Functions for examining measurement invariance via equivalence testing along with adjusted RMSEA (root mean square error of approximation; Steiger & Lind, 1980) cutoff values. In particular, a projection-based method is implemented to test the equality of latent factor means across groups without assuming the equality of intercepts. / GPL-3	noarch
<a href="#">r-equate</a>	2.0.7	Contains methods for observed-score linking and equating under the single-group, equivalent-groups, and nonequivalent-groups with anchor test(s) designs. Equating types include identity, mean, linear, general linear, equipercentile, circle-arc, and composites of these. Equating methods include synthetic, nominal weights, Tucker, Levine observed score, Levine true score, Braun/Holland, frequency estimation, and chained equating. Plotting and summary methods, and methods for multivariate presmoothing and bootstrap error estimation are also provided. / GPL-3	noarch
<a href="#">r-equivnoninf</a>	1.0	Making available in R the complete set of programs accompanying S. Wellek's (2010) monograph "Testing Statistical Hypotheses of Equivalence and Non-inferiority. Second Edition" (Chapman&Hall/CRC). / CC0	noarch
<a href="#">r-equivump</a>	0.1.1	Implementation of uniformly most powerful invariant equivalence tests for one- and two-sample problems (paired and unpaired) as described in Wellek (2010, ISBN:978-1-4398-0818-4). Also one-sided alternatives (non-inferiority and non-superiority tests) are supported. Basically a variant of a t-test with (relaxed) null and alternative hypotheses exchanged. / GPL-2	noarch
<a href="#">r-erboost</a>	1.3	Expectile regression is a nice tool for estimating the conditional expectiles of a response variable given a set of covariates. This package implements a regression tree based gradient boosting estimator for nonparametric multiple expectile regression. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-ercv</a>	1.0.0	Provides a methodology simple and trustworthy for the analysis of extreme values and multiple threshold tests for a generalized Pareto distribution, together with an automatic threshold selection algorithm. See del Castillo, J, Daoudi, J and Lockhart, R (2014) <doi:10.1111/sjos.12037>. / GPL-2	noarch
<a href="#">r-ergmharris</a>	1.0	Data for use with the Sage Introduction to Exponential Random Graph Modeling text by Jenine K. Harris. Network data set consists of 1283 local health departments and the communication links among them along with several attributes. / GPL-3	noarch
<a href="#">r-erm</a>	1.0_0	Fits Rasch models (RM), linear logistic test models (LLTM), rating scale model (RSM), linear rating scale models (LRSM), partial credit models (PCM), and linear partial credit models (LPCM). Missing values are allowed in the data matrix. Additional features are the ML estimation of the person parameters, Andersen's LR-test, item-specific Wald test, Martin-Loef-Test, non-parametric Monte-Carlo Tests, itemfit and personfit statistics including infit and outfit measures, ICC and other plots, automated stepwise item elimination, simulation module for various binary data matrices. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-erpr</a>	0.2.0	This package is dedicated to the analysis of event-related potentials (ERPs). Event-related potentials are the measured brain responses associated with a specific sensory, cognitive, or motor event and are obtained from electroencephalographic (EEG) signal. The erpR package contains a series of functions for importing ERP data, computing traditional ERP measures, exploratory ERP analyses and plotting. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-err	0.2.0	Messages should provide users with readable information about R objects without flooding their console. ‘cc()’ concatenates vector and data frame values into a grammatically correct string using commas, an ellipsis and conjunction. ‘cn()’ allows the user to define a string which varies based on a count. ‘co()’ combines the two to produce a customizable object aware string. The package further facilitates this process by providing five ‘sprintf’-like types such as ‘%n’ for the length of an object and ‘%o’ for its name as well as wrappers for pasting objects and issuing errors, warnings and messages. / MIT	noarch
r-errorizer	0.2.1	Provides a function to convert existing R functions into errorized versions with added logging and handling functionality when encountering errors or warnings. The errorize function accepts an existing R function as its first argument and returns a R function with the exact same arguments and functionality. However, if an error or warning occurs when running that errorized R function, it will save a .Rds file to the current working directory with the relevant objects and information required to immediately recreate the error. / BSD_2_clause	noarch
r-errors	0.3.2	Support for measurement errors in R vectors, matrices and arrays: automatic uncertainty propagation and reporting. Documentation about ‘errors’ is provided in the paper by Ucar, Pebesma & Azcorra (2018, <doi:10.32614/RJ-2018-075>), included in this package as a vignette; see ‘citation(errors)’ for details. / MIT	noarch
r-es	1.0	Implementation of the Edge Selection Algorithm / GPL-2	noarch
r-es.dif	1.0.1	Computes various effect sizes of the difference, their variance, and confidence interval. This package treats Cohen’s d, Hedges’ d, biased/unbiased c (an effect size between a mean and a constant) and e (an effect size between means without assuming the variance equality). / MIT	noarch
r-esc	0.5.0	Implementation of the web-based ‘Practical Meta-Analysis Effect Size Calculator’ from David B. Wilson (< <a href="http://www.campbellcollaboration.org/escalc/html/EffectSizeCalculator-Home.php">http://www.campbellcollaboration.org/escalc/html/EffectSizeCalculator-Home.php</a> >) in R. Based on the input, the effect size can be returned as standardized mean difference, Cohen’s f, Hedges’ g, Pearson’s r or Fisher’s transformation z, odds ratio or log odds, or eta squared effect size. / GPL-3	noarch
r-esdesign	1.0.2	Software of ‘esDesign’ is developed to implement the adaptive enrichment designs with sample size re-estimation. In details, three-proposed trial designs are provided, including the AED1-SSR (or ES1-SSR), AED2-SSR (or ES2-SSR) and AED3-SSR (or ES3-SSR). In addition, this package also contains several widely used adaptive designs, such as the Marker Sequential Test (MaST) design proposed Freidlin et al. (2014) <doi:10.1177/1740774513503739>, the adaptive enrichment designs without early stopping (AED or ES), the sample size re-estimation procedure (SSR) based on the conditional power proposed by Proschan and Hunsberger (1995), and some useful functions. In details, we can calculate the futility and/or efficacy stopping boundaries, the sample size required, calibrate the value of the threshold of the difference between subgroup-specific test statistics, conduct the simulation studies in AED, SSR, AED1-SSR, AED2-SSR and AED3-SSR. / GPL-2	noarch
r-esg	0.1	The package presents a Scenarios class containing general parameters, risk parameters and projection results. Risk parameters are gathered together into a ParamsScenarios sub-object. The general process for using this package is to set all needed parameters in a Scenarios object, use the customPathsGeneration method to proceed to the projection, then use xxx_PriceDistribution() methods to get asset prices. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-eshrink</a>	0.1.0	Computes shrinkage estimators for regression problems. Selects penalty parameter by minimizing bias and variance in the effect estimate, where bias and variance are estimated from the posterior predictive distribution. / GPL-2	noarch
<a href="#">r-esmprep</a>	0.2.0	Support in preparing a raw ESM dataset for statistical analysis. Preparation includes the handling of errors (mostly due to technological reasons) and the generating of new variables that are necessary and/or helpful in meeting the conditions when statistically analyzing ESM data. The functions in ‘esmprep’ are meant to hierarchically lead from bottom, i.e. the raw (separated) ESM dataset(s), to top, i.e. a single ESM dataset ready for statistical analysis. This hierarchy evolved out of my personal experience in working with ESM data. / GPL-2	linux-64, osx-64
<a href="#">r-esreg</a>	0.4.0	Simultaneous modeling of the quantile and the expected shortfall of a response variable given a set of covariates, see Dimitriadis and Bayer (2017) <arXiv:1704.02213>. / GPL-3	linux-64, osx-64
<a href="#">r-essentials</a>	3.6.0	Some essential packages for working with R / Various	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-essentials-mrclient</a>	3.4.3	Essential R packages including MS R Client and MS Machine Learning / Various	linux-64, win-64
<a href="#">r-esshist</a>	1.2.2	Provide an optimal histogram, in the sense of probability density estimation and features detection, by means of multiscale variational inference. In other words, the resulting histogram serves as an optimal density estimator, and meanwhile recovers the features, such as increases or modes, with both false positive and false negative controls. Moreover, it provides a parsimonious representation in terms of the number of blocks, which simplifies data interpretation. The only assumption for the method is that data points are independent and identically distributed, so it applies to fairly general situations, including continuous distributions, discrete distributions, and mixtures of both. For details see Li, Munk, Sieling and Walther (2016) <arXiv:1612.07216>. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-esther</a>	1.0	Our method is a variable selection method to select active components in sparse linear mixed models in order to estimate the heritability. The selection allows us to reduce the size of the data sets which improves the accuracy of the estimations. Our package also provides a confidence interval for the estimated heritability. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-estimability</a>	1.3	Provides tools for determining estimability of linear functions of regression coefficients, and ‘epredict’ methods that handle non-estimable cases correctly. Estimability theory is discussed in many linear-models textbooks including Chapter 3 of Monahan, JF (2008), A Primer on Linear Models, Chapman and Hall (ISBN 978-1-4200-6201-4). / GPL (>= 3)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-estimatr</a>	0.20.0	Fast procedures for small set of commonly-used, design-appropriate estimators with robust standard errors and confidence intervals. Includes estimators for linear regression, instrumental variables regression, difference-in-means, Horvitz-Thompson estimation, and regression improving precision of experimental estimates by interacting treatment with centered pre-treatment covariates introduced by Lin (2013) <doi:10.1214/12-AOAS583>. / MIT	linux-64, osx-64, win-64
<a href="#">r-estout</a>	1.2	This package is intended to speedup the process of creating model-comparing tables common in Macroeconomics. The function collection stores the estimates of several models and formats it to a table of the form estimate starred and std.err. below. The default output is LaTeX but output to CSV for later editing in a spreadsheet tool is possible as well. It works for linear models (lm) and panel models from the plm-package (plm). Two further implemented functions descsto and descstab enable you to export descriptive statistics of data-frames and single variables to LaTeX and CSV. / GPL-2	noarch
<a href="#">r-estsimpdmp</a>	1.2	This package deals with the estimation of the jump rate for piecewise-deterministic Markov processes (PDMPs), from only one observation of the process within a long time. The main functions provide an estimate of this function. The state space may be discrete or continuous. The associated paper has been published in Scandinavian Journal of Statistics and is given in references. Other functions provide a method to simulate random variables from their (conditional) hazard rate, and then to simulate PDMPs. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-estudy2</a>	0.9.0	An implementation of a most commonly used event study methodology, including both parametric and nonparametric tests. It contains variety aspects of the rate of return estimation (the core calculation is done in C), as well as three classical for event study market models: mean adjusted returns, market adjusted returns and single-index market models. There are 6 parametric and 6 nonparametric tests provided, which examine cross-sectional daily abnormal return (see the documentation of the functions for more information). Parametric tests include tests proposed by Brown and Warner (1980) <DOI:10.1016/0304-405X(80)90002-1>, Brown and Warner (1985) <DOI:10.1016/0304-405X(85)90042-X>, Boehmer et al. (1991) <DOI:10.1016/0304-405X(91)90032-F>, Patell (1976) <DOI:10.2307/2490543>, and Lamb (1995) <DOI:10.2307/253695>. Nonparametric tests covered in estudy2 are tests described in Corrado and Zivney (1992) <DOI:10.2307/2331331>, McConnell and Muscarella (1985) <DOI:10.1016/0304-405X(85)90006-6>, Boehmer et al. (1991) <DOI:10.1016/0304-405X(91)90032-F>, Cowan (1992) <DOI:10.1007/BF00939016>, Corrado (1989) <DOI:10.1016/0304-405X(89)90064-0>, Campbell and Wasley (1993) <DOI:10.1016/0304-405X(93)90025-7>, Savickas (2003) <DOI:10.1111/1475-6803.00052>, Kolari and Pynnonen (2010) <DOI:10.1093/rfs/hhq072>. Furthermore, tests for the cumulative abnormal returns proposed by Brown and Warner (1985) <DOI:10.1016/0304-405X(85)90042-X> and Lamb (1995) <DOI:10.2307/253695> are included. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-esvis</a>	0.2.0	A variety of methods are provided to estimate and visualize distributional differences in terms of effect sizes. Particular emphasis is upon evaluating differences between two or more distributions across the entire scale, rather than at a single point (e.g., differences in means). For example, Probability-Probability (PP) plots display the difference between two or more distributions, matched by their empirical CDFs (see Ho and Reardon, 2012; <doi:10.3102/1076998611411918>), allowing for examinations of where on the scale distributional differences are largest or smallest. The area under the PP curve (AUC) is an effect-size metric, corresponding to the probability that a randomly selected observation from the x-axis distribution will have a higher value than a randomly selected observation from the y-axis distribution. Binned effect size plots are also available, in which the distributions are split into bins (set by the user) and separate effect sizes (Cohen's d) are produced for each bin - again providing a means to evaluate the consistency (or lack thereof) of the difference between two or more distributions at different points on the scale. Evaluation of empirical CDFs is also provided, with built-in arguments for providing annotations to help evaluate distributional differences at specific points (e.g., semi-transparent shading). All function take a consistent argument structure. Calculation of specific effect sizes is also possible. The following effect sizes are estimable: (a) Cohen's d, (b) Hedges' g, (c) percentage above a cut, (d) transformed (normalized) percentage above a cut, (e) area under the PP curve, and (f) the V statistic (see Ho, 2009; <doi:10.3102/1076998609332755>), which essentially transforms the area under the curve to standard deviation units. By default, effect sizes are calculated for all possible pairwise comparisons, but a reference group (distribution) can be specified. / MIT	noarch

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Name	Version	Summary/License	Platforms
r-etc	1.3	The package allows selecting those treatments of a one-way layout being equivalent to a control. Bonferroni adjusted two one-sided t-tests (TOST) and related simultaneous confidence intervals are given for both differences or ratios of means of normally distributed data. For the case of equal variances and balanced sample sizes for the treatment groups, the single-step procedure of Bofinger and Bofinger (1995) can be chosen. For non-normal data, the Wilcoxon test is applied. / GPL-3	noarch
r-etm	1.0.5	The etm (empirical transition matrix) package permits to estimate the matrix of transition probabilities for any time-inhomogeneous multistate model with finite state space using the Aalen-Johansen estimator. Functions for data preparation and for displaying are also included (Allignol et al., 2011 <doi:10.18637/jss.v038.i04>). Functionals of the Aalen-Johansen estimator, e.g., excess length-of-stay in an intermediate state, can also be computed (Allignol et al. 2011 <doi:10.1007/s00180-010-0200-x>). / MIT	linux-64, osx-64, win-64
r-etma	1.1_1	Traditional meta-regression based method has been developed for using meta-analysis data, but it faced the challenge of inconsistent estimates. This package purpose a new statistical method to detect epistasis using incomplete information summary, and have proven it not only successfully let consistency of evidence, but also increase the power compared with traditional method (Detailed tutorial is shown in website). / GPL-3	noarch
r-etrunc	0.1	Computes moments of univariate truncated t distribution. There is only one exported function, e_trunc(), which should be seen for details. / MIT	noarch
r-etseed	0.1.0	Client to interact with the 'etcd' 'key-value' data store < <a href="https://github.com/coreos/etcd">https://github.com/coreos/etcd</a> >. Functions included for managing directories, keys, nodes, and getting statistics. / MIT	noarch
r-europop	0.3.1	This dataset contains population estimates of all European cities with at least 10,000 inhabitants during the period 1500-1800. These data are adapted from Jan De Vries, European Urbanization, 1500-1800 (1984). / CC0	noarch
r-eurosarcbayes	1.1	Bayesian sample size calculation software and examples for EuroSARC clinical trials which utilise Bayesian methodology. These trials rely on binomial based endpoints so the majority of programs found here relate to this sort of endpoint. Developed as part of the EuroSARC FP7 grant. / GPL-2	noarch
r-evaluate	0.13	Parsing and evaluation tools that make it easy to recreate the command line behaviour of R. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-evaluationmeasures	1.1.0	Provides Some of the most important evaluation measures for evaluating a model. Just by giving the real and predicted class, measures such as accuracy, sensitivity, specificity, ppv, npv, fmeasure, mcc and ... will be returned. / GPL-3	noarch
r-evapotranspiration	1.14	Uses data and constants to calculate potential evapotranspiration (PET) and actual evapotranspiration (AET) from 21 different formulations including Penman, Penman-Monteith FAO 56, Priestley-Taylor and Morton formulations. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-evcombr	0.1_2	Package for combining pieces of evidence / MIT	noarch
r-evd	2.3_3	Extends simulation, distribution, quantile and density functions to univariate and multivariate parametric extreme value distributions, and provides fitting functions which calculate maximum likelihood estimates for univariate and bivariate maxima models, and for univariate and bivariate threshold models. / GPL-3	linux-64, osx-64
r-evdbayes	1.1_1	Provides functions for the bayesian analysis of extreme value models, using MCMC methods. / GPL-2	linux-64, osx-64
r-eventdatar	0.2.0	Event dataset repository including both real-life and artificial event logs. They can be used in combination with functionalities provided by the 'bupaR' packages 'edeaR', 'processmapR', etc. / MIT	noarch
r-eventinterval	1.3	Functions for analysis of rate changes in sequential events. / GPL-2	noarch
r-events	0.5	Stores, manipulates, aggregates and otherwise messes with event data from KEDS/TABARI or any other extraction tool with similar output / GPL-3	noarch
r-evir	1.7_4	Functions for extreme value theory, which may be divided into the following groups; exploratory data analysis, block maxima, peaks over thresholds (univariate and bivariate), point processes, gev/gpd distributions. / GPL-2	noarch
r-evmix	2.12	The usual distribution functions, maximum likelihood inference and model diagnostics for univariate stationary extreme value mixture models are provided. Kernel density estimation including various boundary corrected kernel density estimation methods and a wide choice of kernels, with cross-validation likelihood based bandwidth estimator. Reasonable consistency with the base functions in the 'evd' package is provided, so that users can safely interchange most code. / GPL-3	noarch
r-evolvability	1.1.0	An implementation of the evolvability parameters defined in Hansen and Houle (2008). / GPL-2	noarch
r-evorag	2.0	Uses maximum likelihood to estimate rates of trait evolution across environmental gradients. / GPL-2	noarch
r-ew	1.1	Edgeworth Expansion calculation. / GPL-3	noarch
r-ewgof	2.2.2	Contains a large number of the goodness-of-fit tests for the Exponential and Weibull distributions classified into families: the tests based on the empirical distribution function, the tests based on the probability plot, the tests based on the normalized spacings, the tests based on the Laplace transform and the likelihood based tests. / GPL (>= 2.0)	linux-64, osx-64, win-64
r-exact	1.7	Performs unconditional exact tests and power calculations for 2x2 contingency tables. Unconditional exact tests are often more powerful than conditional exact tests and asymptotic tests. / GPL-2	noarch
r-exactcidiff	1.3	This is a package for exact Confidence Intervals for the difference between two independent or dependent proportions. / GPL-2	noarch
r-exactloglintest	1.4.2	Monte Carlo and MCMC goodness of fit tests for log-linear models / GPL-3	linux-64, osx-64, win-64
r-exactmeta	1.0_2	Perform exact fixed effect meta analysis for rare events data without the need of artificial continuity correction. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-exactranktests</a>	0.8_30	Computes exact conditional p-values and quantiles using an implementation of the Shift-Algorithm by Streitberg & Roehmel. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-excel.link</a>	0.9.8	Allows access to data in running instance of Microsoft Excel (e. g. 'xl[a1] = xl[b2]*3' and so on). Graphics can be transferred with 'xl[a1] = current.graphics()'. Additionally there are function for reading/writing 'Excel' files - 'xl.read.file'/'xl.save.file'. They are not fast but able to read/write '*.xlsb'-files and password-protected files. There is an Excel workbook with examples of calling R from Excel in the 'doc' folder. It tries to keep things as simple as possible - there are no needs in any additional installations besides R, only 'VBA' code in the Excel workbook. Microsoft Excel is required for this package. / GPL-2	win-64
<a href="#">r-excelr</a>	0.3.0	An R interface to 'jExcel' library to create web-based interactive tables and spreadsheets compatible with 'Excel' or any other spreadsheet software. / MIT	noarch
<a href="#">r-excerptpr</a>	2.0.0	This is an R interface to the python package 'excerpts' (< <a href="https://pypi.python.org/pypi/excerpts">https://pypi.python.org/pypi/excerpts</a> >). / BSD_2_clause	noarch
<a href="#">r-excessmass</a>	1.0	Implementation of a function which calculates the empirical excess mass for given eqn{lambda} and given maximal number of modes (excessm()). Offering powerful plot features to visualize empirical excess mass (exmplot()). This includes the possibility of drawing several plots (with different maximal number of modes / cut off values) in a single graph. / LGPL-3	noarch
<a href="#">r-excon</a>	0.2.5	Interactive tools to explore topographic-like data sets. Such data sets take the form of a matrix in which the rows and columns provide location/frequency information, and the matrix elements contain altitude/response information. Such data is found in cartography, 2D spectroscopy and chemometrics. The functions in this package create interactive web pages showing the contoured data, possibly with slices from the original matrix parallel to each dimension. The interactive behavior is created using the 'D3.js' 'JavaScript' library by Mike Bostock. / GPL-3	noarch
<a href="#">r-excursions</a>	2.4.4	Functions that compute probabilistic excursion sets, contour credibility regions, contour avoiding regions, and simultaneous confidence bands for latent Gaussian random processes and fields. The package also contains functions that calculate these quantities for models estimated with the INLA package. The main references for excursions are Bolin and Lindgren (2015) <doi:10.1111/rssb.12055>, Bolin and Lindgren (2017) <doi:10.1080/10618600.2016.1228537>, and Bolin and Lindgren (2018) <doi:10.18637/jss.v086.i05>. These can be generated by the citation function in R. / GPL-3	linux-64, osx-64

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Name	Version	Summary/License	Platforms
r-exdex	1.0.1	Performs frequentist inference for the extremal index of a stationary time series. Two types of methodology are used. One type is based on a model that relates the distribution of block maxima to the marginal distribution of series and leads to the semiparametric maxima estimators described in Northrop (2015) <doi:10.1007/s10687-015-0221-5> and Berghaus and Bucher (2018) <doi:10.1214/17-AOS1621>. Sliding block maxima are used to increase precision of estimation. The other type of methodology uses a model for the distribution of threshold inter-exceedance times (Ferro and Segers (2003) <doi:10.1111/1467-9868.00401>). Two versions of this type of approach are provided, following Suveges (2007) <doi:10.1007/s10687-007-0034-2> and Suveges and Davison (2010) <doi:10.1214/09-AOAS292>. / GPL-2	linux-64, osx-64
r-exif	0.1.0	Extracts Exchangeable Image File Format (EXIF) metadata, such as camera make and model, ISO speed and the date-time the picture was taken on, from JPEG images. Incorporates the ‘easyexif’ ( <a href="https://github.com/mayanklahiri/easyexif">https://github.com/mayanklahiri/easyexif</a> ) library. / BSD_2_clause	linux-64, osx-64
r-exiftoolr	0.1.2	Reads, writes, and edits EXIF and other file metadata using ExifTool < <a href="http://www.sno.phy.queensu.ca/~phil/exiftool/">http://www.sno.phy.queensu.ca/~phil/exiftool/</a> >, returning read results as a data frame. ExifTool supports many different metadata formats including EXIF, GPS, IPTC, XMP, JFIF, GeoTIFF, ICC Profile, Photoshop IRB, FlashPix, AFCP and ID3, as well as the maker notes of many digital cameras by Canon, Casio, DJI, FLIR, FujiFilm, GE, GoPro, HP, JVC/Victor, Kodak, Leaf, Minolta/Konica-Minolta, Motorola, Nikon, Nintendo, Olympus/Epson, Panasonic/Leica, Pentax/Asahi, Phase One, Reconyx, Ricoh, Samsung, Sanyo, Sigma/Foveon and Sony. / GPL-2	noarch
r-expde	0.1.4	Modular implementation of the Differential Evolution algorithm for experimenting with different types of operators. / GPL-2	noarch
r-experiment	1.2.0	Provides various statistical methods for designing and analyzing randomized experiments. One functionality of the package is the implementation of randomized-block and matched-pair designs based on possibly multivariate pre-treatment covariates. The package also provides the tools to analyze various randomized experiments including cluster randomized experiments, two-stage randomized experiments, randomized experiments with noncompliance, and randomized experiments with missing data. / GPL-2	linux-64, osx-64
r-expert	1.0_0	Expert opinion (or judgment) is a body of techniques to estimate the distribution of a random variable when data is scarce or unavailable. Opinions on the quantiles of the distribution are sought from experts in the field and aggregated into a final estimate. The package supports aggregation by means of the Cooke, Mendel-Sheridan and predefined weights models. / GPL-2	noarch
r-expint	0.1_5	The exponential integrals $E_1(x)$ , $E_2(x)$ , $E_n(x)$ and $Ei(x)$ , and the incomplete gamma function $G(a, x)$ defined for negative values of its first argument. The package also gives easy access to the underlying C routines through an API; see the package vignette for details. A test package included in subdirectory example_API provides an implementation. C routines derived from the GNU Scientific Library < <a href="https://www.gnu.org/software/gsl/">https://www.gnu.org/software/gsl/</a> >. / GPL-2	linux-64, osx-64
r-expm	0.999	Computation of the matrix exponential, logarithm, sqrt, and related quantities. / GPL-2	linux-64, osx-64
r-expokit	0.9.4	An R-interface to the Fortran package Expokit. / GPL-2	linux-64, osx-64

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Name	Version	Summary/License	Platforms
r-expperm	1.6	A set of functions for computing expected permutation matrices given a matrix of likelihoods for each individual assignment. It has been written to accompany the forthcoming paper ‘Computing expectations and marginal likelihoods for permutations’. Publication details will be updated as soon as they are finalized. / GPL-3	linux-64, osx-64, win-64
r-exprep	1.0	Allows to calculate the probabilities of occurrences of an event in a great number of repetitions of Bernoulli experiment, through the application of the local and the integral theorem of De Moivre Laplace, and the theorem of Poisson. Gives the possibility to show the results graphically and analytically, and to compare the results obtained by the application of the above theorems with those calculated by the direct application of the Binomial formula. Is basically useful for educational purposes. / Unlimited	noarch
r-expss	0.9.1	Package computes and displays tables with support for ‘SPSS’-style labels, multiple and nested banners, weights, multiple-response variables and significance testing. There are facilities for nice output of tables in ‘knitr’, ‘Shiny’, ‘*.xlsx’ files, R and ‘Jupyter’ notebooks. Methods for labelled variables add value labels support to base R functions and to some functions from other packages. Additionally, the package brings popular data transformation functions from ‘SPSS’ Statistics and ‘Excel’: ‘RECODE’, ‘COUNT’, ‘COMPUTE’, ‘DO IF’, ‘COUNTIF’, ‘VLOOKUP’ and etc. These functions are very useful for data processing in marketing research surveys. Package intended to help people to move data processing from ‘Excel’ and ‘SPSS’ to R. / GPL-2	noarch
r-expptest	1.2	Tests for the composite hypothesis of exponentiality / GPL-3	noarch
r-exrq	1.0	Estimation for high conditional quantiles based on quantile regression. / GPL-3	noarch
r-exsic	1.1.1	The package provides tools for botanists, plant taxonomists, curators of plant genebanks and perhaps other biological collections. / MIT	noarch
r-exteriormatch	1.0.0	If one treated group is matched to one control reservoir in two different ways to produce two sets of treated-control matched pairs, then the two control groups may be entwined, in the sense that some control individuals are in both control groups. The exterior match is used to compare the two control groups. / GPL-2	noarch
r-extlasso	0.2	The package estimates coefficients of extended LASSO penalized linear regression and generalized linear models. Currently lasso and elastic net penalized linear regression and generalized linear models are considered. The package currently utilizes an accurate approximation of L1 penalty and then a modified Jacobi algorithm to estimate the coefficients. There is provision for plotting of the solutions and predictions of coefficients at given values of lambda. The package also contains functions for cross validation to select a suitable lambda value given the data. The package also provides a function for estimation in fused lasso penalized linear regression. / GPL-2	noarch
r-extmallows	0.1.0	For multiple full/partial ranking lists, R package ‘ExtMallows’ can (1) detect whether the input ranking lists are over-correlated, and (2) use the Mallows model or extended Mallows model to integrate the ranking lists, and (3) use hierarchical extended Mallows model for rank integration if there are groups of over-correlated ranking lists. / GPL-2	noarch
r-extrabinomial	2.1	This package tests for differences in minor allele frequency between groups and is based on an extra-binomial variation model for pooled sequencing data. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-extradistr</a>	1.8.1	Density, distribution function, quantile function and random generation for a number of univariate and multivariate distributions. This package implements the following distributions: Bernoulli, beta-binomial, beta-negative binomial, beta prime, Bhattacharjee, Birnbaum-Saunders, bivariate normal, bivariate Poisson, categorical, Dirichlet, Dirichlet-multinomial, discrete gamma, discrete Laplace, discrete normal, discrete uniform, discrete Weibull, Frechet, gamma-Poisson, generalized extreme value, Gompertz, generalized Pareto, Gumbel, half-Cauchy, half-normal, half-t, Huber density, inverse chi-squared, inverse-gamma, Kumaraswamy, Laplace, location-scale t, logarithmic, Lomax, multivariate hypergeometric, multinomial, negative hypergeometric, non-standard beta, normal mixture, Poisson mixture, Pareto, power, reparametrized beta, Rayleigh, shifted Gompertz, Skellam, slash, triangular, truncated binomial, truncated normal, truncated Poisson, Tukey lambda, Wald, zero-inflated binomial, zero-inflated negative binomial, zero-inflated Poisson. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-extrafontdb</a>	1.0	Package for holding the database for the extrafont package / GPL-2	noarch
<a href="#">r-extratrees</a>	1.0.5	Classification and regression based on an ensemble of decision trees. The package also provides extensions of ExtraTrees to multi-task learning and quantile regression. Uses Java implementation of the method. / Apache License 2.0	noarch
<a href="#">r-extremebounds</a>	0.1.6	An implementation of Extreme Bounds Analysis (EBA), a global sensitivity analysis that examines the robustness of determinants in regression models. The package supports both Leamer's and Sala-i-Martin's versions of EBA, and allows users to customize all aspects of the analysis. / GPL-2	noarch
<a href="#">r-extremefit</a>	1.0.2	Extreme value theory, nonparametric kernel estimation, tail conditional probabilities, extreme conditional quantile, adaptive estimation, quantile regression, survival probabilities. / GPL-2	noarch
<a href="#">r-extremis</a>	0.90	Conducts inference in statistical models for extreme values (de Carvalho et al (2012), <doi:10.1080/03610926.2012.709905>; de Carvalho and Davison (2014), <10.1080/01621459.2013.872651>; Einmahl et al (2016), <doi:10.1111/rssb.12099>). / GPL-3	linux-64, osx-64, win-64
<a href="#">r-extremogram</a>	1.0.2	Estimation of the sample univariate, cross and return time extremograms. The package can also adds empirical confidence bands to each of the extremogram plots via a permutation procedure under the assumption that the data are independent. Finally, the stationary bootstrap allows us to construct credible confidence bands for the extremograms. / GPL-3	noarch
<a href="#">r-extweibquant</a>	1.1	It implements the subjectively censored Weibull MLE and censored Weibull mixture methods for the lower quantile estimation. Quantile estimates from these two methods are robust to model misspecification in the lower tail. It also includes functions to evaluation the standard error of the resulting quantile estimates. Also, the methods here can be used to fit the Weibull or Weibull mixture for the Type-I or Type-II right censored data. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-eyetracking</a>	1.1	Misc function for working with eyetracking data / GPL-3	noarch
<a href="#">r-ezglm</a>	1.0	This package implements a simplified version of least squares, and logistic regression for efficiently selecting the significant non-additive interactions between two variables. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-ezknitr</a>	0.6	An extension of ‘knitr’ that adds flexibility in several ways. One common source of frustration with ‘knitr’ is that it assumes the directory where the source file lives should be the working directory, which is often not true. ‘ezknitr’ addresses this problem by giving you complete control over where all the inputs and outputs are, and adds several other convenient features to make rendering markdown/HTML documents easier. / MIT	noarch
<a href="#">r-fabci</a>	0.1	Frequentist assisted by Bayes (FAB) confidence interval construction. See ‘Adaptive multigroup confidence intervals with constant coverage’ by Yu and Hoff < <a href="https://arxiv.org/abs/1612.08287">https://arxiv.org/abs/1612.08287</a> >. / GPL-3	noarch
<a href="#">r-fabricatr</a>	0.10.0	Helps you imagine your data before you collect it. Hierarchical data structures and correlated data can be easily simulated, either from random number generators or by resampling from existing data sources. This package is faster with ‘data.table’ and ‘mvnfast’ installed. / MIT	noarch
<a href="#">r-facebook.s4</a>	1.1.0	Provides an interface to the Facebook API and builds collections of elements that reflects the graph architecture of Facebook. See < <a href="https://developers.facebook.com/docs/graph-api">https://developers.facebook.com/docs/graph-api</a> > for more information. / MIT	noarch
<a href="#">r-factmixtanalysis</a>	1.0	The package estimates Factor Mixture Analysis via the EM algorithm / GPL-2	noarch
<a href="#">r-factorial2x2</a>	0.1.0	Used for the design and analysis of a 2x2 factorial trial for a time-to-event endpoint. Performs power calculations and significance testing. Important reference papers include Slud EV. (1994) < <a href="https://www.ncbi.nlm.nih.gov/pubmed/8086609">https://www.ncbi.nlm.nih.gov/pubmed/8086609</a> > Lin DY, Gong J, Gallo P, Bunn PH, Couper D. (2016) <DOI:10.1111/biom.12507> Leifer ES, Troendle JF, Kolecki A, Follmann DA. (2019) < <a href="https://github.com/EricSLeifer/factorial2x2/blob/master/Leifer%20et%20al%20Factorial.pdf">https://github.com/EricSLeifer/factorial2x2/blob/master/Leifer%20et%20al%20Factorial.pdf</a> >. / GPL-2	noarch
<a href="#">r-factorplot</a>	1.1_2	Methods to calculate, print, summarize and plot pairwise differences from GLMs, GLHT or Multinomial Logit models. / GPL-2	noarch
<a href="#">r-factorqr</a>	0.1_4	Package to fit Bayesian quantile regression models that assume a factor structure for at least part of the design matrix. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-factorsr</a>	1.4	It identifies the factors significantly related to species richness, and their relative contribution, using multiple regressions and support vector machine models. It uses an output file of ‘ModestR’ (< <a href="http://www.ipez.es/ModestR">http://www.ipez.es/ModestR</a> >) with data of richness of the species and environmental variables in a cell size defined by the user. The residuals of the support vector machine model are shown on a map. Negative residuals may be potential areas with undiscovered and/or unregistered species, or areas with decreased species richness due to the negative effect of anthropogenic factors. / GPL-2	noarch
<a href="#">r-factualr</a>	0.5	Per the Factual.com website, Factual is a platform where anyone can share and mash open, living data on any subject. The data is in the form of tables and is accessible via REST API. The factualR package is a thin wrapper around the Factual.com API, to make it even easier for people working with R to explore Factual.com data sets. / Apache License 2.0	noarch
<a href="#">r-fadist</a>	2.2	Probability distributions that are sometimes useful in hydrology. / GPL-2	noarch
<a href="#">r-fahrmeir</a>	2016.5	Data and functions for the book Multivariate Statistical Modelling Based on Generalized Linear Models, first edition, by Ludwig Fahrmeir and Gerhard Tutz. Useful when using the book. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-fail	1.3	More comfortable interface to work with R data or source files in a key-value fashion. / BSD_3_clause	noarch
r-faisalconjoint	1.15	It is used for systematic analysis of decisions based on attributes and its levels. / GPL-3	noarch
r-falcon	0.2	This is a method for Allele-specific DNA Copy Number Profiling using Next-Generation Sequencing. Given the allele-specific coverage at the variant loci, this program segments the genome into regions of homogeneous allele-specific copy number. It requires, as input, the read counts for each variant allele in a pair of case and control samples. For detection of somatic mutations, the case and control samples can be the tumor and normal sample from the same individual. / GPL-2	linux-64, osx-64, win-64
r-falconx	0.2	This is a method for Allele-specific DNA Copy Number profiling for whole-Exome sequencing data. Given the allele-specific coverage and site biases at the variant loci, this program segments the genome into regions of homogeneous allele-specific copy number. It requires, as input, the read counts for each variant allele in a pair of case and control samples, as well as the site biases. For detection of somatic mutations, the case and control samples can be the tumor and normal sample from the same individual. The implemented method is based on the paper: Chen, H., Jiang, Y., Maxwell, K., Nathanson, K. and Zhang, N. (under review). Allele-specific copy number estimation by whole Exome sequencing. / GPL-2	linux-64, osx-64, win-64
r-fam.recrisk	0.1	Given vectors of family sizes and number of affecteds per family, calculates the risk of disease recurrence in an unaffected person, conditional on a family having at least k affected members. Methods also model heterogeneity of disease risk across families by fitting a mixture model, allowing for high and low risk families. / GPL-2	noarch
r-famle	1.3.5	Estimate parameters of univariate probability distributions with maximum likelihood and Bayesian methods. / GPL-2	linux-64, osx-64, win-64
r-fanc	2.2	Computes the penalized maximum likelihood estimates of factor loadings and unique variances for various tuning parameters. The pathwise coordinate descent along with EM algorithm is used. This package also includes a new graphical tool which outputs path diagram, goodness-of-fit indices and model selection criteria for each regularization parameter. The user can change the regularization parameter by manipulating scrollbars, which is helpful to find a suitable value of regularization parameter. / GPL-2	linux-64, osx-64, win-64
r-fancova	0.5_1	This package contains a collection of R functions to perform nonparametric analysis of covariance for regression curves or surfaces. Testing the equality or parallelism of nonparametric curves or surfaces is equivalent to analysis of variance (ANOVA) or analysis of covariance (ANCOVA) for one-sample functional data. Three different testing methods are available in the package, including one based on L-2 distance, one based on an ANOVA statistic, and one based on variance estimators. / GPL-3	noarch
r-fancycut	0.1.2	Provides the function fancycut() which is like cut() except you can mix left open and right open intervals with point values, intervals that are closed on both ends and intervals that are open on both ends. / CC0	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-fanplot</a>	3.4.1	Visualise sequential distributions using a range of plotting styles. Sequential distribution data can be input as either simulations or values corresponding to percentiles over time. Plots are added to existing graphic devices using the fan function. Users can choose from four different styles, including fan chart type plots, where a set of coloured polygon, with shadings corresponding to the percentile values are layered to represent different uncertainty levels. / GPL-2	noarch
<a href="#">r-fansi</a>	0.4.0	Counterparts to R string manipulation functions that account for the effects of ANSI text formatting control sequences. / GPL (>= 2)	linux-64, osx-64, win-32, win-64
<a href="#">r-far</a>	0.6.5	Modelizations and previsions functions for Functional AutoRegressive processes using nonparametric methods: functional kernel, estimation of the covariance operator in a subspace, ... / LGPL-2.1	linux-64, osx-64, win-64
<a href="#">r-faraway</a>	1.0.7	Books are Practical Regression and ANOVA in R on CRAN, Linear Models with R published 1st Ed. August 2004, 2nd Ed. July 2014 by CRC press, ISBN 9781439887332, and Extending the Linear Model with R published by CRC press in 1st Ed. December 2005 and 2nd Ed. March 2016, ISBN 9781584884248. / GPL-3	noarch
<a href="#">r-farmtest</a>	1.0.3	Performs robust multiple testing for means in the presence of known and unknown latent factors. It implements a robust procedure to estimate distribution parameters using the Huber's loss function and accounts for strong dependence among coordinates via an approximate factor model. This method is particularly suitable for high dimensional data when there are many variables but only a small number of observations available. Moreover, the method is tailored to cases when the underlying distribution deviates from Gaussian, which is commonly assumed in the literature. Besides the results of hypotheses testing, the estimated underlying factors and diagnostic plots are also output. Multiple comparison correction is done after estimating the proportion of true null hypotheses using the method in Storey (2015) < <a href="https://github.com/jdstorey/qvalue">https://github.com/jdstorey/qvalue</a> >. For detailed description of methods and further references, see the papers on the 'FarmTest' method: Fan et al. (2017) <arXiv:1711.05386> and Zhou et al. (2017) <arXiv:1711.05381>. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-farver</a>	1.1.0	The encoding of colour can be handled in many different ways, using different colour spaces. As different colour spaces have different uses, efficient conversion between these representations are important. The 'farver' package provides a set of functions that gives access to very fast colour space conversion and comparisons implemented in C, and offers 100-fold speed improvements over the 'convertColor' function in the 'grDevices' package. / MIT	linux-64, osx-64, win-64
<a href="#">r-faseg</a>	0.1.9	It contains a function designed to the joint segmentation in the mean of several correlated series. The method is described in the paper X. Collilieux, E. Lebarbier and S. Robin. A factor model approach for the joint segmentation with between-series correlation (2015) <arXiv:1505.05660>. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-fasjem	1.1.2	This is an R implementation of A Fast and Scalable Joint Estimator for Learning Multiple Related Sparse Gaussian Graphical Models (FASJEM). The FASJEM algorithm can be used to estimate multiple related precision matrices. For instance, it can identify context-specific gene networks from multi-context gene expression datasets. By performing data-driven network inference from high-dimensional and heterogonous data sets, this tool can help users effectively translate aggregated data into knowledge that take the form of graphs among entities. Please run demo(fasjem) to learn the basic functions provided by this package. For more details, please see < <a href="http://proceedings.mlr.press/v54/wang17e/wang17e.pdf">http://proceedings.mlr.press/v54/wang17e/wang17e.pdf</a> >. / GPL-2	noarch
r-fast	0.64	The Fourier Amplitude Sensitivity Test (FAST) is a method to determine global sensitivities of a model on parameter changes with relatively few model runs. This package implements this sensitivity analysis method. / GPL-2	noarch
r-fasta	0.1.0	A collection of acceleration schemes for proximal gradient methods for estimating penalized regression parameters described in Goldstein, Studer, and Baraniuk (2016) <arXiv:1411.3406>. Schemes such as Fast Iterative Shrinkage and Thresholding Algorithm (FISTA) by Beck and Teboulle (2009) <doi:10.1137/080716542> and the adaptive stepsize rule introduced in Wright, Nowak, and Figueiredo (2009) <doi:10.1109/TSP.2009.2016892> are included. You provide the objective function and proximal mappings, and it takes care of the issues like stepsize selection, acceleration, and stopping conditions for you. / MIT	noarch
r-fastadaboost	1.0.0	Implements Adaboost based on C backend code. This is blazingly fast and especially useful for large, in memory data sets. The package uses decision trees as weak classifiers. Once the classifiers have been trained, they can be used to predict new data. Currently, we support only binary classification tasks. The package implements the Adaboost.M1 algorithm and the real Adaboost(SAMME.R) algorithm. / MIT	linux-64, osx-64, win-64
r-fastbandchol	0.1.1	Fast and numerically stable estimation of a covariance matrix by banding the Cholesky factor using a modified Gram-Schmidt algorithm implemented in RcppArmadillo. See < <a href="http://stat.umn.edu/~molst029">http://stat.umn.edu/~molst029</a> > for details on the algorithm. / GPL-2	linux-64, osx-64, win-64
r-fastclime	1.4.1	Provides a method of recovering the precision matrix efficiently and solving for the dantzig selector by applying the parametric simplex method. The computation is based on a linear optimization solver. It also contains a generic LP solver and a parameterized LP solver using parametric simplex method. / GPL-2	linux-64, osx-64, win-64
r-fastcluster	1.1.25	This is a two-in-one package which provides interfaces to both R and 'Python'. It implements fast hierarchical, agglomerative clustering routines. Part of the functionality is designed as drop-in replacement for existing routines: linkage() in the 'SciPy' package 'scipy.cluster.hierarchy', hclust() in R's 'stats' package, and the 'flashClust' package. It provides the same functionality with the benefit of a much faster implementation. Moreover, there are memory-saving routines for clustering of vector data, which go beyond what the existing packages provide. For information on how to install the 'Python' files, see the file INSTALL in the source distribution. Based on the present package, Christoph Dalitz also wrote a pure 'C' interface to 'fastcluster': < <a href="http://informatik.hsnr.de/~dalitz/data/hclust">http://informatik.hsnr.de/~dalitz/data/hclust</a> >. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-fastcmh</a>	0.2.7	A method which uses the Cochran-Mantel-Haenszel test with significant pattern mining to detect intervals in binary genotype data which are significantly associated with a particular phenotype, while accounting for categorical covariates. / GPL-2   GPL-3	linux-64, osx-64, win-64
<a href="#">r-fastcmprsk</a>	1.1.1	In competing risks regression, the proportional subdistribution hazards (PSH) model is popular for its direct assessment of covariate effects on the cumulative incidence function. This package allows for both penalized and unpenalized PSH regression in linear time using a novel forward-backward scan. Penalties include Ridge, Least Absolute Shrinkage and Selection Operator (LASSO), Smoothly Clipped Absolute Deviation (SCAD), Minimax Concave Plus (MCP), and elastic net. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-fastcox</a>	1.1.3	We implement a cocktail algorithm, a good mixture of coordinate decent, the majorization-minimization principle and the strong rule, for computing the solution paths of the elastic net penalized Cox's proportional hazards model. The package is an implementation of Yang, Y. and Zou, H. (2013) DOI: <doi:10.4310/SII.2013.v6.n2.a1>. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-fastdigest</a>	0.6_3	Provides an R interface to Bob Jenkin's streaming, non-cryptographic 'SpookyHash' hash algorithm for use in digest-based comparisons of R objects. 'fastdigest' plugs directly into R's internal serialization machinery, allowing digests of all R objects the serialize() function supports, including reference-style objects via custom hooks. Speed is high and scales linearly by object size; memory usage is constant and negligible. / Artistic-2.0	linux-64, osx-64, win-64
<a href="#">r-fasteraster</a>	1.1.1	If there is a need to recognise edges on a raster image or a bitmap or any kind of a matrix, one can find packages that does only 90 degrees vectorization. Typically the nature of artefact images is linear and can be vectorized in much more efficient way than draw a series of 90 degrees lines. The fasteraster package does recognition of lines using only one pass. It also allows to calculate mass and the mass centers for the recognized zones or polygons. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-fasterelasticnet</a>	1.1.2	Fit Elastic Net, Lasso, and Ridge regression and do cross-validation in a fast way. We build the algorithm based on Least Angle Regression by Bradley Efron, Trevor Hastie, Iain Johnstone, etc. (2004)(<doi:10.1214/009053604000000067 >) and some algorithms like Givens rotation and Forward/Back Substitution. In this way, many matrices to be computed are retained as triangular matrices which can eventually speed up the computation. The fitting algorithm for Elastic Net is written in C using Armadillo linear algebra library. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-fasterize</a>	1.0.0	Provides a drop-in replacement for rasterize() from the 'raster' package that takes 'sf'-type objects, and is much faster. There is support for the main options provided by the rasterize() function, including setting the field used and background value, and options for aggregating multi-layer rasters. Uses the scan line algorithm attributed to Wylie et al. (1967) <doi:10.1145/1465611.1465619>. / MIT	linux-64, osx-64, win-64
<a href="#">r-fastghquad</a>	1.0	Fast, numerically-stable Gauss-Hermite quadrature rules and utility functions for adaptive GH quadrature. See Liu, Q. and Pierce, D. A. (1994) <doi:10.2307/2337136> for a reference on these methods. / MIT	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-fastglm</a>	0.0.1	Fits generalized linear models efficiently using ‘RcppEigen’. The iteratively reweighted least squares implementation utilizes the step-halving approach of Marschner (2011) <doi:10.32614/RJ-2011-012> to help safeguard against convergence issues. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-fastgraph</a>	2.1	Provides functionality to produce graphs of probability density functions and cumulative distribution functions with few keystrokes, allows shading under the curve of the probability density function to illustrate concepts such as p-values and critical values, and fits a simple linear regression line on a scatter plot with the equation as the main title. / GPL-3	noarch
<a href="#">r-fasthcs</a>	0.0.6	The FastHCS algorithm of Schmitt and Vakili (2014) <doi:10.1007/s11222-015-9602-5> for high-dimensional, robust PCA modelling and associated outlier detection and diagnostic tools. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-fasthica</a>	1.0.2	It implements HICA (Hierarchical Independent Component Analysis) algorithm. This approach, obtained through the integration between treelets and Independent Component Analysis, is able to provide a multi-scale non-orthogonal data-driven basis, whose elements have a phenomenological interpretation according to the problem under study. / GPL-2	noarch
<a href="#">r-fastica</a>	1.2.1	Implementation of FastICA algorithm to perform Independent Component Analysis (ICA) and Projection Pursuit. / GPL-2   GPL-3	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-fastimputation</a>	2.0	TrainFastImputation() uses training data to describe a multivariate normal distribution that the data approximates or can be transformed into approximating and stores this information as an object of class ‘FastImputationPatterns’. FastImputation() function uses this ‘FastImputationPatterns’ object to impute (make a good guess at) missing data in a single line or a whole data frame of data. This approximates the process used by ‘Amelia’ < <a href="http://gking.harvard.edu/amelia/">http://gking.harvard.edu/amelia/</a> > but is much faster when filling in values for a single line of data. / GPL-2	noarch
<a href="#">r-fastjt</a>	1.0.5	This ‘Rcpp’-based package implements highly efficient functions for the calculation of the Jonckheere-Terpstra statistic. It can be used for a variety of applications, including feature selection in machine learning problems, or to conduct genome-wide association studies (GWAS) with multiple quantitative phenotypes. The code leverages ‘OpenMP’ directives for multi-core computing to reduce overall processing time. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-fastlzero	2018.12.10	Estimate spike times from calcium imaging data using an L0 penalty. / GPL-3	linux-64, osx-64, win-64
r-fastm	0.0_4	Implements the new algorithm for fast computation of M-scatter matrices using a partial Newton-Raphson procedure for several estimators. The algorithm is described in Duembgen, Nordhausen and Schuhmacher (2016) <doi:10.1016/j.jmva.2015.11.009>. / GPL-2	linux-64, osx-64, win-64
r-fastmap	1.0.0	Fast implementation of a key-value store. Environments are commonly used as key-value stores, but every time a new key is used, it is added to R's global symbol table, causing a small amount of memory leakage. This can be problematic in cases where many different keys are used. Fastmap avoids this memory leak issue by implementing the map using data structures in C. / MIT	linux-64, osx-64, win-64
r-fastmatch	1.1_0	Package providing a fast match() replacement for cases that require repeated look-ups. It is slightly faster than R's built-in match() function on first match against a table, but extremely fast on any subsequent lookup as it keeps the hash table in memory. / GPL-2	linux-64, osx-64, win-64
r-fastnaivebayes	2.1.0	This is an extremely fast implementation of a Naive Bayes classifier. This package is currently the only package that supports a Bernoulli distribution, a Multinomial distribution, and a Gaussian distribution, making it suitable for both binary features, frequency counts, and numerical features. Another feature is the support of a mix of different event models. Only numerical variables are allowed, however, categorical variables can be transformed into dummies and used with the Bernoulli distribution. The implementation is largely based on the paper A comparison of event models for Naive Bayes anti-spam e-mail filtering written by K.M. Schneider (2003) <doi:10.3115/1067807>. Any issues can be submitted to: <https://github.com/mskogholt/fastNaiveBayes/issues>. / GPL-3	noarch
r-fastpcs	0.1.3	The FastPCS algorithm of Vakili and Schmitt (2014) <doi:10.1016/j.csda.2013.07.021> for robust estimation of multivariate location and scatter and multivariate outliers detection. / GPL-2	linux-64, osx-64, win-64
r-fastpseudo	0.1	Computes pseudo-observations for survival analysis on right-censored data based on restricted mean survival time. / GPL-2	noarch
r-fastres	0.0.8	The FastRCS algorithm of Vakili and Schmitt (2014) for robust fit of the multivariable linear regression model and outliers detection. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-fastrweb	1.1_1	Infrastructure for creating rich, dynamic web content using R scripts while maintaining very fast response time. / GPL-2	linux-64, osx-64
r-fastsum	1.0.0	Functions for computing spillover measures, especially spillover tables and spillover indices, as well as their average, minimal, and maximal values. / GPL-2	linux-64, osx-64, win-64
r-fasttext	1.0	An interface to the ‘fastText’ library < <a href="https://github.com/facebookresearch/fastText">https://github.com/facebookresearch/fastText</a> >. The package can be used for text classification and to learn word vectors. The install folder contains the ‘PATENTS’ file. An example how to use ‘fastTextR’ can be found in the ‘README’ file. / BSD_3_clause	linux-64, osx-64, win-64
r-fasttime	1.0_2	Fast functions for timestamp manipulation that avoid system calls and take shortcuts to facilitate operations on very large data. / GPL-2	linux-64, osx-64, win-64
r-favnums	1.0.0	A dataset of favourite numbers, selected from an online poll of over 30,000 people by Alex Bellos ( <a href="http://pages.bloomsbury.com/favouritenumber">http://pages.bloomsbury.com/favouritenumber</a> ). / CC0	noarch
r-fbasics	3042.89	Provides a collection of functions to explore and to investigate basic properties of financial returns and related quantities. The covered fields include techniques of explorative data analysis and the investigation of distributional properties, including parameter estimation and hypothesis testing. Even more there are several utility functions for data handling and management. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
r-fbfsearch	1.1	We propose an objective Bayesian algorithm for searching the space of Gaussian directed acyclic graph (DAG) models. The algorithm proposed makes use of moment fractional Bayes factors (MFBF) and thus it is suitable for learning sparse graph. The algorithm is implemented by using Armadillo: an open-source C linear algebra library. / GPL-2	linux-64, osx-64, win-64
r-fbn	1.5.1	Normalizes the data from a file containing the raw values of the SNP probes of microarray data by using the FISH probes and their corresponding CNs. / GPL-2	noarch
r-fbonds	3042.78	implements the Nelson-Siegel and the Nelson-Siegel-Svensson term structures. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-fbranks</a>	2.0	This package uses time dependent Poisson regression and a record of goals scored in matches to rank teams via estimated attack and defense strengths. The statistical model is based on Dixon and Coles (1997) Modeling Association Football Scores and Inefficiencies in the Football Betting Market, Applied Statistics, Volume 46, Issue 2, 265-280. The package has a some web scrapers to assist in the development and updating of a match database. If the match database contains unconnected clusters (i.e. sets of teams that have only played each other and not played teams from other sets), each cluster is ranked separately relative to the median team strength in the cluster. The package contains functions for predicting and simulating tournaments and leagues from estimated models. The package allows fitting via the <code>glm()</code> , <code>speedglm()</code> , and <code>glmnet()</code> functions. The latter allows fast and efficient fitting of very large numbers of teams. The fitting algorithm will analyze the match data and determine which teams form a cluster (a set of teams where there is a path of matches connecting every team) and fit each cluster separately. / GPL-2	noarch
<a href="#">r-fc</a>	0.1.0	Provides a streamlined, standard evaluation-based approach to multivariate function composition. Allows for chaining commands via a forward-pipe operator, <code>%&gt;%</code> . / GPL-2	noarch
<a href="#">r-fcd</a>	0.1	Efficient procedures for community detection in network studies, especially for sparse networks with not very obvious community structure. The algorithms impose penalties on the differences of the coordinates which represent the community labels of the nodes. / GPL (>= 2.0)	noarch
<a href="#">r-fclust</a>	2.1	Algorithms for fuzzy clustering, cluster validity indices and plots for cluster validity and visualizing fuzzy clustering results. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-fcmapper</a>	1.1	Provides several functions to create and manipulate fuzzy cognitive maps. It is based on 'FCMapper' for Excel, distributed at <a href="http://www.fcmapers.net/joomla/">http://www.fcmapers.net/joomla/</a> , developed by Michael Bachhofer and Martin Wildenberg. Maps are inputted as adjacency matrices. Attributes of the maps and the equilibrium values of the concepts (including with user-defined constrained values) can be calculated. The maps can be graphed with a function that calls 'igraph'. Multiple maps with shared concepts can be aggregated. / GPL-2	noarch
<a href="#">r-fcros</a>	1.6.1	A fold change rank based method is presented to search for genes with changing expression and to detect recurrent chromosomal copy number aberrations. This method may be useful for high-throughput biological data (micro-array, sequencing, ...). Probabilities are associated with genes or probes in the data set and there is no problem of multiple tests when using this method. For array-based comparative genomic hybridization data, segmentation results are obtained by merging the significant probes detected. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-fda	2.4.8	These functions were developed to support functional data analysis as described in Ramsay, J. O. and Silverman, B. W. (2005) Functional Data Analysis. New York: Springer. They were ported from earlier versions in Matlab and S-PLUS. An introduction appears in Ramsay, J. O., Hooker, Giles, and Graves, Spencer (2009) Functional Data Analysis with R and Matlab (Springer). The package includes data sets and script files working many examples including all but one of the 76 figures in this latter book. Matlab versions of the code and sample analyses are no longer distributed through CRAN, as they were when the book was published. For those, ftp from <a href="http://www.psych.mcgill.ca/misc/fda/downloads/FDAfuns/">http://www.psych.mcgill.ca/misc/fda/downloads/FDAfuns/</a> There you find a set of .zip files containing the functions and sample analyses, as well as two .txt files giving instructions for installation and some additional information. The changes from Version 2.4.1 are fixes of bugs in density.fd and removal of functions create.polynomial.basis, polynompen, and polynomial. These were deleted because the monomial basis does the same thing and because there were errors in the code. / GPL-2	noarch
r-fdakma	1.2.1	It performs simultaneously clustering and alignment of a multidimensional or unidimensional functional dataset by means of k-mean alignment. / GPL-3	noarch
r-fdamixed	0.6	Likelihood based analysis of 1-dimension functional data in a mixed-effects model framework. Matrix computation are approximated by semi-explicit operator equivalents with linear computational complexity. Markussen (2013) <doi:10.3150/11-BEJ389>. / GPL-2	linux-64, osx-64, win-64
r-fdrcti	2.1	FDR functions for permutation-based estimators, including pi0 as well as FDR confidence intervals. The confidence intervals account for dependencies between tests by the incorporation of an overdispersion parameter, which is estimated from the permuted data. / Artistic-2.0	noarch
r-fdrsampsiz	1.0	Defines a collection of functions to compute average power and sample size for studies that use the false discovery rate as the final measure of statistical significance. / GPL-2	noarch
r-fdrtool	1.2.1	Estimates both tail area-based false discovery rates (Fdr) as well as local false discovery rates (fdr) for a variety of null models (p-values, z-scores, correlation coefficients, t-scores). The proportion of null values and the parameters of the null distribution are adaptively estimated from the data. In addition, the package contains functions for non-parametric density estimation (Grenander estimator), for monotone regression (isotonic regression and antitonic regression with weights), for computing the greatest convex minorant (GCM) and the least concave majorant (LCM), for the half-normal and correlation distributions, and for computing empirical higher criticism (HC) scores and the corresponding decision threshold. / GPL-3	linux-64, osx-64, win-64
r-fdth	1.2.1	Perform frequency distribution tables, associated histograms and polygons from vector, data.frame and matrix objects for numerical and categorical variables. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-feather</a>	0.3.3	Read and write feather files, a lightweight binary columnar data store designed for maximum speed. / Apache License 2.0	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-featurehashing</a>	0.9.1	Feature hashing, also called as the hashing trick, is a method to transform features of a instance to a vector. Thus, it is a method to transform a real dataset to a matrix. Without looking up the indices in an associative array, it applies a hash function to the features and uses their hash values as indices directly. The method of feature hashing in this package was proposed in Weinberger et al. (2009) <arXiv:0902.2206>. The hashing algorithm is the murmurhash3 from the 'digest' package. Please see the README in < <a href="https://github.com/wush978/FeatureHashing">https://github.com/wush978/FeatureHashing</a> > for more information. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-featurizer</a>	0.2	A collection of functions that would help one to build features based on external data. Very useful for Data Scientists in data to day work. Many functions create features using parallel computation. Since the nitty gritty of parallel computation is hidden under the hood, the user need not worry about creating clusters and shutting them down. / GPL-2	noarch
<a href="#">r-fechner</a>	1.0.3	Functions and example datasets for Fechnerian scaling of discrete object sets. User can compute Fechnerian distances among objects representing subjective dissimilarities, and other related information. See package?fechner for an overview. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-federalregister</a>	0.2.0	Access data from the Federal Register API < <a href="https://www.federalregister.gov/developers/api/v1">https://www.federalregister.gov/developers/api/v1</a> >. / GPL-2	noarch
<a href="#">r-fedreporter</a>	0.2.1	Downloads data from Federal 'RePORTER' < <a href="https://api.federalreporter.nih.gov/">https://api.federalreporter.nih.gov/</a> > using the Federal 'RePORTER' API. Allows the user to search job projects from different government agencies. / GPL-3	noarch
<a href="#">r-fenmlm</a>	2.4.2	Efficient estimation of maximum likelihood models with multiple fixed-effects. Standard-errors can easily and flexibly be clustered and estimations exported. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-fermicatsr</a>	1.4	Data from various catalogs of astrophysical gamma-ray sources detected by NASA's Large Area Telescope (The Astrophysical Journal, 697, 1071, 2009 June 1), on board the Fermi gamma-ray satellite. More information on Fermi and its data products is available from the Fermi Science Support Center ( <a href="http://fermi.gsfc.nasa.gov/ssc/">http://fermi.gsfc.nasa.gov/ssc/</a> ). / CC0	noarch
<a href="#">r-fextremes</a>	3042.82	Provides functions for analysing and modelling extreme events in financial time Series. The topics include: (i) data pre-processing, (ii) explorative data analysis, (iii) peak over threshold modelling, (iv) block maxima modelling, (v) estimation of VaR and CVaR, and (vi) the computation of the extreme index. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-ff	2.2.14	The ff package provides data structures that are stored on disk but behave (almost) as if they were in RAM by transparently mapping only a section (page-size) in main memory - the effective virtual memory consumption per ff object. ff supports R's standard atomic data types 'double', 'logical', 'raw' and 'integer' and non-standard atomic types boolean (1 bit), quad (2 bit unsigned), nibble (4 bit unsigned), byte (1 byte signed with NAs), ubyte (1 byte unsigned), short (2 byte signed with NAs), ushort (2 byte unsigned), single (4 byte float with NAs). For example 'quad' allows efficient storage of genomic data as an 'A','T','G','C' factor. The unsigned types support 'circular' arithmetic. There is also support for close-to-atomic types 'factor', 'ordered', 'POSIXct', 'Date' and custom close-to-atomic types. ff not only has native C-support for vectors, matrices and arrays with flexible dimorder (major column-order, major row-order and generalizations for arrays). There is also a ffd class not unlike data.frames and import/export filters for csv files. ff objects store raw data in binary flat files in native encoding, and complement this with metadata stored in R as physical and virtual attributes. ff objects have well-defined hybrid copying semantics, which gives rise to certain performance improvements through virtualization. ff objects can be stored and reopened across R sessions. ff files can be shared by multiple ff R objects (using different data en/de-coding schemes) in the same process or from multiple R processes to exploit parallelism. A wide choice of finalizer options allows to work with 'permanent' files as well as creating/removing 'temporary' ff files completely transparent to the user. On certain OS/Filesystem combinations, creating the ff files works without notable delay thanks to using sparse file allocation. Several access optimization techniques such as Hybrid Index Preprocessing and Virtualization are implemented to achieve good performance even with large datasets, for example virtual matrix transpose without touching a single byte on disk. Further, to reduce disk I/O, 'logicals' and non-standard data types get stored native and compact on binary flat files i.e. logicals take up exactly 2 bits to represent TRUE, FALSE and NA. Beyond basic access functions, the ff package also provides compatibility functions that facilitate writing code for ff and ram objects and support for batch processing on ff objects (e.g. as.ram, as.ff, ffapply). ff interfaces closely with functionality from package 'bit': chunked looping, fast bit operations and coercions between different objects that can store subscript information ('bit', 'bitwhich', ff 'boolean', ri range index, hi hybrid index). This allows to work interactively with selections of large datasets and quickly modify selection criteria. Further high-performance enhancements can be made available upon request. / GPL-2	linux-64, osx-64, win-64
r-ffield	0.1.0	Force field simulation of interaction of set of points. Very useful for placing text labels on graphs, such as scatterplots. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-ffmanova</a>	1.1.0	General linear modeling with multiple responses (MANCOVA). An overall p-value for each model term is calculated by the 50-50 MANOVA method by Langsrud (2002) <doi:10.1111/1467-9884.00320>, which handles collinear responses. Rotation testing, described by Langsrud (2005) <doi:10.1007/s11222-005-4789-5>, is used to compute adjusted single response p-values according to familywise error rates and false discovery rates (FDR). The approach to FDR is described in the appendix of Moen et al. (2005) <doi:10.1128/AEM.71.4.2086-2094.2005>. Unbalanced designs are handled by Type II sums of squares as argued in Langsrud (2003) <doi:10.1023/A:1023260610025>. Furthermore, the Type II philosophy is extended to continuous design variables as described in Langsrud et al. (2007) <doi:10.1080/02664760701594246>. This means that the method is invariant to scale changes and that common pitfalls are avoided. / GPL-2	noarch
<a href="#">r-ffmetadata</a>	1.0.0	A collection of functions that allows users to retrieve metadata for the Fragile Families challenge via a Web API (< <a href="http://api.metadata.fragilefamilies.princeton.edu">http://api.metadata.fragilefamilies.princeton.edu</a> >). Users can select and search metadata for relevant variables by filtering on different attribute names. / MIT	noarch
<a href="#">r-ffstream</a>	0.1.6	An implementation of the adaptive forgetting factor scheme described in Bodenham and Adams (2016) <doi:10.1007/s11222-016-9684-8> which adaptively estimates the mean and variance of a stream in order to detect multiple changepoints in streaming data. The implementation is in C and uses Rcpp. Additionally, implementations of the fixed forgetting factor scheme from the same paper, as well as the classic CUSUM and EWMA methods, are included. / GPL-2   GPL-3	linux-64, osx-64, win-64
<a href="#">r-fftw</a>	1.0.5	Provides a simple and efficient wrapper around the fastest Fourier transform in the west (FFTW) < <a href="http://www.fftw.org/">http://www.fftw.org/</a> > library. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-fftwtools</a>	0.9.8	Provides a wrapper for several ‘FFTW’ functions. This package provides access to the two-dimensional ‘FFT’, the multivariate ‘FFT’, and the one-dimensional real to complex ‘FFT’ using the ‘FFTW3’ library. The package includes the functions fftw() and mvfftw() which are designed to mimic the functionality of the R functions fft() and mvfft(). The ‘FFT’ functions have a parameter that allows them to not return the redundant complex conjugate when the input is real data. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-fgac</a>	0.6.1	Bi-variate data fitting is done by two stochastic components: the marginal distributions and the dependency structure. The dependency structure is modeled through a copula. An algorithm was implemented considering seven families of copulas (Generalized Archimedean Copulas), the best fitting can be obtained looking all copula’s options (totally positive of order 2 and stochastically increasing models). / GPL-3	noarch
<a href="#">r-fgalgorithm</a>	1.0	This is a package for implementation of Flury-Gautschi algorithms. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-fgarch	3042.8	Provides a collection of functions to analyze and model heteroskedastic behavior in financial time series models. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
r-fgeo.x	1.1.4	Access small example datasets from Luquillo, a ForestGEO site in Puerto Rico (< <a href="https://forestgeo.si.edu/sites/north-america/luquillo">https://forestgeo.si.edu/sites/north-america/luquillo</a> >). / GPL-3	noarch
r-fgof	0.2_1	Goodness-of-fit test with multiplier or parametric bootstrap. / GPL-3	noarch
r-fgpt	2.3	A permutation technique to explore and control for spatial autocorrelation. This package contains low level functions for performing permutations and calculating statistics as well as higher level functions. Higher level functions are an easy to use function for performing spatially restricted permutation tests and summarize and plot results. / GPL-3	noarch
r-fgsg	1.0.2	Implement algorithms for feature grouping and selection over an undirected graph, solves problems like graph fused lasso, graph OSCAR and so on. / GPL-2	linux-64, osx-64, win-64
r-fgui	1.0_8	Rapidly create a GUI interface for a function you created by automatically creating widgets for arguments of the function. Automatically parses help routines for context-sensitive help to these arguments. The interface essentially a wrapper to some Tcl/Tk routines to both simplify and facilitate GUI creation. More advanced Tcl/Tk routines/GUI objects can be incorporated into the interface for greater customization for the more experienced. / GPL-3	noarch
r-fhdi	1.3.2	Impute general multivariate missing data with the fractional hot deck imputation based on Jaekwang Kim (2011) <doi:10.1093/biomet/asq073>. / GPL-2	linux-64, osx-64, win-64
r-fhidata	2019.8.27	Provides structural data for Norway. Datasets relating to maps, population in municipalities, vaccination coverage for childhood vaccines, municipality/county matching, and how different municipalities have merged/redistricted over time from 2006 to 2019. / GPL-3	noarch
r-fi	1.0	Provide functions for forest inventory calculations. Common volumetric equations (Smalian, Newton and Huber) as well stacking factor and form / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-fiberld</a>	0.1.6	Routines for estimating tree fiber (tracheid) length distributions in the standing tree based on increment core samples. Two types of data can be used with the package, increment core data measured by means of an optical fiber analyzer (OFA), e.g. such as the Kajaani Fiber Lab, or measured by microscopy. Increment core data analyzed by OFAs consist of the cell lengths of both cut and uncut fibres (tracheids) and fines (such as ray parenchyma cells) without being able to identify which cells are cut or if they are fines or fibres. The microscopy measured data consist of the observed lengths of the uncut fibres in the increment core. A censored version of a mixture of the fine and fiber length distributions is proposed to fit the OFA data, under distributional assumptions (Svensson et al., 2006) <doi:10.1111/j.1467-9469.2006.00501.x>. The package offers two choices for the assumptions of the underlying density functions of the true fiber (fine) lengths of those fibers (fines) that at least partially appear in the increment core, being the generalized gamma and the log normal densities. / GPL-2	noarch
<a href="#">r-filehash</a>	2.4.2	Implements a simple key-value style database where character string keys are associated with data values that are stored on the disk. A simple interface is provided for inserting, retrieving, and deleting data from the database. Utilities are provided that allow ‘filehash’ databases to be treated much like environments and lists are already used in R. These utilities are provided to encourage interactive and exploratory analysis on large datasets. Three different file formats for representing the database are currently available and new formats can easily be incorporated by third parties for use in the ‘filehash’ framework. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-filelock</a>	1.0.2	Place an exclusive or shared lock on a file. It uses ‘LockFile’ on Windows and ‘fcntl’ locks on Unix-like systems. / MIT	linux-64, osx-64, win-64
<a href="#">r-filematrix</a>	1.3	Interface for working with large matrices stored in files, not in computer memory. Supports multiple non-character data types (double, integer, logical and raw) of various sizes (e.g. 8 and 4 byte real values). Access to parts of the matrix is done by indexing, exactly as with usual R matrices. Supports very large matrices. Tested on multi-terabyte matrices. Allows for more than $2^{32}$ rows or columns. Allows for quick addition of extra columns to a filematrix. Cross-platform as the package has R code only. / LGPL-3	noarch
<a href="#">r-filenamer</a>	0.2.3	Create descriptive file names with ease. New file names are automatically (but optionally) time stamped and placed in date stamped directories. Streamline your analysis pipeline with input and output file names that have informative tags and proper file extensions. / GPL-3	noarch
<a href="#">r-files</a>	0.0.1	Functions for printing the contents of a folder as columns in a ragged-bottom data.frame and for viewing the details (size, time created, time modified, etc.) of a folder’s top level contents. / GPL-3	noarch
<a href="#">r-fillr</a>	0.1.1	Edit vectors to fill missing values, based on the vector itself. / MIT	noarch
<a href="#">r-fimport</a>	3042.85	Provides a collection of utility functions to download and manage data sets from the Internet or from other sources. / GPL-2	noarch
<a href="#">r-finana</a>	0.1.2	Functions for financial analysis and financial modeling, including batch graphs generation, beta calculation, descriptive statistics, annuity calculation, bond pricing and financial data download. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-financialinstrument</a>	1.3.1	Infrastructure for defining meta-data and relationships for financial instruments. / GPL-3	noarch
<a href="#">r-financialmath</a>	0.1.1	Contains financial math functions and introductory derivative functions included in the Society of Actuaries and Casualty Actuarial Society ‘Financial Mathematics’ exam, and some topics in the ‘Models for Financial Economics’ exam. / GPL-2	noarch
<a href="#">r-finasymp</a>	1.0	This package accomplishes two tasks: a) it classifies implicit trading activity from quotes in OTC markets using the algorithm of Lee and Ready (1991); b) based on information for trade initiation, the package computes the probability of informed trading of Easley and O’Hara (1987). / GPL-3	noarch
<a href="#">r-fincovregularization</a>	1.1.0	Estimation and regularization for covariance matrix of asset returns. For covariance matrix estimation, three major types of factor models are included: macroeconomic factor model, fundamental factor model and statistical factor model. For covariance matrix regularization, four regularized estimators are included: banding, tapering, hard-thresholding and soft- thresholding. The tuning parameters of these regularized estimators are selected via cross-validation. / GPL-2	noarch
<a href="#">r-findallroots</a>	1.0	Find all root(s) of the equation,including complex roots;Find root(s) of the equation by dichotomy.Besides,in dichotomy, more than one interval can be given at a time. / GPL-2	noarch
<a href="#">r-findpython</a>	1.0.5	Package designed to find an acceptable python binary. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-findr</a>	0.2.1	Scans all directories and subdirectories of a path for code snippets, R scripts, R Markdown, PDF or text files containing a specific pattern. Files found can be copied to a new folder. / GPL-3	noarch
<a href="#">r-finepop</a>	1.5.1	Statistical tool set for population genetics. The package provides following functions: 1) empirical Bayes estimator of Fst and other measures of genetic differentiation, 2) regression analysis of environmental effects on genetic differentiation using bootstrap method, 3) interfaces to read and manipulate ‘GENEPOP’ format data files and allele/haplotype frequency format files. / GPL (>= 2.0)	noarch
<a href="#">r-fingerprint</a>	3.5.7	Functions to manipulate binary fingerprints of arbitrary length. A fingerprint is represented by an object of S4 class ‘fingerprint’ which is internally represented a vector of integers, such that each element represents the position in the fingerprint that is set to 1. The bitwise logical functions in R are overridden so that they can be used directly with ‘fingerprint’ objects. A number of distance metrics are also available (many contributed by Michael Fadock). Fingerprints can be converted to Euclidean vectors (i.e., points on the unit hypersphere) and can also be folded using OR. Arbitrary fingerprint formats can be handled via line handlers. Currently handlers are provided for CDK, MOE and BCI fingerprint data. / GPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-fints	0.4.6	R companion to Tsay (2005) Analysis of Financial Time Series, second edition (Wiley). Includes data sets, functions and script files required to work some of the examples. Version 0.3-x includes R objects for all data files used in the text and script files to recreate most of the analyses in chapters 1-3 and 9 plus parts of chapters 4 and 11. / GPL-2	noarch
r-fire	1.0	The algorithm assigns rareness/ outlieriness score to every sample in voluminous datasets. The algorithm makes multiple estimations of the proximity between a pair of samples, in low-dimensional spaces. To compute proximity, FiRE uses Sketching, a variant of locality sensitive hashing. For more details: Jindal, A., Gupta, P., Jayadeva and Sengupta, D., 2018. Discovery of rare cells from voluminous single cell expression data. Nature Communications, 9(1), p.4719. <doi:10.1038/s41467-018-07234-6>. / GPL-3	linux-64, osx-64, win-64
r-fishdata	0.1.3	A collection of four datasets based around the population dynamics of migratory fish. Datasets contain both basic size information on a per fish basis, as well as otolith data that contains a per day record of fish growth history. All data in this package was collected by the author, from 2015-2016, in the Wellington region of New Zealand. / GPL-3	noarch
r-fisherem	1.5.1	The FisherEM algorithm, proposed by Bouveyron & Brunet (201) <doi:10.1007/s11222-011-9249-9>, is an efficient method for the clustering of high-dimensional data. FisherEM models and clusters the data in a discriminative and low-dimensional latent subspace. It also provides a low-dimensional representation of the clustered data. A sparse version of Fisher-EM algorithm is also provided. / GPL-2	noarch
r-fisheyer	0.9	fisheyeR provides tools for creating Interactive Data Visualizations by implementing ideas from Furnas, Munzner, Costa and Venturini. / GPL-2	noarch
r-fishical	1.1	FisHiCal integrates Hi-C and FISH data, offering a modular and easy-to-use tool for chromosomal spatial analysis. / GPL-3	linux-64, osx-64, win-64
r-fishkirkko2015	1.0.0	Dataset of 302 measurements of 11 fish species to accompany the manuscript Length-weight relationships of six freshwater fish species from lake Kirkkojarvi, Finland. / GPL-3	noarch
r-fishmethods	1.11	Functions for applying a wide range of fisheries stock assessment methods. / GPL-2	noarch
r-fishmod	0.29	Fits models to catch and effort data. Single-species models are 1) delta log-normal, 2) Tweedie, or 3) Poisson-gamma (G)LMs. / GPL-3	linux-64, osx-64, win-64
r-fishtree	0.3.1	An interface to the Fish Tree of Life API to download taxonomies, phylogenies, fossil calibrations, and diversification rate information for ray-finned fishes. / BSD_2_clause	noarch
r-fit.models	0.5.14	The fit.models function and its associated methods (coefficients, print, summary, plot, etc.) were originally provided in the robust package to compare robustly and classically fitted model objects. The aim of the fit.models package is to separate this fitted model object comparison functionality from the robust package and to extend it to support fitting methods (e.g., classical, robust, Bayesian, regularized, etc.) more generally. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-fitbitscraper</a>	0.1.8	Scrapes data from Fitbit <a href="http://www.fitbit.com">http://www.fitbit.com</a> . This does not use the official API, but instead uses the API that the web dashboard uses to generate the graphs displayed on the dashboard after login at <a href="http://www.fitbit.com">http://www.fitbit.com</a> . / MIT	noarch
<a href="#">r-fitdc</a>	0.0.1	A pure R package for decoding activity files written in the FIT (Flexible and Interoperable Data Transfer) format. A format that is fast becoming the standard for recording running and cycling data. Details of the FIT protocol can be found at <a href="https://www.thisisant.com/resources/fit">https://www.thisisant.com/resources/fit</a> . / MIT	noarch
<a href="#">r-fitdrc</a>	1.1.1	Fits Density Ratio Classes to elicited probability-quantile points or intervals. / GPL-2	noarch
<a href="#">r-fitpoly</a>	3.0.0	Genotyping assays for bi-allelic markers (e.g. SNPs) produce signal intensities for the two alleles. ‘fitPoly’ assigns genotypes (allele dosages) to a collection of polyploid samples based on these signal intensities. ‘fitPoly’ replaces the older package ‘fitTetra’ that was limited (a.o.) to only tetraploid populations whereas ‘fitPoly’ accepts any ploidy level. Reference: Voorrips RE, Gort G, Vosman B (2011) <doi:10.1186/1471-2105-12-172>. / GPL-2	noarch
<a href="#">r-fitsio</a>	2.1.0	Utilities to read and write files in the FITS (Flexible Image Transport System) format, a standard format in astronomy (see e.g. <a href="https://en.wikipedia.org/wiki/FITS">https://en.wikipedia.org/wiki/FITS</a> for more information). Present low-level routines allow: reading, parsing, and modifying FITS headers; reading FITS images (multi-dimensional arrays); reading FITS binary and ASCII tables; and writing FITS images (multi-dimensional arrays). Higher-level functions allow: reading files composed of one or more headers and a single (perhaps multidimensional) image or single table; reading tables into data frames; generating vectors for image array axes; scaling and writing images as 16-bit integers. Known incompletenesses are reading random group extensions, as well as bit, complex, and array descriptor data types in binary tables. / GPL-2	noarch
<a href="#">r-fittetra</a>	1.0	Package fitTetra contains three functions that can be used to assign genotypes to a collection of tetraploid samples based on biallelic marker assays. Functions fitTetra (to fit several models for one marker from the data and select the best fitting) or saveMarkerModels (calls fitTetra for multiple markers and saves the results to files) will probably be the most convenient to use. Function CodomMarker offers more control and fits one specified model for a given marker. / GPL (>= 2.2)	noarch
<a href="#">r-fivethirtyeight</a>	0.5.0	Datasets and code published by the data journalism website ‘FiveThirtyEight’ available at <a href="https://github.com/fivethirtyeight/data">https://github.com/fivethirtyeight/data</a> . Note that while we received guidance from editors at ‘FiveThirtyEight’, this package is not officially published by ‘FiveThirtyEight’. / MIT	noarch
<a href="#">r-fixedpoint</a>	0.6.1	For functions that take and return vectors (or scalars), this package provides 8 algorithms for finding fixed point vectors (vectors for which the inputs and outputs to the function are the same vector). These algorithms include Anderson (1965) acceleration <doi:10.1145/321296.321305>, epsilon extrapolation methods (Wynn 1962 <doi:10.2307/2004051>) and minimal polynomial methods (Cabay and Jackson 1976 <doi:10.1137/0713060>). / MIT	noarch
<a href="#">r-fixedtimeevents</a>	1.0	Distribution functions and test for over-representation of short distances in the Liland distribution. Simulation functions are included for comparison. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-fixest</a>	0.1.0	Fast and user-friendly estimation of econometric models with multiple fixed-effects. Includes ordinary least squares (OLS), generalized linear models (GLM) and the negative binomial. The core of the package is based on optimized parallel C code, scaling especially well for large data sets. The method to obtain the fixed-effects coefficients is based on Berge (2018) < <a href="https://www.en.uni.lu/content/download/110162/1299525/file/2018_13">https://www.en.uni.lu/content/download/110162/1299525/file/2018_13</a> >. Further provides tools to export and view the results of several estimations with intuitive design to cluster the standard-errors. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-fixseqmtp</a>	0.1.2	Several generalized / directional Fixed Sequence Multiple Testing Procedures (FSMTPs) are developed for testing a sequence of pre-ordered hypotheses while controlling the FWER, FDR and Directional Error (mdFWER). All three FWER controlling generalized FSMTPs are designed under arbitrary dependence, which allow any number of acceptances. Two FDR controlling generalized FSMTPs are respectively designed under arbitrary dependence and independence, which allow more but a given number of acceptances. Two mdFWER controlling directional FSMTPs are respectively designed under arbitrary dependence and independence, which can also make directional decisions based on the signs of the test statistics. The main functions for each proposed generalized / directional FSMTPs are designed to calculate adjusted p-values and critical values, respectively. For users' convenience, the functions also provide the output option for printing decision rules. / GPL-2	noarch
<a href="#">r-fizzbuzzr</a>	0.1.1	An implementation of the Fizz Buzz algorithm, as defined e.g. in < <a href="https://en.wikipedia.org/wiki/Fizz_buzz">https://en.wikipedia.org/wiki/Fizz_buzz</a> >. It provides the standard algorithm with 3 replaced by Fizz and 5 replaced by Buzz, with the option of specifying start and end numbers, step size and the numbers being replaced by fizz and buzz, respectively. This package gives interviewers the optional answer of I use fizzbuzzR::fizzbuzz() when interviewing rather than having to write an algorithm themselves. / GPL-3	noarch
<a href="#">r-flagr</a>	0.3.2	Three methods are implemented in R to facilitate the aggregations of flags in official statistics. From the underlying flags the highest in the hierarchy, the most frequent, or with the highest total weight is propagated to the flag(s) for EU or other aggregates. Below there are some reference documents for the topic: < <a href="https://sdmx.org/wp-content/uploads/CL_OBS_STATUS_v2_1.docx">https://sdmx.org/wp-content/uploads/CL_OBS_STATUS_v2_1.docx</a> >, < <a href="https://sdmx.org/wp-content/uploads/CL_CONF_STATUS_1_2_2018.docx">https://sdmx.org/wp-content/uploads/CL_CONF_STATUS_1_2_2018.docx</a> >, < <a href="http://ec.europa.eu/eurostat/data/database/information">http://ec.europa.eu/eurostat/data/database/information</a> >, < <a href="http://www.oecd.org/sdd/33869551.pdf">http://www.oecd.org/sdd/33869551.pdf</a> >, < <a href="https://sdmx.org/wp-content/uploads/CL_OBS_STATUS_implementation_20-10-2014.pdf">https://sdmx.org/wp-content/uploads/CL_OBS_STATUS_implementation_20-10-2014.pdf</a> >. / EUPL-1.1	noarch
<a href="#">r-flam</a>	3.2	Implements the fused lasso additive model as proposed in Petersen, A., Witten, D., and Simon, N. (2016). Fused Lasso Additive Model. Journal of Computational and Graphical Statistics, 25(4): 1005-1025. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-flamingos</a>	0.1.0	Provides a variety of original and flexible user-friendly statistical latent variable models for the simultaneous clustering and segmentation of heterogeneous functional data (i.e time series, or more generally longitudinal data, fitted by unsupervised algorithms, including EM algorithms. Functional Latent Data Models for Clustering heterogeneous curves ('FLaMingos') are originally introduced and written in 'Matlab' by Faicel Chamroukhi < <a href="https://github.com/fchamroukhi?utf8=?&amp;tab=repositories&amp;q=mix&amp;type=public&amp;language=matlab">https://github.com/fchamroukhi?utf8=?&amp;tab=repositories&amp;q=mix&amp;type=public&amp;language=matlab</a> >. The references are mainly the following ones. Chamroukhi F. (2010) < <a href="https://chamroukhi.com/FChamroukhi-PhD.pdf">https://chamroukhi.com/FChamroukhi-PhD.pdf</a> >. Chamroukhi F., Same A., Govaert, G. and Aknin P. (2010) <doi:10.1016/j.neucom.2009.12.023>. Chamroukhi F., Same A., Aknin P. and Govaert G. (2011). <doi:10.1109/IJCNN.2011.6033590>. Same A., Chamroukhi F., Govaert G. and Aknin, P. (2011) <doi:10.1007/s11634-011-0096-5>. Chamroukhi F., and Glotin H. (2012) <doi:10.1109/IJCNN.2012.6252818>. Chamroukhi F., Glotin H. and Same A. (2013) <doi:10.1016/j.neucom.2012.10.030>. Chamroukhi F. (2015) < <a href="https://chamroukhi.com/FChamroukhi-HDR.pdf">https://chamroukhi.com/FChamroukhi-HDR.pdf</a> >. Chamroukhi F. and Nguyen H-D. (2019) <doi:10.1002/widm.1298>. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-flare</a>	1.6.0	Provide the implementation of a family of Lasso variants including Dantzig Selector, LAD Lasso, SQRT Lasso, Lq Lasso for estimating high dimensional sparse linear model. We adopt the alternating direction method of multipliers and convert the original optimization problem into a sequential L1 penalized least square minimization problem, which can be efficiently solved by linearization algorithm. A multi-stage screening approach is adopted for further acceleration. Besides the sparse linear model estimation, we also provide the extension of these Lasso variants to sparse Gaussian graphical model estimation including TIGER and CLIME using either L1 or adaptive penalty. Missing values can be tolerated for Dantzig selector and CLIME. The computation is memory-optimized using the sparse matrix output. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-flashclust</a>	1.01	Fast implementation of hierarchical clustering / GPL-2	linux-64, osx-64, win-64
<a href="#">r-flatxml</a>	0.0.2	On import, the XML information is converted to a dataframe that reflects the hierarchical XML structure. Intuitive functions allow to navigate within this transparent XML data structure (without any knowledge of 'XPath'). 'flatXML' also provides tools to extract data from the XML into a flat dataframe that can be used to perform statistical operations. / GPL-3	noarch
<a href="#">r-flexclust</a>	1.4.0	The main function kcca implements a general framework for k-centroids cluster analysis supporting arbitrary distance measures and centroid computation. Further cluster methods include hard competitive learning, neural gas, and QT clustering. There are numerous visualization methods for cluster results (neighborhood graphs, convex cluster hulls, barcharts of centroids, ...), and bootstrap methods for the analysis of cluster stability. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-flexdashboard</a>	0.5.1	Format for converting an R Markdown document to a grid oriented dashboard. The dashboard flexibly adapts the size of it's components to the containing web page. / MIT	noarch

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Table 51 – continued from previous page

Name	Version	Summary/License	Platforms
<a href="#">r-flexdir</a>	1.0	Provides tools to work with the Flexible Dirichlet distribution. The main features are an E-M algorithm for computing the maximum likelihood estimate of the parameter vector and a function based on conditional bootstrap to estimate its asymptotic variance-covariance matrix. It contains also functions to plot graphs, to generate random observations and to handle compositional data. / GPL-2	noarch
<a href="#">r-flexmet</a>	1.0.0	Application of the filtered monotonic polynomial (FMP) item response model to flexibly fit item response models. The package includes tools that allow the item response model to be build on any monotonic transformation of the latent trait metric, as described by Feuerstahler (2016) < <a href="http://hdl.handle.net/11299/182267">http://hdl.handle.net/11299/182267</a> >. / GPL-3	noarch
<a href="#">r-flexmix</a>	2.3_1	A general framework for finite mixtures of regression models using the EM algorithm is implemented. The E-step and all data handling are provided, while the M-step can be supplied by the user to easily define new models. Existing drivers implement mixtures of standard linear models, generalized linear models and model-based clustering. / GPL-2	noarch
<a href="#">r-flexparamcurve</a>	1.5_5	Model selection tools and ‘selfStart’ functions to fit parametric curves in ‘nls’, ‘nlsList’ and ‘nlme’ frameworks. / GPL-2	noarch
<a href="#">r-flexpm</a>	2.0	Estimation of flexible parametric models for survival data. / GPL-2	noarch
<a href="#">r-flickrapi</a>	0.1.0	Provides an interface to the Flickr API < <a href="https://www.flickr.com/services/api/">https://www.flickr.com/services/api/</a> > and allows R users to download data on Flickr. / GPL-2	noarch
<a href="#">r-flipscores</a>	0.2	Provides robust tests for testing in GLMs, by sign-flipping score contributions. The tests are often robust against overdispersion, heteroscedasticity and, in some cases, ignored nuisance variables. See Hemerik and Goeman (2017) < <a href="https://doi.org/10.1007/s11749-017-0571-1">doi:10.1007/s11749-017-0571-1</a> >. / GPL-3	noarch
<a href="#">r-flat</a>	1.2_1	Fits the Fused Lasso Latent Feature model, which is used for modeling multi-sample aCGH data to identify regions of copy number variation (CNV). Produces a set of features that describe the patterns of CNV and a set of weights that describe the composition of each sample. Also provides functions for choosing the optimal tuning parameters and the appropriate number of features, and for estimating the false discovery rate. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-float</a>	0.2_3	R comes with a suite of utilities for linear algebra with numeric (double precision) vectors/matrices. However, sometimes single precision (or less!) is more than enough for a particular task. This package extends R’s linear algebra facilities to include 32-bit float (single precision) data. Float vectors/matrices have half the precision of their numeric-type counterparts but are generally faster to numerically operate on, for a performance vs accuracy trade-off. The internal representation is an S4 class, which allows us to keep the syntax identical to that of base R’s. Interaction between floats and base types for binary operators is generally possible; in these cases, type promotion always defaults to the higher precision. The package ships with copies of the single precision ‘BLAS’ and ‘LAPACK’, which are automatically built in the event they are not available on the system. / BSD_2_clause	linux-64, osx-64, win-64
<a href="#">r-flock</a>	0.7	Implements synchronization between R processes (spawned by using the parallel package for instance) using file locks. Supports both exclusive and shared locking. / Apache License 2.0	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-flower	1.0	Flowering is an important life history trait of flowering plants. It has been mainly analyzed with respect to flowering onset and duration of flowering. This tools provide some functions to compute the temporal distribution of an flowering individual related to other population members. fCV() measures the temporal variation in flowering. Rlind() measures the rank order of flowering for individual plants within a population. SI(), SI2(), SI3(), and SI4() calculate flowering synchrony with different methods. / GPL ( $\geq 1.0$ )	noarch
r-flowfield	1.0	Flow field forecasting draws information from an interpolated flow field of the observed time series to incrementally build a forecast. / GPL-3	noarch
r-flowregenvcost	0.1.1	An application to calculate the daily environmental costs of river flow regulation by dams based on Garc�a de Jalon et al. 2017 <doi:10.1007/s11269-017-1663-0>. / MIT	noarch
r-flows	1.1.1	Selections on flow matrices, statistics on selected flows, map and graph visualisations. / GPL-3	noarch
r-flr	1.0	FLR algorithm for classification / GPL-2	noarch
r-flsa	1.5.1	Implements a path algorithm for the Fused Lasso Signal Approximator. For more details see the help files or the article by Hoeffling (2009) <arXiv:0910.0526>. / GPL-2	linux-64, osx-64, win-64
r-fluosurv	1.0.0	Use spectrophotometry measurements performed on insects as a way to infer pathogens virulence. Insect movements cause fluctuations in fluorescence signal, and functions are provided to estimate when the insect has died as the moment when variance in autofluorescence signal drops to zero. The package provides functions to obtain this estimate together with functions to import spectrophotometry data from a Biotek microplate reader. Details of the method are given in Parthuisot et al. (2018) <doi:10.1101/297929>. / GPL-3	noarch
r-flury	0.1_3	Contains data sets from Bernard Flury (1997) A First Course in Multivariate Statistics, Springer NY / GPL-2	noarch
r-flux	0.3_0	Functions for the calculation of greenhouse gas flux rates from closed chamber concentration measurements. The package follows a modular concept: Fluxes can be calculated in just two simple steps or in several steps if more control in details is wanted. Additionally plot and preparation functions as well as functions for modelling gpp and reco are provided. / GPL-2	noarch
r-fluxweb	0.2.0	Compute energy fluxes in trophic networks, from resources to their consumers, and can be applied to systems ranging from simple two-species interactions to highly complex food webs. It implements the approach described in Gauzens et al. (2017) <doi:10.1101/229450> to calculate energy fluxes, which are also used to calculate equilibrium stability. / GPL ( $\geq 2.0$ )	noarch
r-fmcmc	0.2_0	Provides a friendly (flexible) Markov Chain Monte Carlo (MCMC) framework for implementing Metropolis-Hastings algorithm in a modular way allowing users to specify automatic convergence checker, personalized transition kernels, and out-of-the-box multiple MCMC chains using parallel computing. Most of the methods implemented in this package can be found in Brooks et al. (2011, ISBN 9781420079425). / MIT	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-fmdates</a>	0.1.4	Implements common date calculations relevant for specifying the economic nature of financial market contracts that are typically defined by International Swap Dealer Association (ISDA, < <a href="http://www2.isda.org">http://www2.isda.org</a> >) legal documentation. This includes methods to check whether dates are business days in certain locales, functions to adjust and shift dates and time length (or day counter) calculations. / GPL-2	noarch
<a href="#">r-fmp</a>	1.4	Estimates Filtered Monotonic Polynomial IRT Models as described by Liang and Browne (2015) <DOI:10.3102/1076998614556816>. / GPL-2	noarch
<a href="#">r-fmrs</a>	1.0.9	Provides parameter estimation as well as variable selection in Finite Mixture of Accelerated Failure Time Regression and Finite Mixture of Regression Models. Furthermore, this package provides Ridge Regression and Elastic Net. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-fmsb</a>	0.6.3	Several utility functions for the book entitled Practices of Medical and Health Data Analysis using R (Pearson Education Japan, 2007) with Japanese demographic data and some demographic analysis related functions. / GPL-2	noarch
<a href="#">r-fmsmsnreg</a>	1.0	Fit linear regression models where the random errors follow a finite mixture of of Skew Heavy-Tailed Errors. / GPL-2	noarch
<a href="#">r-fmstable</a>	0.1.2	This package implements some basic procedures for dealing with log maximally skew stable distributions, which are also called finite moment log stable distributions. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-fnn</a>	1.1.3	Cover-tree and kd-tree fast k-nearest neighbor search algorithms and related applications including KNN classification, regression and information measures are implemented. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-fnonlinear</a>	3042.7	Provides a collection of functions for testing various aspects of univariate time series including independence and neglected nonlinearities. Further provides functions to investigate the chaotic behavior of time series processes and to simulate different types of chaotic time series maps. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-foba</a>	0.1	foba is a package that implements forward, backward, and foba sparse learning algorithms for ridge regression, described in the paper Adaptive Forward-Backward Greedy Algorithm for Learning Sparse Representations. / GPL-2	noarch
<a href="#">r-focusedmds</a>	1.3.3	Takes a distance matrix and plots it as an interactive graph. One point is focused at the center of the graph, around which all other points are plotted in their exact distances as given in the distance matrix. All other non-focus points are plotted as best as possible in relation to one another. Double click on any point to choose a new focus point, and hover over points to see their ID labels. If color label categories are given, hover over colors in the legend to highlight only those points and click on colors to highlight multiple groups. For more information on the rationale and mathematical background, as well as an interactive introduction, see < <a href="https://lea-urpa.github.io/focusedMDS.html">https://lea-urpa.github.io/focusedMDS.html</a> >. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-folderfun</a>	0.1.2	If you find yourself working on multiple different projects in R, you'll want a series of folders pointing to raw data, processed data, plot results, intermediate table outputs, etc. This package makes it easier to do that by providing a quick and easy way to create and use functions for project-level directories. / BSD_2_clause	noarch
<a href="#">r-fontbitstreamvera</a>	0.1.1	Provides fonts licensed under the 'Bitstream Vera Fonts' license for the 'fontquiver' package. / file LICENCE (FOSS)	noarch
<a href="#">r-fontcm</a>	1.1	Computer Modern font for use with extrafont package / GPL-2	noarch
<a href="#">r-fontliberation</a>	0.1.0	A placeholder for the Liberation fontset intended for the <i>fontquiver</i> package. This fontset covers the 12 combinations of families (sans, serif, mono) and faces (plain, bold, italic, bold italic) supported in R graphics devices. / file LICENSE (FOSS)	noarch
<a href="#">r-foolbox</a>	0.1.1	Provides functionality for manipulating functions and translating them in metaprogramming. / GPL-3	noarch
<a href="#">r-foptions</a>	3042.86	Provides a collection of functions to valuate basic options. This includes the generalized Black-Scholes option, options on futures and options on commodity futures. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-forcats</a>	0.4.0	Helpers for reordering factor levels (including moving specified levels to front, ordering by first appearance, reversing, and randomly shuffling), and tools for modifying factor levels (including collapsing rare levels into other, 'anonymising', and manually 'recoding'). / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-foreach</a>	1.4.4	Support for the foreach looping construct. Foreach is an idiom that allows for iterating over elements in a collection, without the use of an explicit loop counter. This package in particular is intended to be used for its return value, rather than for its side effects. In that sense, it is similar to the standard lapply function, but doesn't require the evaluation of a function. Using foreach without side effects also facilitates executing the loop in parallel. / Apache License (== 2.0)	linux-32, linux-64, noarch, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
<code>r-forecast</code>	8.6	Methods and tools for displaying and analysing univariate time series forecasts including exponential smoothing via state space models and automatic ARIMA modelling. / GPL-3	linux-32, linux-64, osx-64, win-32, win-64
<code>r-forecastcombinations</code>	1.1	Aim: Supports the most frequently used methods to combine forecasts. Among others: Simple average, Ordinary Least Squares, Least Absolute Deviation, Constrained Least Squares, Variance-based, Best Individual model, Complete subset regressions and Information-theoretic (information criteria based). / GPL-2	noarch
<code>r-forecastsnsts</code>	1.3_0	Methods to compute linear h-step ahead prediction coefficients based on localised and iterated Yule-Walker estimates and empirical mean squared and absolute prediction errors for the resulting predictors. Also, functions to compute autocovariances for AR(p) processes, to simulate tvARMA(p,q) time series, and to verify an assumption from Kley et al. (2019), Electronic of Statistics, forthcoming. Preprint <arXiv:1611.04460>. / GPL-2	linux-64, osx-64, win-64
<code>r-foreign</code>	0.8_7	Reading and writing data stored by some versions of ‘Epi Info’, ‘Minitab’, ‘S’, ‘SAS’, ‘SPSS’, ‘Stata’, ‘Systat’, ‘Weka’, and for reading and writing some ‘dBase’ files. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-forestfit</a>	0.4	Developed for the following tasks. I) Computing the probability density function, cumulative distribution function, random generation, and estimating the parameters of the eleven mixture models including mixture of Birnbaum-Saunders, BurrXII, Chen, F, Frechet, gamma, Gompertz, log-logistic, log-normal, Lomax, and Weibull. II) Point estimation of the parameters of two- and three-parameter Weibull distributions. In the case of two-parameter, twelve methods consist of generalized least square type 1, generalized least square type 2, L-moment, maximum likelihood, logarithmic moment, moment, percentile, rank correlation, least square, weighted maximum likelihood, U-statistic, weighted least square are used and investigated methods for the three-parameter case are: maximum likelihood, modified moment type 1, modified moment type 2, modified moment type 3, modified maximum likelihood type 1, modified maximum likelihood type 2, modified maximum likelihood type 3, modified maximum likelihood type 4, moment, maximum product spacing, T-L moment, and weighted maximum likelihood. III) The Bayesian estimators of the three-parameter Weibull distribution. IV) Estimating parameters of the three-parameter Weibull distribution fitted to grouped data using three methods including approximated maximum likelihood, expectation maximization, and maximum likelihood. V) Estimating the parameters of the gamma, log-normal, and Weibull mixture models fitted to the grouped data through the EM algorithm. VI) Estimating parameters of the non-linear growth curve fitted to the height-diameter observations. / GPL-2	noarch
<a href="#">r-foresthes</a>	1.0_1	Assessing forest ecosystem health is an effective way for forest resource management. The national forest health evaluation system at the forest stand level using analytic hierarchy process, has a high application value and practical significance. The package can effectively and easily realize the total assessment process, and help foresters to further assess and management forest resources. / GPL-2	noarch
<a href="#">r-forestplot</a>	1.9	A forest plot that allows for multiple confidence intervals per row, custom fonts for each text element, custom confidence intervals, text mixed with expressions, and more. The aim is to extend the use of forest plots beyond meta-analyses. This is a more general version of the original 'rmeta' package's forestplot() function and relies heavily on the 'grid' package. / GPL-2	noarch
<a href="#">r-foretell</a>	0.2.0	Project Customer Retention based on Beta Geometric, Beta Discrete Weibull and Latent Class Discrete Weibull Models. This package is based on Fader and Hardie (2007) <doi:10.1002/dir.20074> and Fader and Hardie et al. (2018) <doi:10.1016/j.intmar.2018.01.002>. / GPL-3	noarch
<a href="#">r-forge</a>	0.2.0	Helper functions with a consistent interface to coerce and verify the types and shapes of values for input checking. / Apache License (>= 2.0)	noarch
<a href="#">r-forit</a>	1.0	This package provides estimates of tree volume and biomass from Italian NFI models / GPL-3	noarch
<a href="#">r-formalseries</a>	1.0	Implemented, addition, subtracking, multiplication, division in formal series rings of any number of variables (except division is only to 3 variables). Also are available [ <- operators. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-formatr</a>	1.6	Provides a function <code>tidy_source()</code> to format R source code. Spaces and indent will be added to the code automatically, and comments will be preserved under certain conditions, so that R code will be more human-readable and tidy. There is also a Shiny app as a user interface in this package (see <code>tidy_app()</code> ). / GPL	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-formattable</a>	0.2.0	Provides functions to create formattable vectors and data frames. ‘Formattable’ vectors are printed with text formatting, and formattable data frames are printed with multiple types of formatting in HTML to improve the readability of data presented in tabular form rendered in web pages. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-formula</a>	1.2_3	Infrastructure for extended formulas with multiple parts on the right-hand side and/or multiple responses on the left-hand side (see <DOI:10.18637/jss.v034.i01>). / GPL-2   GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-fortunes</a>	1.5_4	A collection of fortunes from the R community. / GPL-2   GPL-3	noarch
<a href="#">r-forward</a>	1.0.4	Robust analysis using forward search in linear and generalized linear regression models, as described in Atkinson, A.C. and Riani, M. (2000), Robust Diagnostic Regression Analysis, First Edition. New York: Springer. / GPL-2	noarch
<a href="#">r-forwards</a>	0.1.3	Anonymized data from surveys conducted by Forwards < <a href="https://forwards.github.io/">https://forwards.github.io/</a> >, the R Foundation task force on women and other under-represented groups. Currently, a single data set of responses to a survey of attendees at useR! 2016 < <a href="https://www.r-project.org/useR-2016/">https://www.r-project.org/useR-2016/</a> >, the R user conference held at Stanford University, Stanford, California, USA, June 27 - June 30 2016. / CC0	noarch
<a href="#">r-forwardsearch</a>	1.0	Forward Search analysis of time series regressions. Implements the asymptotic theory developed in Johansen and Nielsen (2013, 2014). / GPL-3	noarch
<a href="#">r-foto</a>	1.0.0	The Fourier Transform Textural Ordination method uses a principal component analysis on radially averaged two dimensional Fourier spectra to characterize image texture. / AGPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-fourgametep</a>	0.1.0	The four-gamete test is based on the infinite-sites model which assumes that the probability of the same mutation occurring twice (recurrent or parallel mutations) and the probability of a mutation back to the original state (reverse mutations) are close to zero. Without these types of mutations, the only explanation for observing the four dilocus genotypes (example below) is recombination (Hudson and Kaplan 1985, Genetics 111:147-164). Thus, the presence of all four gametes is also called phylogenetic incompatibility. / GPL-2	noarch
<a href="#">r-fourierin</a>	0.2.4	Computes Fourier integrals of functions of one and two variables using the Fast Fourier transform. The Fourier transforms must be evaluated on a regular grid for fast evaluation. / MIT	linux-64, osx-64, win-64
<a href="#">r-fourpno</a>	1.0.5	Estimate Barton & Lord's (1981) <doi:10.1002/j.2333-8504.1981.tb01255.x> four parameter IRT model with lower and upper asymptotes using Bayesian formulation described by Culpepper (2016) <doi:10.1007/s11336-015-9477-6>. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-fourscores</a>	1.5.1	A game for two players: Who gets first four in a row (horizontal, vertical or diagonal) wins. As board game published by Milton Bradley, designed by Howard Wexler and Ned Strongin. / GPL-3	noarch
<a href="#">r-fpca2d</a>	1.0	Compute the two dimension functional principal component scores for a series of two dimension images. / GPL-3	noarch
<a href="#">r-fpca3d</a>	1.0	Run three dimensional functional principal component analysis and return the three dimensional functional principal component scores. The details of the method are explained in Lin et al.(2015) <doi:10.1371/journal.pone.0132945>. / GPL-2   GPL-3	noarch
<a href="#">r-fpcompare</a>	0.2.3	Comparisons of floating point numbers are problematic due to errors associated with the binary representation of decimal numbers. Despite being aware of these problems, people still use numerical methods that fail to account for these and other rounding errors (this pitfall is the first to be highlighted in Circle 1 of Burns (2012) 'The R Inferno' < <a href="http://www.burns-stat.com/pages/Tutor/R_inferno.pdf">http://www.burns-stat.com/pages/Tutor/R_inferno.pdf</a> >). This package provides new relational operators useful for performing floating point number comparisons with a set tolerance. / GPL-3	noarch
<a href="#">r-fpeek</a>	0.1.1	Tools to help text files importation. It can return the number of lines; print the first and last lines; convert encoding. Operations are made without reading the entire file before starting, resulting in good performances with large files. This package provides an alternative to a simple use of the 'head', 'tail', 'wc' and 'iconv' programs that are not always available on machine where R is installed. / MIT	linux-64, osx-64, win-64
<a href="#">r-fpest</a>	0.1.1	Given the values of sampled units and selection probabilities the desraj function in the package computes the estimated value of the total as well as estimated variance. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-fpop	2019.08.26	Dynamic programming algorithm for the fast segmentation of univariate signals into piecewise constant profiles. The ‘fpop’ package is a wrapper to a C implementation of the fpop (Functional Pruning Optimal Partitioning) algorithm described in Maidstone et al. 2017 <doi:10.1007/s11222-016-9636-3>. The problem of detecting changepoints in an univariate sequence is formulated in terms of minimising the mean squared error over segmentations. The fpop algorithm exactly minimizes the mean squared error for a penalty linear in the number of changepoints. / LGPL-2.1	linux-64, osx-64, win-64
r-fpow	0.0_2	Returns the noncentrality parameter of the noncentral F distribution if probability of type I and type II error, degrees of freedom of the numerator and the denominator are given. It may be useful for computing minimal detectable differences for general ANOVA models. This program is documented in the paper of A. Baharev, S. Kemeny, On the computation of the noncentral F and noncentral beta distribution; Statistics and Computing, 2008, 18 (3), 333-340. / CC0	linux-64, osx-64, win-64
r-fptdapprox	2.1	Efficient approximation of first-passage-time densities for diffusion processes based on the First-Passage-Time Location (FPTL) function. / GPL-2	noarch
r-fracdiff	1.4_2	Maximum likelihood estimation of the parameters of a fractionally differenced ARIMA(p,d,q) model (Haslett and Raftery, Appl.Statistics, 1989). / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
r-fracprolif	1.0.7	Functions for fitting data to a quiescent growth model, i.e. a growth process that involves members of the population who stop dividing or propagating. / GPL-2	noarch
r-fractaldim	0.8_4	Implements various methods for estimating fractal dimension of time series and 2-dimensional data. / GPL-2	noarch
r-fractalparameterestimation	1.1.2	The parameters p and q are estimated with the aid of a randomized Sierpinski Carpet which is built on a [p-p-p-q]-model. Thereby, for three times a simulation with a p-value and once with a q-value is assumed. Hence, these parameters are estimated and displayed. Moreover, functions for simulating random Sierpinski-Carpets with constant and variable probabilities are included. For more details on the method please see Hermann et al. (2015) <doi:10.1002/sim.6497>. / GPL-2	noarch
r-fraction	1.0	This is the package which can help you turn numeric,dataframe,matrix into fraction form. / GPL-2	noarch
r-fractional	0.1.3	The main function of this package allows numerical vector objects to be displayed with their values in vulgar fractional form. This is convenient if patterns can then be more easily detected. In some cases replacing the components of a numeric vector by a rational approximation can also be expected to remove some component of round-off error. The main functions form a re-implementation of the functions ‘fractions’ and ‘rational’ of the MASS package, but using a radically improved programming strategy. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-fragman</a>	1.0.9	Performs fragment analysis using genetic data coming from capillary electrophoresis machines. These are files with FSA extension which stands for FASTA-type file, and .txt files from Beckman CEQ 8000 system, both contain DNA fragment intensities read by machinery. In addition to visualization, it performs automatic scoring of SSRs (Sample Sequence Repeats; a type of genetic marker very common across the genome) and other type of PCR markers (standing for Polymerase Chain Reaction) in biparental populations such as F1, F2, BC (backcross), and diversity panels (collection of genetic diversity). / GPL-3	noarch
<a href="#">r-frailtyhl</a>	2.2	Implements the h-likelihood estimation procedures for general frailty models including competing-risk models and joint models. / Unlimited	noarch
<a href="#">r-frambgrowth</a>	0.1.0	Generation of theoretical size distributions of framboidal or sunflower pyrite. The growth mechanisms used are surface and supply controlled and dependent or independent of size. The algorithms are fully described in the published work in Mineralogy and Petrology journal: Theoretical growth of framboidal and sunflower pyrite using the R-package frambgrowth The authors Merinero, R., and Cardenes, V. (2018). <DOI:10.1007/s00710-017-0535-x>. / GPL-2	noarch
<a href="#">r-franc</a>	1.1.2	With no external dependencies and support for 335 languages; all languages spoken by more than one million speakers. ‘Franc’ is a port of the ‘JavaScript’ project of the same name, see < <a href="https://github.com/woorm/franc">https://github.com/woorm/franc</a> >. / MIT	noarch
<a href="#">r-frapplot</a>	0.1.3	Automatically process Fluorescence Recovery After Photobleaching (FRAP) data and generate consistent, publishable figures. Note: this package does not replace ‘ImageJ’ (or its equivalence) in raw image quantification. Some references about the methods: Sprague, Brian L. (2004) <doi:10.1529/biophysj.103.026765>; Day, Charles A. (2012) <doi:10.1002/0471142956.cy0219s62>. / MIT	noarch
<a href="#">r-frbs</a>	3.1.0	An implementation of various learning algorithms based on fuzzy rule-based systems (FRBSs) for dealing with classification and regression tasks. Moreover, it allows to construct an FRBS model defined by human experts. FRBSs are based on the concept of fuzzy sets, proposed by Zadeh in 1965, which aims at representing the reasoning of human experts in a set of IF-THEN rules, to handle real-life problems in, e.g., control, prediction and inference, data mining, bioinformatics data processing, and robotics. FRBSs are also known as fuzzy inference systems and fuzzy models. During the modeling of an FRBS, there are two important steps that need to be conducted: structure identification and parameter estimation. Nowadays, there exists a wide variety of algorithms to generate fuzzy IF-THEN rules automatically from numerical data, covering both steps. Approaches that have been used in the past are, e.g., heuristic procedures, neuro-fuzzy techniques, clustering methods, genetic algorithms, squares methods, etc. Furthermore, in this version we provide a universal framework named ‘frbsPMML’, which is adopted from the Predictive Model Markup Language (PMML), for representing FRBS models. PMML is an XML-based language to provide a standard for describing models produced by data mining and machine learning algorithms. Therefore, we are allowed to export and import an FRBS model to/from ‘frbsPMML’. Finally, this package aims to implement the most widely used standard procedures, thus offering a standard package for FRBS modeling to the R community. / GPL-2	noarch
<a href="#">r-frecc</a>	1.0	This package implements the functions associated with Fast Regularized Canonical Correlation Analysis. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-freegroup	1.1.0	Provides functionality for manipulating elements of the free group (juxtaposition is represented by a plus) including inversion, multiplication by a scalar, group-theoretic power operation, and Tietze forms. The package is fully vectorized. / GPL-2	noarch
r-freeknotsplines	1.0.1	Algorithms for fitting free-knot splines for data with one independent variable and one dependent variable. Four free-knot spline algorithms are provided for the case where the number of knots is known in advance. A knot-search algorithm is provided for the case where the number of knots is not known in advance. In addition, methods are available to compute the fitted values, the residuals, and the coefficients of the splines, and to plot the results, along with a method to summarize the results. / GPL-2	linux-64, osx-64, win-64
r-freestats	0.0.3	A collections of useful statistical functions used in Columbia course W4240/W4400. / BSD_3_clause	noarch
r-freesurferformats	0.1.0	Provides functions to read data from neuroimaging files in 'FreeSurfer' < <a href="http://freesurfer.net/">http://freesurfer.net/</a> > binary formats. This includes the following file formats: 1) MGH/MGZ format files, which can contain multi-dimensional images or other data. Typically they contain time-series of three-dimensional brain scans acquired by magnetic resonance imaging (MRI). They can also contain vertex-wise measures of surface morphometry data. The MGH format is named after the Massachusetts General Hospital, and the MGZ format is a compressed version of the same format. 2) 'FreeSurfer' morphometry data files in binary 'curv' format. These contain vertex-wise surface measures, i.e., one scalar value for each vertex of a brain surface mesh. These are typically values like the cortical thickness or brain surface area at each vertex. / MIT	noarch
r-fregression	3042.82	A collection of functions for linear and non-linear regression modelling. It implements a wrapper for several regression models available in the base and contributed packages of R. / GPL-2	noarch
r-freq	1.0	Real capture frequencies will be fitted to various distributions which provide the basis of estimating population sizes, their standard error, and symmetric as well as asymmetric confidence intervals. / GPL-2	noarch
r-freqdist	0.1	Generates a frequency distribution. The frequency distribution includes raw frequencies, percentages in each category, and cumulative frequencies. The frequency distribution can be stored as a data frame. / GPL-2	noarch
r-frlr	1.1	When fitting a set of linear regressions which have some same variables, we can separate the matrix and reduce the computation cost. This package aims to fit a set of repeated linear regressions faster. More details can be found in this blog Lijun Wang (2017) < <a href="https://stats.hohoweiya.xyz/2017/09/26/An-R-Package-Fit-Repeated-Linear-Regressions/">https://stats.hohoweiya.xyz/2017/09/26/An-R-Package-Fit-Repeated-Linear-Regressions/</a> >. / GPL-2	linux-64, osx-64, win-64
r-frm	1.2.2	Estimation and specification analysis of one- and two-part fractional regression models and calculation of partial effects. / GPL-2	noarch
r-frmhet	1.1.3	Estimation and specification analysis of fractional regression models with neglected heterogeneity and/or endogenous covariates. / GPL-2	noarch
r-frmpd	1.1.0	Estimation of panel data regression models for fractional responses. / GPL-2	noarch
r-fromo	0.2.1	Fast, numerically robust computation of weighted moments via 'Rcpp'. Supports computation on vectors and matrices, and Monoidal append of moments. Moments and cumulants over running fixed length windows can be computed, as well as over time-based windows. Moment computations are via a generalization of Welford's method, as described by Bennett et. (2009) <doi:10.1109/CLUSTER.2009.5289161>. / LGPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-frost	0.0.4	A compilation of empirical methods used by farmers and agronomic engineers to predict the minimum temperature to detect a frost night. These functions use variables such as environmental temperature, relative humidity, and dew point. See < <a href="http://sedici.unlp.edu.ar/handle/10915/72102">http://sedici.unlp.edu.ar/handle/10915/72102</a> > < <a href="http://www.fao.org/docrep/008/y7223e/y7223e0b.htm#bm11.8">http://www.fao.org/docrep/008/y7223e/y7223e0b.htm#bm11.8</a> > for details. / MIT	noarch
r-frt	0.1	Perform full randomization tests. / GPL-2	noarch
r-fs	1.2.7	A cross-platform interface to file system operations, built on top of the 'libuv' C library. / GPL-3	linux-64, osx-64, win-32, win-64
r-fsadata	0.3.8	The datasets to support the Fish Stock Assessment ('FSA') package. / GPL-2	noarch
r-fselectorrccpp	0.3.1	'Rccpp' (free of 'Java'/'Weka') implementation of 'FSelector' entropy-based feature selection algorithms based on an MDL discretization (Fayyad U. M., Irani K. B.: Multi-Interval Discretization of Continuous-Valued Attributes for Classification Learning. In 13'th International Joint Conference on Uncertainty in Artificial Intelligence (IJCAI93), pages 1022-1029, Chambéry, France, 1993.) < <a href="https://www.ijcai.org/Proceedings/93-2/Papers/022.pdf">https://www.ijcai.org/Proceedings/93-2/Papers/022.pdf</a> > with a sparse matrix support. It is also equipped with a parallel backend. / GPL-2	linux-64, osx-64, win-64
r-fsia	1.1.1	Import data of tests and questionnaires from FormScanner. FormScanner is an open source software that converts scanned images to data using optical mark recognition (OMR) and it can be downloaded from < <a href="http://sourceforge.net/projects/formscanner/">http://sourceforge.net/projects/formscanner/</a> >. The spreadsheet file created by FormScanner is imported in a convenient format to perform the analyses provided by the package. These analyses include the conversion of multiple responses to binary (correct/incorrect) data, the computation of the number of corrected responses for each subject or item, scoring using weights, the computation and the graphical representation of the frequencies of the responses to each item and the report of the responses of a few subjects. / GPL-3	noarch
r-fsinteract	0.1.2	Performs fast detection of interactions in large-scale data using the method of random intersection trees introduced in Shah, R. D. and Meinshausen, N. (2014) < <a href="http://www.jmlr.org/papers/v15/shah14a.html">http://www.jmlr.org/papers/v15/shah14a.html</a> >. The algorithm finds potentially high-order interactions in high-dimensional binary two-class classification data, without requiring lower order interactions to be informative. The search is particularly fast when the matrices of predictors are sparse. It can also be used to perform market basket analysis when supplied with a single binary data matrix. Here it will find collections of columns which for many rows contain all 1's. / GPL-2	linux-64, osx-64, win-64
r-fst	0.9.0	Multithreaded serialization of compressed data frames using the 'fst' format. The 'fst' format allows for random access of stored data and compression with the LZ4 and ZSTD compressors created by Yann Collet. The ZSTD compression library is owned by Facebook Inc. / AGPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-fstability	0.1.2	Has two functions to help with calculating feature selection stability. ‘Lump’ is a function that groups subset vectors into a dataframe, and adds NA to shorter vectors so they all have the same length. ‘ASM’ is a function that takes a dataframe of subset vectors and the original vector of features as inputs, and calculates the Stability of the feature selection. The calculation for ‘asm’ uses the Adjusted Stability Measure proposed in: ‘Lustgarten’, ‘Gopalakrishnan’, & ‘Visweswaran’ (2009)< <a href="https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2815476/">https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2815476/</a> >. / GPL-3	noarch
r-fsthet	1.0.1	A program to generate smoothed quantiles for the Fst-heterozygosity distribution. Designed for use with large numbers of loci (e.g., genome-wide SNPs). The best case for analyzing the Fst-heterozygosity distribution is when many populations (>10) have been sampled. See Flanagan & Jones (2017) <doi:10.1093/jhered/esx048>. / GPL-2	noarch
r-fticrms	0.8	This package was developed partially with funding from the NIH Training Program in Biomolecular Technology (2-T32-GM08799). / GPL-2	noarch
r-ftnonpar	0.1_88	The package contains R-functions to perform the methods in nonparametric regression and density estimation, described in Davies, P. L. and Kovac, A. (2001) Local Extremes, Runs, Strings and Multiresolution (with discussion) Annals of Statistics. 29. p1-65 Davies, P. L. and Kovac, A. (2004) Densities, Spectral Densities and Modality Annals of Statistics. Annals of Statistics. 32. p1093-1136 Kovac, A. (2006) Smooth functions and local extreme values. Computational Statistics and Data Analysis (to appear) Dumbgen, L. and Kovac, A. (2006) Extensions of smoothing via taut strings Davies, P. L. (1995) Data features. Statistica Neerlandica 49,185-245. / GPL-2	linux-64, osx-64, win-64
r-ftrading	3042.79	A collection of functions for trading and rebalancing financial instruments. It implements various technical indicators to analyse time series such as moving averages or stochastic oscillators. / GPL-2	noarch
r-fts	0.9.9.3	Fast operations for time series objects. / GPL-3	linux-64, osx-64, win-64
r-fueleconomy	0.1	Fuel economy data from the EPA, 1985-2015, conveniently packaged for consumption by R users. / CC0	noarch
r-fugue	0.1.7	As in music, a fugue statistic repeats a theme in small variations. Here, the psi-function that defines an m-statistic is slightly altered to maintain the same design sensitivity in matched sets of different sizes. The main functions in the package are sen() and senCI(). For sensitivity analyses for m-statistics, see Rosenbaum (2007) Biometrics 63 456-464 <doi:10.1111/j.1541-0420.2006.00717.x>. / GPL-2	noarch
r-fun	0.2	This is a collection of R games and other funny stuff, such as the classic Mine sweeper and sliding puzzles. / GPL-3	noarch
r-funchir	0.1.4	A set of functions, some subset of which I use in every .R file I write. Examples are table2(), which adds useful functionalities to base table (sorting, built-in proportion argument, etc.); lyx.xtable(), which converts xtable() output to a format more easily copy-pasted into LyX; pdf2(), which writes a plot to file while also displaying it in the RStudio plot window; and abbr_to_colClass(), which is a much more concise way of feeding many types to a colClass argument in a data reader. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-funchisq</a>	2.4.8	Statistical hypothesis testing methods for inferring model-free functional dependency using asymptotic chi-squared or exact distributions. Functional test statistics are asymmetric and functionally optimal, unique from other related statistics. Tests in this package reveal evidence for causality based on the causality-by-functionality principle. They include asymptotic functional chi-squared tests ('Zhang & Song' 2013) <arXiv:1311.2707> and an exact functional test ('Zhong & Song' 2019) <doi:10.1109/TCBB.2018.2809743>. The normalized functional chi-squared test was used by Best Performer 'NMSUSongLab' in HPN-DREAM (DREAM8) Breast Cancer Network Inference Challenges ('Hill et al' 2016) <doi:10.1038/nmeth.3773>. A function index ('Zhong & Song' in press) ('Kumar et al' 2018) <doi:10.1109/BIBM.2018.8621502> derived from the functional test statistic offers a new effect size measure for the strength of functional dependency, a better alternative to conditional entropy in many aspects. For continuous data, these tests offer an advantage over regression analysis when a parametric functional form cannot be assumed; for categorical data, they provide a novel means to assess directional dependency not possible with symmetrical Pearson's chi-squared or Fisher's exact tests. / LGPL-3	linux-64, osx-64, win-64
<a href="#">r-functional</a>	0.6	Curry, Compose, and other higher-order functions / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-functools</a>	0.2.0	Extends functional programming in R by providing support to the usual higher order functional suspects (Map, Reduce, Filter, etc.). / MIT	noarch
<a href="#">r-funique</a>	0.0.1	Similar to base's unique function, only optimized for working with data frames, especially those that contain date-time columns. / MIT	noarch
<a href="#">r-funitroots</a>	3042.7	Provides four addons for analyzing trends and unit roots in financial time series: (i) functions for the density and probability of the augmented Dickey-Fuller Test, (ii) functions for the density and probability of MacKinnon's unit root test statistics, (iii) reimplementations for the ADF and MacKinnon Test, and (iv) an 'urca' Unit Root Test Interface for Pfaff's unit root test suite. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-funr</a>	0.3.2	A small utility which wraps Rscript and provides access to all R functions from the shell. / MIT	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-funreg</a>	1.2	Performs functional regression, and some related approaches, for intensive longitudinal data (see the book by Walls & Schafer, 2006, Models for Intensive Longitudinal Data, Oxford) when such data is not necessarily observed on an equally spaced grid of times. The approach generally follows the ideas of Goldsmith, Bobb, Crainiceanu, Caffo, and Reich (2011)<DOI:10.1198/jcgs.2010.10007> and the approach taken in their sample code, but with some modifications to make it more feasible to use with long rather than wide, non-rectangular longitudinal datasets with unequal and potentially random measurement times. It also allows easy plotting of the correlation between the smoothed covariate and the outcome as a function of time, which can add additional insights on how to interpret a functional regression. Additionally, it also provides several permutation tests for the significance of the functional predictor. The heuristic interpretation of “time” is used to describe the index of the functional predictor, but the same methods can equally be used for another unidimensional continuous index, such as space along a north-south axis. The development of this package was part of a research project supported by Award R03 CA171809-01 from the National Cancer Institute and Award P50 DA010075 from the National Institute on Drug Abuse. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institute on Drug Abuse, the National Cancer Institute, or the National Institutes of Health. / GPL-2	noarch
<a href="#">r-funta</a>	0.1.0	Computes the functional tangential angle pseudo-depth and its robustified version from the paper by Kuhnt and Rehage (2016). See Kuhnt, S.; Rehage, A. (2016): An angle-based multivariate functional pseudo-depth for shape outlier detection, JMVA 146, 325-340, <doi:10.1016/j.jmva.2015.10.016> for details. / GPL-3	noarch
<a href="#">r-fusionclust</a>	1.0.0	Provides the Big Merge Tracker and COSCI algorithms for convex clustering and feature screening using L1 fusion penalty. See Radchenko, P. and Mukherjee, G. (2017) <doi:10.1111/rssb.12226> and T.Banerjee et al. (2017) <doi:10.1016/j.jmva.2017.08.001> for more details. / GPL-2	noarch
<a href="#">r-fusionlearn</a>	0.1.1	The fusion learning method uses a model selection algorithm to learn from multiple data sets across different experimental platforms through group penalization. The responses of interest may include a mix of discrete and continuous variables. The responses may share the same set of predictors, however, the models and parameters differ across different platforms. Integrating information from different data sets can enhance the power of model selection. Package is based on Xin Gao, Raymond J. Carroll (2017) <arXiv:1610.00667v1>. / GPL-2	noarch
<a href="#">r-futile.options</a>	1.0.1	A scoped options management framework. Used in other packages. / LGPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-futility</a>	0.4	Randomized clinical trials commonly follow participants for a time-to-event efficacy endpoint for a fixed period of time. Consequently, at the time when the last enrolled participant completes their follow-up, the number of observed endpoints is a random variable. Assuming data collected through an interim timepoint, simulation-based estimation and inferential procedures in the standard right-censored failure time analysis framework are conducted for the distribution of the number of endpoints—in total as well as by treatment arm—at the end of the follow-up period. The future (i.e., yet unobserved) enrollment, endpoint, and dropout times are generated according to mechanisms specified in the <code>simTrial()</code> function in the ‘seqDesign’ package. A Bayesian model for the endpoint rate, offering the option to specify a robust mixture prior distribution, is used for generating future data (see the vignette for details). Inference can be restricted to participants who received treatment according to the protocol and are observed to be at risk for the endpoint at a specified timepoint. Plotting functions are provided for graphical display of results. / GPL-2	noarch
<a href="#">r-fuzzyahp</a>	0.9.1	Calculation of AHP (Analytic Hierarchy Process - <a href="http://en.wikipedia.org/wiki/Analytic_hierarchy_process">http://en.wikipedia.org/wiki/Analytic_hierarchy_process</a> ) with classic and fuzzy weights based on Saaty’s pairwise comparison method for determination of weights. / LGPL-3	noarch
<a href="#">r-fuzzyfdr</a>	1.0	Exact calculation of fuzzy decision rules for multiple testing. Choose to control FDR (false discovery rate) using the Benjamini and Hochberg method, or FWER (family wise error rate) using the Bonferroni method. Kulinskaya and Lewin (2007). / GPL-3	noarch
<a href="#">r-fuzzynumbers</a>	0.4.6	S4 classes and methods to deal with fuzzy numbers. They allow for computing any arithmetic operations (e.g., by using the Zadeh extension principle), performing approximation of arbitrary fuzzy numbers by trapezoidal and piecewise linear ones, preparing plots for publications, computing possibility and necessity values for comparisons, etc. / LGPL-3	noarch
<a href="#">r-fuzzyr</a>	2.1	Design and simulate fuzzy logic systems using Type 1 Fuzzy Logic. This toolkit includes with graphical user interface (GUI) and an adaptive neuro-fuzzy inference system (ANFIS). This toolkit is a continuation from the previous package (‘FuzzyToolkitUoN’). Produced by the Intelligent Modelling & Analysis Group, University of Nottingham. / GPL-2	noarch
<a href="#">r-fuzzyranktests</a>	0.3.1	Does fuzzy tests and confidence intervals (following Geyer and Meeden, Statistical Science, 2005, <doi:10.1214/088342305000000340>) for sign test and Wilcoxon signed rank and rank sum tests. / MIT	linux-64, osx-64, win-64
<a href="#">r-fuzzysim</a>	2.0	Functions to calculate fuzzy versions of species’ occurrence patterns based on presence-absence data (including inverse distance interpolation, trend surface analysis and prevalence-independent favourability GLM), and pair-wise fuzzy similarity (based on fuzzy versions of commonly used similarity indices) among those occurrence patterns. Includes also functions for model comparison (overlap and fuzzy similarity, loss or gain), and for data preparation, such as obtaining unique abbreviations of species names, converting species lists (long format) to presence-absence tables (wide format), transposing part of a data frame, assessing the false discovery rate, or analysing and dealing with multicollinearity among variables. Includes also sample datasets for providing practical examples. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-fuzzystattra	1.0	The aim of the package is to provide some basic functions for doing statistics with trapezoidal fuzzy numbers. In particular, the package contains several functions for simulating trapezoidal fuzzy numbers, as well as for calculating some central tendency measures (mean and two types of median), some scale measures (variance, ADD, MDD, Sn, Qn, Tn and some M-estimators) and one diversity index and one inequality index. Moreover, functions for calculating the 1-norm distance, the mid/spr distance and the (phi,theta)-wabl/ldev/rdev distance between fuzzy numbers are included, and a function to calculate the value phi-wabl given a sample of trapezoidal fuzzy numbers. / GPL-2	noarch
r-fuzzytoolkituon	1.0	A custom framework for working with Type 1 Fuzzy Logic, produced by the University of Nottingham IMA Group. / GPL-2	noarch
r-fuzzywuzzyr	1.0.3	Fuzzy string matching implementation of the ‘fuzzywuzzy’ < <a href="https://github.com/seatgeek/fuzzywuzzy">https://github.com/seatgeek/fuzzywuzzy</a> > ‘python’ package. It uses the Levenshtein Distance < <a href="https://en.wikipedia.org/wiki/Levenshtein_distance">https://en.wikipedia.org/wiki/Levenshtein_distance</a> > to calculate the differences between sequences. / GPL-2	noarch
r-fwdselect	2.1.0	A simple method to select the best model or best subset of variables using different types of data (binary, Gaussian or Poisson) and applying it in different contexts (parametric or non-parametric). / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-fwi.fbp	1.7	Provides three functions to calculate the outputs of the two main components of the Canadian Forest Fire Danger Rating System (CFFDRS): the Fire Weather Index (FWI) System and the Fire Behaviour Prediction (FBP) System. / GPL-2	noarch
r-fwsim	0.3.4	Simulates a population under the Fisher-Wright model (fixed or stochastic population size) with a one-step neutral mutation process (stepwise mutation model, logistic mutation model and exponential mutation model supported). The stochastic population sizes are random Poisson distributed and different kinds of population growth are supported. For the stepwise mutation model, it is possible to specify locus and direction specific mutation rate (in terms of upwards and downwards mutation rate). Intermediate generations can be saved in order to study e.g. drift. / GPL-2	linux-64, osx-64, win-64
r-g.data	2.4	Create and maintain delayed-data packages (ddp’s). Data stored in a ddp are available on demand, but do not take up memory until requested. You attach a ddp with g.data.attach(), then read from it and assign to it in a manner similar to S-PLUS, except that you must run g.data.save() to actually commit to disk. / GPL-3	noarch
r-g1dbn	3.1.1	G1DBN performs DBN inference using 1st order conditional dependencies. / GPL-2	noarch
r-g3viz	1.1.2	R interface for ‘g3-lollipop’ JavaScript library. Visualize genetic mutation data using an interactive lollipop diagram in RStudio or your browser. / MIT	noarch

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Name	Version	Summary/License	Platforms
r-ga	3.2	Flexible general-purpose toolbox implementing genetic algorithms (GAs) for stochastic optimisation. Binary, real-valued, and permutation representations are available to optimize a fitness function, i.e. a function provided by users depending on their objective function. Several genetic operators are available and can be combined to explore the best settings for the current task. Furthermore, users can define new genetic operators and easily evaluate their performances. Local search using general-purpose optimisation algorithms can be applied stochastically to exploit interesting regions. GAs can be run sequentially or in parallel, using an explicit master-slave parallelisation or a coarse-grain islands approach. / GPL-2	linux-64, osx-64, win-64
r-gad	1.1.1	This package analyses complex ANOVA models with any combination of orthogonal/nested and fixed/random factors, as described by Underwood (1997). There are two restrictions: (i) data must be balanced; (ii) fixed nested factors are not allowed. Homogeneity of variances is checked using Cochran's C test and 'a posteriori' comparisons of means are done using Student-Newman-Keuls (SNK) procedure. / GPL (>= 2.0)	noarch
r-gadag	0.99.0	Sparse large Directed Acyclic Graphs learning with a combination of a convex program and a tailored genetic algorithm (see Champion et al. (2017) < <a href="https://hal.archives-ouvertes.fr/hal-01172745v2/document">https://hal.archives-ouvertes.fr/hal-01172745v2/document</a> >). / GPL-2	linux-64, osx-64, win-64
r-gadifpt	1.0	In this package we consider Gaussian Diffusion processes and smooth thresholds. After evaluating the mean of the process to check the subthreshold regimen hypothesis, the FPT density function is reconstructed via the numerical quadrature of the integral equation in (Buonocore 1987); first passage times are also generated by the method in (Buonocore 2014) and results are compared. The timestep of the simulations can iteratively be refined. User should provide the functional form for the drift and the infinitesimal variance in the script 'userfunc.R' and for the threshold in the script 'userthresh.R'. All the parameters required by the implementation are to be set in the script 'userparam.R'. Example scripts for common drifts and thresholds are given. / GPL-2	noarch
r-gafit	0.5.1	A group of sample points are evaluated against a user-defined expression, the sample points are lists of parameters with values that may be substituted into that expression. The genetic algorithm attempts to make the result of the expression as low as possible (usually this would be the sum of residuals squared). / GPL-2	linux-64, osx-64, win-64
r-gains	1.2	Constructs gains tables and lift charts for prediction algorithms. Gains tables and lift charts are commonly used in direct marketing applications. The method is described in Drozdenko and Drake (2002), Optimal Database Marketing, Chapter 11. / GPL-3	noarch
r-gaipe	1.0	GAIPE implements graphical representation of accuracy in parameter estimation (AIPE) on RMSEA for sample size planning in structural equation modeling. Sample sizes suggested by RMSEA with AIPE method and power analysis approach can also be obtained separately using the provided functions. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-galgo	1.4	Build multivariate predictive models from large datasets having far larger number of features than samples such as in functional genomics datasets. Trevino and Falciani (2006) <doi:10.1093/bioinformatics/btl074>. / GPL-2	linux-64, osx-64, win-64
r-gam	1.16	Functions for fitting and working with generalized additive models, as described in chapter 7 of Statistical Models in S (Chambers and Hastie (eds), 1991), and Generalized Additive Models (Hastie and Tibshirani, 1990). / GPL-2	linux-64, osx-64, win-64
r-gamair	1.0_2	Data sets and scripts used in the book ‘Generalized Additive Models: An Introduction with R’, Wood (2006,2017) CRC. / GPL-2	noarch
r-gambin	2.4.1	Fits unimodal and multimodal gambin distributions to species-abundance distributions from ecological data, as in in Matthews et al. (2014) <DOI:10.1111/ecog.00861>. ‘gambin’ is short for ‘gamma-binomial’. The main function is fit_abundances(), which estimates the ‘alpha’ parameter(s) of the gambin distribution using maximum likelihood. Functions are also provided to generate the gambin distribution and for calculating likelihood statistics. / GPL-3	noarch
r-gamboost	1.2_3	This package provides routines for fitting generalized linear and and generalized additive models by likelihood based boosting, using penalized B-splines / GPL-2	linux-64, osx-64, win-64
r-games	1.1.2	Provides estimation and analysis functions for strategic statistical models. / GPL-2	noarch
r-gamesga	1.1.3_6	Finds adaptive strategies for sequential symmetric games using a genetic algorithm. Currently, any symmetric two by two matrix is allowed, and strategies can remember the history of an opponent’s play from the previous three rounds of moves in iterated interactions between players. The genetic algorithm returns a list of adaptive strategies given payoffs, and the mean fitness of strategies in each generation. / MIT	linux-64, osx-64, win-64
r-gamlr	1.13_5	The gamma lasso algorithm provides regularization paths corresponding to a range of non-convex cost functions between L0 and L1 norms. As much as possible, usage for this package is analogous to that for the glmnet package (which does the same thing for penalization between L1 and L2 norms). For details see: Taddy (2017 JCGS), One-Step Estimator Paths for Concave Regularization, <arXiv:1308.5623>. / GPL-3	linux-64, osx-64, win-64
r-gamlss.data	5.1_4	Data used as examples to demonstrate GAMLSS models. / GPL-2   GPL-3	noarch
r-gamlss.dist	5.1_4	A set of distributions which can be used for modelling the response variables in Generalized Additive Models for Location Scale and Shape, Rigby and Stasinopoulos (2005), <doi:10.1111/j.1467-9876.2005.00510.x>. The distributions can be continuous, discrete or mixed distributions. Extra distributions can be created, by transforming, any continuous distribution defined on the real line, to a distribution defined on ranges 0 to infinity or 0 to 1, by using a ‘log’ or a ‘logit’ transformation respectively. / GPL-2   GPL-3	linux-64, osx-64, win-64
r-gamm4	0.2_5	Estimate generalized additive mixed models via a version of function gamm() from ‘mgcv’, using ‘lme4’ for estimation. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-gammslice	2.0.2	Uses a slice sampling-based Markov chain Monte Carlo to conduct Bayesian fitting and inference for generalized additive mixed models. Generalized linear mixed models and generalized additive models are also handled as special cases of generalized additive mixed models. The methodology and software is described in Pham, T.H. and Wand, M.P. (2018). Australian and New Zealand Journal of Statistics, 60, 279-330 <DOI:10.1111/ANZS.12241>. / GPL-2	linux-64, osx-64, win-64
r-gamrr	0.6.0	To calculate the relative risk (RR) for the generalized additive model. / GPL-3	noarch
r-ganpadata	1.0	This is a dataset package for GANPA, which implements a network-based gene weighting approach to pathway analysis. This package includes data useful for GANPA, such as a functional association network, pathways, an expression dataset and multi-subunit proteins. / GPL-2	noarch
r-gap	1.2.1	It is designed as an integrated package for genetic data analysis of both population and family data. Currently, it contains functions for sample size calculations of both population-based and family-based designs, probability of familial disease aggregation, kinship calculation, statistics in linkage analysis, and association analysis involving genetic markers including haplotype analysis with or without environmental covariates. / GPL-2	linux-64, osx-64, win-64
r-gap.datasets	0.0.4	Datasets associated with the 'gap' package. Currently, it includes an example data for regional association plot (CDKN), an example data for a genomewide association meta-analysis (OPG), Manhattan plots with (hr1420, mhtdata) and without (w4) gene annotations. / GPL-2	noarch
r-gaparsimony	0.9.2	Methodology that combines feature selection, model tuning, and parsimonious model selection with Genetic Algorithms (GA) proposed in {Martinez-de-Pison} (2015) <DOI:10.1016/j.asoc.2015.06.012>. To this objective, a novel GA selection procedure is introduced based on separate cost and complexity evaluations. / GPL-2	noarch
r-gar	1.1	The functions included are used to obtain initial authentication with Google Analytics as well as simple and organized data retrieval from the API. Allows for retrieval from multiple profiles at once. / GPL-2	noarch
r-garray	1.1.2	Organize a so-called ragged array as generalized arrays, which is simply an array with sub-dimensions denoting the subdivision of dimensions (grouping of members within dimensions). By the margins (names of dimensions and sub-dimensions) in generalized arrays, operators and utility functions provided in this package automatically match the margins, doing map-reduce style parallel computation along margins. Generalized arrays are also cooperative to R's native functions that work on simple arrays. / GPL-3	noarch
r-gaselect	1.0.7	Provides a genetic algorithm for finding variable subsets in high dimensional data with high prediction performance. The genetic algorithm can use ordinary least squares (OLS) regression models or partial least squares (PLS) regression models to evaluate the prediction power of variable subsets. By supporting different cross-validation schemes, the user can fine-tune the tradeoff between speed and quality of the solution. / GPL-2	linux-64, osx-64, win-64
r-gatepoints	0.1.3	Allows user to choose/gate a region on the plot and returns points within it. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-gausscov	0.0.2	Given the standard linear model the traditional way of deciding whether to include the $j$ th covariate is to apply the F-test to decide whether the corresponding beta coefficient is zero. The Gaussian covariate method is completely different. The question as to whether the beta coefficient is or is not zero is replaced by the question as to whether the covariate is better or worse than i.i.d. Gaussian noise. The P-value for the covariate is the probability that Gaussian noise is better. Surprisingly this can be given exactly and it is the same as the P-value for the classical model based on the F-distribution. The Gaussian covariate P-value is model free, it is the same for any data set. Using the idea it is possible to do covariate selection for a small number of covariates 25 by considering all subsets. Post selection inference causes no problems as the P-values hold whatever the data. The idea extends to stepwise regression again with exact probabilities. In the simplest version the only parameter is a specified cut-off P-value which can be interpreted as the probability of a false positive being included in the final selection. For more information see the website below and the accompanying papers: L. Davies and L. Duembgen, A Model-free Approach to Linear Least Squares Regression with Exact Probabilities and Applications to Covariate Selection, 2019, <arXiv:1906.01990>. L. Davies, Lasso, Knockoff and Gaussian covariates: A comparison, 2018, <arXiv:1807.09633v4>. / GPL-3	linux-64, osx-64, win-64
r-gaussdiff	1.1	A collection difference measures for multivariate Gaussian probability density functions, such as the Euclidean mean, the Mahalanobis distance, the Kullback-Leibler divergence, the J-Coefficient, the Minkowski L2-distance, the Chi-square divergence and the Hellinger Coefficient. / GPL-2	noarch
r-gaussfacts	0.0.2	Display a random fact about Carl Friedrich Gauss based on the collection curated by Mike Cavers via the < <a href="http://gaussfacts.com">http://gaussfacts.com</a> > site. / GPL-2	noarch
r-gaussianhmm1d	1.0.1	Inference, goodness-of-fit test, and prediction densities and intervals for univariate Gaussian Hidden Markov Models (HMM). The goodness-of-fit is based on a Cramer-von Mises statistic and uses parametric bootstrap to estimate the p-value. The description of the methodology is taken from Chapter 10.2 of Remillard (2013) <doi:10.1201/b14285>. / GPL-2	noarch
r-gb	2.3.3	A collection of algorithms and functions for fitting data to a generalized lambda distribution via moment matching methods, and generalized bootstrapping. / Unlimited	linux-64, osx-64, win-64
r-gbm	2.1.5	An implementation of extensions to Freund and Schapire's AdaBoost algorithm and Friedman's gradient boosting machine. Includes regression methods for least squares, absolute loss, t-distribution loss, quantile regression, logistic, multinomial logistic, Poisson, Cox proportional hazards partial likelihood, AdaBoost exponential loss, Huberized hinge loss, and Learning to Rank measures (LambdaMart). Originally developed by Greg Ridgeway. / GPL-2	linux-64, osx-64, win-64
r-gbrd	0.4.1	Provides utilities for processing Rd objects and files. Extract argument descriptions and other parts of the help pages of functions. / GPL-2	noarch
r-gcai.bias	1.0	Many inherited biases and effects exist in RNA-seq due to both biological and technical effects. We observed the biological variance of testing target transcripts can influence the yield of sequencing reads, which might indicate a resource competition existing in RNA-seq. We developed this package to capture the bias depending on local sequence and perform the correction of this type of bias by borrowing information from spike-in measurement. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-gcat	0.1	These are two-sample tests for categorical data utilizing similarity information among the categories. They are useful when there is underlying structure on the categories. / GPL-2	linux-64, osx-64, win-64
r-gcd	4.0.4	Contains the Global Charcoal database data. Data include charcoal series (age, depth, charcoal quantity, associated units and methods) and information on sedimentary sites (localisation, depositional environment, biome, etc.) as well as publications informations. Since 4.0.0 the GCD mirrors the online SQL database at < <a href="http://paleofire.org">http://paleofire.org</a> >. / GPL-2	noarch
r-gcdnet	1.0.5	A generalized coordinate descent (GCD) algorithm for computing the solution path of the hybrid Huberized support vector machine (HHSVM) and its generalization, including the LASSO and elastic net (adaptive) penalized least squares, logistic regression, HHSVM, squared hinge loss SVM and expectile regression. / GPL-2	linux-64, osx-64, win-64
r-gckrig	1.1.3	Provides a variety of functions to analyze and model geostatistical count data with Gaussian copulas, including 1) data simulation and visualization; 2) correlation structure assessment (here also known as the Normal To Anything); 3) calculate multivariate normal rectangle probabilities; 4) likelihood inference and parallel prediction at predictive locations. / GPL-2	linux-64, osx-64, win-64
r-gclus	1.3.2	Orders panels in scatterplot matrices and parallel coordinate displays by some merit index. Package contains various indices of merit, ordering functions, and enhanced versions of pairs and parcoord which color panels according to their merit level. / GPL-2	noarch
r-gconcord	0.41	Estimates a sparse inverse covariance matrix from a convex pseudo-likelihood function with L1 penalty / GPL-2	linux-64, osx-64, win-64
r-gcookbook	2.0	Data sets used in the book R Graphics Cookbook by Winston Chang, published by O'Reilly Media. / GPL-2	noarch
r-gcpm	1.2.2	Analyze the default risk of credit portfolios. Commonly known models, like CreditRisk or the CreditMetrics model are implemented in their very basic settings. The portfolio loss distribution can be achieved either by simulation or analytically in case of the classic CreditRisk model. Models are only implemented to respect losses caused by defaults, i.e. migration risk is not included. The package structure is kept flexible especially with respect to distributional assumptions in order to quantify the sensitivity of risk figures with respect to several assumptions. Therefore the package can be used to determine the credit risk of a given portfolio as well as to quantify model sensitivities. / GPL-2	linux-64, osx-64, win-64
r-gd	1.7	Geographical detectors for measuring spatial stratified heterogeneity, as described in Jinfeng Wang (2010) <doi:10.1080/13658810802443457> and Jinfeng Wang (2016) <doi:10.1016/j.ecolind.2016.02.052>. Includes the optimal discretization of continuous data, four primary functions of geographical detectors, comparison of size effects of spatial unit and the visualizations of results. The descriptions of the package, methods and case datasets refer to the citation information below. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-gdadata	0.93	Datasets used in the book ‘Graphical Data Analysis with R’ (Antony Unwin, CRC Press 2015). / GPL-2	noarch
r-gdata	2.18.0	Various R programming tools for data manipulation, including: - medical unit conversions (‘ConvertMedUnits’, ‘MedUnits’), - combining objects (‘bindData’, ‘cbindX’, ‘combine’, ‘interleave’), - character vector operations (‘centerText’, ‘startsWith’, ‘trim’), - factor manipulation (‘levels’, ‘reorder.factor’, ‘mapLevels’), - obtaining information about R objects (‘object.size’, ‘elem’, ‘env’, ‘humanReadable’, ‘is.what’, ‘ll’, ‘keep’, ‘ls.funs’, ‘Args’, ‘nPairs’, ‘nobs’), - manipulating MS-Excel formatted files (‘read.xls’, ‘installXLSX-support’, ‘sheetCount’, ‘xlsFormats’), - generating fixed-width format files (‘write.fwf’), - extricating components of date & time objects (‘getYear’, ‘getMonth’, ‘getDay’, ‘getHour’, ‘getMin’, ‘getSec’), - operations on columns of data frames (‘matchcols’, ‘rename.vars’), - matrix operations (‘unmatrix’, ‘upperTriangle’, ‘lowerTriangle’), - operations on vectors (‘case’, ‘unknown-ToNA’, ‘duplicated2’, ‘trimSum’), - operations on data frames (‘frameApply’, ‘wideByFactor’), - value of last evaluated expression (‘ans’), and - wrapper for ‘sample’ that ensures consistent behavior for both scalar and vector arguments (‘resample’). / GPL-2	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-gdistance	1.2_2	Calculate distances and routes on geographic grids. / GPL-2	noarch
r-gdmp	0.2.0	Manage and analyze high-dimensional SNP data from chips with multiple densities. / GPL-2	linux-64, osx-64, win-64
r-gdns	0.3.1	To address the problem of insecurity of ‘UDP’-based ‘DNS’ requests, ‘Google Public DNS’ offers ‘DNS’ resolution over an encrypted ‘HTTPS’ connection. ‘DNS-over-HTTPS’ greatly enhances privacy and security between a client and a recursive resolver, and complements ‘DNSSEC’ to provide end-to-end authenticated ‘DNS’ lookups. Functions that enable querying individual requests that bulk requests that return detailed responses and bulk requests are both provided. Support for reverse lookups is also provided. See < <a href="https://developers.google.com/speed/public-dns/docs/dns-over-https">https://developers.google.com/speed/public-dns/docs/dns-over-https</a> > for more information. / AGPL-3	noarch
r-gdpc	1.1.0	Functions to compute the Generalized Dynamic Principal Components introduced in Peña and Yohai (2016) <DOI:10.1080/01621459.2015.1072542>. / GPL-2	linux-64, osx-64, win-64
r-gds	0.1.0	Contains a function called gds() which accepts three input parameters like lower limits, upper limits and the frequencies of the corresponding classes. The gds() function calculate and return the values of mean (‘gmean’), median (‘gmedian’), mode (‘gmode’), variance (‘gvar’), standard deviation (‘gstdev’), coefficient of variance (‘gcv’), quartiles (‘gq1’, ‘gq2’, ‘gq3’), inter-quartile range (‘gIQR’), skewness (‘g1’), and kurtosis (‘g2’) which facilitate effective data analysis. For skewness and kurtosis calculations we use moments. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-gee	4.13.0	Generalized Estimation Equation solver. / GPL-2	linux-64, osx-64, win-64
r-gee4	0.1.0.0	Fit joint mean-covariance models for longitudinal data within the framework of (weighted) generalised estimating equations (GEE/WGEE). The models and their components are represented using S4 classes and methods. The core computational algorithms are implemented using the 'Armadillo' C library for numerical linear algebra and 'RcppArmadillo' glue. / GPL-2	linux-64, osx-64, win-64
r-geem	0.10.1	IGEE estimation of the parameters in mean structures with possible correlation between the outcomes. User-specified mean link and variance functions are allowed, along with observation weighting. The 'M' in the name 'geeM' is meant to emphasize the use of the Matrix package, which allows for an implementation based fully in R. / GPL-3	noarch
r-geepack	1.2.1	Generalized estimating equations solver for parameters in mean, scale, and correlation structures, through mean link, scale link, and correlation link. Can also handle clustered categorical responses. / GPL-3	linux-64, osx-64, win-64
r-geigen	2.3	Functions to compute generalized eigenvalues and eigenvectors, the generalized Schur decomposition and the generalized Singular Value Decomposition of a matrix pair, using Lapack routines. / GPL-2	linux-64, osx-64, win-64
r-gelnet	1.2.1	Implements several extensions of the elastic net regularization scheme. These extensions include individual feature penalties for the L1 term, feature-feature penalties for the L2 term, as well as translation coefficients for the latter. / GPL-3	linux-64, osx-64, win-64
r-gen2stage	1.0	One can find single-stage and two-stage designs for a phase II single-arm study with either efficacy or safety/toxicity endpoints as described in Kim and Wong (2019) <doi:10.29220/CSAM.2019.26.2.163>. / GPL-2	noarch
r-genalg	0.2.0	R based genetic algorithm for binary and floating point chromosomes. / GPL-2	noarch
r-genbinomapps	1.0.2	Density, distribution function, quantile function and random generation for the Generalized Binomial Distribution. Functions to compute the Clopper-Pearson Confidence Interval and the required sample size. Enhanced model for burn-in studies, where failures are tackled by countermeasures. / GPL-3	noarch
r-gendata	1.1	Set of functions to create datasets using a correlation matrix. / GPL-3	noarch
r-genderizer	2.1.1	Utilizes the 'genderize.io' Application Programming Interface to predict gender from first names extracted from a text vector. The accuracy of prediction could be controlled by two parameters: counts of a first name in the database and probability of prediction. / MIT	noarch

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Name	Version	Summary/License	Platforms
r-gendist	2.0	Computes the probability density function (pdf), cumulative distribution function (cdf), quantile function (qf) and generates random values (rg) for the following general models : mixture models, composite models, folded models, skewed symmetric models and arc tan models. / GPL-2	noarch
r-genef	1.0	This package implements several generalized F-statistics. The current version includes a generalized F-statistic based on the flexible isotonic/monotonic regression or order restricted hypothesis testing. / GPL-2	noarch
r-genelistpie	1.0	geneListPie package is for mapping a gene list to function categories defined in GOSlim or Kegg. The results can be plotted as a pie chart to provide a quick view of the genes distribution of the gene list among the function categories. The gene list must contain a list of gene symbols. The package contains a set of pre-processed gene sets obtained from Gene Ontology and MSigDB including human, mouse, rat and yeast. To provide a high level concise view, only GO slim and kegg are provided. The gene sets are regularly updated. User can also use customized gene sets. User can use the R Pie() or Pie3D() function for plotting the pie chart. Users can also choose to output the gene function mapping results and use external software such as Excel(R) for plotting. / GPL-3	noarch
r-genemodel	1.1.0	Using simple input, this package creates plots of gene models. Users can create plots of alternatively spliced gene variants and the positions of mutations and other gene features. / GPL-2	noarch
r-genepi	1.0.1	Functions for Genetic Epi Methods Developed at MSKCC / GPL-2	linux-64, osx-64, win-64
r-genepop	1.1.3	Makes the Genepop software available in R. This software implements a mixture of traditional population genetic methods and some more focused developments: it computes exact tests for Hardy-Weinberg equilibrium, for population differentiation and for genotypic disequilibrium among pairs of loci; it computes estimates of F-statistics, null allele frequencies, allele size-based statistics for microsatellites, etc.; and it performs analyses of isolation by distance from pairwise comparisons of individuals or population samples. / CeCILL-2	linux-64, osx-64, win-64
r-generalhoslem	1.3.4	Functions to assess the goodness of fit of binary, multinomial and ordinal logistic models. Included are the Hosmer-Lemeshow tests (binary, multinomial and ordinal) and the Lipsitz and Pulkstenis-Robinson tests (ordinal). / GPL-2	noarch
r-generalizedhyperbolic	0.8.4	Functions for the hyperbolic and related distributions. Density, distribution and quantile functions and random number generation are provided for the hyperbolic distribution, the generalized hyperbolic distribution, the generalized inverse Gaussian distribution and the skew-Laplace distribution. Additional functionality is provided for the hyperbolic distribution, normal inverse Gaussian distribution and generalized inverse Gaussian distribution, including fitting of these distributions to data. Linear models with hyperbolic errors may be fitted using hyperblmFit. / GPL-2	noarch
r-generalaoxaca	1.0	Perform the Blinder-Oaxaca decomposition for generalized linear model with bootstrapped standard errors. The twofold and threefold decomposition are given, even the generalized linear model output in each group. / GPL-2	noarch
r-generator	0.1.0	Allows users to quickly and easily generate fake data containing Personally Identifiable Information (PII) through convenience functions. / MIT	noarch

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Name	Version	Summary/License	Platforms
r-generics	0.0.2	In order to reduce potential package dependencies and conflicts, generics provides a number of commonly used S3 generics. / GPL-2	linux-32, linux-64, noarch, osx-64, win-64
r-genesignaturefinder	2014.02.15	Tool for finding an ensemble gene-signature by a steepest ascending algorithm partially supervised by survival time data. / GPL-2	noarch
r-genesysr	0.9.2	Access data on plant genetic resources from genebanks around the world published on Genesys (< <a href="https://www.genesys-pgr.org">https://www.genesys-pgr.org</a> >). Your use of data is subject to terms and conditions available at < <a href="https://www.genesys-pgr.org/content/legal/terms">https://www.genesys-pgr.org/content/legal/terms</a> >. / Apache License 2.0	noarch
r-genetics	1.3.8	Classes and methods for handling genetic data. Includes classes to represent genotypes and haplotypes at single markers up to multiple markers on multiple chromosomes. Function include allele frequencies, flagging homo/heterozygotes, flagging carriers of certain alleles, estimating and testing for Hardy-Weinberg disequilibrium, estimating and testing for linkage disequilibrium, ... / GPL-3	noarch
r-geneticssubsetter	0.8	Finds subsets of sets of genotypes with a high Heterozygosity, and Mean of Transformed Kinships (MTK), measures that can indicate a subset would be beneficial for rare-trait discovery and genome-wide association scanning, respectively. / GPL-2	noarch
r-genie	1.0.4	A new hierarchical clustering linkage criterion: the Genie algorithm links two clusters in such a way that a chosen economic inequity measure (e.g., the Gini index) of the cluster sizes does not increase drastically above a given threshold. Benchmarks indicate a high practical usefulness of the introduced method: it most often outperforms the Ward or average linkage in terms of the clustering quality while retaining the single linkage speed, see (Gagolewski et al. 2016a <DOI:10.1016/j.ins.2016.05.003>, 2016b <DOI:10.1007/978-3-319-45656-0_16>) for more details. / GPL-3	linux-64, osx-64, win-64
r-genkern	1.2_60	Computes generalised KDEs / GPL-2	linux-64, osx-64, win-64
r-genlasso	1.4	Provides fast algorithms for computing the solution path for generalized lasso problems. Important use cases are the fused lasso over an arbitrary graph, and trend fitting of any given polynomial order. Specialized implementations for the latter two problems are given to improve stability and speed. / GPL (>= 2.0)	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<code>r-genmeta</code>	0.1	Generalized meta-analysis is a technique for estimating parameters associated with a multiple regression model through meta-analysis of studies which may have information only on partial sets of the regressors. It estimates the effects of each variable while fully adjusting for all other variables that are measured in at least one of the studies. Using algebraic relationships between regression parameters in different dimensions, a set of moment equations is specified for estimating the parameters of a maximal model through information available on sets of parameter estimates from a series of reduced models available from the different studies. The specification of the equations requires a reference dataset to estimate the joint distribution of the covariates. These equations are solved using the generalized method of moments approach, with the optimal weighting of the equations taking into account uncertainty associated with estimates of the parameters of the reduced models. The proposed framework is implemented using iterated reweighted least squares algorithm for fitting generalized linear regression models. For more details about the method, please see pre-print version of the manuscript on generalized meta-analysis by Prosenjit Kundu, Runlong Tang and Nilanjan Chatterjee (2018) <arXiv:1708.03818>. / GPL-3	noarch
<code>r-genodds</code>	1.0.0	Calculates Agresti's (1980) < <a href="https://www.jstor.org/stable/2530495">https://www.jstor.org/stable/2530495</a> > generalized odds ratios. For a randomly selected pair of observations from two groups, calculates the odds that the second group will have a higher scoring outcome than that of the first group. Package provides hypothesis testing for if this odds ratio is significantly different to 1 (equal chance). / GPL-2	linux-64, osx-64, win-64
<code>r-genomic.autocorr</code>	1.0.1	Local structure in genomic data often induces dependence between observations taken at different genomic locations. Ignoring this dependence leads to underestimation of the standard error of parameter estimates. This package uses block bootstrapping to estimate asymptotically correct standard errors of parameters from any standard generalised linear model that may be fit by the <code>glm()</code> function. / GPL-2	noarch
<code>r-genomicper</code>	1.6	Circular genomic permutation approach uses GWAS results to establish the significance of pathway/gene-set associations whilst accounting for genomic structure. All SNPs in the GWAS are placed in a 'circular genome' according to their location. Then the complete set of SNP association p-values are permuted by rotation with respect to the SNPs' genomic locations. Two testing frameworks are available: permutations at the gene level, and permutations at the SNP level. The permutation at the gene level uses fisher's combination test to calculate a single gene p-value, followed by the hypergeometric test. The SNP count methodology maps each SNP to pathways/gene-sets and calculates the proportion of SNPs for the real and the permuted datasets above a pre-defined threshold. Genomicper requires a matrix of GWAS association p-values. The SNPs annotation and pathways annotations can be performed within the package or provided by the user. / GPL-2	noarch
<code>r-genopltr</code>	0.8.9	Draws gene or genome maps and comparisons between these, in a publication-grade manner. Starting from simple, common files, it will draw postscript or PDF files that can be sent as such to journals. / GPL-2	noarch
<code>r-genord</code>	1.4.0	A gaussian copula based procedure for generating samples from discrete random variables with prescribed correlation matrix and marginal distributions. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-gensa	1.1.7	Performs search for global minimum of a very complex non-linear objective function with a very large number of optima. / GPL-2	linux-64, osx-64, win-64
r-gensemble	1.0.1	Generalized ensemble methods allowing arbitrary underlying models to be used. Currently only bagging is supported. / GPL-2	noarch
r-gensurv	1.0.3	Generation of survival data with one (binary) time-dependent covariate. Generation of survival data arising from a progressive illness-death model. / GPL-2	linux-64, osx-64, win-64
r-gensvm	0.1.1	The GenSVM classifier is a generalized multiclass support vector machine (SVM). This classifier aims to find decision boundaries that separate the classes with as wide a margin as possible. In GenSVM, the loss function is very flexible in the way that misclassifications are penalized. This allows the user to tune the classifier to the dataset at hand and potentially obtain higher classification accuracy than alternative multiclass SVMs. Moreover, this flexibility means that GenSVM has a number of other multiclass SVMs as special cases. One of the other advantages of GenSVM is that it is trained in the primal space, allowing the use of warm starts during optimization. This means that for common tasks such as cross validation or repeated model fitting, GenSVM can be trained very quickly. Based on: G.J.J. van den Burg and P.J.F. Groenen (2018) < <a href="http://www.jmlr.org/papers/v17/14-526.html">http://www.jmlr.org/papers/v17/14-526.html</a> >. / GPL-2	linux-64, win-64
r-gentag	1.0	Implement a coherent and flexible protocol for animal color tagging. ‘GenTag’ provides a simple computational routine with low CPU usage to create color sequences for animal tag. First, a single-color tag sequence is created from an algorithm selected by the user, followed by verification of the combination uniqueness. Three methods to produce color tag sequences are provided. Users can modify the main function core to allow a wide range of applications. / GPL-2	noarch
r-genwin	0.1	Defines window or bin boundaries for the analysis of genomic data. Boundaries are based on the inflection points of a cubic smoothing spline fitted to the raw data. Along with defining boundaries, a technique to evaluate results obtained from unequally-sized windows is provided. Applications are particularly pertinent for, though not limited to, genome scans for selection based on variability between populations (e.g. using Wright’s fixations index, Fst, which measures variability in subpopulations relative to the total population). / MIT	noarch
r-geoboxplot	1.0	Make geographic box plot as detailed in Willmott et al. (2007). / GPL-2	noarch
r-geocount	1.150	This package provides a variety of functions to analyze and model geostatistical count data with generalized linear spatial models, including 1) simulate and visualize the data; 2) posterior sampling with robust MCMC algorithms (in serial or parallel way); 3) perform prediction for unsampled locations; 4) conduct Bayesian model checking procedure to evaluate the goodness of fitting; 5) conduct transformed residual checking procedure. In the package, seamlessly embedded C programs and parallel computing techniques are implemented to speed up the computing processes. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-geode	1.0	Given expression data this package calculate a multivariate geometrical characterization of the differential expression and can also perform gene-set enrichment. / GPL-2	noarch
r-geodist	0.0.3	Dependency-free, ultra fast calculation of geodesic distances. Includes the reference nanometre-accuracy geodesic distances of Karney (2013) <doi:10.1007/s00190-012-0578-z>, as used by the ‘sf’ package, as well as Haversine and Vincenty distances. Default distance measure is the Mapbox cheap ruler which is generally more accurate than Haversine or Vincenty for distances out to a few hundred kilometres, and is considerably faster. The main function accepts one or two inputs in almost any generic rectangular form, and returns either matrices of pairwise distances, or vectors of sequential distances. / MIT	linux-64, osx-64, win-64
r-geohashtools	0.2.4	Tools for working with Gustavo Niemeyer’s geohash coordinate system, ported to R from Hiroaki Kawai’s ‘Python’ implementation and embellished to sit naturally in the R ecosystem. / MIT	linux-64, osx-64, win-64
r-geojsonr	1.0.7	Includes functions for processing GeoJson objects < <a href="https://en.wikipedia.org/wiki/GeoJSON">https://en.wikipedia.org/wiki/GeoJSON</a> > relying on ‘RFC 7946’ < <a href="https://tools.ietf.org/pdf/rfc7946.pdf">https://tools.ietf.org/pdf/rfc7946.pdf</a> >. The geojson encoding is based on ‘json11’, a tiny JSON library for ‘C11’ < <a href="https://github.com/dropbox/json11">https://github.com/dropbox/json11</a> >. Furthermore, the source code is exported in R through the ‘Rcpp’ and ‘RcppArmadillo’ packages. / MIT	linux-64, osx-64, win-64
r-geomapdata	1.0_4	Set of data for use in package GEOMap. Includes world map, USA map, Coso map, Japan Map, ETOPO5 / GPL-3	noarch
r-geomedb	2.0.0	The Genomic Observatory Metadatabase (GeOMe Database) is an open access repository for geographic and ecological metadata associated with sequenced samples. This package is used to retrieve GeOMe data for analysis. See < <a href="http://www.geome-db.org">http://www.geome-db.org</a> > for more information regarding GeOMe. / GPL-3	noarch
r-geometa	0.5_0	Provides facilities to handle reading and writing of geographic metadata defined with OGC/ISO 19115, 11119 and 19110 geographic information metadata standards, and encoded using the ISO 19139 (XML) standard. It includes also a facility to check the validity of ISO 19139 XML encoded metadata. / MIT	noarch
r-geometry	0.4.1	Makes the qhull library ( <a href="http://www.qhull.org">www.qhull.org</a> ) available in R, in a similar manner as in Octave and MATLAB. Qhull computes convex hulls, Delaunay triangulations, halfspace intersections about a point, Voronoi diagrams, furthest-site Delaunay triangulations, and furthest-site Voronoi diagrams. It runs in 2-d, 3-d, 4-d, and higher dimensions. It implements the Quickhull algorithm for computing the convex hull. Qhull does not support constrained Delaunay triangulations, or mesh generation of non-convex objects, but the package does include some R functions that allow for this. Currently the package only gives access to Delaunay triangulation and convex hull computation. / GPL (>= 3)	linux-32, linux-64, osx-64, win-32, win-64
r-geonames	0.999	The web service at < <a href="https://www.geonames.org/">https://www.geonames.org/</a> > provides a number of spatial data queries, including administrative area hierarchies, city locations and some country postal code queries. A (free) username is required and rate limits exist. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-geoops	0.2.0	Tools for doing calculations and manipulations on ‘GeoJSON’, a ‘geospatial’ data interchange format (< <a href="https://tools.ietf.org/html/rfc7946">https://tools.ietf.org/html/rfc7946</a> >). ‘GeoJSON’ is also valid ‘JSON’. / MIT	linux-64, osx-64, win-64
r-geosapi	0.4.0	Provides an R interface to the GeoServer REST API, allowing to upload and publish data in a GeoServer web-application and expose data to OGC Web-Services. The package currently supports all CRUD (Create,Read,Update,Delete) operations on GeoServer workspaces, namespaces, datastores (stores of vector data), featuretypes, layers, styles, as well as vector data upload operations. For more information about the GeoServer REST API, see < <a href="http://docs.geoserver.org/stable/en/user/rest/">http://docs.geoserver.org/stable/en/user/rest/</a> >. / MIT	noarch
r-geoscale	2.0	Function for adding the geological timescale to bivariate plots. / GPL-2	noarch
r-geosed	0.1.1	Find the smallest circle that contains all longitude and latitude input points. From the generated center and radius, variable side polygons can be created, navigation based on bearing and distance can be applied, and more. Based on a modified version of Welzl’s algorithm for smallest circle. Distance calculations are based on the haversine formula. Calculations for distance, midpoint, bearing and more are derived from < <a href="https://www.movable-type.co.uk">https://www.movable-type.co.uk</a> >. / MIT	noarch
r-geosphere	1.5.1	Spherical trigonometry for geographic applications. That is, compute distances and related measures for angular (longitude/latitude) locations. / GPL-3	linux-64, osx-64, win-64
r-geostatsp	1.7.8	Geostatistical modelling facilities using Raster and SpatialPoints objects are provided. Non-Gaussian models are fit using INLA, and Gaussian geostatistical models use Maximum Likelihood Estimation. For details see Brown (2015) <doi:10.18637/jss.v063.i12>. / GPL-3	linux-64, osx-64, win-64
r-geotech	1.0	A compilation of functions for performing calculations and creating plots that commonly arise in geotechnical engineering and soil mechanics. The types of calculations that are currently included are: (1) phase diagrams and index parameters, (2) grain-size distributions, (3) plasticity, (4) soil classification, (5) compaction, (6) groundwater, (7) subsurface stresses (geostatic and induced), (8) Mohr circle analyses, (9) consolidation settlement and rate, (10) shear strength, (11) bearing capacity, (12) lateral earth pressures, (13) slope stability, and (14) subsurface explorations. Geotechnical engineering students, educators, researchers, and practitioners will find this package useful. / GPL-3	noarch
r-geotools	0.1	Tools / GPL-3	noarch
r-geozoo	0.5.1	Geometric objects defined in ‘geozoo’ can be simulated or displayed in the R package ‘tourr’. / GPL-2	noarch
r-gepaf	0.1.1	Encode and decode the Google Encoded Polyline Algorithm Format (< <a href="https://developers.google.com/maps/documentation/utilities/polylinealgorithm">https://developers.google.com/maps/documentation/utilities/polylinealgorithm</a> >). / GPL-3	noarch
r-gesca	1.0.4	Fit a variety of component-based structural equation models. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-gestalt	0.1.8	Provides a suite of function-building tools centered around a (forward) composition operator, <code>%&gt;&gt;&gt;%</code> , which extends the semantics of the ‘magrittr’ <code>%&gt;%</code> operator and supports ‘tidyverse’ quasiquotation. It enables you to construct composite functions that can be inspected and transformed as list-like objects. In conjunction with <code>%&gt;&gt;&gt;%</code> , a compact function constructor, <code>fn()</code> , and a function that performs partial application, <code>partial()</code> , are also provided. Both support quasiquotation. / MIT	noarch
r-gethr	0.1.0	Full access to the Geth command line interface for running full Ethereum nodes. With gethr it is possible to carry out different tasks such as mine ether, transfer funds, create contacts, explore block history, etc. The package also provides access to all the available APIs. The officially exposed by Ethereum blockchains (eth, shh, web3, net) and some provided directly by Geth (admin, debug, miner, personal, txpool). For more details on Ethereum, access the project website < <a href="https://www.ethereum.org/">https://www.ethereum.org/</a> >. For more details on the Geth client, access the project website < <a href="https://github.com/ethereum/go-ethereum/wiki/geth/">https://github.com/ethereum/go-ethereum/wiki/geth/</a> >. / MIT	noarch
r-getopt	1.20.3	Package designed to be used with Rscript to write “#!” shebang scripts that accept short and long flags/options. Many users will prefer using instead the packages optparse or argparse which add extra features like automatically generated help option and usage, support for default values, positional argument support, etc. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-getpass	0.2_2	A micro-package for reading passwords, i.e. reading user input with masking, so that the input is not displayed as it is typed. Currently we have support for ‘RStudio’, the command line (every OS), and any platform where ‘tcltk’ is present. / BSD_2_clause	linux-64, osx-64, win-64
r-gets	0.19	Automated General-to-Specific (GETS) modelling of the mean and variance of a regression, and indicator saturation methods for detecting and testing for structural breaks in the mean. / GPL-2	noarch
r-gettz	0.0.3	A function to retrieve the system timezone on Unix systems which has been found to find an answer when ‘Sys.timezone()’ has failed. It is based on an answer by Duane McCully posted on ‘StackOverflow’, and adapted to be callable from R. The package also builds on Windows, but just returns NULL. / GPL-2	linux-64, osx-64, win-64
r-gevcdn	1.1.6	Implements a flexible nonlinear modelling framework for nonstationary generalized extreme value analysis in hydroclimatology following Cannon (2010) < <a href="https://doi.org/10.1002/hyp.7506">doi:10.1002/hyp.7506</a> >. / GPL-2	noarch
r-gexp	1.0_0	Generates experiments - simulating structured or experimental data as: completely randomized design, randomized block design, latin square design, factorial and split-plot experiments (Ferreira, 2008, ISBN:8587692526; Naes et al., 2007 < <a href="https://doi.org/10.1002/qre.841">doi:10.1002/qre.841</a> >; Rencher et al., 2007, ISBN:9780471754985; Montgomery, 2001, ISBN:0471316490). / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-gfa</a>	1.0.3	Factor analysis implementation for multiple data sources, i.e., for groups of variables. The whole data analysis pipeline is provided, including functions and recommendations for data normalization and model definition, as well as missing value prediction and model visualization. The model group factor analysis (GFA) is inferred with Gibbs sampling, and it has been presented originally by Virtanen et al. (2012), and extended in Klami et al. (2015) <DOI:10.1109/TNNLS.2014.2376974> and Bunte et al. (2016) <DOI:10.1093/bioinformatics/btw207>; for details, see the citation info. / MIT	noarch
<a href="#">r-gforce</a>	0.1.4	A complete suite of computationally efficient methods for high dimensional clustering and inference problems in G-Latent Models (a type of Latent Variable Gaussian graphical model). The main feature is the FORCE (First-Order, Certifiable, Efficient) clustering algorithm which is a fast solver for a semi-definite programming (SDP) relaxation of the K-means problem. For certain types of graphical models (G-Latent Models), with high probability the algorithm not only finds the optimal clustering, but produces a certificate of having done so. This certificate, however, is model independent and so can also be used to certify data clustering problems. The ‘GFORCE’ package also contains implementations of inferential procedures for G-Latent graphical models using n-fold cross validation. Also included are native code implementations of other popular clustering methods such as Lloyd’s algorithm with kmeans initialization and complete linkage hierarchical clustering. The FORCE method is due to Eisenach and Liu (2019) <arxiv:1806.00530>. / GPL-2	linux-64, win-64
<a href="#">r-gglasso</a>	1.4	A unified algorithm, blockwise-majorization-descent (BMD), for efficiently computing the solution paths of the group-lasso penalized least squares, logistic regression, Huberized SVM and squared SVM. The package is an implementation of Yang, Y. and Zou, H. (2015) DOI: <doi:10.1007/s11222-014-9498-5>. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-ggm</a>	2.3	Functions and datasets for maximum likelihood fitting of some classes of graphical Markov models. / GPL-2	noarch
<a href="#">r-ggmridge</a>	1.1	Estimation of partial correlation matrix using ridge penalty followed by thresholding and reestimation. Under multivariate Gaussian assumption, the matrix constitutes an Gaussian graphical model (GGM). / GPL-2	noarch
<a href="#">r-ggmselect</a>	0.1.1	Graph estimation in Gaussian Graphical Models. The main functions return the adjacency matrix of an undirected graph estimated from a data matrix. / GPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-ggplot2	3.1.1	A system for ‘declaratively’ creating graphics, based on The Grammar of Graphics. You provide the data, tell ‘ggplot2’ how to map variables to aesthetics, what graphical primitives to use, and it takes care of the details. / GPL-2   file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-ggplot2movies	0.0.1	A dataset about movies. This was previously contained in ggplot2, but has been moved its own package to reduce the download size of ggplot2. / GPL-3	noarch
r-ggroups	1.2.1	Calculates additive and dominance genetic relationship matrices and their inverses, in matrix and tabular-sparse formats. It includes functions for checking and processing pedigree, as well as functions to calculate the matrix of genetic group contributions (Q), and adding those contributions to the genetic merit of animals (Quaas (1988) <doi:10.3168/jds.S0022-0302(88)79691-5>). Calculation of Q is computationally extensive. There are computationally optimized functions to calculate Q. / GPL-3	noarch
r-ggversa	0.0.1	A collection of datasets for the upcoming book Graficas versatiles con ggplot: Analisis visuales de datos, by Raymond L. Tremblay and Julian Hernandez-Serano. / GPL-2	noarch
r-ggvis	0.4.4	An implementation of an interactive grammar of graphics, taking the best parts of ‘ggplot2’, combining them with the reactive framework of ‘shiny’ and drawing web graphics using ‘vega’. / GPL-2   file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-gh	1.0.1	Minimal client to access the ‘GitHub’ ‘API’. / MIT file LICENSE	noarch
r-ghibli	0.3.0	Colour palettes inspired by Studio Ghibli < <a href="https://en.wikipedia.org/wiki/Studio_Ghibli">https://en.wikipedia.org/wiki/Studio_Ghibli</a> > films, ported to R for your enjoyment. / MIT	noarch
r-ghs	0.1	Draw posterior samples to estimate the precision matrix for multivariate Gaussian data. Posterior means of the samples is the graphical horseshoe estimate by Li, Bhadra and Craig(2017) <arXiv:1707.06661>. The function uses matrix decomposition and variable change from the Bayesian graphical lasso by Wang(2012) <doi:10.1214/12-BA729>, and the variable augmentation for sampling under the horseshoe prior by Makalic and Schmidt(2016) <arXiv:1508.03884>. Structure of the graphical horseshoe function was inspired by the Bayesian graphical lasso function using blocked sampling, authored by Wang(2012) <doi:10.1214/12-BA729>. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-ghyp</a>	1.5.7	Detailed functionality for working with the univariate and multivariate Generalized Hyperbolic distribution and its special cases (Hyperbolic (hyp), Normal Inverse Gaussian (NIG), Variance Gamma (VG), skewed Student-t and Gaussian distribution). Especially, it contains fitting procedures, an AIC-based model selection routine, and functions for the computation of density, quantile, probability, random variates, expected shortfall and some portfolio optimization and plotting routines as well as the likelihood ratio test. In addition, it contains the Generalized Inverse Gaussian distribution. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-gibbs.met</a>	1.1_3	This package provides two generic functions for performing Markov chain sampling in a naive way for a user-defined target distribution, which involves only continuous variables. The function <code>gibbs_met</code> performs Gibbs sampling with each 1-dimensional distribution sampled with Metropolis update using Gaussian proposal distribution centered at the previous state. The function <code>met_gaussian</code> updates the whole state with Metropolis method using independent Gaussian proposal distribution centered at the previous state. The sampling is carried out without considering any special tricks for improving efficiency. This package is aimed at only routine applications of MCMC in moderate-dimensional problems. / GPL-2	noarch
<a href="#">r-gibbsacov</a>	1.1	Gibbs sampler for one-way linear mixed-effects models (ANOVA, ANCOVA) with homoscedasticity of errors and uniform priors. / GPL-2	noarch
<a href="#">r-gifi</a>	0.3_9	Implements categorical principal component analysis ('PRINCALS'), multiple correspondence analysis ('HOMALS'), monotone regression analysis ('MORALS'). It replaces the 'homals' package. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-gifski</a>	0.8.6	Multi-threaded GIF encoder written in Rust: < <a href="https://gif.ski/">https://gif.ski/</a> >. Converts images to GIF animations using pngquant's efficient cross-frame palettes and temporal dithering with thousands of colors per frame. / MIT	osx-64, win-64
<a href="#">r-gifti</a>	0.7.5	Functions to read in the geometry format under the 'Neuroimaging' 'Informat-ics' Technology Initiative ('NIFTI'), called 'GIFTI' < <a href="https://www.nitrc.org/projects/gifti/">https://www.nitrc.org/projects/gifti/</a> >. These files contain surfaces of brain imaging data. / GPL-2	noarch
<a href="#">r-gigrvg</a>	0.5	Generator and density function for the Generalized Inverse Gaussian (GIG) distribution. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-gillespiessa</a>	0.6.1	Provides a simple to use, intuitive, and extensible interface to several stochastic simulation algorithms for generating simulated trajectories of finite population continuous-time model. Currently it implements Gillespie's exact stochastic simulation algorithm (Direct method) and several approximate methods (Explicit tau-leap, Binomial tau-leap, and Optimized tau-leap). The package also contains a library of template models that can be run as demo models and can easily be customized and extended. Currently the following models are included, 'Decaying-Dimerization' reaction set, linear chain system, logistic growth model, 'Lotka' predator-prey model, Rosenzweig-MacArthur predator-prey model, 'Kermack-McKendrick' SIR model, and a 'metapopulation' SIRS model. Pineda-Krch et al. (2008) <doi:10.18637/jss.v025.i12>. / GPL-3	noarch
<a href="#">r-gim</a>	0.11.0	Implements the generalized integration model, which integrates individual-level data and summary statistics under a generalized linear model framework. It supports continuous and binary outcomes to be modeled by the linear and logistic regression models. / MIT	noarch
<a href="#">r-giniwegneg</a>	1.0.1	Gini-based coefficients and plot of the ordinary and generalized curve of maximum inequality in the presence of weighted and negative attributes. / GPL-3	noarch
<a href="#">r-gipfrm</a>	3.1	Maximum likelihood estimation under relational models, with or without the overall effect. / GPL-2	noarch
<a href="#">r-giraf</a>	1.0	Allows calculation on, and sampling from Gibbs Random Fields, and more precisely general homogeneous Potts model. The primary tool is the exact computation of the intractable normalising constant for small rectangular lattices. Beside the latter function, it contains method that give exact sample from the likelihood for small enough rectangular lattices or approximate sample from the likelihood using MCMC samplers for large lattices. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-gistr</a>	0.4.2	Work with 'GitHub' 'gists' from 'R' (e.g., < <a href="http://en.wikipedia.org/wiki/GitHub#Gist">http://en.wikipedia.org/wiki/GitHub#Gist</a> >, < <a href="https://help.github.com/articles/about-gists/">https://help.github.com/articles/about-gists/</a> >). A 'gist' is simply one or more files with code/text/images/etc. This package allows the user to create new 'gists', update 'gists' with new files, rename files, delete files, get and delete 'gists', star and 'un-star' 'gists', fork 'gists', open a 'gist' in your default browser, get embed code for a 'gist', list 'gist' 'commits', and get rate limit information when 'authenticated'. Some requests require authentication and some do not. 'Gists' website: < <a href="https://gist.github.com/">https://gist.github.com/</a> >. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-git2r</a>	0.25.2	Interface to the 'libgit2' library, which is a pure C implementation of the 'Git' core methods. Provides access to 'Git' repositories to extract data and running some basic 'Git' commands. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-git2rdata</a>	0.13	Make versioning of data.frame easy and efficient using git repositories. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-gitlink</a>	0.1.3	Provides helpers to add ‘Git’ links to ‘shiny’ applications, ‘rmarkdown’ documents, and other ‘HTML’ based resources. This is most commonly used for ‘GitHub’ ribbons. / MIT	noarch
<a href="#">r-gk2011</a>	0.1.3	Implementations of the treatment effect estimators for hybrid (self-selection) experiments, as developed by Brian J. Gaines and James H. Kuklinski, (2011), Experimental Estimation of Heterogeneous Treatment Effects Related to Self-Selection, American Journal of Political Science 55(3): 724-736. / GPL-2	noarch
<a href="#">r-glaciersmbm</a>	0.1	A fully distributed glacier surface mass balance model developed for the simulation of accumulation and ablation processes on debris-free as well as debris-covered glaciers. / GPL-3	noarch
<a href="#">r-glamlasso</a>	3.0	Functions capable of performing efficient design matrix free penalized estimation in large scale 2 and 3-dimensional generalized linear array model framework. The generic glamlasso() function solves the penalized maximum likelihood estimation (PMLE) problem in a pure generalized linear array model (GLAM) as well as in a GLAM containing a non-tensor component. Currently Lasso or Smoothly Clipped Absolute Deviation (SCAD) penalized estimation is possible for the followings models: The Gaussian model with identity link, the Binomial model with logit link, the Poisson model with log link and the Gamma model with log link. Furthermore this package also contains two functions that can be used to fit special cases of GLAMs, see glamlassoRR() and glamlassoS(). The procedure underlying these functions is based on the gdpg algorithm from Lund et al. (2017) <doi:10.1080/10618600.2017.1279548>. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-glarma</a>	1.6_0	Functions are provided for estimation, testing, diagnostic checking and forecasting of generalized linear autoregressive moving average (GLARMA) models for discrete valued time series with regression variables. These are a class of observation driven non-linear non-Gaussian state space models. The state vector consists of a linear regression component plus an observation driven component consisting of an autoregressive-moving average (ARMA) filter of past predictive residuals. Currently three distributions (Poisson, negative binomial and binomial) can be used for the response series. Three options (Pearson, score-type and unscaled) for the residuals in the observation driven component are available. Estimation is via maximum likelihood (conditional on initializing values for the ARMA process) optimized using Fisher scoring or Newton Raphson iterative methods. Likelihood ratio and Wald tests for the observation driven component allow testing for serial dependence in generalized linear model settings. Graphical diagnostics including model fits, autocorrelation functions and probability integral transform residuals are included in the package. Several standard data sets are included in the package. / GPL-2	noarch
<a href="#">r-glassdoor</a>	0.8.1	Interacts with the ‘Glassdoor’ API < <a href="https://www.glassdoor.com/developer/index.htm">https://www.glassdoor.com/developer/index.htm</a> >. Allows the user to search job statistics, employer statistics, and job progression, where ‘Glassdoor’ provides a breakdown of other jobs a person did after their current one. / GPL-2	noarch
<a href="#">r-glasso</a>	1.10	Estimation of a sparse inverse covariance matrix using a lasso (L1) penalty. Facilities are provided for estimates along a path of values for the regularization parameter. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-glassofast</a>	1.0	A fast and improved implementation of the graphical LASSO. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-glba</a>	0.2	Analyses response times and accuracies from psychological experiments with the linear ballistic accumulator (LBA) model from Brown and Heathcote (2008). The LBA model is optionally fitted with explanatory variables on the parameters such as the drift rate, the boundary and the starting point parameters. A log-link function on the linear predictors can be used to ensure that parameters remain positive when needed. / GPL-3	noarch
<a href="#">r-gldm</a>	1.6.4	Enables calculation of image textures (Haralick 1973) <doi:10.1109/TSMC.1973.4309314> from grey-level co-occurrence matrices (GLCMs). Supports processing images that cannot fit in memory. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-gldex</a>	2.0.0	The fitting algorithms considered in this package have two major objectives. One is to provide a smoothing device to fit distributions to data using the weight and unweighted discretised approach based on the bin width of the histogram. The other is to provide a definitive fit to the data set using the maximum likelihood and quantile matching estimation. Other methods such as moment matching, starship method, L moment matching are also provided. Diagnostics on goodness of fit can be done via qqplots, KS-resample tests and comparing mean, variance, skewness and kurtosis of the data with the fitted distribution. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-gldrm</a>	1.5	Fits a generalized linear density ratio model (GLDRM). A GLDRM is a semiparametric generalized linear model. In contrast to a GLM, which assumes a particular exponential family distribution, the GLDRM uses a semiparametric likelihood to estimate the reference distribution. The reference distribution may be any discrete, continuous, or mixed exponential family distribution. The model parameters, which include both the regression coefficients and the cdf of the unspecified reference distribution, are estimated by maximizing a semiparametric likelihood. Regression coefficients are estimated with no loss of efficiency, i.e. the asymptotic variance is the same as if the true exponential family distribution were known. Huang (2014) <doi:10.1080/01621459.2013.824892>. Huang and Rathouz (2012) <doi:10.1093/biomet/asr075>. Rathouz and Gao (2008) <doi:10.1093/biostatistics/kxn030>. / MIT	noarch
<a href="#">r-glide</a>	1.0.2	Functions evaluate global and individual tests for direct effects in Mendelian randomization studies. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-glinternet</a>	1.0.10	Group-Lasso INTERAction-NET. Fits linear pairwise-interaction models that satisfy strong hierarchy: if an interaction coefficient is estimated to be nonzero, then its two associated main effects also have nonzero estimated coefficients. Accommodates categorical variables (factors) with arbitrary numbers of levels, continuous variables, and combinations thereof. Implements the machinery described in the paper Learning interactions via hierarchical group-lasso regularization (JCGS 2015, Volume 24, Issue 3). Michael Lim & Trevor Hastie (2015) <DOI:10.1080/10618600.2014.938812>. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-gllm</a>	0.37	Routines for log-linear models of incomplete contingency tables, including some latent class models, via EM and Fisher scoring approaches. Allows bootstrapping. See Espeland and Hui (1987) <doi:10.2307/2531553> for general approach. / GPL-2   GPL-3	linux-64, osx-64, win-64
<a href="#">r-glm.deploy</a>	1.0.4	Provides two functions that generate source code implementing the predict function of fitted glm objects. In this version, code can be generated for either 'C' or 'Java'. The idea is to provide a tool for the easy and fast deployment of glm predictive models into production. The source code generated by this package implements two function/methods. One of such functions implements the equivalent to predict(type=response), while the second implements predict(type=link). Source code is written to disk as a .c or .java file in the specified path. In the case of c, an .h file is also generated. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-glm.predict</a>	3.1_0	Functions to calculate predicted values and the difference between the two cases with confidence interval for lm() [linear model], glm() [general linear model], glm.nb() [negative binomial model], polr() [ordinal logistic model] and multinom() [multinomial model] using Monte Carlo simulations. Reference: Bennet A. Zelner (2009) <doi:10.1002/smj.783>. / GPL-2	noarch
<a href="#">r-glm2</a>	1.2.1	Fits generalized linear models using the same model specification as glm in the stats package, but with a modified default fitting method that provides greater stability for models that may fail to converge using glm. / GPL-2	noarch
<a href="#">r-glmaspu</a>	1.0	Several tests for high dimensional generalized linear models have been proposed recently. In this package, we implemented a new test called adaptive sum of powered score (aSPU) for high dimensional generalized linear models, which is often more powerful than the existing methods in a wide scenarios. We also implemented permutation based version of several existing methods for research purpose. We recommend users use the aSPU test for their real testing problem. You can learn more about the tests implemented in the package via the following papers: 1. Pan, W., Kim, J., Zhang, Y., Shen, X. and Wei, P. (2014) <DOI:10.1534/genetics.114.165035> A powerful and adaptive association test for rare variants, Genetics, 197(4). 2. Guo, B., and Chen, S. X. (2016) <DOI:10.1111/rssb.12152>. Tests for high dimensional generalized linear models. Journal of the Royal Statistical Society: Series B. 3. Goeman, J. J., Van Houwelingen, H. C., and Finos, L. (2011) <DOI:10.1093/biomet/asr016>. Testing against a high-dimensional alternative in the generalized linear model: asymptotic type I error control. Biometrika, 98(2). / GPL-2	linux-64, osx-64, win-64
<a href="#">r-glmbb</a>	0.3	Find all hierarchical models of specified generalized linear model with information criterion (AIC, BIC, or AICc) within specified cutoff of minimum value. Alternatively, find all such graphical models. Use branch and bound algorithm so we do not have to fit all models. / MIT	noarch

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Name	Version	Summary/License	Platforms
r-glmc	0.3.1	Fits generalized linear models where the parameters are subject to linear constraints. The model is specified by giving a symbolic description of the linear predictor, a description of the error distribution, and a matrix of constraints on the parameters. / GPL-2	noarch
r-glmdm	2.60	This package contains functions to perform generalized linear mixed Dirichlet models using posterior simulation. / GPL-3	noarch
r-glmgraph	1.0.3	We propose to use sparse regression model to achieve variable selection while accounting for graph-constraints among coefficients. Different linear combination of a sparsity penalty(L1) and a smoothness(MCP) penalty has been used, which induces both sparsity of the solution and certain smoothness on the linear coefficients. / GPL-2	linux-64, osx-64, win-64
r-glmlep	0.2	Efficient algorithms for fitting regularization paths for linear or logistic regression models penalized by LEP. / GPL-2	linux-64, osx-64, win-64
r-glmmadaptive	0.6.0	Fits generalized linear mixed models for a single grouping factor under maximum likelihood approximating the integrals over the random effects with an adaptive Gaussian quadrature rule; Jose C. Pinheiro and Douglas M. Bates (1995) <doi:10.1080/10618600.1995.10474663>. / GPL-3	noarch
r-glmmboot	0.4.0	Performs bootstrap resampling for most models that update() works for. There are two primary functions: bootstrap_model() performs block resampling if random effects are present, and case resampling if not; bootstrap_ci() converts output from bootstrap model runs into confidence intervals and p-values. By default, bootstrap_model() calls bootstrap_ci(). Package motivated by Humphrey and Swingley (2018) <arXiv:1805.08670>. / AGPL-3	noarch
r-glmmlasso	1.5.1	A variable selection approach for generalized linear mixed models by L1-penalized estimation is provided. / GPL-2	noarch
r-glmmml	1.1.0	Binomial and Poisson regression for clustered data, fixed and random effects with bootstrapping. / GPL-3	linux-64, osx-64, win-64
r-glmmrr	0.2.0	Generalized Linear Mixed Model (GLMM) for Binary Randomized Response Data. Includes Cauchit, Compl. Log-Log, Logistic, and Probit link functions for Bernoulli Distributed RR data. RR Designs: Warner, Forced Response, Unrelated Question, Kuk, Crosswise, and Triangular. / GPL-2   GPL-3	noarch
r-glmmstr	0.2.3	Conduct inference about generalized linear mixed models, with a choice about which method to use to approximate the likelihood. In addition to the Laplace and adaptive Gaussian quadrature approximations, which are borrowed from 'lme4', the likelihood may be approximated by the sequential reduction approximation, or an importance sampling approximation. These methods provide an accurate approximation to the likelihood in some situations where it is not possible to use adaptive Gaussian quadrature. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-glmnet</a>	2.0.16	Extremely efficient procedures for fitting the entire lasso or elastic-net regularization path for linear regression, logistic and multinomial regression models, Poisson regression and the Cox model. Two recent additions are the multiple-response Gaussian, and the grouped multinomial regression. The algorithm uses cyclical coordinate descent in a path-wise fashion, as described in the paper linked to via the URL below. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-glmnetcr</a>	1.0.4	Penalized methods are useful for fitting over-parameterized models. This package includes functions for restructuring an ordinal response dataset for fitting continuation ratio models for datasets where the number of covariates exceeds the sample size or when there is collinearity among the covariates. The glmnet fitting algorithm is used to fit the continuation ratio model after data restructuring. / GPL-2	noarch
<a href="#">r-glmnetutils</a>	1.1.2	Provides a formula interface for the ‘glmnet’ package for elasticnet regression, a method for cross-validating the alpha parameter, and other quality-of-life tools. / GPL-2	noarch
<a href="#">r-glmpath</a>	0.98	A path-following algorithm for L1 regularized generalized linear models and Cox proportional hazards model. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-glmsdata</a>	1.0.0	Data sets from the book Generalized Linear Models with Examples in R by Dunn and Smyth. / GPL-2	noarch
<a href="#">r-glmtlp</a>	1.1	It provides an extremely efficient procedure for fitting the entire truncated lasso regularization path for linear regression, logistic and multinomial regression models, Poisson regression and the Cox model. The algorithm uses the difference of convex technique. The detail of the algorithm is described in Shen, Pan and Zhu (2012) <doi:10.1080/01621459.2011.645783>. The package is inherited from a popular R package ‘glmnet’ and many functions in ‘glmnet’ can be directly used in ‘glmtlp’. You can learn more details by the online manual (< <a href="http://wuchong.org/glmtlp.html">http://wuchong.org/glmtlp.html</a> >). / GPL-2	noarch
<a href="#">r-glmulti</a>	1.0.7	Automated model selection and model-averaging. Provides a wrapper for glm and other functions, automatically generating all possible models (under constraints set by the user) with the specified response and explanatory variables, and finding the best models in terms of some Information Criterion (AIC, AICc or BIC). Can handle very large numbers of candidate models. Features a Genetic Algorithm to find the best models when an exhaustive screening of the candidates is not feasible. / GPL-2	noarch
<a href="#">r-glmx</a>	0.1.1	Extended techniques for generalized linear models (GLMs), especially for binary responses, including parametric links and heteroskedastic latent variables. / GPL-2   GPL-3	noarch
<a href="#">r-globalgsa</a>	1.0	Implementation of three different Gene set analysis (GSA) algorithms for combining the individual pvalues of a set of genetic variats (SNPs) in a gene level pvalue. The implementation includes the selection of the best inheritance model for each SNP. / GPL-2	noarch
<a href="#">r-globaloptions</a>	0.1.0	It provides more configurations on the option values such as validation and filtering on the values, making options invisible or private. / MIT	noarch

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Name	Version	Summary/License	Platforms
r-globals	0.12.4	Identifies global (unknown or free) objects in R expressions by code inspection using various strategies, e.g. conservative or liberal. The objective of this package is to make it as simple as possible to identify global objects for the purpose of exporting them in distributed compute environments. / LGPL-2.1	noarch
r-globe	1.2.0	Basic functions for plotting 2D and 3D views of a sphere, by default the Earth with its major coastline, and additional lines and points. / GPL (>= 2.0)	noarch
r-glogis	1.0.1	Tools for the generalized logistic distribution (Type I, also known as skew-logistic distribution), encompassing basic distribution functions (p, q, d, r, score), maximum likelihood estimation, and structural change methods. / GPL-2   GPL-3	noarch
r-glrt	2.0	Functions to conduct four generalized logrank tests and a score test under a proportional hazards model / GPL-2	noarch
r-glrrth	0.2.0	Likelihood ratio tests for genome-wide association and genome-wide linkage analysis under heterogeneity. / GPL-3	noarch
r-glsme	1.0.4	Performs linear regression with correlated predictors, responses and correlated measurement errors in predictors and responses, correcting for biased caused by these. / GPL-2	noarch
r-glue	1.3.1	An implementation of interpreted string literals, inspired by Python's Literal String Interpolation < <a href="https://www.python.org/dev/peps/pep-0498/">https://www.python.org/dev/peps/pep-0498/</a> > and Docstrings < <a href="https://www.python.org/dev/peps/pep-0257/">https://www.python.org/dev/peps/pep-0257/</a> > and Julia's Triple-Quoted String Literals < <a href="https://docs.julialang.org/en/stable/manual/strings/#triple-quoted-string-literals">https://docs.julialang.org/en/stable/manual/strings/#triple-quoted-string-literals</a> >. / MIT file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
r-gmac	3.0	Performs genomic mediation analysis with adaptive confounding adjustment (GMAC) proposed by Yang et al. (2017) <doi:10.1101/078683>. It implements large scale mediation analysis and adaptively selects potential confounding variables to adjust for each mediation test from a pool of candidate confounders. The package is tailored for but not limited to genomic mediation analysis (e.g., cis-gene mediating trans-gene regulation pattern where an eQTL, its cis-linking gene transcript, and its trans-gene transcript play the roles as treatment, mediator and the outcome, respectively), restricting to scenarios with the presence of cis-association (i.e., treatment-mediator association) and random eQTL (i.e., treatment). / GPL-3	noarch
r-gmapsdistance	3.4	Get distance and travel time between two points from Google Maps. Four possible modes of transportation (bicycling, walking, driving and public transportation). / GPL-2	noarch
r-gmdatabase	0.5.0	A template for a geometallurgical database and a fast and easy interface for accessing it is provided in this package. / GPL-2   LGPL-2	noarch
r-gmdh	1.6	Group method of data handling (GMDH) - type neural network algorithm is the heuristic self-organization method for modelling the complex systems. In this package, GMDH-type neural network algorithms are applied to make short term forecasting for a univariate time series. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-gmdhreg	0.2.0	Regression using GMDH algorithms from Prof. Alexey G. Ivakhnenko. Group Method of Data Handling (GMDH), or polynomial neural networks, is a family of inductive algorithms that performs gradually complicated polynomial models and selecting the best solution by an external criterion. In other words, inductive GMDH algorithms give possibility finding automatically interrelations in data, and selecting an optimal structure of model or network. The package includes GMDH Combinatorial, GMDH MIA (Multilayered Iterative Algorithm), GMDH GIA (Generalized Iterative Algorithm) and GMDH Combinatorial with Active Neurons. An introduction of GMDH algorithms: Farlow, S.J. (1981): The GMDH algorithm of Ivakhnenko, The American Statistician, 35(4), pp. 210-215. <doi:10.2307/2683292> Ivakhnenko A.G. (1968): The Group Method of Data Handling - A Rival of the Method of Stochastic Approximation, Soviet Automatic Control, 13(3), pp. 43-55. / GPL-3	noarch
r-gmediation	0.1.1	Current version of this R package conducts mediation path analysis for multiple mediators in two stages. / GPL-2   GPL-3	noarch
r-gmfd	1.0.1	Some methods for the inference and clustering of univariate and multivariate functional data, using a generalization of Mahalanobis distance, along with some functions useful for the analysis of functional data. For further details, see Martino A., Ghigletti, A., Ieva, F. and Paganoni A. M. (2017) <arXiv:1708.00386>. / GPL-3	noarch
r-gmm	1.6_2	It is a complete suite to estimate models based on moment conditions. It includes the two step Generalized method of moments (Hansen 1982; <doi:10.2307/1912775>), the iterated GMM and continuous updated estimator (Hansen, Eaton and Yaron 1996; <doi:10.2307/1392442>) and several methods that belong to the Generalized Empirical Likelihood family of estimators (Smith 1997; <doi:10.1111/j.0013-0133.1997.174.x>, Kitamura 1997; <doi:10.1214/aos/1069362388>, Newey and Smith 2004; <doi:10.1111/j.1468-0262.2004.00482.x>, and Anatolyev 2005 <doi:10.1111/j.1468-0262.2005.00601.x>). / GPL-2	noarch
r-gmmboost	1.1.2	Likelihood-based Boosting for Generalized mixed models / GPL-2	noarch
r-gmodels	2.18.1	Various R programming tools for model fitting. / GPL-2	noarch
r-gmp	0.5_1	Multiple Precision Arithmetic (big integers and rationals, prime number tests, matrix computation), arithmetic without limitations using the C library GMP (GNU Multiple Precision Arithmetic). / GPL	linux-32, linux-64, osx-64, win-32, win-64
r-gmt	2.0_1	Interface between the GMT map-making software and R, enabling the user to manipulate geographic data within R and call GMT commands to draw and annotate maps in postscript format. The gmt package is about interactive data analysis, rapidly visualizing subsets and summaries of geographic data, while performing statistical analysis in the R console. / GPL-2	noarch
r-gnorm	1.0.0	Functions for obtaining generalized normal/exponential power distribution probabilities, quantiles, densities and random deviates. The generalized normal/exponential power distribution was introduced by Subbotin (1923) and rediscovered by Nadarajah (2005). The parametrization given by Nadarajah (2005) <doi:10.1080/02664760500079464> is used. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-gnumeric	0.7_8	Read data files readable by 'gnumeric' into 'R'. Can read whole sheet or a range, from several file formats, including the native format of 'gnumeric'. Reading is done by using 'ssconvert' (a file converter utility included in the 'gnumeric' distribution < <a href="http://projects.gnome.org/gnumeric/">http://projects.gnome.org/gnumeric/</a> >) to convert the requested part to CSV. From 'gnumeric' files (but not other formats) can list sheet names and sheet sizes or read all sheets. / GPL-2	noarch
r-gofkernel	2.1_1	Tests of goodness-of-fit based on a kernel smoothing of the data. / GPL-3	noarch
r-gogarch	0.7_2	Implementation of the GO-GARCH model class / GPL-2	noarch
r-gomms	1.0	A zero-inflated quasi-Poisson factor model to display similarity between samples visually in a low (2 or 3) dimensional space. / GPL-2	noarch
r-goodmankruskal	0.0.2	Association analysis between categorical variables using the Goodman and Kruskal tau measure. This asymmetric association measure allows the detection of asymmetric relations between categorical variables (e.g., one variable obtained by re-grouping another). / MIT	noarch
r-googleformr	0.0.3	GET and POST data to Google Forms; an API to Google Forms, allowing users to POST data securely to Google Forms without needing authentication or permissioning. / GPL-2	noarch
r-googleknowledgegraphr	0.1.0	Allows you to retrieve information from the 'Google Knowledge Graph' API < <a href="https://www.google.com/intl/bn/insidesearch/features/search/knowledge.html">https://www.google.com/intl/bn/insidesearch/features/search/knowledge.html</a> > and process it in R in various forms. The 'Knowledge Graph Search' API lets you find entities in the 'Google Knowledge Graph'. The API uses standard 'schema.org' types and is compliant with the 'JSON-LD' specification. / MIT	noarch
r-googlevis	0.6.4	R interface to Google's chart tools, allowing users to create interactive charts based on data frames. Charts are displayed locally via the R HTTP help server. A modern browser with an Internet connection is required and for some charts a Flash player. The data remains local and is not uploaded to Google. / GPL-2	noarch
r-goric	1.1_0	Generalized Order-Restricted Information Criterion (GORIC) value for a set of hypotheses in multivariate linear models and generalised linear models. / GPL-2	noarch
r-govstatjpn	0.1	This package purposes to deal with public survey data of Japanese government via their Application Programming Interface ( <a href="http://statdb.nstac.go.jp/">http://statdb.nstac.go.jp/</a> ) / GPL-3	noarch
r-gower	0.2.0	Compute Gower's distance (or similarity) coefficient between records. Compute the top-n matches between records. Core algorithms are executed in parallel on systems supporting OpenMP. / GPL-3	linux-32, linux-64, osx-64, win-32, win-64
r-gparotation	2014.11.1	Gradient Projection Algorithm Rotation for Factor Analysis. See ?GPArotation.Intro for more details. / GPL-2	noarch
r-gpca	1.0	This package implements guided principal components analysis for the detection of batch effects in high-throughput data. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-gpctest	0.4	This package computes the bootstrap goodness-of-fit test for the generalized Pareto distribution by Villasenor-Alva and Gonzalez-Estrada (2009). The null hypothesis includes heavy and non-heavy tailed gPd's. A function for fitting the gPd to data using the parameter estimation methods proposed in the same article is also provided. / GPL-2	noarch
r-gpk	1.0	Collection of datasets as prepared by Profs. A.P. Gore, S.A. Paranjape, and M.B. Kulkarni of Department of Statistics, Poona University, India. With their permission, first letter of their names forms the name of this package, the package has been built by me and made available for the benefit of R users. This collection requires a rich class of models and can be a very useful building block for a beginner. / GPL-2	noarch
r-gplots	3.0.1	Various R programming tools for plotting data, including: - calculating and plotting locally smoothed summary function as ('bandplot', 'wapply'), - enhanced versions of standard plots ('barplot2', 'boxplot2', 'heatmap.2', 'smartlegend'), - manipulating colors ('col2hex', 'colorpanel', 'redgreen', 'greenred', 'bluered', 'redblue', 'rich.colors'), - calculating and plotting two-dimensional data summaries ('ci2d', 'hist2d'), - enhanced regression diagnostic plots ('lplot2', 'residplot'), - formula-enabled interface to 'stats::lowess' function ('lowess'), - displaying textual data in plots ('textplot', 'sinkplot'), - plotting a matrix where each cell contains a dot whose size reflects the relative magnitude of the elements ('balloonplot'), - plotting Venn diagrams ('venn'), - displaying Open-Office style plots ('ooplot'), - plotting multiple data on same region, with separate axes ('overplot'), - plotting means and confidence intervals ('plotCI', 'plotmeans'), - spacing points in an x-y plot so they don't overlap ('space'). / GPL-2	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-gpltr	1.2	Combining a generalized linear model with an additional tree part on the same scale. A four-step procedure is proposed to fit the model and test the joint effect of the selected tree part while adjusting on confounding factors. We also proposed an ensemble procedure based on the bagging to improve prediction accuracy and computed several scores of importance for variable selection. / GPL (>= 2.0)	noarch
r-gpr	1.1	This package provides a minimalistic functionality necessary to apply Gaussian Process in R. They provide a selection of functionalities of GPML Matlab library. / GPL-3	noarch
r-gprofiler	0.6.8	This package has been deprecated and will not be updated. New users should use the package 'gprofiler2' (< <a href="https://CRAN.R-project.org/package=gprofiler2">https://CRAN.R-project.org/package=gprofiler2</a> >) for up-to-date data and improved functionality. Functional enrichment analysis, gene identifier conversion and mapping homologous genes across related organisms via the 'g:Profiler' toolkit (< <a href="https://biit.cs.ut.ee/gprofiler/">https://biit.cs.ut.ee/gprofiler/</a> >). / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-graddescent	3.0	An implementation of various learning algorithms based on Gradient Descent for dealing with regression tasks. The variants of gradient descent algorithm are : Mini-Batch Gradient Descent (MBGD), which is an optimization to use training data partially to reduce the computation load. Stochastic Gradient Descent (SGD), which is an optimization to use a random data in learning to reduce the computation load drastically. Stochastic Average Gradient (SAG), which is a SGD-based algorithm to minimize stochastic step to average. Momentum Gradient Descent (MGD), which is an optimization to speed-up gradient descent learning. Accelerated Gradient Descent (AGD), which is an optimization to accelerate gradient descent learning. Adagrad, which is a gradient-descent-based algorithm that accumulate previous cost to do adaptive learning. Adadelata, which is a gradient-descent-based algorithm that use hessian approximation to do adaptive learning. RMSprop, which is a gradient-descent-based algorithm that combine Adagrad and Adadelata adaptive learning ability. Adam, which is a gradient-descent-based algorithm that mean and variance moment to do adaptive learning. Stochastic Variance Reduce Gradient (SVRG), which is an optimization SGD-based algorithm to accelerates the process toward converging by reducing the gradient. Semi Stochastic Gradient Descent (SSGD), which is a SGD-based algorithm that combine GD and SGD to accelerates the process toward converging by choosing one of the gradients at a time. Stochastic Recursive Gradient Algorithm (SARAH), which is an optimization algorithm similarly SVRG to accelerates the process toward converging by accumulated stochastic information. Stochastic Recursive Gradient Algorithm (SARAHPlus), which is a SARAH practical variant algorithm to accelerates the process toward converging provides a possibility of earlier termination. / GPL-2	noarch
r-grade	0.2.1	Provides functions for matching student-answers to teacher answers for a variety of data types. / GPL-2	noarch
r-grader	1.0.1	After being given the location of your students' submissions and a test file, the function runs each .R file, and evaluates the results from all the given tests. Results are neatly returned in a data frame that has a row for each student, and a column for each test. / MIT	noarch
r-gradientpickerd3	0.1.0.0	Widget for an interactive selection and modification of a color gradient. 'gradientPickerD3' allows addition, removal and replacement of color ticks. List of numeric values will automatically translate in their corresponding tick position within the numeric range. App returns a data.frame containing tick values, colors and the positions in percent (0.0 to 1.0) for each color tick in the gradient. The original JS 'jquery-gradient-picker' was implemented by Matt Crinklaw-Vogt (nick: tantaman) < <a href="https://github.com/tantaman/">https://github.com/tantaman/</a> >. Widget and JS modifications were done by CD. Peikert. / GPL-3	noarch
r-gramevol	2.1.3	A native R implementation of grammatical evolution (GE). GE facilitates the discovery of programs that can achieve a desired goal. This is done by performing an evolutionary optimisation over a population of R expressions generated via a user-defined context-free grammar (CFG) and cost function. / GPL-2	noarch
r-grangers	0.1.0	Contains five functions performing the calculation of unconditional and conditional Granger-causality spectra, bootstrap inference on both, and inference on the difference between them via the bootstrap approach of Farne' and Montanari, 2018 <arXiv:1803.00374>. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-grape	0.1.1	Gene-Ranking Analysis of Pathway Expression (GRAPE) is a tool for summarizing the consensus behavior of biological pathways in the form of a template, and for quantifying the extent to which individual samples deviate from the template. GRAPE templates are based only on the relative rankings of the genes within the pathway and can be used for classification of tissue types or disease subtypes. GRAPE can be used to represent gene-expression samples as vectors of pathway scores, where each pathway score indicates the departure from a given collection of reference samples. The resulting pathway- space representation can be used as the feature set for various applications, including survival analysis and drug-response prediction. Users of GRAPE should use the following citation: Klein MI, Stern DF, and Zhao H. GRAPE: A pathway template method to characterize tissue-specific functionality from gene expression profiles. BMC Bioinformatics, 18:317 (June 2017). / GPL-2	noarch
r-grapes	1.0.0	Turn arbitrary functions into binary operators. / GPL-3	noarch
r-grapfa	1.0	gRapfa is for modelling discrete longitudinal data using acyclic probabilistic finite automata (APFA). The package contains functions for constructing APFA models from a given data using penalized likelihood methods. For graphical display of APFA models, gRapfa depends on 'igraph package'. gRapfa also contains an interface function to Beagle software that implements an efficient model selection algorithm. / GPL-2	noarch
r-grapher	1.9_86	A multi-platform user interface for drawing highly customizable graphs in R. It aims to be a valuable help to quickly draw publishable graphs without any knowledge of R commands. Six kinds of graph are available: histogram, box-and-whisker plot, bar plot, pie chart, curve and scatter plot. / GPL-2	noarch
r-graphfactor	1.1	A Network Implementation of Fuzzy Sets: Build Network Objects from Multivariate Flat Files. For more information on fuzzy sets, refer to: Zadeh, L.A. (1964) <DOI:10.1016/S0019-9958(65)90241-X>. / GPL-2	noarch
r-graphicsqc	1.0_8	Functions to generate graphics files, compare them with model files, and report the results, including visual and textual diffs of any differences. / GPL-2	noarch
r-grassmannoptim	2.0	Optimizing a function F(U), where U is a semi-orthogonal matrix and F is invariant under an orthogonal transformation of U / GPL-2	noarch
r-graticule	0.1.2	Create graticule lines and labels for maps. Control the creation of lines by setting their placement (at particular meridians and parallels) and extent (along parallels and meridians). Labels are created independently of lines. / GPL-3	noarch
r-grcdata	1.0	We implement two main functions. The first function uses a given grouped and/or right-censored grouping scheme and empirical data to infer parameters, and implements chi-square goodness-of-fit tests. The second function searches for the global optimal grouping scheme of grouped and/or right-censored count responses in surveys. / GPL-3	noarch
r-greedyexperimentaldesign	1.0	These are GreedyExperimentalDesign Java dependency libraries. Note: this package has no functionality of its own and should not be installed as a standalone package without GreedyExperimentalDesign. / GPL-3	noarch
r-greenclust	1.0.0	Implements a method of iteratively collapsing the rows of a contingency table, two at a time, by selecting the pair of categories whose combination yields a new table with the smallest loss of chi-squared, as described by Greenacre, M.J. (1988) <doi:10.1007/BF01901670>. The result is compatible with the class of object returned by the 'stats' package's hclust() function and can be used similarly (plotted as a dendrogram, cut, etc.). Additional functions are provided for automatic cutting and diagnostic plotting. / MIT	noarch

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Name	Version	Summary/License	Platforms
r-gremlin	0.1.0	Fit linear mixed-effects models using restricted (or residual) maximum likelihood (REML) and with generalized inverse matrices to specify covariance structures for random effects. In particular, the package is suited to fit quantitative genetic mixed models, often referred to as ‘animal models’ (Kruuk. 2004 <DOI: 10.1098/rstb.2003.1437>). Implements the average information algorithm as the main tool to maximize the restricted likelihood, but with other algorithms available (Meyer. 1997. Genet Sel Evol 29:97; Meyer and Smith. 1998. Genet Sel Evol 28:23.). / GPL-3	noarch
r-grex	1.9	Convert ‘Ensembl’ gene identifiers from Genotype-Tissue Expression (GTEx) data to identifiers in other annotation systems, including ‘Entrez’, ‘HGNC’, and ‘UniProt’. / GPL-3	noarch
r-gridbase	0.4_7	Integration of base and grid graphics / GPL	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-gridbezier	1.1_1	Functions for rendering Bezier curves (Pomax, 2018) < <a href="https://pomax.github.io/bezierinfo/">https://pomax.github.io/bezierinfo/</a> > in ‘grid’. There is support for both quadratic and cubic Bezier curves. There are also functions for calculating points on curves, tangents to curves, and normals to curves. / GPL-2	noarch
r-gridextra	2.3	Provides a number of user-level functions to work with grid graphics, notably to arrange multiple grid-based plots on a page, and draw tables. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-gridgraphics	0.4_1	Functions to convert a page of plots drawn with the ‘graphics’ package into identical output drawn with the ‘grid’ package. The result looks like the original ‘graphics’-based plot, but consists of ‘grid’ grobs and viewports that can then be manipulated with ‘grid’ functions (e.g., edit grobs and revisit viewports). / GPL-2	noarch
r-gridsvg	1.7_0	Functions to export graphics drawn with package grid to SVG format. Additional functions provide access to SVG features that are not available in standard R graphics, such as hyperlinks, animation, filters, masks, clipping paths, and gradient and pattern fills. / GPL-3	noarch
r-grimport	0.9_2	Functions for converting, importing, and drawing PostScript pictures in R plots. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-grimport2	0.1.5	Functions for importing external vector images and drawing them as part of ‘R’ plots. This package is different from the ‘grImport’ package because, where that package imports ‘PostScript’ format images, this package imports ‘SVG’ format images. Furthermore, this package imports a specific subset of ‘SVG’, so external images must be preprocessed using a package like ‘rsvg’ to produce ‘SVG’ that this package can import. ‘SVG’ features that are not supported by ‘R’ graphics, e.g., gradient fills, can be imported and then exported via the ‘gridSVG’ package. / GPL-2	noarch
r-grnn	0.1.0	The program GRNN implements the algorithm proposed by Specht (1991). / AGPL-3	noarch
r-grouped	0.6.0	Regression models for grouped and coarse data, under the Coarsened At Random assumption. / GPL-2	noarch
r-groupica	0.1.1	Contains an implementation of an independent component analysis (ICA) for grouped data. The main function groupICA() performs a blind source separation, by maximizing an independence across sources and allows to adjust for varying confounding for user-specified groups. Additionally, the package contains the function uwedge() which can be used to approximately jointly diagonalize a list of matrices. For more details see the project website < <a href="https://sweichwald.de/groupICA/">https://sweichwald.de/groupICA/</a> >. / AGPL-3	noarch
r-grouptest	1.0.1	Contains functions for a two-stage multiple testing procedure for grouped hypothesis, aiming at controlling both the total posterior false discovery rate and within-group false discovery rate. / GPL-3	noarch
r-growthmodels	1.2.0	A compilation of nonlinear growth models used in many areas / GPL-3	noarch
r-growthrate	1.3	A nonparametric empirical Bayes method for recovering gradients (or growth velocities) from observations of smooth functions (e.g., growth curves) at isolated time points. / GPL-3	noarch
r-grplasso	0.4.6	Fits user-specified (GLM-) models with group lasso penalty. / GPL-3	noarch
r-grpreg	3.2.1	Efficient algorithms for fitting the regularization path of linear or logistic regression models with grouped penalties. This includes group selection methods such as group lasso, group MCP, and group SCAD as well as bi-level selection methods such as the group exponential lasso, the composite MCP, and the group bridge. / GPL-3	linux-32, linux-64, osx-64, win-32, win-64
r-grpregoverlap	2.2.0	Fit the regularization path of linear, logistic or Cox models with overlapping grouped covariates based on the latent group lasso approach. Latent group MCP/SCAD as well as bi-level selection methods, namely the group exponential lasso and the composite MCP are also available. This package serves as an extension of R package ‘grpreg’ (by Dr. Patrick Breheny < <a href="mailto:patrick-breheny@uiowa.edu">patrick-breheny@uiowa.edu</a> >) for grouped variable selection involving overlaps between groups. / GPL-3	noarch
r-grpss	3.0.1	Contains the tools to screen grouped variables, and select screened grouped variables afterwards. The main function grpss() can perform the grouped variables screening as well as selection for ultra-high dimensional data with group structure. The screening step is primarily used to reduce the dimensions of data so that the selection procedure can easily handle the moderate or low dimensions instead of ultra-high dimensions. / GPL-2   GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-grpstring	0.3.2	Methods include converting series of event names to strings, finding common patterns in a group of strings, discovering featured patterns when comparing two groups of strings as well as the number and starting position of each pattern in each string, obtaining transition matrix, computing transition entropy, statistically comparing the difference between two groups of strings, and clustering string groups. Event names can be any action names or labels such as events in log files or areas of interest (AOIs) in eye tracking research. / GPL-2	noarch
r-grs.test	1.1	Computational resources for test proposed by Gibbons, Ross, Shanken (1989)<DOI:10.2307/1913625>. It also has the functions for the power analysis and the choice of the optimal level of significance. The optimal level is determined by minimizing the expected loss from hypothesis testing. / GPL-2	noarch
r-grt	0.2.1	Functions to generate and analyze data for psychology experiments based on the General Recognition Theory. / GPL-2	noarch
r-grto	1.3	Offers functions for the comparison of Gutenberg-Richter b-values. Several functions in GRT0 are helpful for the assessment of the quality of seismicity catalogs. / GPL-3	noarch
r-gsa	1.03.1	Gene Set Analysis. / LGPL-3	noarch
r-gsafishercombined	1.0	Provides the p-value for a joint test of association between a phenotype and a set of genetic variants (SNPs) by combining marginal p-values using the Fisher method. See Fisher, R.A. (1925,ISBN:0-05-002170-2) Statistical Methods for Research Workers. / GPL-2	noarch
r-gsalib	2.1	This package contains utility functions used by the Genome Analysis Toolkit (GATK) to load tables and plot data. The GATK is a toolkit for variant discovery in high-throughput sequencing data. / MIT	noarch
r-gsaq	1.0	Computation of Quantitative Trait Loci hits in the selected gene set. Performing gene set validation with Quantitative Trait Loci information. Performing gene set enrichment analysis with available Quantitative Trait Loci data and computation of statistical significance value from gene set analysis. Obtaining the list of Quantitative Trait Loci hit genes along with their overlapped Quantitative Trait Loci names. / GPL-2	noarch
r-gsarima	0.1_4	Write SARIMA models in (finite) AR representation and simulate generalized multiplicative seasonal autoregressive moving average (time) series with Normal / Gaussian, Poisson or negative binomial distribution. / GPL-2	noarch
r-gseg	0.6	Using an approach based on similarity graph to estimate change-point(s) and the corresponding p-values. Can be applied to any type of data (high-dimensional, non-Euclidean, etc.) as long as a reasonable similarity measure is available. / GPL-2	noarch
r-gsg	2.0	gsg (gam selection gradients) provides a unified approach to the regression analysis of selection from longitudinal data collected from natural populations. / GPL-2	noarch
r-gsheet	0.4.2	Simple package to download Google Sheets using just the sharing link. Spreadsheets can be downloaded as a data frame, or as plain text to parse manually. Google Sheets is the new name for Google Docs Spreadsheets. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-gsl</a>	2.1_6	An R wrapper for the special functions and quasi random number generators of the Gnu Scientific Library ( <a href="http://www.gnu.org/software/gsl/">http://www.gnu.org/software/gsl/</a> ). See <code>gsl-package.Rd</code> for details of overall package organization, and <code>Misc.Rd</code> for some functions that are widely used in the package, and some tips on installation. / GPL-3	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-gsloid</a>	0.1.0	Contains published data sets for global benthic d18O data for 0-5.3 Myr <doi:10.1029/2004PA001071> and global sea levels based on marine sediment core data for 0-800 ka <doi:10.5194/cp-12-1-2016>. / MIT	noarch
<a href="#">r-gsm</a>	1.3.2	Implementation of a Bayesian approach for estimating a mixture of gamma distributions in which the mixing occurs over the shape parameter. This family provides a flexible and novel approach for modeling heavy-tailed distributions, it is computationally efficient, and it only requires to specify a prior distribution for a single parameter. / GPL-2	noarch
<a href="#">r-gsmx</a>	1.3	Estimating trait heritability and handling overfitting. This package includes a collection of functions for (1) estimating genetic variance-covariances and calculate trait heritability; and (2) handling overfitting by calculating the variance components and the heritability through cross validation. / GPL-2	noarch
<a href="#">r-gss</a>	2.1_9	A comprehensive package for structural multivariate function estimation using smoothing splines. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-gstream</a>	0.2.0	Uses an approach based on k-nearest neighbor information to sequentially detect change-points. Offers analytic approximations for false discovery control given user-specified average run length. Can be applied to any type of data (high-dimensional, non-Euclidean, etc.) as long as a reasonable similarity measure is available. See references (1) Chen, H. (2019) Sequential change-point detection based on nearest neighbors. The Annals of Statistics, 47(3):1381-1407. (2) Chu, L. and Chen, H. (2018) Sequential change-point detection for high-dimensional and non-Euclidean data <arXiv:1810.05973>. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-gsubfn	0.7	The gsubfn function is like gsub but can take a replacement function or certain other objects instead of the replacement string. Matches and back references are input to the replacement function and replaced by the function output. gsubfn can be used to split strings based on content rather than delimiters and for quasi-perl-style string interpolation. The package also has facilities for translating formulas to functions and allowing such formulas in function calls instead of functions. This can be used with R functions such as apply, sapply, lapply, optim, integrate, xyplot, Filter and any other function that expects another function as an input argument or functions like cat or sql calls that may involve strings where substitution is desirable. There is also a facility for returning multiple objects from functions and a version of transform that allows the RHS to refer to LHS used in the same transform. / GPL-2	noarch
r-gsw	1.0_5	Provides an interface to the Gibbs ‘SeaWater’ (‘TEOS-10’) C library, version 3.05-4 (commit ‘5b4d959e54031f9e972f3e863f63e67fa4f5bfec’, dated 2017-08-07, available at < <a href="https://github.com/TEOS-10/GSW-C">https://github.com/TEOS-10/GSW-C</a> >, which stems from ‘Matlab’ and other code written by members of Working Group 127 of ‘SCOR’/‘IAPSO’ (Scientific Committee on Oceanic Research / International Association for the Physical Sciences of the Oceans). / GPL (>= 2)   file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
r-gt4ireval	2.0	Provides tools to measure the reliability of an Information Retrieval test collection. It allows users to estimate reliability using Generalizability Theory and map those estimates onto well-known indicators such as Kendall tau correlation or sensitivity. / MIT	noarch
r-gtable	0.3.0	Tools to make it easier to work with tables of ‘grobs’. The ‘gtable’ package defines a ‘gtable’ grob class that specifies a grid along with a list of grobs and their placement in the grid. Further the package makes it easy to manipulate and combine ‘gtable’ objects so that complex compositions can be build up sequentially. / GPL-2	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-gtcorr	0.2_1	This package provides functions to calculate the efficiencies (expected tests per unit) of hierarchical and matrix group testing procedures. Efficiencies can be calculated in the presense of correlated responses under multiple arrangements of clusters. Efficiencies can also be evaluated in the presense of test error. / GPL-3	noarch
r-gtests	0.2	Four graph-based tests are provided for testing whether two samples are from the same distribution. It works for both continuous data and discrete data. / GPL-2	noarch
r-gtheory	0.1.2	Estimates variance components, generalizability coefficients, universe scores, and standard errors when observed scores contain variation from one or more measurement facets (e.g., items and raters). / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-gtools	3.8.1	Functions to assist in R programming, including: - assist in developing, updating, and maintaining R and R packages ('ask', 'checkRVersion', 'getDependencies', 'keywords', 'scat'), - calculate the logit and inverse logit transformations ('logit', 'inv.logit'), - test if a value is missing, empty or contains only NA and NULL values ('invalid'), - manipulate R's .Last function ('addLast'), - define macros ('defmacro'), - detect odd and even integers ('odd', 'even'), - convert strings containing non-ASCII characters (like single quotes) to plain ASCII ('ASCIIify'), - perform a binary search ('binsearch'), - sort strings containing both numeric and character components ('mixedsort'), - create a factor variable from the quantiles of a continuous variable ('quantcut'), - enumerate permutations and combinations ('combinations', 'permutation'), - calculate and convert between fold-change and log-ratio ('foldchange', 'logratio2foldchange', 'foldchange2logratio'), - calculate probabilities and generate random numbers from Dirichlet distributions ('rdirichlet', 'ddirichlet'), - apply a function over adjacent subsets of a vector ('running'), - modify the TCP_NODELAY ('de-Nagle') flag for socket objects, - efficient 'rbind' of data frames, even if the column names don't match ('smartbind'), - generate significance stars from p-values ('stars.pval'), - convert characters to/from ASCII codes. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
r-gtwas	1.1.0	Quantitative trait loci mapping and genome wide association analysis are used to find candidate molecular marker or region associated with phenotype based on linkage analysis and linkage disequilibrium. Gene expression quantitative trait loci mapping is used to find candidate molecular marker or region associated with gene expression. In this package, we applied the method in Liu W. (2011) <doi:10.1007/s00122-011-1631-7> and Gusev A. (2016) <doi:10.1038/ng.3506> to genome and transcriptome wide association study, which is aimed at revealing the association relationship between phenotype and molecular markers, expression levels, molecular markers nested within different related expression effect and expression effect nested within different related molecular marker effect. F test based on full and reduced model are performed to obtain p value or likelihood ratio statistic. The best linear model can be obtained by stepwise regression analysis. / GPL-2	noarch
r-gtx	0.0.8	Assorted tools for genetic association analyses. The current focus is on implementing (either exactly or approximately) regression analyses using summary statistics instead of using subject-specific data. So far, functions exist to support multi-SNP risk score analyses, multi-SNP conditional regression analyses, and multi-phenotype analyses, using summary statistics. There are helper functions for reading and manipulating subject-specific genotype data, which provide a platform for calculating the summary statistics, or for using R to conduct other analyses not supported by specific GWAS analysis tools. / GPL-2	noarch
r-guardianr	0.9	Provides an interface to the Open Platform's Content API of the Guardian Media Group. It retrieves content from news outlets The Observer, The Guardian, and guardian.co.uk from 1999 to current day. / GPL-2	noarch
r-guerry	1.6.1	This package comprises maps of France in 1830, multivariate data from A.-M. Guerry and others, and statistical and graphic methods related to Guerry's Moral Statistics of France. The goal is to facilitate the exploration and development of statistical and graphic methods for multivariate data in a geo-spatial context of historical interest. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-guide	1.2.7	A nice GUI for financial DERivatives in R. / GPL-2	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-gumbel	1.10	Provides probability functions (cumulative distribution and density functions), simulation function (Gumbel copula multivariate simulation) and estimation functions (Maximum Likelihood Estimation, Inference For Margins, Moment Based Estimation and Canonical Maximum Likelihood). / GPL-2	noarch
r-gustave	0.4.0	Provides a toolkit for analytical variance estimation in survey sampling. Apart from the implementation of standard variance estimators, its main feature is to help the sampling expert produce easy-to-use variance estimation wrappers, where systematic operations (linearization, domain estimation) are handled in a consistent and transparent way. / GPL-3	noarch
r-gvarx	1.1	Perform the estimation and inference of stationary Global Vector Autoregression model (GVAR) of Pesaran, Schuermann and Weiner (2004) <DOI:10.1198/073500104000000019> and Dees, di Mauro, Pesaran and Smith (2007) <DOI:10.1002/jae.932>. / GPL-2	noarch
r-gvc	0.5.2	Several tools for Global Value Chain ('GVC') analysis are implemented. / GPL-3	noarch
r-gvcm.cat	1.9	Generalized structured regression models with regularized categorical effects, categorical effect modifiers, continuous effects and smooth effects. / GPL-2	noarch
r-gvlma	1.0.0	Methods from the paper: Pena, EA and Slate, EH, Global Validation of Linear Model Assumptions, J. American Statistical Association, 101(473):341-354, 2006. / GPL-3	noarch
r-gweram	1.0	This package provides functions to calculate the significance threshold for controlling the type I error rate in mixed-model association mapping analyses. / GPL-2	noarch
r-gwg	1.0	Based on calculations of 758 women this package calculates positive predictive values (PPV) and negative predictive values (NPV) for inadequate and excessive gestational weight gain (GWG) for different prevalences for different BMI categories. / GPL-2	noarch
r-gwidgets	0.0_54	Provides a toolkit-independent API for building interactive GUIs. At least one of the 'gWidgetsXXX packages', such as gWidgetstcltk, needs to be installed. Some icons are on loan from the scigraphica project < <a href="http://scigraphica.sourceforge.net">http://scigraphica.sourceforge.net</a> >. / GPL-2	noarch
r-gwidgets2	1.0_8	Re-implementation of the 'gWidgets' API. The API is defined in this package. A second, toolkit-specific package is required to use it. There are three in development: 'gWidgets2RGtk2', 'gWidgets2Qt', and 'gWidgets2tcltk'. / GPL-3	noarch
r-gworm	2.1.0	Statistical functions to fit, validate and describe a Generalized Waring Regression Model (GWRM). / GPL-2   GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-gwrpvr	1.0	Computes the sample probability value (p-value) for the estimated coefficient from a standard genome-wide univariate regression. It computes the exact finite-sample p-value under the assumption that the measured phenotype (the dependent variable in the regression) has a known Bernoulli-normal mixture distribution. Finite-sample genome-wide regression p-values (Gwrpv) with a non-normally distributed phenotype (Gregory Connor and Michael O'Neill, bioRxiv 204727 <doi:10.1101/204727>). / GPL-3	noarch
r-gwsignif	1.2	The correlations and linkage disequilibrium between tests can vary as a function of minor allele frequency thresholds used to filter variants, and also varies with different choices of test statistic for region-based tests. Appropriate genome-wide significance thresholds can be estimated empirically through permutation on only a small proportion of the whole genome. / GPL-2	noarch
r-gxm	1.1	Quantifying and testing gene-by-measured-environment interaction in behavior genetic designs. / GPL-2	noarch
r-gym	0.1.0	OpenAI Gym is a open-source Python toolkit for developing and comparing reinforcement learning algorithms. This is a wrapper for the OpenAI Gym API, and enables access to an ever-growing variety of environments. For more details on OpenAI Gym, please see here: < <a href="https://github.com/openai/gym">https://github.com/openai/gym</a> >. For more details on the OpenAI Gym API specification, please see here: < <a href="https://github.com/openai/gym-http-api">https://github.com/openai/gym-http-api</a> >. / MIT	noarch
r-h2o	3.26.0	Interface for 'H2O', the scalable open source machine learning platform that offers parallelized implementations of many supervised and unsupervised machine learning algorithms such as Generalized Linear Models, Gradient Boosting Machines (including XGBoost), Random Forests, Deep Neural Networks (Deep Learning), Stacked Ensembles, Naive Bayes, Cox Proportional Hazards, K-Means, PCA, Word2Vec, as well as a fully automatic machine learning algorithm (AutoML). / Apache License (== 2.0)	noarch
r-h2o4gpu	0.2.0	Interface to 'H2O4GPU' < <a href="https://github.com/h2oai/h2o4gpu">https://github.com/h2oai/h2o4gpu</a> >, a collection of 'GPU' solvers for machine learning algorithms. / Apache License 2.0	noarch
r-hac	1.0.5	Package provides the estimation of the structure and the parameters, sampling methods and structural plots of Hierarchical Archimedean Copulae (HAC). / GPL-3	noarch
r-hadoopstreaming	0.2	Provides a framework for writing map/reduce scripts for use in Hadoop Streaming. Also facilitates operating on data in a streaming fashion, without Hadoop. / GPL-3	noarch
r-hail	0.1.1	Read data from the City of Portland's 'HYDRA' < <a href="http://or.water.usgs.gov/precip/">http://or.water.usgs.gov/precip/</a> > rainfall datasets within R. / MIT	noarch
r-halfcircle	0.1.0	There are growing concerns on flow data in diverse fields including trade, migration, knowledge diffusion, disease spread, and transportation. The package is an effective visual support to learn the pattern of flow which is called halfcircle diagram. The flow between two nodes placed on the center line of a circle is represented using a half circle drawn from the origin to the destination in a clockwise direction. Through changing the order of nodes, the halfcircle diagram enables users to examine the complex relationship between bidirectional flow and each potential determinants. Furthermore, the halfmeancenter function, which calculates (un) weighted mean center of half circles, makes the comparison easier. / MIT	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-hamlet</a>	0.9.6	Various functions and algorithms are provided here for solving optimal matching tasks in the context of preclinical cancer studies. Further, various helper and plotting functions are provided for unsupervised and supervised machine learning as well as longitudinal mixed-effects modeling of tumor growth response patterns. / GPL-2	noarch
<a href="#">r-handtill2001</a>	0.2_1	An S4 implementation of Eq. (3) and Eq. (7) by David J. Hand and Robert J. Till (2001) <DOI:10.1023/A:1010920819831>. / GPL-2	noarch
<a href="#">r-handypLOTS</a>	1.1.3	Several handy plots for quickly looking at the relationship between two numeric vectors of equal length. Quickly visualize scatter plots, residual plots, qq-plots, box plots, confidence intervals, and prediction intervals. / GPL-2	noarch
<a href="#">r-hapim</a>	1.3	The package provides a set of functions whose aim is to propose 4 methods of QTL detection. HAPimLD is an interval-mapping method designed for unrelated individuals with no family information that makes use of linkage disequilibrium. HAPimLDL is an interval-mapping method for design of half-sib families. It combines linkage analysis and linkage disequilibrium. HaploMax is based on an analysis of variance with a dose haplotype effect. HaploMaxHS is based on an analysis of variance with a sire effect and a dose haplotype effect in half-sib family design. Fundings for the package development were provided to the LDLmapQTL project by the ANR GENANIMAL program and APIS-GENE. / GPL-3	noarch
<a href="#">r-haploReconstruct</a>	0.1.2	Reconstruction of founder haplotype blocks from time series data. / GPL-3	noarch
<a href="#">r-haploSim</a>	1.8.4	Simulate haplotypes through meioses. Allows specification of population parameters. / GPL-2	noarch
<a href="#">r-haplotyper</a>	0.1	Function to identify haplotypes within QTL (Quantitative Trait Loci). One haplotype is a combination of SNP (Single Nucleotide Polymorphisms) within the QTL. This function groups together all individuals of a population with the same haplotype. Each group contains individual with the same allele in each SNP, whether or not missing data. Thus, haplotyper groups individuals, that to be imputed, have a non-zero probability of having the same alleles in the entire sequence of SNP's. Moreover, haplotyper calculates such probability from relative frequencies. / GPL-3	noarch
<a href="#">r-happytime</a>	0.1.0	There are two interesting games in this package, one is 2048 games(for windows), using up and down to control the direction until there is a 2048 figure. And the other is 'what to eat today',preparing for people who choose difficulties, including most of the delicious Cantonese cuisine. / GPL-2	noarch
<a href="#">r-harmonicRegression</a>	1.0	Fits the first harmonics in a Fourier expansion to one or more time series. Trend elimination can be performed. Computed values include estimates of amplitudes and phases, as well as confidence intervals and p-values for the null hypothesis of Gaussian noise. / MIT	noarch
<a href="#">r-hartools</a>	0.0.5	The goal of 'HARtools' is to provide a simple set of functions to read/parse, write and visualise HTTP Archive ('HAR') files in R. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-harvest.tree</a>	1.1	Aimed at applying the Harvest classification tree algorithm, modified algorithm of classic classification tree. The harvested tree has advantage of deleting redundant rules in trees, leading to a simplify and more efficient tree model. It was firstly used in drug discovery field, but it also performs well in other kinds of data, especially when the region of a class is disconnected. This package also improves the basic harvest classification tree algorithm by extending the field of data of algorithm to both continuous and categorical variables. To learn more about the harvest classification tree algorithm, you can go to <a href="http://www.stat.ubc.ca/Research/TechReports/techreports/220.pdf">http://www.stat.ubc.ca/Research/TechReports/techreports/220.pdf</a> for more information. / GPL-2	noarch
<a href="#">r-hash</a>	2.2.6	Implements a data structure similar to hashes in Perl and dictionaries in Python but with a purposefully R flavor. For objects of appreciable size, access using hashes outperforms native named lists and vectors. / GPL-2	noarch
<a href="#">r-hashids</a>	0.9.0	An R port of the hashids library. hashids generates YouTube-like hashes from integers or vector of integers. Hashes generated from integers are relatively short, unique and non-sequential. hashids can be used to generate unique ids for URLs and hide database row numbers from the user. By default hashids will avoid generating common English cursewords by preventing certain letters being next to each other. hashids are not one-way: it is easy to encode an integer to a hashid and decode a hashid back into an integer. / MIT	noarch
<a href="#">r-haven</a>	2.1.0	Import foreign statistical formats into R via the embedded 'ReadStat' C library, < <a href="https://github.com/WizardMac/ReadStat">https://github.com/WizardMac/ReadStat</a> >. / MIT file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-hazer</a>	1.1.1	Provides a set of functions to estimate haziness of an image based on RGB bands. It returns a haze factor, varying from 0 to 1, a metric for fogginess and cloudiness. The package also presents additional functions to estimate brightness, darkness and contrast rasters of the RGB image. This package can be used for several applications such as inference of weather quality data and performing environmental studies from interpreting digital images. / AGPL-3	noarch
<a href="#">r-hazus</a>	0.1	Damage Functions (DFs), also known as Vulnerability Functions, associate the physical damage to a building or a structure (and also its contents and inventory) from natural disasters to financial damage. The Federal Emergency Management Agency (FEMA) in USA developed several thousand DFs and these serve as a benchmark in natural catastrophe modeling, both in academia and industry. However, these DFs and their documentation are buried within the HAZUS software are not easily accessible for analysis and visualization. This package provides more than 1300 raw DFs used by FEMA's HAZUS software and also functionality to extract and visualize DFs specific to the flood hazard. The vignette included with this package demonstrates its use. / GPL-2	noarch
<a href="#">r-hbim</a>	1.0.3	Calculate expected relative risk and proportion protected assuming normally distributed log10 transformed antibody dose for several component vaccine. Uses Hill models for each component which are combined under Bliss independence. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-hbm</a>	1.0	A package for building hierarchical block matrices from association matrices and for performing multi-scale analysis. It specifically targets chromatin contact maps, generated from high-throughput chromosome conformation capture data, such as 5C and Hi-C, and provides methods for detecting movements and for computing chain hierarchy and region communicability across scales. / GPL-2	noarch
<a href="#">r-hbsae</a>	1.0	Functions to compute small area estimates based on a basic area or unit-level model. The model is fit using restricted maximum likelihood, or in a hierarchical Bayesian way. In the latter case numerical integration is used to average over the posterior density for the between-area variance. The output includes the model fit, small area estimates and corresponding MSEs, as well as some model selection measures. Additional functions provide means to compute aggregate estimates and MSEs, to minimally adjust the small area estimates to benchmarks at a higher aggregation level, and to graphically compare different sets of small area estimates. / GPL-3	noarch
<a href="#">r-hbstm</a>	1.0.1	This package fits Hierarchical Bayesian space-Time models for Gaussian data. Furthermore, its functions have been implemented for analysing the fitting qualities of those models. / GPL (>= 2.0)	noarch
<a href="#">r-hcandersenr</a>	0.2.0	Texts for H.C. Andersens fairy tales, ready for text analysis. Fairy tales in German, Danish, English, Spanish and French. / MIT	noarch
<a href="#">r-hcc</a>	0.54	A new diagnostic check for model adequacy in regression and generalized linear models is implemented. / GPL-2	noarch
<a href="#">r-hccci</a>	1.0.0	This package calculates the interval estimates for the parameters of linear models heteroscedastic regression using bootstrap - (Wild Bootstrap) and double bootstrap-t (Wild Bootstrap). It is also possible to calculate confidence intervals using the percentile bootstrap and percentile bootstrap double. It is possible to calculate consistent estimates of the covariance matrix of the parameters of linear regression models with heteroskedasticity of unknown form. The package also provides function to calculate consistently the covariance matrix of the parameters of linear models with heteroskedasticity of unknown form. / GPL-2	noarch
<a href="#">r-hchinamap</a>	0.1.0	By binding R functions and the ‘Highmaps’ < <a href="https://www.highcharts.com.cn/products/highmaps">https://www.highcharts.com.cn/products/highmaps</a> > chart library, ‘hchinamap’ package provides a simple way to map China and its provinces. The map of China drawn by this package contains complete Chinese territory, especially the Nine-dotted line, South Tibet, Hong Kong, Macao and Taiwan. / MIT	noarch
<a href="#">r-hcp</a>	0.1	Estimation of parameters in 3-segment (i.e. 2 change-point) regression models with heteroscedastic variances is provided based on both likelihood and hybrid Bayesian approaches, with and without continuity constraints at the change points. / GPL-2   GPL-3	noarch
<a href="#">r-hcr</a>	0.1.1	This code provides a method to fit the hidden compact representation model as well as to identify the causal direction on discrete data. We implement an effective solution to recover the above hidden compact representation under the likelihood framework. Please see the Causal Discovery from Discrete Data using Hidden Compact Representation from NIPS 2018 by Ruichu Cai, Jie Qiao, Kun Zhang, Zhenjie Zhang and Zhifeng Hao (2018) < <a href="https://nips.cc/Conferences/2018/Schedule?showEvent=11274">https://nips.cc/Conferences/2018/Schedule?showEvent=11274</a> > for a description of some of our methods. / GPL-2	noarch
<a href="#">r-hda</a>	0.2.1	Functions to perform dimensionality reduction for classification if the covariance matrices of the classes are unequal. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-hdci</a>	1.0.2	Fits regression models on high dimensional data to estimate coefficients and use bootstrap method to obtain confidence intervals. Choices for regression models are Lasso, LassoOLS, Lasso partial ridge, LassoOLS partial ridge. / GNU General Public License version 2	noarch
<a href="#">r-hdfqlr</a>	0.6.1	Provides an interface to 'HDFql' < <a href="http://www.hdfql.com/">http://www.hdfql.com/</a> > and helper functions for reading data from and writing data to 'HDF5' files. 'HDFql' provides a high-level language for managing 'HDF5' data that is platform independent. For more information, see the reference manual < <a href="http://www.hdfql.com/resources/HDFqlReferenceManual.pdf">http://www.hdfql.com/resources/HDFqlReferenceManual.pdf</a> >. / GPL-3	noarch
<a href="#">r-hdinterval</a>	0.2.0	A generic function and a set of methods to calculate highest density intervals for a variety of classes of objects which can specify a probability density distribution, including MCMC output, fitted density objects, and functions. / GPL-3	noarch
<a href="#">r-hdmd</a>	1.2	High Dimensional Molecular Data (HDMD) typically have many more variables or dimensions than observations or replicates ( $D \gg N$ ). This can cause many statistical procedures to fail, become intractable, or produce misleading results. This package provides several tools to reduce dimensionality and analyze biological data for meaningful interpretation of results. Factor Analysis (FA), Principal Components Analysis (PCA) and Discriminant Analysis (DA) are frequently used multivariate techniques. However, PCA methods prcomp and princomp do not reflect the proportion of total variation of each principal component. Loadings.variation displays the relative and cumulative contribution of variation for each component by accounting for all variability in data. When $D \gg N$ , the maximum likelihood method cannot be applied in FA and the the principal axes method must be used instead, as in factor.pa of the psych package. The factor.pa.ginv function in this package further allows for a singular covariance matrix by applying a general inverse method to estimate factor scores. Moreover, factor.pa.ginv removes and warns of any variables that are constant, which would otherwise create an invalid covariance matrix. Promax.only further allows users to define rotation parameters during factor estimation. Similar to the Euclidean distance, the Mahalanobis distance estimates the relationship among groups. pairwise.mahalanobis computes all such pairwise Mahalanobis distances among groups and is useful for quantifying the separation of groups in DA. Genetic sequences are composed of discrete alphabetic characters, which makes estimates of variability difficult. MolecularEntropy and MolecularMI calculate the entropy and mutual information to estimate variability and covariability, respectively, of DNA or Amino Acid sequences. Functional grouping of amino acids (Atchley et al 1999) is also available for entropy and mutual information estimation. Mutual information values can be normalized by NMI to account for the background distribution arising from the stochastic pairing of independent, random sites. Alternatively, discrete alphabetic sequences can be transformed into biologically informative metrics to be used in various multivariate procedures. FactorTransform converts amino acid sequences using the amino acid indices determined by Atchley et al 2005. / GPL-2	noarch
<a href="#">r-hdpca</a>	1.0.0	In high-dimensional settings: Estimate the number of distant spikes based on the Generalized Spiked Population (GSP) model. Estimate the population eigenvalues, angles between the sample and population eigenvectors, correlations between the sample and population PC scores, and the asymptotic shrinkage factors. Adjust the shrinkage bias in the predicted PC scores. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-heatex</a>	1.0	The heatex package calculates heat storage in the body and the components of heat exchange (conductive, convective, radiative, and evaporative) between the body and the environment during physical activity based on the principles of partitional calorimetry. The program enables heat exchange calculations for a range of environmental conditions when wearing various clothing ensembles. / GPL-3	noarch
<a href="#">r-heatmap.plus</a>	1.3	Allows heatmap matrix to have non-identical X- and Y-dimensions. Allows multiple tracks of annotation for RowSideColors and ColSideColors. / GPL-3	noarch
<a href="#">r-heatmapfit</a>	2.0.4	Generates a fit plot for diagnosing misspecification in models of binary dependent variables, and calculates the related heatmap fit statistic described in Esarey and Pierce (2012) <DOI:10.1093/pan/mps026>. / GPL-2	noarch
<a href="#">r-hedgehog</a>	0.1	Hedgehog will eat all your bugs. ‘Hedgehog’ is a property-based testing package in the spirit of ‘QuickCheck’. With ‘Hedgehog’, one can test properties of their programs against randomly generated input, providing far superior test coverage compared to unit testing. One of the key benefits of ‘Hedgehog’ is integrated shrinking of counterexamples, which allows one to quickly find the cause of bugs, given salient examples when incorrect behaviour occurs. / MIT	noarch
<a href="#">r-hellno</a>	0.0.1	Base R’s default setting for ‘stringsAsFactors’ within ‘data.frame()’ and ‘as.data.frame()’ is supposedly the most often complained about piece of code in the R infrastructure. The ‘hellno’ package provides an explicit solution without changing R itself or having to mess around with options. It tries to solve this problem by providing alternative ‘data.frame()’ and ‘as.data.frame()’ functions that are in fact simple wrappers around base R’s ‘data.frame()’ and ‘as.data.frame()’ with ‘stringsAsFactors’ option set to ‘HELLNO’ ( which in turn equals FALSE ) by default. / MIT	noarch
<a href="#">r-hellojavaworld</a>	0.0_9	A dummy package to demonstrate how to interface to a jar file that resides inside an R package. / GPL-3	noarch
<a href="#">r-helminthr</a>	1.0.7	Access to large host-parasite data is often hampered by the availability of data and difficulty in obtaining it in a programmatic way to encourage analyses. ‘helminthR’ provides a programmatic interface to the London Natural History Museum’s host-parasite database, one of the largest host-parasite databases existing currently < <a href="http://www.nhm.ac.uk/research-curation/scientific-resources/taxonomy-systematics/host-parasites/">http://www.nhm.ac.uk/research-curation/scientific-resources/taxonomy-systematics/host-parasites/</a> >. The package allows the user to query by host species, parasite species, and geographic location. / GPL-3	noarch
<a href="#">r-helpersmg</a>	3.7	Contains many functions useful for managing ‘NetCDF’ files (see < <a href="http://en.wikipedia.org/wiki/NetCDF">http://en.wikipedia.org/wiki/NetCDF</a> >), get tide levels on any point of the globe, get moon phase and time for sun rise and fall, analyse and reconstruct periodic time series of temperature with irregular sinusoidal pattern, show scales and wind rose in plot with change of color of text, Metropolis-Hastings algorithm for Bayesian MCMC analysis, plot graphs or boxplot with error bars, search files in disk by there names or their content, read the contents of all files from a folder at one time. / GPL-2	noarch
<a href="#">r-helsinki</a>	0.9.29	Tools for accessing various open data sources in the Helsinki region in Finland. Current data sources include the Real Estate Department (< <a href="http://ptp.hel.fi/avoindata/">http://ptp.hel.fi/avoindata/</a> >), Service Map API (< <a href="http://api.hel.fi/servicemap/v1/">http://api.hel.fi/servicemap/v1/</a> >), Linked Events API (< <a href="http://api.hel.fi/linkedevents/v0.1/">http://api.hel.fi/linkedevents/v0.1/</a> >), Helsinki Region Infoshare statistics API (< <a href="https://dev.hel.fi/stats/">https://dev.hel.fi/stats/</a> >). / BSD_2_clause	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-here</a>	0.1	Constructs paths to your project's files. The 'here()' function uses a reasonable heuristics to find your project's files, based on the current working directory at the time when the package is loaded. Use it as a drop-in replacement for 'file.path()', it will always locate the files relative to your project root. / GPL-3	noarch
<a href="#">r-heritability</a>	1.2	Implements marker-based estimation of heritability when observations on genetically identical replicates are available. These can be either observations on individual plants or plot-level data in a field trial. Heritability can then be estimated using a mixed model for the individual plant or plot data. For comparison, also mixed-model based estimation using genotypic means and estimation of repeatability with ANOVA are implemented. For illustration the package contains several datasets for the model species <i>Arabidopsis thaliana</i> . / GPL-3	noarch
<a href="#">r-hermite</a>	1.1.2	Probability functions and other utilities for the generalized Hermite distribution. / GPL-2	noarch
<a href="#">r-hero</a>	0.0.3	Data and data-generating functions related to the paper Fast Bivariate Penalized Splines by Xiao et al. (2012) <doi:10.1111/rssb.12007>. A hero is a specific type of sandwich. Dictionary.com (2018) <https://www.dictionary.com> describes a hero as: a large sandwich, usually consisting of a small loaf of bread or long roll cut in half lengthwise and containing a variety of ingredients, as meat, cheese, lettuce, and tomatoes. / GPL-2	noarch
<a href="#">r-het.test</a>	0.1	An implementation of White's Test for Heteroskedasticity as outlined in Doornik (1996). / GPL-2	noarch
<a href="#">r-hett</a>	0.3_2	Functions for the fitting and summarizing of heteroscedastic t-regression. / GPL-2	noarch
<a href="#">r-hexbin</a>	1.27	Binning and plotting functions for hexagonal bins. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-hexview</a>	0.3_4	Functions to view files in raw binary form like in a hex editor. Additional functions to specify and read arbitrary binary formats. / GPL-2	noarch
<a href="#">r-hflights</a>	0.1	A data only package containing commercial domestic flights that departed Houston (IAH and HOU) in 2011. / CC0	noarch
<a href="#">r-hglm.data</a>	1.0_1	This data-only package was created for distributing data used in the examples of the 'hglm' package. / GPL-2	noarch
<a href="#">r-hgnchelper</a>	0.7.1	Contains functions for identifying and correcting HGNC human gene symbols and MGI mouse gene symbols which have been converted to date format by Excel, withdrawn, or aliased. Also contains functions for reversibly converting between HGNC symbols and valid R names. / GPL (>= 2.0)	noarch
<a href="#">r-hgsl</a>	1.0.0	Estimation of high-dimensional multi-response regression with heterogeneous noises under Heterogeneous group square-root Lasso penalty. For details see: Ren, Z., Kang, Y., Fan, Y. and Lv, J. (2018)<arXiv:1606.03803>. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-hiddenf</a>	2.0	Computes the ACMIF test and Bonferroni-adjusted p-value of interaction in two-factor studies. Produces corresponding interaction plot and analysis of variance tables and p-values from several other tests of non-additivity. / GPL-2	noarch
<a href="#">r-hierdiversity</a>	0.1	Hierarchical group-wise partitioning of phenotypic diversity into within-group (alpha), among-group (beta), and pooled-total (gamma) components using Hill numbers. Turnover and overlap are also calculated as standardized alternatives to beta diversity. Hierarchical bootstrapping is used to approximate uncertainty around each diversity component. / GPL-2	noarch
<a href="#">r-hiertest</a>	1.1	Implementation of the convex hierarchical testing (CHT) procedure introduced in Bien, Simon, and Tibshirani (2015) Convex Hierarchical Testing of Interactions. Annals of Applied Statistics. Vol. 9, No. 1, 27-42. / GPL-3	noarch
<a href="#">r-hiest</a>	2.0	Uses likelihood to estimate ancestry and heterozygosity. Evaluates simple hybrid classifications (parentals, F1, F2, backcrosses). Estimates genomic clines. / GPL-3	noarch
<a href="#">r-highcharter</a>	0.7.0	A wrapper for the 'Highcharts' library including shortcut functions to plot R objects. 'Highcharts' < <a href="http://www.highcharts.com/">http://www.highcharts.com/</a> > is a charting library offering numerous chart types with a simple configuration syntax. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-highlight</a>	0.5.0	Syntax highlighter for R code based on the results of the R parser. Rendering in HTML and latex markup. Custom Sweave driver performing syntax highlighting of R code chunks. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-highlighthtml</a>	0.2.1	A tool to format R markdown with CSS ids for HTML output. The tool may be most helpful for those using markdown to create reproducible documents. The biggest limitations in formatting is the knowledge of CSS by the document authors. / MIT	noarch
<a href="#">r-highmean</a>	3.0	Provides various tests for comparing high-dimensional mean vectors in two sample populations. / GPL-2	noarch
<a href="#">r-highr</a>	0.8	Provides syntax highlighting for R source code. Currently it supports LaTeX and HTML output. Source code of other languages is supported via Andre Simon's highlight package (< <a href="http://www.andre-simon.de">http://www.andre-simon.de</a> >). / GPL	linux-32, linux-64, noarch, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-highscreen</a>	0.3	Can be used to carry out extraction, normalization, quality control (QC), candidate hits identification and visualization for plate based assays, in drug discovery. This project was funded by the Division of Allergy, Immunology, and Transplantation, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Department of Health and Human Services, under contract No. HHSN272201400054C entitled Adjuvant Discovery For Vaccines Against West Nile Virus and Influenza, awarded to Duke University and lead by Drs. Herman Staats and Soman Abraham. / GPL-3	noarch
<a href="#">r-hightttest</a>	1.1	Implements the method developed by Cao and Kosorok (2011) for the significance analysis of thousands of features in high-dimensional biological studies. It is an asymptotically valid data-driven procedure to find critical values for rejection regions controlling the k-familywise error rate, false discovery rate, and the tail probability of false discovery proportion. / GPL-2	noarch
<a href="#">r-higrad</a>	0.1.0	Implements the Hierarchical Incremental GRADient Descent (HiGrad) algorithm, a first-order algorithm for finding the minimizer of a function in online learning just like stochastic gradient descent (SGD). In addition, this method attaches a confidence interval to assess the uncertainty of its predictions. See Su and Zhu (2018) <arXiv:1802.04876> for details. / GPL-3	noarch
<a href="#">r-hilmm</a>	1.1	Estimation of heritability with confidence intervals in linear mixed models. / GPL-2	noarch
<a href="#">r-hindexcalculator</a>	1.0.0	H(x) is the h-index for the past x years. Here, the h(x) of a scientist/department/etc. can be calculated using the exported excel file from a Web of Science citation report of a search. Also calculated is the year of first publication, total number of publications, and sum of times cited for the specified period. Therefore, for h-10: the date of first publication, total number of publications, and sum of times cited in the past 10 years are calculated. Note: the excel file has to first be saved in a .csv format. / AGPL-3	noarch
<a href="#">r-histdata</a>	0.8_4	The ‘HistData’ package provides a collection of small data sets that are interesting and important in the history of statistics and data visualization. The goal of the package is to make these available, both for instructional use and for historical research. Some of these present interesting challenges for graphics or analysis in R. / GPL-3	noarch
<a href="#">r-histogram</a>	0.0_25	Automatic construction of regular and irregular histograms as described in Rozenholc/Mildenberger/Gather (2010). / GPL-2	noarch
<a href="#">r-historydata</a>	0.1	These sample data sets are intended for historians learning R. They include population, institutional, religious, military, and prosopographical data suitable for mapping, quantitative analysis, and network analysis. / MIT	noarch
<a href="#">r-hiv.lifetables</a>	0.1	The functions in this package produce a complete set of mortality rates as a function of a combination of HIV prevalence and either life expectancy at birth (e0), child mortality (5q0), or child mortality with adult mortality (45q15) / Unlimited	noarch
<a href="#">r-hive</a>	0.2_0	Hadoop InteractiVE facilitates distributed computing via the MapReduce paradigm through R and Hadoop. An easy to use interface to Hadoop, the Hadoop Distributed File System (HDFS), and Hadoop Streaming is provided. / GPL-3	noarch
<a href="#">r-hk80</a>	0.0.2	This is a collection of functions for converting coordinates between WGS84UTM, WGS84GEO, HK80UTM, HK80GEO and HK1980GRID Coordinate Systems used in Hong Kong SAR, based on the algorithms described in Explanatory Notes on Geodetic Datums in Hong Kong by Survey and Mapping Office Lands Department, Hong Kong Government (1995). / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-hkclustering</a>	1.0.1	Implements an ensemble algorithm for clustering combining a k-means and a hierarchical clustering approach. / GPL-2	noarch
<a href="#">r-hkex.api</a>	0.1	A set of functions helps to retrieve data from HKEX (Hong Kong Stock Exchange), see < <a href="https://www.hkex.com.hk/">https://www.hkex.com.hk/</a> > for more information. In addition, a function generates insert SQL statements from a dataframe. / GPL-3	noarch
<a href="#">r-hmdhfdplus</a>	1.9.1	Utilities for reading data from the Human Mortality Database (< <a href="https://www.mortality.org/">https://www.mortality.org/</a> >), Human Fertility Database (< <a href="https://www.humanfertility.org/">https://www.humanfertility.org/</a> >), and similar databases from the web or locally into an R session as data.frame objects. These are the two most widely used sources of demographic data to study basic demographic change, trends, and develop new demographic methods. Other supported databases at this time include the Human Fertility Collection (< <a href="http://www.fertilitydata.org/">http://www.fertilitydata.org/</a> >), The Japanese Mortality Database (< <a href="http://www.ipss.go.jp/p-toukei/JMD/">http://www.ipss.go.jp/p-toukei/JMD/</a> >), and the Canadian Human Mortality Database (< <a href="http://www.bdlc.umontreal.ca/chmd/">http://www.bdlc.umontreal.ca/chmd/</a> >). Arguments and data are standardized. / GPL-2	noarch
<a href="#">r-hmeasure</a>	1.0.2	Classification performance metrics that are derived from the ROC curve of a classifier. The package includes the H-measure performance metric as described in < <a href="http://link.springer.com/article/10.1007/s10994-009-5119-5">http://link.springer.com/article/10.1007/s10994-009-5119-5</a> >, which computes the minimum total misclassification cost, integrating over any uncertainty about the relative misclassification costs, as per a user-defined prior. It also offers a one-stop-shop for other scalar metrics of performance, including sensitivity, specificity and many others, and also offers plotting tools for ROC curves and related statistics. / MIT	noarch
<a href="#">r-hmisc</a>	4.2.0	Contains many functions useful for data analysis, high-level graphics, utility operations, functions for computing sample size and power, importing and annotating datasets, imputing missing values, advanced table making, variable clustering, character string manipulation, conversion of R objects to LaTeX and html code, and recoding variables. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-hmm</a>	1.0	Easy to use library to setup, apply and make inference with discrete time and discrete space Hidden Markov Models / GPL-2	noarch
<a href="#">r-hmmcont</a>	1.0	The package includes the functions designed to analyse continuous observations processes with the Hidden Markov Model approach. They include Baum-Welch and Viterbi algorithms and additional visualisation functions. The observations are assumed to have Gaussian distribution and to be weakly stationary processes. The package was created for analyses of financial time series, but can also be applied to any continuous observations processes. / GPL-3	noarch
<a href="#">r-hmmpa</a>	1.0.1	Analysing time-series accelerometer data to quantify length and intensity of physical activity using hidden Markov models. It also contains the traditional cut-off point method. Witowski V, Foraita R, Pitsiladis Y, Pigeot I, Wirsik N (2014)< <a href="https://doi.org/10.1371/journal.pone.0114089">doi:10.1371/journal.pone.0114089</a> >. / GPL-3	noarch
<a href="#">r-hmr</a>	0.4.2	Statistical analysis of static chamber concentration data for trace gas flux estimation. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-hms	0.4.2	Implements an S3 class for storing and formatting time-of-day values, based on the 'difftime' class. / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-hmstimer	0.0.2	Tracks elapsed clock time using a 'hms()' scalar (inherits from 'difftime()') with seconds as the unit). / MIT	noarch
r-hmvd	1.0	Perform association test between a group of variable and the outcome. / GPL-3	noarch
r-hnp	1.2_6	Generates (half-)normal plots with simulation envelopes using different diagnostics from a range of different fitted models. A few example datasets are included. / GPL-2	noarch
r-hoardr	0.5.2	Suite of tools for managing cached files, targeting use in other R packages. Uses 'rappdirs' for cross-platform paths. Provides utilities to manage cache directories, including targeting files by path or by key; cached directories can be compressed and uncompressed easily to save disk space. / MIT	noarch
r-holdem	1.2	Simulates hands and tournaments of Texas Holdem, the most popular form of poker. For examples of probability problems involving Texas Holdem and a brief explanation of the game see Schoenberg, F. (2011). An Introduction to Probability with Texas Hold'em Examples. Taylor and Francis, New York, ISBN-13: 978-1439827680. / GPL-2	noarch
r-homer	0.3.0	A collection of functions useful for the analysis of building physics experiments. / GPL-2	noarch
r-homeric	0.1_3	A simple implementation of doughnut plots - pie charts with a blank center. The package is named after Homer Simpson - arguably the best-known lover of doughnuts. / GPL-2	noarch
r-homtest	1.0_5	A collection of homogeneity tests described in: Viglione A., Laio F., Claps P. (2007) "A comparison of homogeneity tests for regional frequency analysis", Water Resources Research, 43, W03428, doi:10.1029/2006WR005095. More on Regional Frequency Analysis can be found in package nsRFA. / GPL-2	noarch
r-horizon	1.2	Calculates horizon elevation angle and sky view factor from a digital terrain model (Dozier and Frew, 1990). / GPL-2	noarch
r-hornpa	1.0	A stand-alone function that generates a user specified number of random datasets and computes eigenvalues using the random datasets (i.e., implements Horn's parallel analysis). Users then compare the resulting eigenvalues (the mean or the specified percentile) from the random datasets (i.e., eigenvalues resulting from noise) to the eigenvalues generated with the user's data. Can be used for both principal components analysis (PCA) and common/exploratory factor analysis (EFA). The output table shows how large eigenvalues can be as a result of merely using randomly generated datasets. If the user's own dataset has actual eigenvalues greater than the corresponding eigenvalues, that lends support to retain that factor/component. In other words, if the i(th) eigenvalue from the actual data was larger than the percentile of the (i)th eigenvalue generated using randomly generated data, empirical support is provided to retain that factor/component. Horn, J. (1965). A rationale and test for the number of factors in factor analysis. Psychometrika, 32, 179-185. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-horseshoe	0.2.0	Contains functions for applying the horseshoe prior to high- dimensional linear regression, yielding the posterior mean and credible intervals, amongst other things. The key parameter tau can be equipped with a prior or estimated via maximum marginal likelihood estimation (MMLE). The main function, horseshoe, is for linear regression. In addition, there are functions specifically for the sparse normal means problem, allowing for faster computation of for example the posterior mean and posterior variance. Finally, there is a function available to perform variable selection, using either a form of thresholding, or credible intervals. / GPL-3	noarch
r-hotelling	1.0_5	A set of R functions which implements Hotelling's $T^2$ test and some variants of it. Functions are also included for Aitchison's additive log ratio and centred log ratio transformations. / GPL-2	noarch
r-hotspot	1.0	Contains data for software hotspot analysis, along with a function performing the analysis itself. / GPL-2	noarch
r-housingdata	0.3.0	Monthly median home listing, sale price per square foot, and number of units sold for 2984 counties in the contiguous United States From 2008 to January 2016. Additional data sets containing geographical information and links to Wikipedia are also included. / CC0	noarch
r-howmany	0.3_1	When testing multiple hypotheses simultaneously, this package provides functionality to calculate a lower bound for the number of correct rejections (as a function of the number of rejected hypotheses), which holds simultaneously -with high probability- for all possible number of rejections. As a special case, a lower bound for the total number of false null hypotheses can be inferred. Dependent test statistics can be handled for multiple tests of associations. For independent test statistics, it is sufficient to provide a list of p-values. / GPL-3	noarch
r-hpackedbubble	0.1.0	By binding R functions and the 'Highcharts' < <a href="http://www.highcharts.com/">http://www.highcharts.com/</a> > charting library, 'hpackedbubble' package provides a simple way to draw split packed bubble charts. / MIT	noarch
r-hpbayes	0.1	This package provides all the functions necessary to estimate the 8 parameters of the Heligman Pollard mortality model using a Bayesian Melding procedure with IMIS as well as to convert those parameters into age-specific probabilities of death and a corresponding life table / Unlimited	noarch
r-hqmisc	0.1_1	This package contains some miscellaneous convenience functions, to create a matrix of dummy columns from a factor, to determine whether x lies in range [a,b], to add a rectangular bracket to an existing plot, and to convert frequencies between Hz, semitones, mel and Bark. This package also contains an example data set of a stratified sample of 80 talkers of Dutch. / GPL-2	noarch
r-hripw	0.1.2	Estimates the log hazard ratio associated with a binary exposure using a Cox PH model weighted by the propensity score. Propensity model is estimated using a simple logistic regression. Variance estimation takes into account the propensity score estimation step with the method proposed by Hajage et al. (2018) < <a href="https://doi.org/10.1002/bimj.201700330">doi:10.1002/bimj.201700330</a> >. Both the average treatment effect on the overall (ATE) or the treated (ATT) population can be estimated. For the ATE estimation, both unstabilized and stabilized weights can be used. / GPL-2	noarch
r-hrw	1.0_3	The book Semiparametric Regression with R by J. Harezlak, D. Ruppert & M.P. Wand (2018, Springer; ISBN: 978-1-4939-8851-8) makes use of datasets and scripts to explain semiparametric regression concepts. Each of the book's scripts are contained in this package as well as datasets that are not within other R packages. Functions that aid semiparametric regression analysis are also included. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-hsaur</a>	1.3_9	Functions, data sets, analyses and examples from the book “A Handbook of Statistical Analyses Using R” (Brian S. Everitt and Torsten Hothorn, Chapman & Hall/CRC, 2006). The first chapter of the book, which is entitled “An Introduction to R”, is completely included in this package, for all other chapters, a vignette containing all data analyses is available. / GPL-3	noarch
<a href="#">r-hsaur2</a>	1.1_1	Functions, data sets, analyses and examples from the second edition of the book “A Handbook of Statistical Analyses Using R” (Brian S. Everitt and Torsten Hothorn, Chapman & Hall/CRC, 2008). The first chapter of the book, which is entitled “An Introduction to R”, is completely included in this package, for all other chapters, a vignette containing all data analyses is available. In addition, the package contains Sweave code for producing slides for selected chapters (see HSAUR2/inst/slides). / GPL-2	noarch
<a href="#">r-hsaur3</a>	1.0_9	Functions, data sets, analyses and examples from the third edition of the book “A Handbook of Statistical Analyses Using R” (Torsten Hothorn and Brian S. Everitt, Chapman & Hall/CRC, 2014). The first chapter of the book, which is entitled “An Introduction to R”, is completely included in this package, for all other chapters, a vignette containing all data analyses is available. In addition, Sweave source code for slides of selected chapters is included in this package (see HSAUR3/inst/slides). The publishers web page is ‘< <a href="http://www.crcpress.com/product/isbn/9781482204582">http://www.crcpress.com/product/isbn/9781482204582</a> >’. / GPL-2	noarch
<a href="#">r-hsiccca</a>	1.0	Canonical correlation analysis that extracts nonlinear correlation through the use of Hilbert Schmidt Independence Criterion and Centered Kernel Target Alignment. / GPL-2	noarch
<a href="#">r-hssvd</a>	1.2	A data mining tool for discovering subgroups of patients and genes that simultaneously display unusual levels of variability compared to other genes and patients. Based on sparse singular value decomposition (SSVD), the method can detect both mean and variance biclusters in the presence of heterogeneous residual variance. / GPL-2	noarch
<a href="#">r-htm2txt</a>	2.1.1	Convert a html document to simple plain texts by removing all html tags. This package utilizes regular expressions to strip off html tags. It also offers gettxt() and browse() function, which enables you to get or browse texts at a certain web page. / GPL-2	noarch
<a href="#">r-htmltab</a>	0.7.1	HTML tables are a valuable data source but extracting and recasting these data into a useful format can be tedious. This package allows to collect structured information from HTML tables. It is similar to readHTMLTable() of the XML package but provides three major advantages. First, the function automatically expands row and column spans in the header and body cells. Second, users are given more control over the identification of header and body rows which will end up in the R table, including semantic header information that appear throughout the body. Third, the function preprocesses table code, corrects common types of malformations, removes unneeded parts and so helps to alleviate the need for tedious post-processing. / MIT	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-htmltable</a>	1.13.1	Tables with state-of-the-art layout elements such as row spanners, column spanners, table spanners, zebra striping, and more. While allowing advanced layout, the underlying css-structure is simple in order to maximize compatibility with word processors such as ‘MS Word’ or ‘LibreOffice’. The package also contains a few text formatting functions that help outputting text compatible with HTML/LaTeX. / GPL (>= 3)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-htmltools</a>	0.3.6	Tools for HTML generation and output. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-htmlwidgets</a>	1.3	A framework for creating HTML widgets that render in various contexts including the R console, ‘R Markdown’ documents, and ‘Shiny’ web applications. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-httpcache</a>	1.1.0	In order to improve performance for HTTP API clients, ‘httpcache’ provides simple tools for caching and invalidating cache. It includes the HTTP verb functions GET, PUT, PATCH, POST, and DELETE, which are drop-in replacements for those in the ‘httr’ package. These functions are cache-aware and provide default settings for cache invalidation suitable for RESTful APIs; the package also enables custom cache-management strategies. Finally, ‘httpcache’ includes a basic logging framework to facilitate the measurement of HTTP request time and cache performance. / MIT	noarch
<a href="#">r-httpcode</a>	0.2.0	Find and explain the meaning of ‘HTTP’ status codes. Functions included for searching for codes by full or partial number, by message, and get appropriate dog and cat images for many status codes. / MIT	noarch
<a href="#">r-httprequest</a>	0.0.10	HTTP Request protocols. Implements the GET, POST and multipart POST request. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-httptest</a>	3.2.2	Testing and documenting code that communicates with remote servers can be painful. Dealing with authentication, server state, and other complications can make testing seem too costly to bother with. But it doesn't need to be that hard. This package enables one to test all of the logic on the R sides of the API in your package without requiring access to the remote service. Importantly, it provides three contexts that mock the network connection in different ways, as well as testing functions to assert that HTTP requests were—or were not—made. It also allows one to safely record real API responses to use as test fixtures. The ability to save responses and load them offline also enables one to write vignettes and other dynamic documents that can be distributed without access to a live server. / MIT	noarch
<a href="#">r-httpuv</a>	1.5.1	Provides low-level socket and protocol support for handling HTTP and Web-Socket requests directly from within R. It is primarily intended as a building block for other packages, rather than making it particularly easy to create complete web applications using httpuv alone. httpuv is built on top of the libuv and http-parser C libraries, both of which were developed by Joyent, Inc. (See LICENSE file for libuv and http-parser license information.) / GPL (>= 2)   file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-httr</a>	1.4.0	Useful tools for working with HTTP organised by HTTP verbs (GET(), POST(), etc). Configuration functions make it easy to control additional request components (authenticate(), add_headers() and so on). / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-hues</a>	0.1	Creating effective colour palettes for figures is challenging. This package generates and plot palettes of optimally distinct colours in perceptually uniform colour space, based on 'iwanthue' < <a href="http://tools.medialab.sciences-po.fr/iwanthue/">http://tools.medialab.sciences-po.fr/iwanthue/</a> >. This is done through k-means clustering of CIE Lab colour space, according to user-selected constraints on hue, chroma, and lightness. / LGPL-3	noarch
<a href="#">r-humanformat</a>	1.0	Format quantities of time or bytes into human-friendly strings. / MIT	noarch
<a href="#">r-humanize</a>	0.2.0	An almost direct port of the 'python' 'humanize' package < <a href="https://github.com/jmoiron/humanize">https://github.com/jmoiron/humanize</a> >. This package contains utilities to convert values into human readable forms. / MIT	noarch
<a href="#">r-humidity</a>	0.1.4	Vapor pressure, relative humidity, absolute humidity, specific humidity, and mixing ratio are commonly used water vapor measures in meteorology. This R package provides functions for calculating saturation vapor pressure (hPa), partial water vapor pressure (Pa), relative humidity (%), absolute humidity (kg/m^3), specific humidity (kg/kg), and mixing ratio (kg/kg) from temperature (K) and dew point (K). Conversion functions between humidity measures are also provided. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-hunspell</a>	3.0	Low level spell checker and morphological analyzer based on the famous ‘hunspell’ library < <a href="https://hunspell.github.io">https://hunspell.github.io</a> >. The package can analyze or check individual words as well as parse text, latex, html or xml documents. For a more user-friendly interface use the ‘spelling’ package which builds on this package to automate checking of files, documentation and vignettes in all common formats. / GPL-2   LGPL-2.1   MPL-1.1	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-hurdlr</a>	0.1	When considering count data, it is often the case that many more zero counts than would be expected of some given distribution are observed. It is well established that data such as this can be reliably modelled using zero-inflated or hurdle distributions, both of which may be applied using the functions in this package. Bayesian analysis methods are used to best model problematic count data that cannot be fit to any typical distribution. The package functions are flexible and versatile, and can be applied to varying count distributions, parameter estimation with or without explanatory variable information, and are able to allow for multiple hurdles as it is also not uncommon that count data have an abundance of large-number observations which would be considered outliers of the typical distribution. In lieu of throwing out data or misspecifying the typical distribution, these extreme observations can be applied to a second, extreme distribution. With the given functions of this package, such a two-hurdle model may be easily specified in order to best manage data that is both zero-inflated and over-dispersed. / GPL-2	noarch
<a href="#">r-hw.pval</a>	1.0	HW.pval calculates plain and fully conditional root-mean-square, chi-square, and log likelihood-ratio P-values for the user-provided genotypic counts to be consistent with the Hardy-Weinberg equilibrium model. For further information on the Hardy-Weinberg equilibrium model and the pseudocode, refer to the paper Testing Hardy-Weinberg equilibrium with a simple root-mean-square statistic by Rachel Ward. / GPL-3	noarch
<a href="#">r-hwde</a>	0.67	Fits models for genotypic disequilibria, as described in Huttley and Wilson (2000), Weir (1996) and Weir and Wilson (1986). Contrast terms are available that account for first order interactions between loci. Also implements, for a single locus in a single population, a conditional exact test for Hardy-Weinberg equilibrium. / GPL-2	noarch
<a href="#">r-hweintrinsic</a>	1.2.2	General (multi-allelic) Hardy-Weinberg equilibrium problem from an objective Bayesian testing standpoint. This aim is achieved through the identification of a class of priors specifically designed for this testing problem. A class of intrinsic priors under the full model is considered. This class is indexed by a tuning quantity, the training sample size, as discussed in Consonni, Moreno and Venturini (2010). These priors are objective, satisfy Savage’s continuity condition and have proved to behave extremely well for many statistical testing problems. / GPL-2	noarch
<a href="#">r-hwriter</a>	1.3.2	Easy-to-use and versatile functions to output R objects in HTML format / LGPL-2.1	noarch
<a href="#">r-hybridhclust</a>	1.0_5	Hybrid hierarchical clustering via mutual clusters. A mutual cluster is a set of points closer to each other than to all other points. Mutual clusters are used to enrich top-down hierarchical clustering. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-hydra	0.1.0	Calculate an optimal embedding of a set of data points into low-dimensional hyperbolic space. This uses the strain-minimizing hyperbolic embedding of Keller-Ressel and Nargang (2019), see <arXiv:1903.08977>. / GPL-2	noarch
r-hydrogeo	0.6.1	Contains one function for drawing Piper diagrams (also called Piper-Hill diagrams) of water analyses for major ions. / BSD_2_clause	noarch
r-hydrostats	0.2.7	Calculates a suite of hydrologic indices for daily time series data that are widely used in hydrology and stream ecology. / GPL-2	noarch
r-hyperbolicdist	0.6.2	This package provides functions for the hyperbolic and related distributions. Density, distribution and quantile functions and random number generation are provided for the hyperbolic distribution, the generalized hyperbolic distribution, the generalized inverse Gaussian distribution and the skew-Laplace distribution. Additional functionality is provided for the hyperbolic distribution, including fitting of the hyperbolic to data. / GPL-2	noarch
r-hypercube	0.1.0	Provides methods for organizing data in a hypercube (i.e. a multi-dimensional cube). Cubes are generated from molten data frames. Each cube can be manipulated with five operations: rotation (changeDimensionOrder()), dicing and slicing (add.selection(), remove.selection()), drilling down (add.aggregation()), and rolling up (remove.aggregation()). / GPL-3	noarch
r-hypergate	0.8.1	Given a high-dimensional dataset that typically represents a cytometry dataset, and a subset of the datapoints, this algorithm outputs an hyperrectangle so that datapoints within the hyperrectangle best correspond to the specified subset. In essence, this allows the conversion of clustering algorithms' outputs to gating strategies outputs. / GPL-3	noarch
r-hypergeo	1.2.1	The Gaussian hypergeometric function for complex numbers. / GPL-2	noarch
r-hypersampleplan	0.1.1	Implements an algorithm for efficient and exact calculation of hypergeometric and binomial probabilities using Chebyshev polynomials, while other algorithm use an approximation when N is large. A useful applications is also considered in this package for the construction of attribute sampling plans which is an important field of statistical quality control. The quantile, and the confidence limit for the attribute sampling plan are also implemented in this package. The hypergeometric distribution can be represented in terms of Chebyshev polynomials. This representation is particularly useful in the calculation of exact values of hypergeometric variables. / GPL-2	noarch
r-hyphy	1.0	A Bay Area high level phylogenetic analysis package mostly using the birth-death process. Analysis of species tree branching times and simulation of species trees under a number of different time variable birth-death processes. Analysis of gene tree species tree reconciliations and simulations of gene trees in species trees. / GPL-2	noarch
r-hypothesetest	1.0	Compute the confidence interval of the population mean with one sample or of the difference of population means of two samples from normal distributions or t-distributions. Compute the confidence interval of population variance with one sample or of the difference of population variances of two samples by chi-square tests. Test for population mean or the differences of two normal samples under normality with the given null hypothesis H0, which depends on the user, so that he can know if he can reject H0 or not at the significance level alpha. Do the chi-square tests with one or two samples which have multinomial distributions by using an approximate chi-square distribution when n is large enough. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-iabin</a>	1.0	In randomized-controlled trials, interim analyses are often planned for possible early trial termination to claim superiority or futility of a new therapy. Blinded data also have information about the potential treatment difference between the groups. We developed a blinded data monitoring tool that enables investigators to predict whether they observe such an unblinded interim analysis results that supports early termination of the trial. Investigators may skip some of the planned interim analyses if an early termination is unlikely. This tool will provide reference information about N: Sample size at interim analysis, and T: Total number of responders at interim analysis for decision on performing an interim analysis. / GPL-2	noarch
<a href="#">r-iadapt</a>	0.1.0	Simulate and implement early phase two-stage adaptive dose-finding design developed by Chiuzan et al. (2018) <DOI:10.1080/19466315.2018.1462727>. / LGPL-3	noarch
<a href="#">r-ialsasynthesis</a>	0.1.6	Synthesizes information across collaborating research. Created specifically for Integrative Analysis of Longitudinal Studies of Aging (IALSA). / GPL-2	noarch
<a href="#">r-iasd</a>	1.1	Calculate AIC's and AICc's of unimodal model (one normal distribution) and bimodal model(a mixture of two normal distributions) which fit the distribution of indices of asymmetry (IAS), and plot their density, to help determine IAS distribution is unimodal or bimodal. / GPL-2	noarch
<a href="#">r-iatanalytics</a>	0.1.1	Quickly score raw data outputted from an Implicit Association Test (IAT; Greenwald, McGhee, & Schwartz, 1998) <doi:10.1037/0022-3514.74.6.1464>. IAT scores are calculated as specified by Greenwald, Nosek, and Banaji (2003) <doi:10.1037/0022-3514.85.2.197>. The output of this function is a data frame that consists of four rows containing the following information: (1) the overall IAT effect size for the participant's dataset, (2) the effect size calculated for odd trials only, (3) the effect size calculated for even trials only, and (4) the proportion of trials with reaction times under 300ms (which is important for exclusion purposes). Items (2) and (3) allow for a measure of the internal consistency of the IAT. Specifically, you can use the subsetting IAT effect sizes for odd and even trials to calculate Cronbach's alpha across participants in the sample. The input function consists of three arguments. First, indicate the name of the dataset to be analyzed. This is the only required input. Second, indicate the number of trials in your entire IAT (the default is set to 220, which is typical for most IATs). Last, indicate whether congruent trials (e.g., flowers and pleasant) or incongruent trials (e.g., guns and pleasant) were presented first for this participant (the default is set to congruent). Data files should consist of six columns organized in order as follows: Block (0-6), trial (0-19 for training blocks, 0-39 for test blocks), category (dependent on your IAT), the type of item within that category (dependent on your IAT), a dummy variable indicating whether the participant was correct or incorrect on that trial (0=correct, 1=incorrect), and the participant's reaction time (in milliseconds). A sample dataset (titled 'sampledata') is included in this package to practice with. / MIT	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-iatscore</a>	0.1.1	This minimalist package is designed to quickly score raw data outputted from an Implicit Association Test (IAT; Greenwald, McGhee, & Schwartz, 1998) <doi:10.1037/0022-3514.74.6.1464>. IAT scores are calculated as specified by Greenwald, Nosek, and Banaji (2003) <doi:10.1037/0022-3514.85.2.197>. Outputted values can be interpreted as effect sizes. The input function consists of three arguments. First, indicate the name of the dataset to be analyzed. This is the only required input. Second, indicate the number of trials in your entire IAT (the default is set to 219, which is typical for most IATs). Last, indicate whether congruent trials (e.g., flowers and pleasant) or incongruent trials (e.g., guns and pleasant) were presented first for this participant (the default is set to congruent). The script will tell you how long it took to run the code, the effect size for the participant, and whether that participant should be excluded based on the criteria outlined by Greenwald et al. (2003). Data files should consist of six columns organized in order as follows: Block (0-6), trial (0-19 for training blocks, 0-39 for test blocks), category (dependent on your IAT), the type of item within that category (dependent on your IAT), a dummy variable indicating whether the participant was correct or incorrect on that trial (0=correct, 1=incorrect), and the participant's reaction time (in milliseconds). Three sample datasets are included in this package (labeled 'IAT', 'TooFastIAT', and 'BriefIAT') to practice with. / MIT	noarch
<a href="#">r-ibdhaplortools</a>	1.8	Functions to analyze, plot, and store the output of running IBD_Haplo software package. More information regarding IBD_Haplo can be found at <a href="http://www.stat.washington.edu/thompson/Genepi/pangaea.shtml">http://www.stat.washington.edu/thompson/Genepi/pangaea.shtml</a> . / GPL-3	noarch
<a href="#">r-ibdlabels</a>	1.1	Convert label, lexicographic, jacquard and vec, full state description vector. All conversions are done to and from label, as used in IBD_Haplo. More information regarding IBD_Haplo can be found at <a href="http://www.stat.washington.edu/thompson/Genepi/pangaea.shtml">http://www.stat.washington.edu/thompson/Genepi/pangaea.shtml</a> . / GPL-3	noarch
<a href="#">r-ibelief</a>	1.2	Some basic functions to implement belief functions including: transformation between belief functions using the method introduced by Philippe Smets (arXiv:1304.1122 [cs.AI]), evidence combination, evidence discounting, decision-making, and constructing masses. Currently, thirteen combination rules and five decision rules are supported. It can also be used to generate different types of random masses when working on belief combination and conflict management. / GPL-2	noarch
<a href="#">r-ibmsunburst</a>	0.1.1	Generates Personality Insights sunburst diagrams based on 'IBM Watson' Personality Insights service output. / MIT	noarch
<a href="#">r-ibrokers</a>	0.9.1	Provides native R access to Interactive Brokers Trader Workstation API. / GPL-3	noarch
<a href="#">r-ic10trainingdata</a>	1.3.1	Training datasets for iC10; which implements the classifier described in the paper 'Genome-driven integrated classification of breast cancer validated in over 7,500 samples' (Ali HR et al., Genome Biology 2014). It uses copy number and/or expression from breast cancer data, trains a pamr classifier (Tibshirani et al.) with the features available and predicts the iC10 group. Genomic annotation for the training dataset has been obtained from Mark Dunning's IlluminaHumanv3.db package. / GPL-3	noarch
<a href="#">r-ic2</a>	1.0.1	Lorenz and concentration curves; Atkinson, Generalized entropy and SGini indices (with decomposition) / GPL-2	noarch
<a href="#">r-ic50</a>	1.4.2	Calculation of IC50 values, automatic drawing of dose-response curves and validation of compound screens on 96- and 384-well plates. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-ica	1.0.2	Independent Component Analysis (ICA) using various algorithms: FastICA, Information-Maximization (Infomax), and Joint Approximate Diagonalization of Eigenmatrices (JADE). / GPL-2	noarch
r-icaff	1.0.1	Imperialist Competitive Algorithm (ICA) < <a href="http://en.wikipedia.org/wiki/Imperialist_competitive_algorithm">http://en.wikipedia.org/wiki/Imperialist_competitive_algorithm</a> > is a computational method that is used to solve optimization problems of different types and it is the mathematical model and the computer simulation of human social evolution. The package provides a minimum value for the cost function and the best value for the optimization variables by Imperialist Competitive Algorithm. Users can easily define their own objective function depending on the problem at hand. This version has been successfully applied to solve optimization problems, for continuous functions. / GPL-2	noarch
r-icarus	0.3.1	Provides user-friendly tools for calibration in survey sampling. The package is production-oriented, and its interface is inspired by the famous popular macro ‘Calmar’ for SAS, so that ‘Calmar’ users can quickly get used to ‘icarus’. In addition to calibration (with linear, raking and logit methods), ‘icarus’ features functions for calibration on tight bounds and penalized calibration. / GPL-3	noarch
r-icc	2.3.0	Assist in the estimation of the Intraclass Correlation Coefficient (ICC) from variance components of a one-way analysis of variance and also estimate the number of individuals or groups necessary to obtain an ICC estimate with a desired confidence interval width. / GPL-2	noarch
r-icc.sample.size	1.0	Provides functions to calculate the requisite sample size for studies where ICC is the primary outcome. Can also be used for calculation of power. In both cases it allows the user to test the impact of changing input variables by calculating the outcome for several different values of input variables. Based off the work of Zou. Zou, G. Y. (2012). Sample size formulas for estimating intraclass correlation coefficients with precision and assurance. Statistics in medicine, 31(29), 3972-3981. / GPL-3	noarch
r-iccbin	1.1.1	Assists in generating binary clustered data, estimates of Intraclass Correlation coefficient (ICC) for binary response in 16 different methods, and 5 different types of confidence intervals. / GPL-2	noarch
r-icd.data	1.0	Data from the United States Center for Medicare and Medicaid Services (CMS) is included in this package. There are ICD-9 and ICD-10 diagnostic and procedure codes, and lists of the chapter and sub-chapter headings and the ranges of ICD codes they encompass. There are also two sample datasets. These data are used by the ‘icd’ package for finding comorbidities. / GPL-3	noarch
r-icdglm	1.0.0	Provides an estimator for generalized linear models with incomplete data for discrete covariates. The estimation is based on the EM algorithm by the method of weights by Ibrahim (1990) <DOI:10.2307/2290013>. / GPL-2	noarch
r-icebox	1.1.2	Implements Individual Conditional Expectation (ICE) plots, a tool for visualizing the model estimated by any supervised learning algorithm. ICE plots refine Friedman’s partial dependence plot by graphing the functional relationship between the predicted response and a covariate of interest for individual observations. Specifically, ICE plots highlight the variation in the fitted values across the range of a covariate of interest, suggesting where and to what extent they may exist. / GPL-2   GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-iceinfer</a>	1.1	Given two unbiased samples of patient level data on cost and effectiveness for a pair of treatments, make head-to-head treatment comparisons by (i) generating the bivariate bootstrap resampling distribution of ICE uncertainty for a specified value of the shadow price of health, lambda, (ii) form the wedge-shaped ICE confidence region with specified confidence fraction within [0.50, 0.99] that is equivariant with respect to changes in lambda, (iii) color the bootstrap outcomes within the above confidence wedge with economic preferences from an ICE map with specified values of lambda, beta and gamma parameters, (iv) display VAGR and ALICE acceptability curves, and (v) illustrate variation in ICE preferences by displaying potentially non-linear indifference(iso-preference) curves from an ICE map with specified values of lambda, beta and either gamma or eta parameters. / GPL-3	noarch
<a href="#">r-icemelt</a>	1.0	Estimates the parameters of the semiparametric linear transformation model using imputation method, naive method and regression calibration method when time-to-event is interval-censored and a covariate is measured with error. A right censoring indicator must be available. The methods implemented in this package can be found in Mandal, S., Wang, S. and Sinha, S. (2019). Analysis of Linear Transformation Models with Covariate Measurement Error and Interval Censoring. (accepted, Statistics In Medicine). / GPL-2	linux-64, osx-64, win-64
<a href="#">r-icensmis</a>	1.3.1	We consider studies in which information from error-prone diagnostic tests or self-reports are gathered sequentially to determine the occurrence of a silent event. Using a likelihood-based approach incorporating the proportional hazards assumption, we provide functions to estimate the survival distribution and covariate effects. We also provide functions for power and sample size calculations for this setting. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-icesadvice</a>	2.0.0	A collection of functions that facilitate computational steps related to advice for fisheries management, according to ICES guidelines. These include methods for calculating reference points and model diagnostics. / GPL-2	noarch
<a href="#">r-icesdatras</a>	1.3.0	R interface to access the web services of the ICES (International Council for the Exploration of the Sea) DATRAS trawl survey database < <a href="https://datras.ices.dk/WebServices/Webservices.aspx">https://datras.ices.dk/WebServices/Webservices.aspx</a> >. / GPL-2	noarch
<a href="#">r-icestaf</a>	3.1.1	Functions to support the ICES Transparent Assessment Framework < <a href="http://taf.ices.dk">http://taf.ices.dk</a> > to organize data, methods, and results used in ICES assessments. ICES is an organization facilitating international collaboration in marine science. / GPL-2	noarch
<a href="#">r-icesvocab</a>	1.1.4	R interface to access the RECO POX web services of the ICES (International Council for the Exploration of the Sea) Vocabularies database < <a href="https://vocab.ices.dk/services/POX.aspx">https://vocab.ices.dk/services/POX.aspx</a> >. / GPL-2	noarch
<a href="#">r-icge</a>	0.3	ICGE is a package that helps to estimate the number of real clusters in data as well as to identify atypical units. The underlying methods are based on distances rather than on unit x variables. / GPL-2	noarch
<a href="#">r-iciter</a>	0.1.0	A minimal wrapper around the NIH's 'iCite' API (< <a href="https://icite.od.nih.gov/api">https://icite.od.nih.gov/api</a> >). Given a vector of pubmed IDs, this package returns a dataframe of the information yielded by the 'iCite' API. The primary metric yielded by 'iCite' is the paper's relative citation ratio, but the API also returns other meta-data from the paper, including author names, publication journal, publication year, paper title, doi, and a number of other citation metrics. / MIT	noarch
<a href="#">r-icluster</a>	2.1.0	Integrative clustering of multiple genomic data types using a joint latent variable model. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-icods</a>	1.0	Sieve semiparametric likelihood methods for analyzing interval-censored failure time data from an outcome-dependent sampling (ODS) design and from a case-cohort design. Zhou, Q., Cai, J., and Zhou, H. (2018) <doi:10.1111/biom.12744>; Zhou, Q., Zhou, H., and Cai, J. (2017) <doi:10.1093/biomet/asw067>. / GPL-2	noarch
<a href="#">r-icpsrdata</a>	0.4.0	Reproducible, programmatic retrieval of datasets from the Inter-university Consortium for Political and Social Research archive. / MIT	noarch
<a href="#">r-icr</a>	0.6.0	Provides functions to compute and plot Krippendorff's inter-coder reliability coefficient alpha and bootstrapped uncertainty estimates (Krippendorff 2004, ISBN:0761915443). The bootstrap routines are set up to make use of parallel threads where supported. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-icranks</a>	3.1	Algorithms to construct simultaneous confidence intervals for the ranks of means $\mu_1, \dots, \mu_n$ based on an independent Gaussian sample using multiple testing techniques. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-icsw</a>	1.0.0	Provides the necessary tools to estimate average treatment effects with an instrumental variable by re-weighting observations using a model of compliance. / MIT	noarch
<a href="#">r-icv</a>	1.0	Functions for computing the global and local Gaussian density estimates based on the ICV bandwidth. See the article of Savchuk, O.Y., Hart, J.D., Sheather, S.J. (2010). Indirect cross-validation for density estimation. Journal of the American Statistical Association, 105(489), 415-423 <doi:10.1198/jasa.2010.tm08532>. / GPL-2	noarch
<a href="#">r-idbg</a>	1.0	An interactive R debugger / GPL-2	noarch
<a href="#">r-idcard</a>	0.3.0	The digits of the old version (before 2000 year) of 'Chinese ID Card Number' is 15, this package aims to update to the current version of 18 digits. Besides, this package can help check whether the given 'ID' is right or not. / GPL-3	noarch
<a href="#">r-idendr0</a>	1.5.3	Interactive dendrogram that enables the user to select and color clusters, to zoom and pan the dendrogram, and to visualize the clustered data not only in a built-in heat map, but also in 'GGobi' interactive plots and user-supplied plots. This is a backport of Qt-based 'idendro' (< <a href="https://github.com/tsieger/idendro">https://github.com/tsieger/idendro</a> >) to base R graphics and Tcl/Tk GUI. / GPL-2	noarch
<a href="#">r-identity</a>	0.2_1	Calculate identity coefficients, based on Mark Abney's C code. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-idetect</a>	0.1.0	Provides efficient implementation of the Isolate-Detect methodology for the consistent estimation of the number and location of multiple change-points in one-dimensional data sequences from the deterministic noise model. For details on the Isolate-Detect methodology, please see Anastasiou and Fryzlewicz (2018) < <a href="https://docs.wixstatic.com/ugd/24cdcc_6a0866c574654163b8255e272bc0001b.pdf">https://docs.wixstatic.com/ugd/24cdcc_6a0866c574654163b8255e272bc0001b.pdf</a> >. Currently implemented scenarios are: piecewise-constant signal with Gaussian noise, piecewise-constant signal with heavy-tailed noise, continuous piecewise-linear signal with Gaussian noise, continuous piecewise-linear signal with heavy-tailed noise. / GPL-3	noarch
<a href="#">r-idiogramfish</a>	1.0.0	Plot idiograms of several karyotypes having a set of dataframes for chromosome data and optionally mark data. Includes also a function to plot holocentrics and its marks supporting micrometers and Mb. Marks can have square or dot form, its legend (label) can be drawn inline or to the right of karyotypes. It is possible to calculate chromosome indices by Levan et al. (1964) <doi:10.1111/j.1601-5223.1964.tb01953.x>, karyotype indices of Watanabe et al. (1999) <doi:10.1007/PL00013869> and Romero-Zarco (1986) <doi:10.2307/1221906> and classify chromosomes by morphology Guerra (1986) and Levan et al. (1964). / GPL-2	noarch
<a href="#">r-idmining</a>	1.0.6	Contains techniques for mining large and high-dimensional data sets by using the concept of Intrinsic Dimension (ID). Here the ID is not necessarily an integer. It is extended to fractal dimensions. And the Morisita estimator is used for the ID estimation, but other tools are included as well. / CC BY-NC-SA 4.0	noarch
<a href="#">r-idmtpreg</a>	1.1	Modeling of regression effects for transition probabilities in a progressive illness-death model. Azarang, Scheike, and de Una-Alvarez (2017) <doi:10.1002/sim.7245>. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-idpmisc</a>	1.1.19	Different high-level graphics functions for displaying large datasets, displaying circular data in a very flexible way, finding local maxima, brewing color ramps, drawing nice arrows, zooming 2D-plots, creating figures with differently colored margin and plot region. In addition, the package contains auxiliary functions for data manipulation like omitting observations with irregular values or selecting data by logical vectors, which include NAs. Other functions are especially useful in spectroscopy and analyses of environmental data: robust baseline fitting, finding peaks in spectra, converting humidity measures. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-idr</a>	1.2	This is a package for estimating the copula mixture model and plotting correspondence curves in Measuring reproducibility of high-throughput experiments (2011), Annals of Applied Statistics, Vol. 5, No. 3, 1752-1779, by Li, Brown, Huang, and Bickel / GPL (>= 2.0)	noarch
<a href="#">r-ids</a>	1.0.1	Generate random or human readable and pronounceable identifiers. / MIT	noarch
<a href="#">r-idx2r</a>	1.0.0	Convert files to and from IDX format to vectors, matrices and arrays. IDX is a very simple file format designed for storing vectors and multidimensional matrices in binary format. The format is described on the website from Yann LeCun < <a href="http://yann.lecun.com/exdb/mnist/">http://yann.lecun.com/exdb/mnist/</a> >. / MIT	noarch
<a href="#">r-ieeeeround</a>	0.2_0	A pair of functions for getting and setting the IEEE rounding mode for floating point computations. / GPL-2	linux-64, osx-64

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Name	Version	Summary/License	Platforms
<a href="#">r-iemisdata</a>	0.6.1	Miscellaneous data sets [Engineering Economics, Environmental/ Water Resources Engineering, US Presidential Elections]. / GPL-3	noarch
<a href="#">r-iemisctext</a>	0.9.99	The eclectic collection includes the following written pieces: The War Prayer by Mark Twain, War Is A Racket by Major General Smedley Butler, The Mask of Anarchy: Written on the Occasion of the Massacre at Manchester by Percy Bysshe Shelley, Connect the D.O.T.S. by Obiora Embry, Untitled: Climate Strange by Irucka Ajani Embry, and Untitled: Us versus Them or People Screwing over Other People (as we all live on one Earth and there is no us versus them in the actual Ultimate Reality) by Irucka Ajani Embry. / GPL-3	noarch
<a href="#">r-ifa</a>	7.0	The package performs Independent Factor Analysis / GPL-2	linux-64, osx-64, win-64
<a href="#">r-ifctools</a>	0.3.2	Provides utility functions to deal with Italian fiscal code ('codice fiscale'). / GPL-3	linux-64, osx-64, win-64
<a href="#">r-ifs</a>	0.1.5	Iterated Function Systems Estimator. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-ig.vancouver.2014.topcolours</a>	0.1.2.0	A dataset of the top colours of photos from Instagram taken in 2014 in the topcolours of Vancouver, British Columbia, Canada. It consists of: top colour and counts data. This data was obtained using the Instagram API. Instagram is a web photo sharing service. It can be found at: < <a href="https://instagram.com">https://instagram.com</a> >. The Instagram API is documented at: < <a href="https://instagram.com/developer/">https://instagram.com/developer/</a> >. / CC0	noarch
<a href="#">r-igasso</a>	1.4	A collection of statistical tests for genetic association studies. / GPL-2	noarch
<a href="#">r-igor</a>	0.8.1	Provides function to read data from the 'Igor Pro' data analysis program by Wavemetrics. The data formats supported are 'Igor' packed experiment format (pxp) and 'Igor' binary wave (ibw). See: <a href="http://www.wavemetrics.com/">http://www.wavemetrics.com/</a> for details. Also includes functions to load special pxp files produced by the 'Igor Pro' 'Neuromatic' and 'Nclamp' packages for recording and analysing neuronal data. See <a href="http://www.neuromatic.thinkrandom.com/">http://www.neuromatic.thinkrandom.com/</a> for details. / GPL-2	noarch
<a href="#">r-igraph</a>	1.2.4	Routines for simple graphs and network analysis. It can handle large graphs very well and provides functions for generating random and regular graphs, graph visualization, centrality methods and much more. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-igraphdata</a>	1.0.1	A small collection of various network data sets, to use with the ‘igraph’ package: the Enron email network, various food webs, interactions in the immunoglobulin protein, the karate club network, Koenigsberg’s bridges, visuotactile brain areas of the macaque monkey, UK faculty friendship network, domestic US flights network, etc. / CC BY-SA 4.0 file LICENSE	noarch
<a href="#">r-igraphinshiny</a>	0.1	Using ‘shiny’ to demo ‘igraph’ package makes learning graph theory easy and fun. / GPL-2	noarch
<a href="#">r-igraph-tonia</a>	1.0	This program facilitates exporting igraph graphs to the SoNIA file format / GPL-2	noarch
<a href="#">r-igsea</a>	1.2	To integrate multiple GSEA studies, we propose a hybrid strategy, iGSEA-AT, for choosing random effects (RE) versus fixed effect (FE) models, with an attempt to achieve the potential maximum statistical efficiency as well as stability in performance in various practical situations. In addition to iGSEA-AT, this package also provides options to perform integrative GSEA with testing based on a FE model (iGSEA-FE) and testing based on a RE model (iGSEA-RE). The approaches account for different set sizes when testing a database of gene sets. The function is easy to use, and the three approaches can be applied to both binary and continuous phenotypes. / GPL-2	noarch
<a href="#">r-ihs</a>	1.0	Density, distribution function, quantile function and random generation for the inverse hyperbolic sine distribution. This package also provides a function that can fit data to the inverse hyperbolic sine distribution using maximum likelihood estimation. / GPL-3	noarch
<a href="#">r-iilasso</a>	0.0.2	Efficient algorithms for fitting linear / logistic regression model with Independently Interpretable Lasso. Takada, M., Suzuki, T., & Fujisawa, H. (2018). Independently Interpretable Lasso: A New Regularizer for Sparse Regression with Uncorrelated Variables. AISTATS. < <a href="http://proceedings.mlr.press/v84/takada18a/takada18a.pdf">http://proceedings.mlr.press/v84/takada18a/takada18a.pdf</a> >. / MIT	linux-64, osx-64, win-64
<a href="#">r-im</a>	1.0	Compute moments of images and perform reconstruction from moments. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-image</a>	1.0	Performs mQTL (methylation quantitative-trait locus) mapping in bisulfite sequencing studies by fitting a binomial mixed model and then incorporating the allelic-specific methylation pattern. Based on Fan, Yue; Vilgalys, Tauras P.; Sun, Shiquan; Peng, Qinke; Tung, Jenny; Zhou, Xiang (2019) < <a href="https://doi.org/10.1101/615039">doi:10.1101/615039</a> >. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-imageviewer</a>	0.1.0	Display a 2D-matrix data as a interactive zoomable gray-scale image viewer, providing tools for manual data inspection. The viewer window shows cursor guiding lines and a corresponding data slices for both axes at the current cursor position. A tool-bar allows adjusting image display brightness/contrast through WebGL filters and performing basic high-pass/low-pass filtering. / MIT	noarch

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Name	Version	Summary/License	Platforms
r-imagine	1.5.2	Provides fast application of image filters to data matrices, using R and C algorithms. / GPL-2	linux-64, osx-64, win-64
r-imak	1.2.2	This is an Automatic Item Generator for Psychological Assessment. Items created with the ‘IMak’ package should not be used in applied settings as part of the working protocol without ensuring first that the items meet the required psychometric quality standards (see Blum & Holling, 2018) <DOI:10.3389/fpsyg.2018.01286>. / GPL-3	noarch
r-imap	1.32	Zoom in and out of maps or any supplied lines or points, with control for color, poly fill, and aspect. / GPL-2	noarch
r-imfdata	0.2.0	Search, extract and formulate IMF’s datasets. / MIT	noarch
r-imgur	1.0.3	A complete API client for the image hosting service Imgur.com, including the an imgur graphics device, enabling the easy upload and sharing of plots. / GPL-3	noarch
r-imgw	0.2.0	Download Polish meteorological and hydrological data from the Institute of Meteorology and Water Management - National Research Institute (< <a href="https://dane.imgw.pl/">https://dane.imgw.pl/</a> >). This package also allows for adding geographical coordinates for each observation. / MIT	noarch
r-imis	0.1	IMIS algorithm draws samples from the posterior distribution. The user has to define the following R functions in advance: prior(x) calculates prior density of x, likelihood(x) calculates the likelihood of x, and sample.prior(n) draws n samples from the prior distribution. / GPL-2	noarch
r-immailgun	0.1.2	Send emails using the ‘mailgun’ api. To use this package you will need an account from < <a href="https://www.mailgun.com/">https://www.mailgun.com/</a> > . / GPL-3	noarch
r-immigrate	0.0.2	Based on large margin principle, this package performs feature selection methods: IM4E(Iterative Margin-Maximization under Max-Min Entropy Algorithm); imIM4E(imbalance Iterative Margin-Maximization under Max-Min Entropy Algorithm); Immigrate(Iterative Max-Min Entropy Margin-Maximization with Interaction Terms Algorithm); BIM(Boosted version of IMMIGRATE algorithm); Simba(Iterative Search Margin Based Algorithm); LFE(Local Feature Extraction Algorithm). This package also performs prediction for the above feature selection methods. See Zhao et al. (2018) <arXiv:1810.02658> for more details. / GPL-2	linux-64, osx-64, win-64
r-impact	0.1.1	Implement a multivariate analysis of the impact of items to identify a bias in the questionnaire validation of Likert-type scale variables. The items requires considering a null value (category doesn’t have tendency). Offering frequency, importance and impact of the items. / GPL-2	noarch
r-impactiv	1.0	In this package, you can find two functions proposed in Ding, Geng and Zhou (2011) to estimate direct and indirect causal effects with randomization and multiple-component intervention using instrumental variable method. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-impimp</a>	0.3.1	Imputing blockwise missing data by imprecise imputation, featuring a domain-based, variable-wise, and case-wise strategy. Furthermore, the estimation of lower and upper bounds for unconditional and conditional probabilities based on the obtained imprecise data is implemented. Additionally, two utility functions are supplied: one to check whether variables in a data set contain set-valued observations; and another to merge two already imprecisely imputed data. The method is described in a technical report by Endres, Fink and Augustin (2018, <doi:10.5282/ubm/epub.42423>). / GPL-2   GPL-3	noarch
<a href="#">r-implyr</a>	0.2.4	‘SQL’ back-end to ‘dplyr’ for Apache Impala, the massively parallel processing query engine for Apache ‘Hadoop’. Impala enables low-latency ‘SQL’ queries on data stored in the ‘Hadoop’ Distributed File System ‘(HDFS)’, Apache ‘HBase’, Apache ‘Kudu’, Amazon Simple Storage Service ‘(S3)’, Microsoft Azure Data Lake Store ‘(ADLS)’, and Dell ‘EMC’ ‘Isilon’. See < <a href="https://impala.apache.org">https://impala.apache.org</a> > for more information about Impala. / Apache License 2.0   file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-import</a>	1.1.0	This is an alternative mechanism for importing objects from packages. The syntax allows for importing multiple objects from a package with a single command in an expressive way. The import package bridges some of the gap between using library (or require) and direct (single-object) imports. Furthermore the imported objects are not placed in the current environment. It is also possible to import objects from stand-alone .R files. For more information, refer to the package vignette. / MIT	noarch
<a href="#">r-importar</a>	0.1.1	Enables ‘Python’-like importing/loading of packages or functions with aliasing to prevent namespace conflicts. / GPL-3	noarch
<a href="#">r-imprprobest</a>	1.0.1	A minimum distance estimator is calculated for an imprecise probability model. The imprecise probability model consists of upper coherent previsions whose credal sets are given by a finite number of constraints on the expectations. The parameter set is finite. The estimator chooses that parameter such that the empirical measure lies next to the corresponding credal set with respect to the total variation norm. / LGPL-3	noarch
<a href="#">r-impree</a>	0.5.1	Creation of imprecise classification trees. They rely on probability estimation within each node by means of either the imprecise Dirichlet model or the nonparametric predictive inference approach. The splitting variable is selected by the strategy presented in Fink and Crossman (2013) < <a href="http://www.sipta.org/isipta13/index.php?id=paper&amp;paper=014.html">http://www.sipta.org/isipta13/index.php?id=paper&amp;paper=014.html</a> >, but also the original imprecise information gain of Abellan and Moral (2003) <doi:10.1002/int.10143> is covered. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-imputemdr</a>	1.1.2	This package provides various approaches to handling missing values for the MDR analysis to identify gene-gene interactions using biallelic marker data in genetic association studies / GPL-2	linux-64, osx-64, win-64
<a href="#">r-imputemissings</a>	0.0.3	Compute missing values on a training data set and impute them on a new data set. Current available options are median/mode and random forest. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-imputer</a>	2.1	Multivariate Expectation-Maximization (EM) based imputation framework that offers several different algorithms. These include regularisation methods like Lasso and Ridge regression, tree-based models and dimensionality reduction methods like PCA and PLS. / GPL-3	noarch
<a href="#">r-imputeyn</a>	1.3	Method brings less bias and more efficient estimates for AFT models. / GPL-2	noarch
<a href="#">r-imrmc</a>	1.2.0	Do Multi-Reader, Multi-Case (MRMC) analyses of data from imaging studies where clinicians (readers) evaluate patient images (cases). What does this mean? ... Many imaging studies are designed so that every reader reads every case in all modalities, a fully-crossed study. In this case, the data is cross-correlated, and we consider the readers and cases to be cross-correlated random effects. An MRMC analysis accounts for the variability and correlations from the readers and cases when estimating variances, confidence intervals, and p-values. The functions in this package can treat arbitrary study designs and studies with missing data, not just fully-crossed study designs. The initial package analyzes the reader-average area under the receiver operating characteristic (ROC) curve with U-statistics according to Gallas, Bandos, Samuelson, and Wagner 2009 <doi:10.1080/03610920802610084>. Additional functions analyze other endpoints with U-statistics (binary performance and score differences) following the work by Gallas, Pennello, and Myers 2007 <doi:10.1364/JOSAA.24.000B70>. Package development and documentation is at < <a href="https://github.com/DIDSR/iMRMC/tree/master">https://github.com/DIDSR/iMRMC/tree/master</a> >. / CC0	noarch
<a href="#">r-inarmix</a>	0.4	Fits mixtures models for longitudinal data. Appropriate when the data are counts and when the correlation structure is assumed to be AR(1). / GPL-2	linux-64, osx-64, win-64
<a href="#">r-inbreedr</a>	0.3.2	A framework for analysing inbreeding and heterozygosity-fitness correlations (HFCs) based on microsatellite and SNP markers. / GPL-2	noarch
<a href="#">r-inca</a>	0.0.3	Specific functions are provided for rounding real weights to integers and performing an integer programming algorithm for calibration problems. They are useful for census-weights adjustments, or for performing linear regression with integer parameters. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-independencetests</a>	0.2	Functions for testing mutual independence between many numerical random vectors or serial independence of a multivariate stationary sequence. The proposed test works when some or all of the marginal distributions are singular with respect to Lebesgue measure. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-indexnumr</a>	0.1.2	Computes bilateral and multilateral index numbers. It has support for several standard bilateral indices as well as the GEKS multilateral index number methods (see Ivancic, Diewert and Fox (2011) <doi:10.1016/j.jeconom.2010.09.003>). It also supports updating of GEKS indexes using several splicing methods. / GPL-2	noarch
<a href="#">r-indiantaxcalc</a>	1.0.2	Calculate Indian Income Tax liability for Financial years of Individual resident aged below 60 years, Senior Citizen, Super Senior Citizen, Firm, Local Authority, Any Non Resident Individual / Hindu Undivided Family / Association of Persons / Body of Individuals / Artificial Judicial Person, Co-operative Society. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-indirect</a>	0.2.0	Functions are provided to facilitate prior elicitation for Bayesian generalised linear models using independent conditional means priors. The package supports the elicitation of multivariate normal priors for generalised linear models. The approach can be applied to indirect elicitation for a generalised linear model that is linear in the parameters. The package is designed such that the facilitator executes functions within the R console during the elicitation session to provide graphical and numerical feedback at each design point. Various methodologies for eliciting fractiles (equivalently, percentiles or quantiles) are supported, including versions of the approach of Hosack et al. (2017) <doi:10.1016/j.jress.2017.06.011>. For example, experts may be asked to provide central credible intervals that correspond to a certain probability. Or experts may be allowed to vary the probability allocated to the central credible interval for each design point. Additionally, a median may or may not be elicited. / GPL-3	noarch
<a href="#">r-indtestpp</a>	1.0	Several parametric and non-parametric tests and measures to check independence between two or more (homogeneous or nonhomogeneous) point processes in time are provided. Tools for simulating point processes in one dimension with different types of dependence are also implemented. / GPL-3	noarch
<a href="#">r-ineq</a>	0.2.1	Inequality, concentration, and poverty measures. Lorenz curves (empirical and theoretical). / GPL-2   GPL-3	noarch
<a href="#">r-infdim</a>	1.0	This package contains functions to perform calculations of the infinite-dimensional model (IDM) and to produce 95% confidence intervals around the model elements through bootstrapping. / GPL-2	noarch
<a href="#">r-inference</a>	0.1.0	Collection of functions to extract inferential values (point estimates, confidence intervals, p-values, etc) of a fitted model object into a matrix-like object that can be used for table/report generation; transform point estimates via the delta method. / GPL-2	noarch
<a href="#">r-inferencesmr</a>	1.0	The InferenceSMR package provides functions to make inference about the standardized mortality ratio (SMR) when evaluating the effect of a screening program. The package is based on methods described in Sasieni (2003) and Talbot et al. (2011). / GPL-2	noarch
<a href="#">r-interference</a>	1.0.0	Provides methods for estimating causal effects in the presence of interference described in B. Saul and M. Hugdens (2017) <doi:10.18637/jss.v082.i02>. Currently it implements the inverse-probability weighted (IPW) estimators proposed by E.J. Tchetgen Tchetgen and T.J. Vanderweele (2012) <doi:10.1177/0962280210386779>. / GPL-2	noarch
<a href="#">r-infiniumpurify</a>	1.3.1	The proportion of cancer cells in solid tumor sample, known as the tumor purity, has adverse impact on a variety of data analyses if not properly accounted for. We develop ‘InfiniumPurify’, which is a comprehensive R package for estimating and accounting for tumor purity based on DNA methylation Infinium 450k array data. ‘InfiniumPurify’ provides functionalities for tumor purity estimation. In addition, it can perform differential methylation detection and tumor sample clustering with the consideration of tumor purities. / GPL-2	noarch
<a href="#">r-infix</a>	0.1.0	Contains a number of infix binary operators that may be useful in day to day practices. / GPL-3	noarch
<a href="#">r-inflection</a>	1.3.5	Implementation of methods Extremum Surface Estimator (ESE) and Extremum Distance Estimator (EDE) to identify the inflection point of a curve . Christopoulos, DT (2014) <arXiv:1206.5478v2 [math.NA]> . Christopoulos, DT (2016) <https://veltech.edu.in/wp-content/uploads/2016/04/Paper-04-2016.pdf> . Christopoulos, DT (2016) <doi:10.2139/ssrn.3043076> . / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-influence.me</a>	0.9.9	Provides a collection of tools for detecting influential cases in generalized mixed effects models. It analyses models that were estimated using ‘lme4’. The basic rationale behind identifying influential data is that when single units are omitted from the data, models based on these data should not produce substantially different estimates. To standardize the assessment of how influential a (single group of) observation(s) is, several measures of influence are common practice, such as Cook’s Distance. In addition, we provide a measure of percentage change of the fixed point estimates and a simple procedure to detect changing levels of significance. / GPL-3	noarch
<a href="#">r-influence.sem</a>	2.2	A set of tools for evaluating several measures of case influence for structural equation models. / GPL-2	noarch
<a href="#">r-influencer</a>	0.1.0	Provides functionality to compute various node centrality measures on networks. Included are functions to compute betweenness centrality (by utilizing Madduri and Bader’s SNAP library), implementations of Burt’s constraint and effective network size (ENS) metrics, Borgatti’s algorithm to identify key players, and Valente’s bridging metric. On Unix systems, the betweenness, Key Players, and bridging implementations are parallelized with OpenMP, which may run faster on systems which have OpenMP configured. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-infodecompute</a>	0.6.1	The main purpose of this package is to generate the structure of the analysis of variance (ANOVA) table of the two-phase experiments. The user only need to input the design and the relationships of the random and fixed factors using the Wilkinson-Rogers’ syntax, this package can then quickly generate the structure of the ANOVA table with the coefficients of the variance components for the expected mean squares. Thus, the balanced incomplete block design and provides the efficiency factors of the fixed effects can also be studied and compared much easily. / GPL-3	noarch
<a href="#">r-infotheo</a>	1.2.0	This package implements various measures of information theory based on several entropy estimators. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-infotrad</a>	1.2	Estimates the probability of informed trading (PIN) initially introduced by Easley et. al. (1996) <doi:10.1111/j.1540-6261.1996.tb04074.x> . Contribution of the package is that it uses likelihood factorizations of Easley et. al. (2010) <doi:10.1017/S0022109010000074> (EHO factorization) and Lin and Ke (2011) <doi:10.1016/j.finmar.2011.03.001> (LK factorization). Moreover, the package uses different estimation algorithms. Specifically, the grid-search algorithm proposed by Yan and Zhang (2012) <doi:10.1016/j.jbankfin.2011.08.003> , hierarchical agglomerative clustering approach proposed by Gan et. al. (2015) <doi:10.1080/14697688.2015.1023336> and later extended by Ersan and Alici (2016) <doi:10.1016/j.intfin.2016.04.001> . / GPL-3	noarch
<a href="#">r-infra</a>	0.1.2	Takes a data frame containing latitude and longitude coordinates and downloads images from map servers to determine their file size as a proxy of infrastructure / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-ini	0.3.1	Parse simple '.ini' configuration files to an structured list. Users can manipulate this resulting list with lapply() functions. This same structured list can be used to write back to file after modifications. / GPL-3	noarch
r-injector	0.2.4	R dependency injection framework. Dependency injection allows a program design to follow the dependency inversion principle. The user delegates to external code (the injector) the responsibility of providing its dependencies. This separates the responsibilities of use and construction. / LGPL-3	noarch
r-inline	0.3.15	Functionality to dynamically define R functions and S4 methods with 'inlined' C, C or Fortran code supporting the .C and .Call calling conventions. / LGPL	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-inplace	0.1.0	It provides in-place operators for R that are equivalent to '=', '-=', '*=', '/=' in C. Those can be applied on integer/double vectors/matrices. You have also access to sweep operations (in-place). / GPL-3	linux-64, osx-64, win-64
r-insiderode	2.0	insideRODE package includes builtin functions from deSolve, compiled functions from compiler, and C/FORTRAN code interfaces to nlme. It includes nlmLSODA, nlmODE, nlmVODE, nlmLSODE for general purpose; cflSODA, cflSODE, cfODE, cfVODE call C/FORTRAN compiled dll functions. ver2.0 add sink() function into example it helps to directly combine c/fortran source code in R files. Finally, with new compiler package, we generated compiled functions: nlmODEcp, nlmVODEcp, nlmLSODEcp, nlmLSODAc and cpODE, cpLSODA, cpLSODE, cpVODE. They will help to increase speed. / LGPL (> 2.0)	noarch
r-insight	0.5.0	A tool to provide an easy, intuitive and consistent access to information contained in various R models, like model formulas, model terms, information about random effects, data that was used to fit the model or data from response variables. 'insight' mainly revolves around two types of functions: Functions that find (the names of) information, starting with 'find_', and functions that get the underlying data, starting with 'get_'. The package has a consistent syntax and works with many different model objects, where otherwise functions to access these information are missing. / GPL-3	noarch
r-inspectchangept	1.0.1	Provides a data-driven projection-based method for estimating changepoints in high-dimensional time series. Multiple changepoints are estimated using a (wild) binary segmentation scheme. / GPL-3	noarch
r-inspectr	1.0.0	Check one column or multiple columns of a dataframe using the preset basic checks or your own functions. Enables checks without knowledge of lapply() or sapply(). / CC BY-SA 4.0	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-install.load</a>	1.2.1	The function <i>install_load</i> checks the local R library(ies) to see if the required package(s) is/are installed or not. If the package(s) is/are not installed, then the package(s) will be installed along with the required dependency(ies). This function pulls source or binary packages from the Rstudio-sponsored CRAN mirror and/or the USGS GRAN Repository. Lastly, the chosen package(s) is/are loaded. The function <i>load_package</i> simply loads the provided packages. / CC BY-SA 4.0	noarch
<a href="#">r-instar</a>	0.2.4	Provides an interface to the Instagram API < <a href="https://instagram.com/developer/">https://instagram.com/developer/</a> >, which allows R users to download public pictures filtered by hashtag, popularity, user or location, and to access public users' profile data. / GPL-2	noarch
<a href="#">r-insurancedata</a>	1.0	Insurance datasets, which are often used in claims severity and claims frequency modelling. It helps testing new regression models in those problems, such as GLM, GLMM, HGLM, non-linear mixed models etc. Most of the data sets are applied in the project Mixed models in ratemaking supported by grant NN 111461540 from Polish National Science Center. / GPL-2	noarch
<a href="#">r-intccr</a>	1.1.4	Semiparametric regression models on the cumulative incidence function with interval-censored competing risks data as described in Bakoyannis, Yu, & Yiannoutsos (2017) <doi:10.1002/sim.7350>. The main function fits the proportional subdistribution hazards model (Fine-Gray model), the proportional odds model, and other models that belong to the class of semiparametric generalized odds rate transformation models. / GPL-2	noarch
<a href="#">r-integratebs</a>	0.1.0	Integrated B-spline function. / GPL-2	noarch
<a href="#">r-interact</a>	1.1	This package searches for marginal interactions in a binary response model. Interact uses permutation methods to estimate false discovery rates for these marginal interactions and has some, limited visualization capabilities / GPL-3	linux-64, osx-64, win-64
<a href="#">r-interactiontest</a>	1.2	Implements the procedures suggested in Esarey and Sumner (2017) < <a href="http://justinesarey.com/interaction-overconfidence.pdf">http://justinesarey.com/interaction-overconfidence.pdf</a> > for controlling the false discovery rate when constructing marginal effects plots for models with interaction terms. / GPL-3	noarch
<a href="#">r-interactiveigraph</a>	1.0.6	An extension of the package 'igraph'. This package create possibly to work with 'igraph' objects interactively. / GPL-2	noarch
<a href="#">r-interatrix</a>	1.1.1	Chi-square tests are computed with corrections. / GPL-2	noarch
<a href="#">r-intercure</a>	0.1.0	Implementations of semiparametric cure rate estimators for interval censored data in R. The algorithms are based on the promotion time and frailty models, all for interval censoring. For the frailty model, there is also a implementation contemplating clustered data. / GPL-2   GPL-3	noarch
<a href="#">r-interep</a>	0.3.0	Extensive penalized variable selection methods have been developed in the past two decades for analyzing high dimensional omics data, such as gene expressions, single nucleotide polymorphisms (SNPs), copy number variations (CNVs) and others. However, lipidomics data have been rarely investigated by using high dimensional variable selection methods. This package incorporates our recently developed penalization procedures to conduct interaction analysis for high dimensional lipidomics data with repeated measurements. The core module of this package is developed in C. The development of this software package and the associated statistical methods have been partially supported by an Innovative Research Award from Johnson Cancer Research Center, Kansas State University. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-interfaceqpcr</a>	1.0	Graphical User Interface allowing to determine the concentration in the sample in CFU per mL or in number of copies per mL provided to qPCR results after with or without PMA treatment. This package is simply to use because no knowledge in R commands is necessary. A graphic represents the standard curve, and a table containing the result for each sample is created. / GPL-2	noarch
<a href="#">r-interferenceci</a>	1.1	Computes large sample confidence intervals of Liu and Hudgens (2014), exact confidence intervals of Tchetgen Tchetgen and VanderWeele (2012), and exact confidence intervals of Rigdon and Hudgens (2014) for treatment effects on a binary outcome in two-stage randomized experiments with interference. / GPL-3	noarch
<a href="#">r-interim</a>	0.8.0	Allows the simulation of the recruitment and both the event and treatment phase of a clinical trial. Based on these simulations, the timing of interim analyses can be assessed. / GPL-3	noarch
<a href="#">r-interlinear</a>	1.0	Interlinearized glossed texts (IGT) are used in descriptive linguistics for representing a morphological analysis of a text through a morpheme-by-morpheme gloss. ‘InterlinearR’ provide a set of functions that targets several popular formats of IGT (‘SIL Toolbox’, ‘EMELD XML’) and that turns an IGT into a set of data frames following a relational model (the tables represent the different linguistic units: texts, sentences, word, morphemes). The same pieces of software (‘SIL FLEX’, ‘SIL Toolbox’) typically produce dictionaries of the morphemes used in the glosses. ‘InterlinearR’ provide a function for turning the LIFT XML dictionary format into a set of data frames following a relational model in order to represent the dictionary entries, the sense(s) attached to the entries, the example(s) attached to senses, etc. / BSD_3_clause	noarch
<a href="#">r-interp</a>	1.0.3	Bivariate data interpolation on regular and irregular grids, either linear or using splines are the main part of this package. It is intended to provide FOSS replacement functions for the ACM licensed akima::interp and tripack::tri.mesh functions. Currently the piecewise linear interpolation part of akima::interp (and also akima::interp) is implemented in interp::interp, this corresponds to the call akima::interp(..., linear=TRUE) which is the default setting and covers most of akima::interp use cases in depending packages. A re-implementation of Akimas spline interpolation (akima::interp(..., linear=FALSE)) is currently under development and will complete this package in a later version. Estimators for partial derivatives are already available, these are a prerequisite for the spline interpolation. The basic part is currently a GPLed triangulation algorithm (sweep hull algorithm by David Sinclair) providing the starting point for the piecewise linear interpolator. As side effect this algorithm is also used to provide replacements for the basic functions of the tripack package which also suffer from the ACM restrictions. All functions are designed to be backward compatible with their akima / tripack counterparts. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-interpol</a>	1.3.1	A package for numerical encoding as well as for linear and non-linear interpolation of amino acid sequences. / GPL-2	noarch
<a href="#">r-interpol.t</a>	2.1.1	Hourly interpolation of daily minimum and maximum temperature series. Carries out interpolation on multiple series ad once. Requires some hourly series for calibration (alternatively can use default calibration table). / GPL-2	noarch
<a href="#">r-interpret</a>	0.2.4	Compute permutation- based performance measures and create partial dependence plots for (cross-validated) ‘randomForest’ and ‘ada’ models. / GPL-2	noarch
<a href="#">r-interva4</a>	1.7.5	Provides an R version of the ‘InterVA4’ software (< <a href="http://www.interva.net">http://www.interva.net</a> >) for coding cause of death from verbal autopsies. It also provides simple graphical representation of individual and population level statistics. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-interva5</a>	1.0.2	Provides an R version of the ‘InterVA5’ software ( <a href="http://www.interva.net">http://www.interva.net</a> ) for coding cause of death from verbal autopsies. It also provides simple graphical representation of individual and population level statistics. / GPL-3	noarch
<a href="#">r-intervals</a>	0.15.1	Tools for working with and comparing sets of points and intervals. / Artistic-2.0	linux-64, osx-64, win-64
<a href="#">r-intervalsurgeon</a>	1.0	Functions for manipulating integer-bounded intervals including finding overlaps, piling and merging. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-intervcomp</a>	0.1.2	Performs hypothesis testing using the interval estimates (e.g., confidence intervals). The non-overlapping interval estimates indicates the statistical significance. References to these procedures can be found at Noguchi and Marmolejo-Ramos (2016) <doi:10.1080/00031305.2016.1200487>, Bonett and Seier (2003) <doi:10.1198/0003130032323>, and Lemm (2006) <doi:10.1300/J082v51n02_05>. / GPL-3	noarch
<a href="#">r-interventionaldbn</a>	1.2.2	This package allows a dynamic Bayesian network to be inferred from microarray timecourse data with interventions (inhibitors). / GPL-2	noarch
<a href="#">r-intlik</a>	1.0	This package calculates the integrated likelihood numerically. Given the Likelihood function and the prior function, this package integrates out the nuisance parameters by Metropolis-Hastings (MCMC) Algorithm. / GPL-2	noarch
<a href="#">r-intoo</a>	0.3.1	Contains attribute operators (%\$% and %\$%<-), convenience functions and functions for printing objects compactly but informatively. And partly supports nested matrices. / GPL-2	noarch
<a href="#">r-intreggof</a>	0.85	Performs Goodness of Fit for regression models using Integrated Regression method. Works for several different fitting techniques. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-intriniostockapi</a>	0.0.1	Download financial data from the free ‘Intrinio Stock API’ (< <a href="https://intrinio.com/">https://intrinio.com/</a> >). ‘Intrinio’ offers a REST API which provides financial markets data including intra-day stock prices, historical stock prices, technical indicators, company fundamentals, and more. Complete documentation for the ‘Intrinio Stock API’ is available here: < <a href="https://intrinio.com/documentation/api/">https://intrinio.com/documentation/api/</a> >. To access the ‘Intrinio Stock API’, simply create a free account < <a href="https://intrinio.com/">https://intrinio.com/</a> >. / MIT	noarch
<a href="#">r-intrval</a>	0.1_1	Evaluating if values of vectors are within different open/closed intervals ( $x \in ]c(a, b)$ ), or if two closed intervals overlap ( $c(a1, b1) \cap ]c(a2, b2)$ ). Operators for negation and directional relations also implemented. / GPL-2	noarch
<a href="#">r-intrvals</a>	1.0.0	Calculates event rates and compares means and variances of groups of interval data corrected for missed arrival observations. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-intsurv</a>	0.2.1	Contains implementations of integrative survival analysis routines, including regular Cox cure rate model proposed by Kuk and Chen (1992) <doi:10.1093/biomet/79.3.531> via an EM algorithm proposed by Sy and Taylor (2000) <doi:10.1111/j.0006-341X.2000.00227.x>, regularized Cox cure rate model with elastic net penalty following Masud et al. (2018) <doi:10.1177/0962280216677748>, and Zou and Hastie (2005) <doi:10.1111/j.1467-9868.2005.00503.x>, and weighted concordance index for cure models proposed by Asano and Hirakawa (2017) <doi:10.1080/10543406.2017.1293082>. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-intubate</a>	1.0.0	Interface to popular R functions with formulas and data, such as 'lm', so they can be included painlessly in data science pipelines implemented by 'magrittr' with the operator %>%. / GPL-2	noarch
<a href="#">r-inum</a>	1.0.1	Enum-type representation of vectors and representation of intervals, including a method of coercing variables in data frames. / GPL-2	noarch
<a href="#">r-invasioncorrection</a>	0.1	The correction is achieved under the assumption that non-migrating cells of the essay approximately form a quadratic flow profile due to frictional effects, compare law of Hagen-Poiseuille for flow in a tube. The script fits a conical plane to give xyz-coordinates of the cells. It outputs the number of migrated cells and the new corrected coordinates. / GPL-3	noarch
<a href="#">r-invctr</a>	0.1.0	Vector operations between grapes: An infix-only package! The 'invctr' functions perform common and less common operations on vectors, data frames matrices and list objects: - Extracting a value (range), or, finding the indices of a value (range). - Trimming, or padding a vector with a value of your choice. - Simple polynomial regression. - Set and membership operations. - General check & replace function for NAs, Inf and other values. / GPL-3	noarch
<a href="#">r-investr</a>	1.4.0	Functions to facilitate inverse estimation (e.g., calibration) in linear, generalized linear, nonlinear, and (linear) mixed-effects models. A generic function is also provided for plotting fitted regression models with or without confidence/prediction bands that may be of use to the general user. / GPL-2	noarch
<a href="#">r-invgamma</a>	1.1	Light weight implementation of the standard distribution functions for the inverse gamma distribution, wrapping those for the gamma distribution in the stats package. / GPL-2	noarch
<a href="#">r-invlt</a>	0.2.1	Provides two functions for the numerical inversion of Laplace-Transformed functions, returning the value of the standard (time) domain function at a specified value. The first algorithm is the first optimum contour algorithm described by Evans and Chung (2000)[1]. The second algorithm uses the Bromwich contour as per the definition of the inverse Laplace Transform. The latter is unstable for numerical inversion and mainly included for comparison or interest. There are also some additional functions provided for utility, including plotting and some simple Laplace Transform examples, for which there are known analytical solutions. Polar-cartesian conversion functions are included in this package and are used by the inversion functions. [1] Evans & Chung, 2000: Laplace transform inversions using optimal contours in the complex plane; International Journal of Computer Mathematics v73 pp531-543. / MIT	noarch
<a href="#">r-ioncopy</a>	2.1.1	Method for the calculation of copy numbers and calling of copy number alterations. The algorithm uses coverage data from amplicon sequencing of a sample cohort as input. The method includes significance assessment, correction for multiple testing and does not depend on normal DNA controls. Budczies (2016 Mar 15) <doi:10.18632/oncotarget.7451>. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-ionr	0.3.0	Provides item exclusion procedure, which is a formal method to test ‘Indifference Of iNdicator’ (ION). When a latent personality trait-outcome association is assumed, then the association strength should not depend on which subset of indicators (i.e. items) has been chosen to reflect the trait. Personality traits are often measured (reflected) by a sum-score of a certain set of indicators. Item exclusion procedure randomly excludes items from a sum-score and tests, whether the sum-score - outcome correlation changes. ION has been achieved, when any item can be excluded from the sum-score without the sum-score - outcome correlation substantially changing . For more details, see Vainik, Mottus et. al, (2015) Are Trait-Outcome Associations Caused by Scales or Particular Items? Example Analysis of Personality Facets and BMI,European Journal of Personality DOI: <10.1002/per.2009> . / GPL-2	noarch
r-iosmooth	0.94	Density, spectral density, and regression estimation using infinite order flat-top kernels. / GPL-3	noarch
r-iotools	0.2.5	Basic I/O tools for streaming and data parsing. / GPL-2   GPL-3	linux-64, osx-64
r-ipcswitch	1.0.3	Contains functions for formatting clinical trials data and implementing inverse probability of censoring weights to handle treatment switches when estimating causal treatment effect in randomized clinical trials. / GPL-3	noarch
r-ipdmeta	2.4	This package provides functions to estimate an IPD linear mixed effects model for a continuous outcome and any categorical covariate from study summary statistics. There are also functions for estimating the power of a treatment-covariate interaction test in an individual patient data meta-analysis from aggregate data. / GPL-2	noarch
r-ipecc	0.1.2	Calculates the RMS intrinsic and parameter-effects curvatures of a nonlinear regression model. / GPL-2	noarch
r-ipflasso	0.2	The core of the package is cvr2.ipflasso(), an extension of glmnet to be used when the (large) set of available predictors is partitioned into several modalities which potentially differ with respect to their information content in terms of prediction. For example, in biomedical applications patient outcome such as survival time or response to therapy may have to be predicted based on, say, mRNA data, miRNA data, methylation data, CNV data, clinical data, etc. The clinical predictors are on average often much more important for outcome prediction than the mRNA data. The ipflasso method takes this problem into account by using different penalty parameters for predictors from different modalities. The ratio between the different penalty parameters can be chosen by cross-validation. / GPL-3	noarch
r-ipfp	1.0.1	A fast (C) implementation of the iterative proportional fitting procedure. Based on corresponding code from the networkTomography package. / Apache License (== 2.0)	linux-64, osx-64
r-ipmpack	2.1	IPMpack takes demographic vital rates and (optionally) environmental data to build integral projection models. A number of functional forms for growth and survival can be incorporated, as well as a range of reproductive strategies. The package also includes a suite of diagnostic routines, provides classic matrix model output (e.g., lambda, elasticities, sensitivities), and produces post-hoc metrics (e.g., passage time and life expectancy). / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-ipp	1.1	Generates random numbers corresponding to the events on a Poisson point process with changing event rates. This includes the possibility to incorporate additional information such as the number of events occurring or the location of an already known event. It can also generate the probability density functions of specific events in the cases where additional information is available. Based on Hohmann (2019) <arXiv:1901.10754>. / CC BY 4.0	noarch
r-iped	0.9_8	Improved predictive models by indirect classification and bagging for classification, regression and survival problems as well as resampling based estimators of prediction error. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
r-ipmnet	0.1.5	Provides an R interface to the ‘iPTMnet’ database REST API, which can be used to retrieve Post Translational Modification (PTM) data in systems biology context. This package handles all the aspects of communicating with the API, which involve sending the request, checking the error codes and parsing the response in a format that is ready to integrate into existing workflows. / MIT	noarch
r-ipw-survival	0.5	In observational studies, the presence of confounding factors is common and the comparison of different groups of subjects requires adjustment. In this package, we propose simple functions to estimate adjusted survival curves and log-rank test based on inverse probability weighting (IPW). / GPL-2	noarch
r-iql	1.5	Estimate an optimal dynamic treatment regime using Interactive Q-learning. / GPL-2	noarch
r-irace	3.3	Iterated race is an extension of the Iterated F-race method for the automatic configuration of optimization algorithms, that is, (offline) tuning their parameters by finding the most appropriate settings given a set of instances of an optimization problem. / GPL-2	noarch
r-irafnet	1.1_1	Provides a flexible integrative algorithm that allows information from prior data, such as protein protein interactions and gene knock-down, to be jointly considered for gene regulatory network inference. / GPL-2	linux-64, osx-64
r-ircor	1.0	Provides implementation of various correlation coefficients of common use in Information Retrieval. In particular, it includes Kendall (1970, isbn:0852641990) tau coefficient as well as tau_a and tau_b for the treatment of ties. It also includes Yilmaz et al. (2008) <doi:10.1145/1390334.1390435> tauAP correlation coefficient, and versions tauAP_a and tauAP_b developed by Urbano and Marrero (2017) <doi:10.1145/3121050.3121106> to cope with ties. / MIT	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-irdisplay</a>	0.7.0	An interface to the rich display capabilities of ‘Jupyter’ front-ends (e.g. ‘Jupyter Notebook’) < <a href="https://jupyter.org">https://jupyter.org</a> >. Designed to be used from a running ‘IRkernel’ session < <a href="https://irkernel.github.io">https://irkernel.github.io</a> >. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-iregression</a>	1.2.1	Contains some important regression methods for interval-valued variables. For each method, it is available the fitted values, residuals and some goodness-of-fit measures. / GPL-2	noarch
<a href="#">r-irepro</a>	1.1	Calculates intraclass correlation coefficient (ICC) for assessing reproducibility of interval-censored data with two repeated measurements (Kovacic and Varnai (2014) <doi:10.1097/EDE.000000000000139>). ICC is estimated by maximum likelihood from model with one fixed and one random effect (both intercepts). Help in model checking (normality of subjects’ means and residuals) is provided. / GPL-3	noarch
<a href="#">r-irg</a>	0.1.1	Fits a double logistic function to NDVI time series and calculates instantaneous rate of green (IRG) according to methods described in Bischoff et al. (2012) <doi:10.1086/667590>. / GPL-3	noarch
<a href="#">r-irishdirectorates</a>	1.4	Provides the dataset and an implementation of the method illustrated in Friel, N., Rastelli, R., Wyse, J. and Raftery, A.E. (2016) <DOI:10.1073/pnas.1606295113>. / GPL-3	linux-64, osx-64
<a href="#">r-irkernel</a>	0.8.15	The R kernel for the ‘Jupyter’ environment executes R code which the front-end (‘Jupyter Notebook’ or other front-ends) submits to the kernel via the network. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-irlba</a>	2.3.3	Fast and memory efficient methods for truncated singular value decomposition and principal components analysis of large sparse and dense matrices. / GPL-3	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-irr</a>	0.84.1	Coefficients of Interrater Reliability and Agreement for quantitative, ordinal and nominal data: ICC, Finn-Coefficient, Robinson’s A, Kendall’s W, Cohen’s Kappa, ... / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-irregular1</a>	1.0.0	Simulation and density evaluation of irregularly sampled stationary AR(1) processes with Gaussian errors using the algorithms described in Allévius (2018) <arXiv:1801.03791>. / GPL-3	linux-64, osx-64
<a href="#">r-irtdemo</a>	0.1.4	Includes a collection of shiny applications to demonstrate or to explore fundamental item response theory (IRT) concepts such as estimation, scoring, and multidimensional IRT models. / GPL-2	noarch
<a href="#">r-irtrees</a>	0.1.0	Helper functions and example data sets accompanying De Boeck, P. and Partchev, I. (2012) IRTrees: Tree-Based Item Response Models of the GLMM Family, Journal of Statistical Software - Code Snippets, 48(1), 1-28. / GPL-2	noarch
<a href="#">r-isa2</a>	0.3.5	The ISA is a biclustering algorithm that finds modules in an input matrix. A module or bicluster is a block of the reordered input matrix. / CC BY-NC-SA 4.0	linux-64, osx-64
<a href="#">r-isat</a>	1.0.5	Reads the output of the ‘PerkinElmer InForm’ software < <a href="http://www.perkinelmer.com/product/inform-cell-analysis-one-seat-cls135781">http://www.perkinelmer.com/product/inform-cell-analysis-one-seat-cls135781</a> >. In addition to cell-density count, it can derive statistics of intercellular spatial distance for each cell-type. / GPL-2	noarch
<a href="#">r-isbf</a>	0.2.1	Selection of features for sparse regression estimation (like the LASSO). Selection of blocks of features when the regression parameter is sparse and constant by blocks (like the Fused-LASSO). Application to cgh arrays. / GPL-3	linux-64, osx-64
<a href="#">r-isco08conversions</a>	0.1.0	Implementation of functions to assign corresponding common job prestige scores (SIOPS, ISEI), the official job or group title and the ISCO-88 code to given ISCO-08 codes. ISCO-08 is the latest version of the International Standard Classification of Occupations which is used to organise information on labour and jobs. / GPL-2	noarch
<a href="#">r-isdals</a>	2.0.4	Provides datasets for Introduction to Statistical Data Analysis for the Life Sciences / GPL-2	noarch
<a href="#">r-isinglenzmc</a>	0.2.5	Classical Ising Model is a land mark system in statistical physics. The model explains the physics of spin glasses and magnetic materials, and cooperative phenomenon in general, for example phase transitions and neural networks. This package provides utilities to simulate one dimensional Ising Model with Metropolis and Glauber Monte Carlo with single flip dynamics in periodic boundary conditions. Utility functions for exact solutions are provided. / GPL-3	linux-64, osx-64
<a href="#">r-isingsampler</a>	0.2	Sample states from the Ising model and compute the probability of states. Sampling can be done for any number of nodes, but due to the intractability of the Ising model the distribution can only be computed up to ~10 nodes. / GPL-2	linux-64, osx-64
<a href="#">r-island</a>	0.2.4	Tools to develop stochastic models based on the Theory of Island Biogeography (TIB) of MacArthur and Wilson (1967) <DOI:10.1023/A:1016393430551> and extensions. The package implements methods to estimate colonization and extinction rates (including environmental variables) given presence-absence data, simulate community assembly, and perform model selection. / GPL-3	linux-64, osx-64

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Name	Version	Summary/License	Platforms
r-islasso	1.1.0	An implementation of the induced smoothing (IS) idea to lasso regularization models to allow estimation and inference on the model coefficients (currently hypothesis testing only). Linear, logistic, Poisson and gamma regressions with several link functions are implemented. The algorithm is described in the original paper: Cilluffo, G., Sottile, G., La Grutta, S. and Muggeo, V. (2019) The Induced Smoothed lasso: A practical framework for hypothesis testing in high dimensional regression. <doi:10.1177/0962280219842890>, and discussed in a tutorial: Sottile, G., Cilluffo, G., and Muggeo, V. (2019) The R package islasso: estimation and hypothesis testing in lasso regression. <doi:10.13140/RG.2.2.16360.11521>. / GPL-2	linux-64, win-64
r-islr	1.2	We provide the collection of data-sets used in the book ‘An Introduction to Statistical Learning with Applications in R’. / GPL-2	noarch
r-ism	0.1.0	The development of ISM was made by Warfield in 1974. ISM is the process of collaborating distinct or related essentials into a simplified and an organized format. Hence, ISM is a methodology that seeks the interrelationships among the various elements considered and endows with a hierarchical and multilevel structure. To run this package user needs to provide a matrix (VAXO) converted into 0's and 1's. Warfield,J.N. (1974) <doi:10.1109/TSMC.1974.5408524> Warfield,J.N. (1974, E-ISSN:2168-2909). / GPL-3	noarch
r-ismev	1.42	Functions to support the computations carried out in ‘An Introduction to Statistical Modeling of Extreme Values’ by Stuart Coles. The functions may be divided into the following groups; maxima/minima, order statistics, peaks over thresholds and point processes. / GPL-2	noarch
r-isnullptr	1.0.1	Check if an ‘externalptr’ is a null pointer. R does currently not have a native function for that purpose. This package contains a C function that returns TRUE in case of a null pointer. / GPL-3	linux-64, win-64
r-iso	0.0_18	Linear order and unimodal order (univariate) isotonic regression; bivariate isotonic regression with linear order on both variables. / GPL-2	linux-64, win-64
r-isoband	0.2.0	A fast C implementation to generate contour lines (isolines) and contour polygons (isobands) from regularly spaced grids containing elevation data. / MIT	linux-64, win-64
r-isoci	1.1	Some functions for confidence intervals for current status data based on transformations and bootstrap. / GPL-2	noarch
r-isocodes	2019.05.02	ISO language, territory, currency, script and character codes. Provides ISO 639 language codes, ISO 3166 territory codes, ISO 4217 currency codes, ISO 15924 script codes, and the ISO 8859 character codes as well as the UN M.49 area codes. / GPL-2	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-isopat	1.0	The function calculates the isotopic pattern (fine structures) for a given chemical formula. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-isoplotr</a>	3.0	Plots U-Pb data on Wetherill and Tera-Wasserburg concordia diagrams. Calculates concordia and discordia ages. Performs linear regression of measurements with correlated errors using ‘York’, ‘Titterton’ and ‘Ludwig’ approaches. Generates Kernel Density Estimates (KDEs) and Cumulative Age Distributions (CADs). Produces Multidimensional Scaling (MDS) configurations and Shepard plots of multi-sample detrital datasets using the Kolmogorov-Smirnov distance as a dissimilarity measure. Calculates $^{40}\text{Ar}/^{39}\text{Ar}$ ages, isochrons, and age spectra. Computes weighted means accounting for overdispersion. Calculates U-Th-He (single grain and central) ages, logratio plots and ternary diagrams. Processes fission track data using the external detector method and LA-ICP-MS, calculates central ages and plots fission track and other data on radial (a.k.a. ‘Galbraith’) plots. Constructs total Pb-U, Pb-Pb, K-Ca, Re-Os, Sm-Nd, Lu-Hf, Rb-Sr and $^{230}\text{Th}$ -U isochrons as well as $^{230}\text{Th}$ -U evolution plots. / GPL-3	noarch
<a href="#">r-isospecr</a>	2.0.1	IsoSpec is a fine structure calculator used for obtaining the most probable masses of a chemical compound given the frequencies of the composing isotopes and their masses. It finds the smallest set of isotopologues with a given probability. The probability is assumed to be that of the product of multinomial distributions, each corresponding to one particular element and parametrized by the frequencies of finding these elements in nature. These numbers are supplied by IUPAC - the International Union of Pure and Applied Chemistry. / BSD_2_clause	linux-64
<a href="#">r-isotonic.pen</a>	1.0	Given a response y and a one- or two-dimensional predictor, the isotonic regression estimator is calculated with the usual orderings. / GPL-2   GPL-3	noarch
<a href="#">r-isoweek</a>	0.6_2	This is an substitute for the %V and %u formats which are not implemented on Windows. In addition, the package offers functions to convert from standard calender format yyyy-mm-dd to and from ISO 8601 week format yyyy-Www-d. / GPL-2	noarch
<a href="#">r-isqg</a>	1.2	Accomplish high performance simulations in quantitative genetics. The molecular genetic components are represented by R6/C classes and methods. Mimic the meiosis recombination and de novo genetic variability by means a count-location process (Karlin & Liberman, 1978) <doi:10.1073/pnas.75.12.6332>. The core computational algorithm is implemented using ‘Boost’ dynamic bitsets (Schaling, 2014) [ISBN:978-1937434366]. A mix between low and high level interfaces provides great flexibility and allows user defined extensions and a wide range of applications. / GPL-2	linux-64, win-64
<a href="#">r-isr3</a>	0.98	Performs multivariate normal imputation through iterative sequential regression. Conditional dependency structure between imputed variables can be specified a priori to accelerate imputation. / Unlimited	linux-64, win-64
<a href="#">r-istacr</a>	0.1.0	You can access to open data published in Instituto Canario De Estadística (ISTAC) APIs at < <a href="https://www.gobiernodecanarias.org/istac/api/">https://www.gobiernodecanarias.org/istac/api/</a> >. / GPL-3	noarch
<a href="#">r-iswr</a>	2.0_7	Data sets and scripts for text examples and exercises in P. Dalgaard (2008), ‘Introductory Statistics with R’, 2nd ed., Springer Verlag, ISBN 978-0387790534. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-italy</a>	0.1.0	Provides two record linkage data sets on the Italian Survey on Household and Wealth, 2008 and 2010, a sample survey conducted by the Bank of Italy every two years. The 2010 survey covered 13,702 individuals, while the 2008 survey covered 13,734 individuals. The following categorical variables are included in this data set: year of birth, working status, employment status, branch of activity, town size, geographical area of birth, sex, whether or not Italian national, and highest educational level obtained. Unique identifiers are available to assess the accuracy of oneâ€™s method. Please see Steorts (2015) <DOI:10.1214/15-BA965SI> to find more details about the data set. / CC0	noarch
<a href="#">r-iterators</a>	1.0.10	Support for iterators, which allow a programmer to traverse through all the elements of a vector, list, or other collection of data. / Apache License (== 2.0)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-iterpc</a>	0.4.1	Iterator for generating permutations and combinations. They can be either drawn with or without replacement, or with distinct/ non-distinct items (multi-set). The generated sequences are in lexicographical order (dictionary order). The algorithms to generate permutations and combinations are memory efficient. These iterative algorithms enable users to process all sequences without putting all results in the memory at the same time. The algorithms are written in C/C for faster performance. Note: ‘iterpc’ is no longer being maintained. Users are recommended to switch to ‘arrangements’. / GPL-2	noarch
<a href="#">r-itertools</a>	0.1.3	Various tools for creating iterators, many patterned after functions in the Python itertools module, and others patterned after functions in the ‘snow’ package. / GPL-2	noarch
<a href="#">r-itertools2</a>	0.1.1	A port of Python’s excellent itertools module to R for efficient looping. / MIT	noarch
<a href="#">r-itop</a>	1.0.2	Infers a topology of relationships between different datasets, such as multi-omics and phenotypic data recorded on the same samples. We based this methodology on the RV coefficient (Robert & Escoufier, 1976, <doi:10.2307/2347233>), a measure of matrix correlation, which we have extended for partial matrix correlations and binary data (Aben et al., 2018, <doi:10.1101/293993>). / GPL-2	noarch
<a href="#">r-ityree</a>	0.1	This package is based on the code of the rpart package. It extends rpart by adding additional splitting methods emphasizing interpretable/parsimonious trees. Unless indicated otherwise, it is safe to assume that all functions herein are extensions of or copied directly from similar or nearly identical rpart methods. As such, the authors of rpart are authors of this package as well. However, please direct any error reports or other questions about itree to the maintainer of this package; they are welcome and appreciated. / GPL-2   GPL-3	linux-64, win-64

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Name	Version	Summary/License	Platforms
r-itrllearn	1.0_1	Maximin-projection learning (MPL, Shi, et al., 2018) is implemented for recommending a meaningful and reliable individualized treatment regime for future groups of patients based on the observed data from different populations with heterogeneity in individualized decision making. Q-learning and A-learning are implemented for estimating the groupwise contrast function that shares the same marginal treatment effects. The packages contains classical Q-learning and A-learning algorithms for a single stage study as a byproduct. More functions will be added at later versions. / GPL-2	linux-64, win-64
r-itsmr	1.9	Provides functions for modeling and forecasting time series data. Forecasting is based on the innovations algorithm. A description of the innovations algorithm can be found in the textbook Introduction to Time Series and Forecasting by Peter J. Brockwell and Richard A. Davis. < <a href="http://www.springer.com/us/book/9781475777505">http://www.springer.com/us/book/9781475777505</a> >. / FreeBSD	noarch
r-itunesr	0.1.3	To enable ‘iOS’ App Developers to access iTunes App Store Ratings and Reviews using R to extract Basic App Information and Reviews submitted by their App users, Since Apple Store does not provide this straightforward. / CC0	noarch
r-ivfixed	1.0	Fit an Instrumental least square dummy variable model / Artistic-2.0	noarch
r-ivpanel	1.0	Fit the instrumental panel data models: the fixed effects, random effects and between models. / GPL-3	noarch
r-ivprobit	1.1	Compute the instrumental variables probit model using the Amemiya’s Generalized Least Squares estimators (Amemiya, Takeshi, (1978) <doi: 10.2307/1911443>). / GPL-3	noarch
r-jaatha	3.2.1	An estimation method that can use computer simulations to approximate maximum-likelihood estimates even when the likelihood function can not be evaluated directly. It can be applied whenever it is feasible to conduct many simulations, but works best when the data is approximately Poisson distributed. It was originally designed for demographic inference in evolutionary biology. It has optional support for conducting coalescent simulation using the ‘coala’ package. / GPL-3	noarch
r-jacobieigen	0.3_3	Implements the classical Jacobi algorithm for the eigenvalues and eigenvectors of a real symmetric matrix, both in pure ‘R’ and in ‘C’ using ‘Rcpp’. Mainly as a programming example for teaching purposes. / GPL-2	linux-64, win-64
r-jacpop	0.6	Uses the Jaccard similarity index to account for population structure in sequencing studies. This method was specifically designed to detect population stratification based on rare variants, hence it will be especially useful in rare variant analysis. / GPL-3	noarch
r-jade	2.0_2	Cardoso’s JADE algorithm as well as his functions for joint diagonalization are ported to R. Also several other blind source separation (BSS) methods, like AMUSE and SOBI, and some criteria for performance evaluation of BSS algorithms, are given. The package is described in Miettinen, Nordhausen and Taskinen (2017) <doi:10.18637/jss.v076.i02>. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-jaggr	0.1.1	All the data and functions used to produce the book. We do not expect most people to use the package for any other reason than to get simple access to the ‘JAGS’ model files, the data, and perhaps run some of the simple examples. The authors of the book are David Lucy (now sadly deceased) and James Curran. It is anticipated that a manuscript will be provided to Taylor and Francis around February 2020, with bibliographic details to follow at that point. Until such time, further information can be obtained by emailing James Curran. / GPL-2	noarch
r-jaguar	3.0.1	Implements a novel score test that measures 1) the overall shift in the gene expression due to genotype (additive genetic effect), and 2) group-specific changes in gene expression due to genotype (interaction effect) in a mixed-effects model framework. / GPL-2	linux-64, osx-64, win-64
r-janeaustenr	0.1.5	Full texts for Jane Austen’s 6 completed novels, ready for text analysis. These novels are Sense and Sensibility, Pride and Prejudice, Mansfield Park, Emma, Northanger Abbey, and Persuasion. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-jaspar	0.0.1	R modules for JASPAR data processing and visualization / GPL-2	linux-64, osx-64, win-64
r-jep	1.0	Procedures for joint detection of changes in both expectation and variance in univariate sequences. Performs a statistical test of the null hypothesis of the absence of change points. In case of rejection performs an algorithm for change point detection. References - Bivariate change point detection (2019), Michael Messer. / GPL-3	noarch
r-jdmbms	1.3	Black-Scholes model [Black (1973) <doi:10.1086/260062>] is important to calculate option prices in the stock market and a variety of improved models are studied. In this package, I propose methods in order to calculate both Black-Scholes model and Jump diffusion model [Kou (2002) <doi:10.1287/mnsc.48.8.1086.166>] by Monte Carlo methods. This package can be used for computational finance. / GPL-2	noarch
r-jdx	0.1.3	Simplifies and extends data exchange between ‘R’ and ‘Java’. / GPL-2   BSD_3_clause	noarch

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Name	Version	Summary/License	Platforms
r-jeek	1.1.1	Provides a fast and scalable joint estimator for integrating additional knowledge in learning multiple related sparse Gaussian Graphical Models (JEEK). The JEEK algorithm can be used to fast estimate multiple related precision matrices in a large-scale. For instance, it can identify multiple gene networks from multi-context gene expression datasets. By performing data-driven network inference from high-dimensional and heterogeneous data sets, this tool can help users effectively translate aggregated data into knowledge that take the form of graphs among entities. Please run <code>demo(jeek)</code> to learn the basic functions provided by this package. For further details, please read the original paper: Beilun Wang, Arshdeep Sekhon, Yanjun Qi A Fast and Scalable Joint Estimator for Integrating Additional Knowledge in Learning Multiple Related Sparse Gaussian Graphical Models (ICML 2018) <arXiv:1806.00548>. / GPL-2	noarch
r-jenkins	1.0	Manage jobs and builds on your Jenkins CI server < <a href="https://jenkins.io/">https://jenkins.io/</a> >. Create and edit projects, schedule builds, manage the queue, download build logs, and much more. / MIT	noarch
r-jetpack	0.4.3	Manage project dependencies from your DESCRIPTION file. Create a reproducible virtual environment with minimal additional files in your project. Provides tools to add, remove, and update dependencies as well as install existing dependencies with a single function. / MIT	noarch
r-jgl	2.3.1	The Joint Graphical Lasso is a generalized method for estimating Gaussian graphical models/ sparse inverse covariance matrices/ biological networks on multiple classes of data. We solve JGL under two penalty functions: The Fused Graphical Lasso (FGL), which employs a fused penalty to encourage inverse covariance matrices to be similar across classes, and the Group Graphical Lasso (GGL), which encourages similar network structure between classes. FGL is recommended over GGL for most applications. Reference: Danaher P, Wang P, Witten DM. (2013) <doi:10.1111/rssb.12033>. / GPL-2	noarch
r-jiebard	0.1	jiebaR is a package for Chinese text segmentation, keyword extraction and speech tagging. This package provides the data files required by jiebaR. / MIT	noarch
r-jjb	0.1.0	Set of common functions used for manipulating colors, detecting and interacting with 'RStudio', modeling, formatting, determining users' operating system, feature scaling, and more! / GPL-2	noarch
r-jlctree	0.0.1	Implements the tree-based approach to joint modeling of time-to-event and longitudinal data. This approach looks for a tree-based partitioning such that within each estimated latent class defined by a terminal node, the time-to-event and longitudinal responses display a lack of association. See Zhang and Simonoff (2018) <arXiv:1812.01774>. / GPL-3	noarch
r-jm	1.4_8	Shared parameter models for the joint modeling of longitudinal and time-to-event data. / GPL-2	noarch
r-jmdesign	1.1	Performs power calculations for joint modeling of longitudinal and survival data with k-th order trajectories when the variance-covariance matrix, Sigma_theta, is unknown. / GPL-2	noarch
r-jmdl	0.3.0	Fit joint mean-correlation models for discrete longitudinal data (Tang CY,Zhang W, Leng C, 2017 <doi:10.5705/ss.202016.0435>). / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-jmetrik	1.1	The main purpose of this package is to make it easy for userR's to interact with 'jMetrik' an open source application for psychometric analysis. For example it allows userR's to write data frames to file in a format that can be used by 'jMetrik'. It also allows userR's to read *.jmetrik files (e.g. output from an analysis) for follow-up analysis in R. The *.jmetrik format is a flat file that includes a multiline header and the data as comma separated values. The header includes metadata about the file and one row per variable with the following information in each row: variable name, data type, item scoring, special data codes, and variable label. / GPL-3	noarch
r-jmi	0.1.0	Computes the Jackknife Mutual Information (JMI) between two random vectors and provides the p-value for dependence tests. See Zeng, X., Xia, Y. and Tong, H. (2018) <doi:10.1073/pnas.1715593115>. / GPL-2	linux-64, osx-64, win-64
r-jmisc	0.3.1	Some handy function in R / GPL-2	noarch
r-jmotif	1.0.3	Implements time series z-normalization, SAX, HOT-SAX, VSM, SAX-VSM, RePair, and RRA algorithms facilitating time series motif (i.e., recurrent pattern), discord (i.e., anomaly), and characteristic pattern discovery along with interpretable time series classification. / GPL-2	linux-64, osx-64, win-64
r-jmuoutlier	2.2	Performs a permutation test on the difference between two location parameters, a permutation correlation test, a permutation F-test, the Siegel-Tukey test, a ratio mean deviance test. Also performs some graphing techniques, such as for confidence intervals, vector addition, and Fourier analysis; and includes functions related to the Laplace (double exponential) and triangular distributions. Performs power calculations for the binomial test. / GPL-3	noarch
r-jmvcore	1.0.0	A framework for creating rich interactive analyses for the jamovi platform (see < <a href="https://www.jamovi.org">https://www.jamovi.org</a> > for more information). / GPL-2	noarch
r-johnson	1.4	RE.Johnson performs the Johnson Transformation to increase the normality. / GPL-2	noarch
r-joint.cox	3.5	Perform likelihood estimation and dynamic prediction under joint frailty-copula models for tumour progression and death in meta-analysis. A penalized likelihood method is employed for estimating model parameters, where the baseline hazard functions are modeled by smoothing splines. The methods are applicable for meta-analytic data combining several studies. The methods can analyze data having information on both terminal event time (e.g., time-to-death) and non-terminal event time (e.g., time-to-tumour progression). See Emura et al. (2017) <doi:10.1177/0962280215604510> for likelihood estimation, and Emura et al. (2018) <doi:10.1177/0962280216688032> for dynamic prediction. More details on these methods can also be found in a book of Emura et al. (2019) <10.1007/978-981-13-3516-7>. Survival data from ovarian cancer patients are also available. / GPL-2	noarch
r-jointdiag	0.3	Different algorithms to perform approximate joint diagonalization of a finite set of square matrices. Depending on the algorithm, orthogonal or non-orthogonal diagonalizer is found. These algorithms are particularly useful in the context of blind source separation. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-jointmix	1.0	Fits univariate and joint N-mixture models for data on two unmarked site-associated species. Includes functions to estimate latent abundances through empirical Bayes methods. / GPL-2	noarch
r-jointpm	2.3.1	A bivariate integration method to estimate risk caused by two extreme and dependent forcing variables. / GPL-2	noarch
r-josae	0.3.0	Implementation of some unit and area level EBLUP estimators as well as the estimators of their MSE also under heteroscedasticity. The package further documents the publications Breidenbach and Astrup (2012) <DOI:10.1007/s10342-012-0596-7>, Breidenbach et al. (2016) <DOI:10.1016/j.rse.2015.07.026> and Breidenbach et al. (2018 in press). The vignette further explains the use of the implemented functions. / GPL-2	noarch
r-josaplay	0.1.3	Josa in Korean is often determined by judging the previous word. When writing reports using Rmd, a function that prints the appropriate investigation for each case is helpful. The ‘josaplay’ package then evaluates the previous word to determine which josa is appropriate. / MIT	noarch
r-jose	1.0	Read and write JSON Web Keys (JWK, rfc7517), generate and verify JSON Web Signatures (JWS, rfc7515) and encode/decode JSON Web Tokens (JWT, rfc7519). These standards provide modern signing and encryption formats that are the basis for services like OAuth 2.0 or LetsEncrypt and are natively supported by browsers via the JavaScript WebCryptoAPI. / MIT	noarch
r-jousboost	2.1.0	Implements under/oversampling for probability estimation. To be used with machine learning methods such as AdaBoost, random forests, etc. / MIT	linux-64, osx-64, win-64
r-jpeg	0.1_8	This package provides an easy and simple way to read, write and display bitmap images stored in the JPEG format. It can read and write both files and in-memory raw vectors. / GPL-2   GPL-3	linux-32, linux-64, osx-64, win-32, win-64
r-jpen	1.0	A Joint PENalty Estimation of Covariance and Inverse Covariance Matrices. / GPL-2	noarch
r-jqr	1.1.0	Client for ‘jq’, a ‘JSON’ processor (< <a href="https://stedolan.github.io/jq/">https://stedolan.github.io/jq/</a> >), written in C. ‘jq’ allows the following with ‘JSON’ data: index into, parse, do calculations, cut up and filter, change key names and values, perform conditionals and comparisons, and more. / MIT	win-64
r-jrc	0.1.1	An ‘httpuv’ based bridge between R and ‘JavaScript’. Provides an easy way to exchange commands and data between a web page and a currently running R session. / GPL-3	noarch
r-jrf	0.1_4	Simultaneous estimation of multiple related networks. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-jrich</a>	0.60.3	These functions calculate the taxonomic measures presented in Miranda-Esquivel (2016). The package introduces Jack-knife resampling in evolutionary distinctiveness prioritization analysis, as a way to evaluate the support of the ranking in area prioritization, and the persistence of a given area in a conservation analysis. The algorithm is described in: Miranda-Esquivel, D (2016) <DOI:10.1007/978-3-319-22461-9_11>. / GPL-3	noarch
<a href="#">r-jrvfinance</a>	1.4.1	Implements the basic financial analysis functions similar to (but not identical to) what is available in most spreadsheet software. This includes finding the IRR and NPV of regularly spaced cash flows and annuities. Bond pricing and YTM calculations are included. In addition, Black Scholes option pricing and Greeks are also provided. / GPL-2	noarch
<a href="#">r-json64</a>	0.1.3	Encode/Decode 'base64', with support for JSON format, using two functions: j_encode() and j_decode(). 'Base64' is a group of similar binary-to-text encoding schemes that represent binary data in an ASCII string format by translating it into a radix-64 representation, used when there is a need to encode binary data that needs to be stored and transferred over media that are designed to deal with textual data, ensuring that the data will remain intact and without modification during transport. < <a href="https://developer.mozilla.org/en-US/docs/Web/API/WindowBase64/Base64_encoding_and_decoding">https://developer.mozilla.org/en-US/docs/Web/API/WindowBase64/Base64_encoding_and_decoding</a> > On the other side, JSON (JavaScript Object Notation) is a lightweight data-interchange format. Easy to read, write, parse and generate. It is based on a subset of the JavaScript Programming Language. JSON is a text format that is completely language independent but uses conventions that are familiar to programmers of the C-family of languages, including C, C#, Java, JavaScript, Perl, Python, and many others. JSON structure is built around name:value pairs and ordered list of values. < <a href="https://www.json.org">https://www.json.org</a> > The first function, j_encode(), let you transform a data.frame or list to a 'base64' encoded JSON (or JSON string). The j_decode() function takes a 'base64' string (could be an encoded JSON) and transform it to a data.frame (or list, depending of the JSON structure). / MIT	noarch
<a href="#">r-jsonarr</a>	1.1.1	This package enables users to access MongoDB by running queries and returning their results in R data frames. Usually, data in MongoDB is only available in the form of a JSON document. jSonarR uses data processing and conversion capabilities in the jSonar Analytics Platform and the JSON Studio Gateway ( <a href="http://www.jsonstudio.com">http://www.jsonstudio.com</a> ), to convert it to a tabular format which is easy to use with existing R packages. / AGPL-3	noarch
<a href="#">r-jsonlite</a>	1.6	A fast JSON parser and generator optimized for statistical data and the web. Started out as a fork of 'RJSONIO', but has been completely rewritten in recent versions. The package offers flexible, robust, high performance tools for working with JSON in R and is particularly powerful for building pipelines and interacting with a web API. The implementation is based on the mapping described in the vignette (Ooms, 2014). In addition to converting JSON data from/to R objects, 'jsonlite' contains functions to stream, validate, and prettify JSON data. The unit tests included with the package verify that all edge cases are encoded and decoded consistently for use with dynamic data in systems and applications. / MIT file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-jstree</a>	1.0.1	Create and customize interactive trees using the 'jQuery' 'jsTree' < <a href="https://www.jstree.com/">https://www.jstree.com/</a> > plugin library and the 'htmlwidgets' package. These trees can be used directly from the R console, from 'RStudio', in Shiny apps and R Markdown documents. / GPL-2   GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-jtgwas</a>	1.5.1	The core of this ‘Rcpp’ based package is a function to compute standardized Jonckheere-Terpstra test statistics for large numbers of dependent and independent variables, e.g., genome-wide analysis. It implements ‘OpenMP’, allowing the option of computing on multiple threads. Supporting functions are also provided to calculate p-values and summarize results. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-jtrans</a>	0.2.1	Transforming univariate non-normal data to normality using Johnson families of distributions. Johnson family is a comprehensive distribution family that accommodates many kinds of non-normal distributions. A bunch of distributions with various parameters will be fit and the corresponding p-values under a user-specified normality test will be given. The final transformation will be the one with the largest p-value under the given normality test. / GPL-2	noarch
<a href="#">r-julia</a>	1.1	Generates image data for fractals (Julia and Mandelbrot sets) on the complex plane in the given region and resolution. / GPL-3	noarch
<a href="#">r-juliacall</a>	0.16.6	Provides an R interface to ‘Julia’, which is a high-level, high-performance dynamic programming language for numerical computing, see < <a href="https://julialang.org/">https://julialang.org/</a> > for more information. It provides a high-level interface as well as a low-level interface. Using the high level interface, you could call any ‘Julia’ function just like any R function with automatic type conversion. Using the low level interface, you could deal with C-level SEXP directly while enjoying the convenience of using a high-level programming language like ‘Julia’. / MIT	linux-64, osx-64, win-64
<a href="#">r-jumptest</a>	1.1	A fast simulation on stochastic volatility model, with jump tests, p-values pooling, and FDR adjustments. / MIT	linux-64, osx-64, win-64
<a href="#">r-junctions</a>	1.1	Individual based simulations of hybridizing populations, where the accumulation of junctions is tracked. Furthermore, mathematical equations are provided to verify simulation outcomes. Both simulations and mathematical equations are based on Janzen (2018) <doi:10.1101/058107>. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-junr</a>	0.1.3	The ‘Junar’ API is a commercial platform to organize and publish data < <a href="http://www.junar.com">http://www.junar.com</a> >. It has been used in a number of national and local government Open Data initiatives in Latin America and the USA. This package is a wrapper to make it easier to access data made public through the ‘Junar’ API. / MIT	noarch
<a href="#">r-jvcoords</a>	1.0.2	Provides functions to standardize and whiten data, and to perform Principal Component Analysis (PCA). The main advantage of this package over alternatives like prcomp() is, that jvcoords makes it easy to convert (additional) data between the original and the transformed coordinates. The package also provides a class coords, which can represent affine coordinate transformations. This class forms the basis of the transformations provided by the package, but can also be used independently. The implementation has been optimized to be of comparable speed (and sometimes even faster) than existing alternatives. / GPL-3	noarch
<a href="#">r-jvnvar</a>	1.0	Many method to compute, predict and back-test VaR. For more detail, see the report: Value at Risk < <a href="https://researchgate.net">researchgate.net</a> >. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-jwutil</a>	1.2.3	This is a set of simple utilities for various data manipulation and testing tasks. The goal is to use core R tools well, without bringing in many dependencies. Main areas of interest are semi-automated data frame manipulation, such as converting factors in multiple binary indicator columns. There are testing functions which provide ‘testthat’ expectations to permute arguments to function calls. There are functions and data to test extreme numbers, dates, and bad input of various kinds which should allow testing failure and corner cases, which can be used for fuzzing your functions. The test suite has many examples of usage. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-kader</a>	0.0.8	Implementation of various kernel adaptive methods in nonparametric curve estimation like density estimation as introduced in Stute and Srihera (2011) <doi:10.1016/j.spl.2011.01.013> and Eichner and Stute (2013) <doi:10.1016/j.jspi.2012.03.011> for pointwise estimation, and like regression as described in Eichner and Stute (2012) <doi:10.1080/10485252.2012.760737>. / GPL-3	noarch
<a href="#">r-kamila</a>	0.1.1	Implements methods for clustering mixed-type data, specifically combinations of continuous and nominal data. Special attention is paid to the often-overlooked problem of equitably balancing the contribution of the continuous and categorical variables. This package implements KAMILA clustering, a novel method for clustering mixed-type data in the spirit of k-means clustering. It does not require dummy coding of variables, and is efficient enough to scale to rather large data sets. Also implemented is Modha-Spangler clustering, which uses a brute-force strategy to maximize the cluster separation simultaneously in the continuous and categorical variables. For more information, see Foss, Markatou, Ray, & Heching (2016) <doi:10.1007/s10994-016-5575-7> and Foss & Markatou (2018) <doi:10.18637/jss.v083.i13>. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-kaphom</a>	0.3	Tests the homogeneity of intraclass kappa statistics obtained from independent studies or a stratified study with binary results. It is desired to compare the kappa statistics obtained in multi-center studies or in a single stratified study to give a common or summary kappa using all available information. If the homogeneity test of these kappa statistics is not rejected, then it is possible to make inferences over a single kappa statistic that summarizes all the studies. Muammer Albayrak, Kemal Turhan, Yasemin Yavuz, Zeliha Aydin Kasap (2019) <doi:10.1080/03610918.2018.1538457> Jun-mo Nam (2003) <doi:10.1111/j.0006-341X.2003.00118.x> Jun-mo Nam (2005) <doi:10.1002/sim.2321> Mousumi Banerjee, Michelle Capozzoli, Laura McSweeney, Debajyoti Sinha (1999) <doi:10.2307/3315487> Allan Donner, Michael Eliasziw, Neil Klar (1996) <doi:10.2307/2533154>. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-kappalab	0.4.7	S4 tool box for capacity (or non-additive measure, fuzzy measure) and integral manipulation in a finite setting. It contains routines for handling various types of set functions such as games or capacities. It can be used to compute several non-additive integrals: the Choquet integral, the Sugeno integral, and the symmetric and asymmetric Choquet integrals. An analysis of capacities in terms of decision behavior can be performed through the computation of various indices such as the Shapley value, the interaction index, the orness degree, etc. The well-known Möbius transform, as well as other equivalent representations of set functions can also be computed. Kappalab further contains seven capacity identification routines: three least squares based approaches, a method based on linear programming, a maximum entropy like method based on variance minimization, a minimum distance approach and an unsupervised approach based on parametric entropies. The functions contained in Kappalab can for instance be used in the framework of multicriteria decision making or cooperative game theory. / CeCILL	linux-64, osx-64, win-64
r-kappasize	1.2	Contains basic tools for sample size estimation in studies of interobserver/interrater agreement (reliability). Includes functions for both the power-based and confidence interval-based methods, with binary or multinomial outcomes and two through six raters. / GPL-2	noarch
r-kaps	1.0.2	This package provides some routines to conduct the K-adaptive partitioning (kaps) algorithm for survival data. A function kaps is an implementation version of our algorithm. / GPL-3	linux-64, osx-64, win-64
r-kdensity	1.0.1	Handles univariate non-parametric density estimation with parametric starts and asymmetric kernels in a simple and flexible way. Kernel density estimation with parametric starts involves fitting a parametric density to the data before making a correction with kernel density estimation, see Hjort & Glad (1995) <doi:10.1214/aos/1176324627>. Asymmetric kernels make kernel density estimation more efficient on bounded intervals such as (0, 1) and the positive half-line. Supported asymmetric kernels are the gamma kernel of Chen (2000) <doi:10.1023/A:1004165218295>, the beta kernel of Chen (1999) <doi:10.1016/S0167-9473(99)00010-9>, and the copula kernel of Jones & Henderson (2007) <doi:10.1093/biomet/asm068>. User-supplied kernels, parametric starts, and bandwidths are supported. / MIT	noarch
r-kdist	0.2	Density, distribution function, quantile function and random generation for the K-distribution. A plotting function that plots data on Weibull paper and another function to draw additional lines. See results from package in T Lamont-Smith (2018), submitted J. R. Stat. Soc. / GPL-3	noarch
r-kedd	1.0.3	Smoothing techniques and computing bandwidth selectors of the nth derivative of a probability density for one-dimensional data. / GPL-2	noarch
r-keep	1.0	Provides arrays with flexible control over dimension dropping when subscripting. / GPL-3	noarch
r-kendall	2.2	Computes the Kendall rank correlation and Mann-Kendall trend test. See documentation for use of block bootstrap when there is autocorrelation. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-kendl</a>	1.1	Calculate the kernel-smoothed nonparametric estimator for the exposure distribution in presence of detection limits. / GPL-2	noarch
<a href="#">r-keras</a>	2.2.4	Interface to ‘Keras’ < <a href="https://keras.io">https://keras.io</a> >, a high-level neural networks ‘API’. ‘Keras’ was developed with a focus on enabling fast experimentation, supports both convolution based networks and recurrent networks (as well as combinations of the two), and runs seamlessly on both ‘CPU’ and ‘GPU’ devices. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-64
<a href="#">r-kerasr</a>	0.6.1	Provides a consistent interface to the ‘Keras’ Deep Learning Library directly from within R. ‘Keras’ provides specifications for describing dense neural networks, convolution neural networks (CNN) and recurrent neural networks (RNN) running on top of either ‘TensorFlow’ or ‘Theano’. Type conversions between Python and R are automatically handled correctly, even when the default choices would otherwise lead to errors. Includes complete R documentation and many working examples. / LGPL-2	noarch
<a href="#">r-kere</a>	1.0.0	An efficient algorithm inspired by majorization-minimization principle for solving the entire solution path of a flexible nonparametric expectile regression estimator constructed in a reproducing kernel Hilbert space. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-kerndwd</a>	2.0.2	A novel implementation that solves the linear distance weighted discrimination and the kernel distance weighted discrimination. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-kernelknn</a>	1.1.0	Extends the simple k-nearest neighbors algorithm by incorporating numerous kernel functions and a variety of distance metrics. The package takes advantage of ‘RcppArmadillo’ to speed up the calculation of distances between observations. / MIT	linux-64, osx-64, win-64
<a href="#">r-kernlab</a>	0.9_2	Kernel-based machine learning methods for classification, regression, clustering, novelty detection, quantile regression and dimensionality reduction. Among other methods ‘kernlab’ includes Support Vector Machines, Spectral Clustering, Kernel PCA, Gaussian Processes and a QP solver. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-kernscr</a>	1.0.5	Kernel Machine Score Test for Pathway Analysis in the Presence of Semi-Competing Risks. Method is detailed in: Neykov, Hejblum & Sinnott (2018) <doi: 10.1177/0962280216653427>. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-kernsmooth</a>	2.23	Functions for kernel smoothing (and density estimation) corresponding to the book: Wand, M.P. and Jones, M.C. (1995) Kernel Smoothing. / Unlimited	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-kexpmv</a>	0.0.3	Implements functions from ‘EXPOKIT’ (< <a href="https://www.maths.uq.edu.au/expokit/">https://www.maths.uq.edu.au/expokit/</a> >) to calculate matrix exponentials, Sidje RB, (1998) <doi:10.1145/285861.285868>. Includes functions for small dense matrices along with functions for large sparse matrices. The functions for large sparse matrices implement Krylov subspace methods which help minimise the computational complexity for matrix exponentials. ‘Kexpmv’ can be utilised to calculate both the matrix exponential in isolation along with the product of the matrix exponential and a vector. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-keyboardsimulator</a>	2.1.0	Control your keyboard and mouse with R code by simulating key presses and mouse clicks. The input simulation is implemented with the Windows API. / GPL-2	win-64
<a href="#">r-keypress</a>	1.1.1	Wait for a single key press at the ‘R’ prompt. This works in terminals, but does not currently work in the ‘Windows’ ‘GUI’, the ‘OS X’ ‘GUI’ (‘R.app’), in ‘Emacs’ ‘ESS’, in an ‘Emacs’ shell buffer or in ‘R Studio’. In these cases ‘keypress’ stops with an error message. / MIT	linux-64, osx-64, win-64
<a href="#">r-keyringr</a>	0.4.0	Decrypts passwords stored in the Gnome Keyring, macOS Keychain and strings encrypted with the Windows Data Protection API. / MIT	noarch
<a href="#">r-kfas</a>	1.3.7	State space modelling is an efficient and flexible framework for statistical inference of a broad class of time series and other data. KFAS includes computationally efficient functions for Kalman filtering, smoothing, forecasting, and simulation of multivariate exponential family state space models, with observations from Gaussian, Poisson, binomial, negative binomial, and gamma distributions. See the paper by Helske (2017) <doi:10.18637/jss.v078.i10> for details. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-kfda</a>	1.0.0	Kernel Fisher Discriminant Analysis (KFDA) is performed using Kernel Principal Component Analysis (KPCA) and Fisher Discriminant Analysis (FDA). There are some similar packages. First, ‘lfda’ is a package that performs Local Fisher Discriminant Analysis (LFDA) and performs other functions. In particular, ‘lfda’ seems to be impossible to test because it needs the label information of the data in the function argument. Also, the ‘ks’ package has a limited dimension, which makes it difficult to analyze properly. This package is a simple and practical package for KFDA based on the paper of Yang, J., Jin, Z., Yang, J. Y., Zhang, D., and Frangi, A. F. (2004) <DOI:10.1016/j.patcog.2003.10.015>. / GPL-3	noarch
<a href="#">r-kfigr</a>	1.2	A streamlined cross-referencing system for R Markdown documents generated with ‘knitr’. R Markdown is an authoring format for generating dynamic content from R. ‘kfigr’ provides a hook for anchoring code chunks and a function to cross-reference document elements generated from said chunks, e.g. figures and tables. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-kfksds</a>	1.6	Naive implementation of the Kalman filter, smoother and disturbance smoother for state space models. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-kgc</a>	1.0.0.2	Aids in identifying the Koeppen-Geiger (KG) climatic zone for a given location. The Koeppen-Geiger climate zones were first published in 1884, as a system to classify regions of the earth by their relative heat and humidity through the year, for the benefit of human health, plant and agriculture and other human activity [1]. This climate zone classification system, applicable to all of the earths surface, has continued to be developed by scientists up to the present day. Recently one of use (FZ) has published updated, higher accuracy KG climate zone definitions [2]. In this package we use these updated high-resolution maps as the data source [3]. We provide functions that return the KG climate zone for a given longitude and latitude, or for a given United States zip code. In addition the CZUncertainty() function will check climate zones nearby to check if the given location is near a climate zone boundary. In addition an interactive shiny app is provided to define the KG climate zone for a given longitude and latitude, or United States zip code. Digital data, as well as animated maps, showing the shift of the climate zones are provided on the following website < <a href="http://koeppen-geiger.vu-wien.ac.at">http://koeppen-geiger.vu-wien.ac.at</a> >. This work was supported by the DOE-EERE SunShot award DE-EE-0007140. [1] W. Koeppen, (2011) <doi:10.1127/0941-2948/2011/105>. [2] F. Rubel and M. Kottek, (2010) <doi:10.1127/0941-2948/2010/0430>. [3] F. Rubel, K. Brugger, K. Haslinger, and I. Auer, (2016) <doi:10.1127/metz/2016/0816>. / BSD_2_clause	noarch
<a href="#">r-kidney.epi</a>	1.1.0	Contains kidney care oriented functions. Current version contains only function for calculation of Kidney Donor Risk Index and Kidney Donor Profile Index for kidney transplant donors by Rao et al. (2009) <doi:10.1097/TP.0b013e3181ac620b>. Citation: Bikbov B. R open source programming code for calculation of the Kidney Donor Profile Index and Kidney Donor Risk Index. Kidney Diseases (2018) <doi:10.1159/000492427>. / LGPL-2	noarch
<a href="#">r-kimisc</a>	0.4	A collection of useful functions not found anywhere else, mainly for programming: Pretty intervals, generalized lagged differences, checking containment in an interval, and an alternative interface to assign(). / GPL-3	noarch
<a href="#">r-kin.cohort</a>	0.7	Analysis of kin-cohort studies. kin.cohort provides estimates of age-specific cumulative risk of a disease for carriers and noncarriers of a mutation. The cohorts are retrospectively built from relatives of probands for whom the genotype is known. Currently the method of moments and marginal maximum likelihood are implemented. Confidence intervals are calculated from bootstrap samples. Most of the code is a translation from previous ‘MATLAB’ code by N. Chatterjee. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-kinship2	1.8.4	Routines to handle family data with a pedigree object (2014, <doi: 10.1159/000363105>). The initial purpose was to create correlation structures that describe family relationships such as kinship and identity-by-descent, which can be used to model family data in mixed effects models, such as in the coxme function. Also includes a tool for pedigree drawing which is focused on producing compact layouts without intervention. Recent additions include utilities to trim the pedigree object with various criteria, and kinship for the X chromosome. / GPL-2	noarch
r-kirby21.base	1.7.0	Multi-modal magnetic resonance imaging ('MRI') data from the 'Kirby21' 'reproducibility' study < <a href="https://www.nitrc.org/projects/multimodal/">https://www.nitrc.org/projects/multimodal/</a> >, including functional and structural imaging. / GPL-2	noarch
r-kissmig	1.0.3	Simulating species migration and range dynamics under stable or changing environmental conditions based on a simple, raster-based, stochastic migration model. Providing accessibility for considering species migration in niche-based species distribution models. / GPL-3	linux-64, osx-64, win-64
r-kknn	1.3.1	Weighted k-Nearest Neighbors for Classification, Regression and Clustering. / GPL-2	linux-64, osx-64, win-64
r-klin	2007.01.05	The package implements efficient ways to evaluate and solve equations of the form $Ax=b$ , where A is a kronecker product of matrices. Functions to solve least squares problems of this type are also included. / GPL-2	noarch
r-klustr	0.1.0	Used to create dynamic, interactive 'D3.js' based parallel coordinates and principal component plots in 'R'. The plots make visualizing k-means or other clusters simple and informative. / GPL-3	noarch
r-km.ci	0.5.2	Computes various confidence intervals for the Kaplan-Meier estimator, namely: Petos CI, Rothman CI, CI's based on Greenwoods variance, Thomas and Grunkemeier CI and the simultaneous confidence bands by Nair and Hall and Wellner. / GPL-2	noarch
r-kmconfband	0.1	Computes and plots an exact nonparametric band for any user-specified level of confidence from a single-sample survfit object / GPL-2	noarch
r-kmda	1.0	Compute p-values of metabolite differential expression analysis using the kernel-based approach. / GPL-3	noarch
r-kmlcov	1.0.1	'kmlcov' Cluster longitudinal data using the likelihood as a metric of distance. The generalised linear model allow the user to introduce covariates with different level effects (2 levels). / GPL-2	noarch
r-kmodr	0.1.0	An implementation of the 'k-means-' algorithm proposed by Chawla and Gionis, 2013 in their paper, k-means- : A unified approach to clustering and outlier detection. SIAM International Conference on Data Mining (SDM13), and using 'ordering' described by Howe, 2013 in the thesis, Clustering and anomaly detection in tropical cyclones. Useful for creating (potentially) tighter clusters than standard k-means and simultaneously finding outliers inexpensively in multidimensional space. / GPL-3	noarch
r-kmsurv	0.1.5	Data sets and functions for Klein and Moeschberger (1997), Survival Analysis, Techniques for Censored and Truncated Data, Springer. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-knapsacksampling</a>	0.1.0	The <code>sample.mcmc()</code> function creates samples of the feasible region of a knapsack problem with both equalities and inequalities constraints. / GPL-2	noarch
<a href="#">r-knitlatex</a>	0.9.0	Provides several helper functions for working with ‘knitr’ and ‘LaTeX’. It includes ‘xTab’ for creating traditional ‘LaTeX’ tables, ‘lTab’ for generating ‘longtable’ environments, and ‘sTab’ for generating a ‘supertabular’ environment. Additionally, this package contains a <code>knitr_setup()</code> function which fixes a well-known bug in ‘knitr’, which distorts the ‘results=asis’ command when used in conjunction with user-defined commands; and a <code>com</code> command ( <code>&lt;&lt;com=TRUE&gt;&gt;=</code> ) which renders the output from ‘knitr’ as a ‘LaTeX’ command. / GPL-3	noarch
<a href="#">r-knitr</a>	1.22	Provides a general-purpose tool for dynamic report generation in R using Literate Programming techniques. / GPL	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-knitrbootstrap</a>	1.0.2	A framework to create Bootstrap <a href="http://getbootstrap.com/">http://getbootstrap.com/</a> HTML reports from ‘knitr’ ‘rmarkdown’. / MIT	noarch
<a href="#">r-knitrprogressbar</a>	1.1.0	Provides a progress bar similar to ‘dplyr’ that can write progress out to a variety of locations, including <code>stdout()</code> , <code>stderr()</code> , or from <code>file()</code> . Useful when using ‘knitr’ or ‘rmarkdown’, and you still want to see progress of calculations in the terminal. / MIT	noarch
<a href="#">r-knnecat</a>	1.2.2	Scale categorical variables in such a way as to make NN classification as accurate as possible. The code also handles continuous variables and prior probabilities, and does intelligent variable selection and estimation of both error rates and the right number of NN’s. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-knnngarden</a>	1.0.1	Multi-distance based k-Nearest Neighbors Classification with K Threshold Value Check and Same K_i Problem Dealing, Missing Observations Filling / GPL-2	noarch
<a href="#">r-knnindep</a>	2.0	This package provides the implementation of an exact formula of the <i>i</i> th nearest neighbour distance distribution and implementations of tests of independence based on that formula. Furthermore the package provides a general framework to benchmark tests of independence. / GPL-3	noarch
<a href="#">r-knoema</a>	0.1.16	Using this package, users can access to the largest collection of public data and statistics on the Internet featuring about 2.5 billion time series from thousands of sources collected in ‘Knoema’ repository and use rich R calculations in order to analyze the data. Because data in ‘Knoema’ is time series data, ‘Knoema’ function offers data in a number of formats usable in R such as ‘ts’, ‘xts’ or ‘zoo’. For more information about ‘Knoema’ API go to <a href="https://knoema.com/dev/docs">https://knoema.com/dev/docs</a> . / MIT	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-knor</a>	0.0.6	The k-means ‘NUMA’ Optimized Routine library or ‘knor’ is a highly optimized and fast library for computing k-means in parallel with accelerations for Non-Uniform Memory Access (‘NUMA’) architectures. / Apache License 2.0	linux-64, osx-64, win-64
<a href="#">r-knotr</a>	1.0.2	Makes nice pictures of knots using Bezier curves and numerical optimization. / GPL-2	noarch
<a href="#">r-kodama</a>	1.5	KODAMA algorithm is an unsupervised and semi-supervised learning algorithm that performs feature extraction from noisy and high-dimensional data. It facilitates identification of patterns representing underlying groups on all samples in a data set. The algorithm was published by Cacciatore et al. 2014 <DOI:10.1073/pnas.1220873111>. Addition functions was introduced by Cacciatore et al. 2017 <DOI:10.1093/bioinformatics/btw705> to facilitate the identification of key features associated with the generated output and are easily interpretable for the user. Cross-validated techniques are also included in this package. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-kofdata</a>	0.1.3	Read Swiss time series data from the ‘KOF Datenservice’ API, < <a href="https://datenservice.kof.ethz.ch">https://datenservice.kof.ethz.ch</a> >. The API provides macroeconomic survey data, business cycle and further macro economic time series about Switzerland. The package itself is a set of wrappers around the ‘KOF Datenservice’ API. The ‘kofdata’ package is able to consume public information as well as data that requires an API token. / GPL-2	noarch
<a href="#">r-kofnga</a>	1.3	Provides a function that uses a genetic algorithm to search for a subset of size k from the integers 1:n, such that a user-supplied objective function is minimized at that subset. The selection step is done by tournament selection based on ranks, and elitism may be used to retain a portion of the best solutions from one generation to the next. Population objective function values may optionally be evaluated in parallel. / GPL-2	noarch
<a href="#">r-kohonen</a>	3.0.8	Functions to train self-organising maps (SOMs). Also interrogation of the maps and prediction using trained maps are supported. The name of the package refers to Teuvo Kohonen, the inventor of the SOM. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-kolmim</a>	1.0	Provides an alternative, more efficient evaluation of extreme probabilities of Kolmogorov’s goodness-of-fit measure, $D_n$ , when compared to the original implementation of Wang, Marsaglia, and Tsang. These probabilities are used in Kolmogorov-Smirnov tests when comparing two samples. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-komardown</a>	0.2.0	R Markdown templates based on the ‘KOMA-Script’ classes for LaTeX, additionally offering cross-referencing via the ‘bookdown’ package. / GPL-3	noarch
<a href="#">r-komaletter</a>	0.3.1	An R Markdown template for writing beautiful yet versatile letters, using the ‘KOMA-Script’ letter class ‘scrlltr2’ and an adaptation of the ‘pandoc-letter’ template. ‘scrlltr2’ provides layouts for many different window envelope types and the possibility to define your own. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-konpsurv</a>	1.0.1	The K-sample omnibus non-proportional hazards (KONP) tests are powerful non-parametric tests for comparing K ( $\geq 2$ ) hazard functions based on right-censored data (Gorfine, Schlesinger and Hsu, 2019, <arXiv:1901.05739v1>). These tests are consistent against any differences between the hazard functions of the groups. The KONP tests are often more powerful than other existing tests, especially under non-proportional hazard functions. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-kpart</a>	1.2.2	Cubic spline fitting along with knot selection, includes support for additional variables. / GPL-2	noarch
<a href="#">r-kpeaks</a>	0.1.0	The input argument k which is the number of clusters is needed to start all of the partitioning clustering algorithms. In unsupervised learning applications, an optimal value of this argument is widely determined by using the internal validity indexes. Since these indexes suggest a k value which is computed on the clustering results after several runs of a clustering algorithm they are computationally expensive. On the contrary, 'kpeaks' enables to estimate k before running any clustering algorithm. It is based on a simple novel technique using the descriptive statistics of peak counts of the features in a data set. / GPL-2	noarch
<a href="#">r-kpmt</a>	0.1.0	Functions that implement the known population median test. / MIT	noarch
<a href="#">r-kpodclustr</a>	1.0	The kpodclustr package implements the k-POD method for clustering partially observed data. / MIT	noarch
<a href="#">r-kriens</a>	0.1	Provides basic functions for Continuation-Passing Style development. / BSD_3_clause	noarch
<a href="#">r-krige</a>	0.2_1	Estimates kriging models for geographical point-referenced data. Method is described in Monogan and Gill (2016) <doi:10.1017/psrm.2015.5>. / GPL-2	noarch
<a href="#">r-kriging</a>	1.1	Simple and highly optimized ordinary kriging algorithm to plot geographical data / GPL-2	linux-64, osx-64, win-64
<a href="#">r-krls</a>	1.0_0	Package implements Kernel-based Regularized Least Squares (KRLS), a machine learning method to fit multidimensional functions $y=f(x)$ for regression and classification problems without relying on linearity or additivity assumptions. KRLS finds the best fitting function by minimizing the squared loss of a Tikhonov regularization problem, using Gaussian kernels as radial basis functions. For further details see Hainmueller and Hazlett (2014). / GPL-2	noarch
<a href="#">r-krmm</a>	1.0	Solves kernel ridge regression, within the the mixed model framework, for the linear, polynomial, Gaussian, Laplacian and ANOVA kernels. The model components (i.e. fixed and random effects) and variance parameters are estimated using the expectation-maximization (EM) algorithm. All the estimated components and parameters, e.g. BLUP of dual variables and BLUP of random predictor effects for the linear kernel (also known as RR-BLUP), are available. The kernel ridge mixed model (KRMM) is described in Jacquin L, Cao T-V and Ahmadi N (2016) A Unified and Comprehensible View of Parametric and Kernel Methods for Genomic Prediction with Application to Rice. Front. Genet. 7:145. <doi:10.3389/fgene.2016.00145>. / GPL-2   GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-ksamples</a>	1.2.9	Compares k samples using the Anderson-Darling test, Kruskal-Wallis type tests with different rank score criteria, Steel's multiple comparison test, and the Jonckheere-Terpstra (JT) test. It computes asymptotic, simulated or (limited) exact P-values, all valid under randomization, with or without ties, or conditionally under random sampling from populations, given the observed tie pattern. Except for Steel's test and the JT test it also combines these tests across several blocks of samples. Also analyzed are 2 x t contingency tables and their blocked combinations using the Kruskal-Wallis criterion. Steel's test is inverted to provide simultaneous confidence bounds for shift parameters. A plotting function compares tail probabilities obtained under asymptotic approximation with those obtained via simulation or exact calculations. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-ksd</a>	1.0.0	An adaptation of Kernelized Stein Discrepancy, this package provides a goodness-of-fit test of whether a given i.i.d. sample is drawn from a given distribution. It works for any distribution once its score function (the derivative of log-density) can be provided. This method is based on A Kernelized Stein Discrepancy for Goodness-of-fit Tests and Model Evaluation by Liu, Lee, and Jordan, available at < <a href="http://arxiv.org/abs/1602.03253">http://arxiv.org/abs/1602.03253</a> >. / MIT	noarch
<a href="#">r-kseaapp</a>	0.99.0	Infers relative kinase activity from phosphoproteomics data using the method described by Casado et al. (2013) <doi:10.1126/scisignal.2003573>. / MIT	noarch
<a href="#">r-kselection</a>	0.2.0	Selection of k in k-means clustering based on Pham et al. paper "Selection of k in k-means clustering". / GPL-3	noarch
<a href="#">r-ksgeneral</a>	0.1.1	Computes a p-value of the one-sample two-sided (or one-sided, as a special case) Kolmogorov-Smirnov (KS) statistic, for any fixed critical level, and an arbitrary, possibly large sample size for a pre-specified purely discrete, mixed or continuous cumulative distribution function (cdf) under the null hypothesis. If a data sample is supplied, 'KSgeneral' computes the p-value corresponding to the value of the KS test statistic computed based on the user provided data sample. The package 'KSgeneral' implements a novel, accurate and efficient method named Exact-KS-FFT, expressing the p-value as a double-boundary non-crossing probability for a homogeneous Poisson process, which is then efficiently computed using Fast Fourier Transform (FFT). The package can also be used to compute and plot the complementary cdf of the KS statistic which is known to depend on the hypothesized distribution when the latter is discontinuous (i.e. purely discrete or mixed). / GPL (>= 2.0)	linux-64, osx-64
<a href="#">r-ksnn</a>	0.1.2	Prediction with k* nearest neighbor algorithm based on a publication by Anava and Levy (2016) <arXiv:1701.07266>. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-kstatistics</a>	1.0	Methods and tools for estimate (joint) cumulants of a given population distribution using (multivariate) k-statistics and (multivariate) polykays, symmetric unbiased estimators with minimum variance. For more details see Di Nardo E., Guarino G., Senato D. (2009) <arXiv:0807.5008>. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-kstmatrix	0.1.2	Knowledge space theory by Doignon and Falmagne (1999) <doi:10.1007/978-3-642-58625-5> is a set- and order-theoretical framework, which proposes mathematical formalisms to operationalize knowledge structures in a particular domain. The ‘kstMatrix’ package provides basic functionalities to generate, handle, and manipulate knowledge structures and knowledge spaces. Opposed to the ‘kst’ package, ‘kstMatrix’ uses matrix representations for knowledge structures. Furthermore, ‘kstMatrix’ contains several knowledge spaces developed by the research group around Cornelia Dowling through querying experts. / GPL-3	noarch
r-kuiper.2samp	1.0	This function performs the two-sample Kuiper test to assess the anomaly of continuous, one-dimensional probability distributions. References used for this method are (1). Kuiper, N. H. (1960). <DOI:10.1016/S1385-7258(60)50006-0> and (2). Paltani, S. (2004). <DOI:10.1051/0004-6361:20034220>. / AGPL-3	noarch
r-kulife	0.1.1	Provides various functions and data sets from experiments at the Faculty of Life Sciences, University of Copenhagen. This package will be discontinued and archived, and the functions and datasets will be maintained and updated in the MESS package / GPL-2	noarch
r-kvh	1.4.1	The format KVH is a lightweight format that can be read/written both by humans and machines. It can be useful in situations where XML or alike formats seem to be an overkill. We provide an ability to parse KVH files in R pretty fast due to ‘Rcpp’ use. / GPL-2	linux-64, osx-64, win-64
r-kyotil	2018.10.17	Helper functions for creating formatted summary of regression models, writing publication-ready tables to latex files, and running Monte Carlo experiments. / GPL-2	linux-64, osx-64, win-64
r-kza	4.1.0	Time Series Analysis including break detection, spectral analysis, KZ Fourier Transforms. / GPL-3	linux-64, osx-64, win-64
r-kzs	1.4	A spatial smoothing algorithm based on convolutions of finite rectangular kernels that provides sharp resolution in the presence of high levels of noise. / GPL-2	noarch
r-l0ara	0.1.5	An efficient procedure for feature selection for generalized linear models with L0 penalty, including linear, logistic, Poisson, gamma, inverse Gaussian regression. Adaptive ridge algorithms are used to fit the models. / GPL-2	linux-64, osx-64, win-64
r-l1pack	0.38.1	L1 estimation for linear regression, density, distribution function, quantile function and random number generation for univariate and multivariate Laplace distribution. / GPL (>= 2.0)	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-l2boost</a>	1.0.1	Efficient implementation of Friedman’s boosting algorithm with l2-loss function and coordinate direction (design matrix columns) basis functions. / GPL-2	noarch
<a href="#">r-label.switching</a>	1.8	The Bayesian estimation of mixture models (and more general hidden Markov models) suffers from the label switching phenomenon, making the MCMC output non-identifiable. This package can be used in order to deal with this problem using various relabelling algorithms. / GPL-2	noarch
<a href="#">r-labeledloop</a>	0.1	Support labeled loop and escape from nested loop / MIT	noarch
<a href="#">r-labeling</a>	0.3	Provides a range of axis labeling algorithms / MIT file LICENSE   Unlimited	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-labelvector</a>	0.1.0	Labels are a common construct in statistical software providing a human readable description of a variable. While variable names are succinct, quick to type, and follow a language’s naming conventions, labels may be more illustrative and may use plain text and spaces. R does not provide native support for labels. Some packages, however, have made this feature available. Most notably, the ‘Hmisc’ package provides labelling methods for a number of different object. Due to design decisions, these methods are not all exported, and so are unavailable for use in package development. The ‘labelVector’ package supports labels for atomic vectors in a light-weight design that is suitable for use in other packages. / MIT	noarch
<a href="#">r-labrs</a>	0.1.0	Dati, scripts e funzioni per il libro Ricerca sociale con R. Concetti e funzioni base per la ricerca sociale (Datasets, scripts and functions to support the book Ricerca sociale con R. Concetti e funzioni base per la ricerca sociale). / GPL-3	noarch
<a href="#">r-labstatr</a>	1.0.9	Insieme di funzioni di supporto al volume Laboratorio di Statistica con R, Iacus-Masarotto, MacGraw-Hill Italia, 2006. This package contains sets of functions defined in Laboratorio di Statistica con R, Iacus-Masarotto, MacGraw-Hill Italia, 2006. Function names and docs are in italian as well. / GPL-2	noarch
<a href="#">r-labstats</a>	1.0.1	Contains data sets to accompany the book: Lazic SE (2016). Experimental Design for Laboratory Biologists: Maximising Information and Improving Reproducibility. Cambridge University Press. / GPL-3	noarch
<a href="#">r-laeken</a>	0.5.0	Estimation of indicators on social exclusion and poverty, as well as Pareto tail modeling for empirical income distributions. / GPL-2	noarch
<a href="#">r-laercio</a>	1.0.1	The package contains functions to compare and group means. / GPL-3	noarch
<a href="#">r-laf</a>	0.8.0	Methods for fast access to large ASCII files. Currently the following file formats are supported: comma separated format (CSV) and fixed width format. It is assumed that the files are too large to fit into memory, although the package can also be used to efficiently access files that do fit into memory. Methods are provided to access and process files blockwise. Furthermore, an opened file can be accessed as one would an ordinary data.frame. The LaF vignette gives an overview of the functionality provided. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-lagged</a>	0.3.0	Provides classes and methods for lagged objects. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-lagsequential</a>	0.1.1	Lag-sequential analysis is a method of assessing of patterns (what tends to follow what?) in sequences of codes. The codes are typically for discrete behaviors or states. The functions in this package read a stream of codes, or a frequency transition matrix, and produce a variety of lag sequential statistics, including transitional frequencies, expected transitional frequencies, transitional probabilities, z values, adjusted residuals, Yule's Q values, likelihood ratio tests of stationarity across time and homogeneity across groups or segments, transformed kappas for unidirectional dependence, bidirectional dependence, parallel and nonparallel dominance, and significance levels based on both parametric and randomization tests. The methods are described in Bakeman & Quera (2011) <doi:10.1017/CBO9781139017343>, O'Connor (1999) <doi:10.3758/BF03200753>, Wampold & Margolin (1982) <doi:10.1037/0033-2909.92.3.755>, and Wampold (1995, ISBN:0-89391-919-5). / GPL-2	noarch
<a href="#">r-lahman</a>	6.0_0	Provides the tables from the 'Sean Lahman Baseball Database' as a set of R data.frames. It uses the data on pitching, hitting and fielding performance and other tables from 1871 through 2015, as recorded in the 2016 version of the database. / GPL	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-lambda.r</a>	1.2.3	A language extension to efficiently write functional programs in R. Syntax extensions include multi-part function definitions, pattern matching, guard statements, built-in (optional) type safety. / LGPL-3	noarch
<a href="#">r-lambda4</a>	3.0	Currently the package includes 14 methods for calculating internal consistency reliability but is still growing. The package allows users access to whichever reliability estimator is deemed most appropriate for their situation. / GPL-2	noarch
<a href="#">r-lamme</a>	0.0.1	Log-analytic methods intended for testing multiplicative effects. / GPL-3	noarch
<a href="#">r-landest</a>	1.0	Provides functions to estimate survival and a treatment effect using a landmark estimation approach. / GPL-3	noarch
<a href="#">r-landpred</a>	1.0	This package includes functions for landmark prediction of a survival outcome incorporating covariate and short-term event information. For more information about landmark prediction please see: Parast, Layla, Su-Chun Cheng, and Tianxi Cai. Incorporating short-term outcome information to predict long-term survival with discrete markers. Biometrical Journal 53.2 (2011): 294-307. / GPL-3	noarch
<a href="#">r-landscaper</a>	1.2	Simulates categorical maps on actual geographical realms, starting from either empty landscapes or landscapes provided by the user (e.g. land use maps). Allows to tweak or create landscapes while retaining a high degree of control on its features, without the hassle of specifying each location attribute. In this it differs from other tools which generate null or neutral landscapes in a theoretical space. The basic algorithm currently implemented uses a simple agent style/cellular automata growth model, with no rules (apart from areas of exclusion) and von Neumann neighbourhood (four cells, aka Rook case). Outputs are raster dataset exportable to any common GIS format. / GPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-langevin	1.2.1	Estimate drift and diffusion functions from time series and generate synthetic time series from given drift and diffusion coefficients. / GPL-2	linux-64, osx-64, win-64
r-languagelayer	1.2.4	Improve your text analysis with languagelayer < <a href="https://languagelayer.com">https://languagelayer.com</a> >, a powerful language detection API. / MIT	noarch
r-languager	1.5.0	Data sets exemplifying statistical methods, and some facilitatory utility functions used in “Analyzing Linguistic Data: A practical introduction to statistics using R”, Cambridge University Press, 2008. / GPL-2	noarch
r-laplacesdemon	16.1	Provides a complete environment for Bayesian inference using a variety of different samplers (see ?LaplacesDemon for an overview). The README describes the history of the package development process. / MIT	noarch
r-larf	1.4	Provides instrumental variable estimation of treatment effects when both the endogenous treatment and its instrument are binary. Applicable to both binary and continuous outcomes. / GPL-3	noarch
r-largelist	0.3.1	Functions to write or append a R list to a file, as well as read, remove, modify elements from it without restoring the whole list. / GPL-2	linux-64, osx-64, win-64
r-lars	1.2	Efficient procedures for fitting an entire lasso sequence with the cost of a single least squares fit. Least angle regression and infinitesimal forward stagewise regression are related to the lasso, as described in the paper below. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
r-lasso2	1.2_20	Routines and documentation for solving regression problems while imposing an L1 constraint on the estimates, based on the algorithm of Osborne et al. (1998). / GPL-2	linux-64, osx-64, win-64
r-lassopv	0.2.0	Estimate the p-values for predictors x against target variable y in lasso regression, using the regularization strength when each predictor enters the active set of regularization path for the first time as the statistic. This is based on the assumption that predictors (of the same variance) that (first) become active earlier tend to be more significant. Three null distributions are supported: normal and spherical, which are computed separately for each predictor and analytically under approximation, which aims at efficiency and accuracy for small p-values. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-lassosir</a>	0.1.1	Estimate the sufficient dimension reduction space using sparsed sliced inverse regression via Lasso (Lasso-SIR) introduced in Lin, Zhao, and Liu (2017) <arxiv:1611.06655>. The Lasso-SIR is consistent and achieve the optimal convergence rate under certain sparsity conditions for the multiple index models. / GPL-3	noarch
<a href="#">r-latdiag</a>	0.2.4	A graph proposed by Rosenbaum is useful for checking some properties of various sorts of latent scale, this program generates commands to obtain the graph using 'dot' from 'graphviz'. / GPL-2	noarch
<a href="#">r-later</a>	0.8.0	Executes arbitrary R or C functions some time after the current time, after the R execution stack has emptied. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-laterality</a>	0.9.3	Calculates and plots Handedness index (HI), absolute HI, mean HI and z-score which are commonly used indexes for the study of hand preference (laterality) in non-human primates. / GPL (>= 2.0)	noarch
<a href="#">r-latex2exp</a>	0.4.0	Parses and converts LaTeX math formulas to R's plotmath expressions, used to enter mathematical formulas and symbols to be rendered as text, axis labels, etc. throughout R's plotting system. / MIT	noarch
<a href="#">r-latexpdf</a>	0.1.6	Converts table-like objects to stand-alone PDF or PNG. Can be used to embed tables and arbitrary content in PDF or Word documents. Provides a low-level R interface for creating 'LaTeX' code, e.g. <code>command()</code> and a high-level interface for creating PDF documents, e.g. <code>as.pdf.data.frame()</code> . Extensive customization is available via mid-level functions, e.g. <code>as.tabular()</code> . See also 'package?latexpdf'. Support for PNG is experimental; see 'as.png.data.frame'. Adapted from 'metrumrg' < <a href="http://r-forge.r-project.org/R/?group_id=1215">http://r-forge.r-project.org/R/?group_id=1215</a> >. Requires a compatible installation of 'pdflatex', e.g. < <a href="https://miktex.org/">https://miktex.org/</a> >. / GPL-3	noarch
<a href="#">r-lattice</a>	0.20.38	A powerful and elegant high-level data visualization system inspired by Trellis graphics, with an emphasis on multivariate data. Lattice is sufficient for typical graphics needs, and is also flexible enough to handle most nonstandard requirements. See ?Lattice for an introduction. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-latticeextra</a>	0.6_28	Building on the infrastructure provided by the lattice package, this package provides several new high-level functions and methods, as well as additional utilities such as panel and axis annotation functions. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-lava</a>	1.6.5	A general implementation of Structural Equation Models with latent variables (MLE, 2SLS, and composite likelihood estimators) with both continuous, censored, and ordinal outcomes (Holst and Budtz-Joergensen (2013) <doi:10.1007/s00180-012-0344-y>). Mixture latent variable models and non-linear latent variable models (Holst and Budtz-Joergensen (2019) <doi:10.1093/biostatistics/kxy082>). The package also provides methods for graph exploration (d-separation, back-door criterion), simulation of general non-linear latent variable models, and estimation of influence functions for a broad range of statistical models. / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-lavaan</a>	0.6_3	Fit a variety of latent variable models, including confirmatory factor analysis, structural equation modeling and latent growth curve models. / GPL (>= 2)	linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-lazydata</a>	1.1.0	Supplies a LazyData facility for packages which have data sets but do not provide LazyData: true. A single function is included, requireData, which is a drop-in replacement for base::require, but carrying the additional functionality. By default, it suppresses package startup messages as well. See argument 'reallyQuitely'. / GPL-2	noarch
<a href="#">r-lazyeval</a>	0.2.2	An alternative approach to non-standard evaluation using formulas. Provides a full implementation of LISP style 'quasiquote', making it easier to generate code with other code. / GPL-3	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-lazyrmd</a>	0.2.0	An R Markdown html document format that provides the ability to lazily load plot outputs as the user scrolls over them. This is useful for large R Markdown documents with many plots, as it allows for a fast initial page load and defers loading of individual graphics to the time that the user navigates near them. / MIT	noarch

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Table 51 – continued from previous page

Name	Version	Summary/License	Platforms
<a href="#">r-lazysql</a>	0.1.3	Helper functions to build SQL statements for dbGetQuery or dbSendQuery under program control. They are intended to increase speed of coding and to reduce coding errors. Arguments are carefully checked, in particular SQL identifiers such as names of tables or columns. More patterns will be added as required. / MIT	noarch
<a href="#">r-lbreg</a>	1.2	Maximum likelihood estimation of log-binomial regression with special functionality when the MLE is on the boundary of the parameter space. / GPL-2	noarch
<a href="#">r-lca</a>	0.1.1	Performs model fitting and significance estimation for Localised Co-Dependency between pairs of features of a numeric dataset. / GPL-2	noarch
<a href="#">r-lcf</a>	1.7.0	Baseline correction, normalization and linear combination fitting (LCF) of X-ray absorption near edge structure (XANES) spectra. The package includes data loading of .xmu files exported from 'ATHENA' (Ravel and Newville, 2005) <doi:10.1107/S0909049505012719>. Loaded spectra can be background corrected and all standards can be fitted at once. Two linear combination fitting functions can be used: (1) fit_athena(): Simply fitting combinations of standards as in ATHENA, (2) fit_float(): Fitting all standards with changing baseline correction and edge-step normalization parameters. / GPL-3	noarch
<a href="#">r-lcfdata</a>	2.0	This package contains (1) event-related brain potential data recorded from 10 participants at electrodes Fz, Cz, Pz, and Oz (0–300 ms) in the context of Antoine Tremblay's PhD thesis (Tremblay, 2009); (2) ERP amplitudes at electrode Fz restricted to the 100 to 175 millisecond time window; and (3) plotting data generated from a linear mixed-effects model. / GPL-2	noarch
<a href="#">r-lcpm</a>	0.1.0	An implementation of the Log Cumulative Probability Model (LCPM) and Proportional Probability Model (PPM) for which the Maximum Likelihood Estimates are determined using constrained optimization. This implementation accounts for the implicit constraints on the parameter space. Other features such as standard errors, z tests and p-values use standard methods adapted from the results based on constrained optimization. / GPL-3	noarch
<a href="#">r-lcyanalysis</a>	1.0.3	Analysis of stock data ups and downs trend, the stock technical analysis indicators function have trend line, reversal pattern and market trend. / GPL-3	noarch
<a href="#">r-ldbounds</a>	1.1_1	Computations related to group sequential boundaries. Includes calculation of bounds using the Lan-DeMets alpha spending function approach. / GPL-2	noarch
<a href="#">r-ldcorsv</a>	1.3.2	Four measures of linkage disequilibrium are provided: the usual $r^2$ measure, the $r^2_S$ measure ( $r^2$ corrected by the structure sample), the $r^2_V$ ( $r^2$ corrected by the relatedness of genotyped individuals), the $r^2_{VS}$ measure ( $r^2$ corrected by both the relatedness of genotyped individuals and the structure of the sample). / GPL-2	noarch
<a href="#">r-ldlinkr</a>	1.0.0	Provides access to the LDlink API (< <a href="https://ldlink.nci.nih.gov/?tab=apiaccess">https://ldlink.nci.nih.gov/?tab=apiaccess</a> >) using the R console. This programmatic access facilitates researchers who are interested in performing batch queries in 1000 Genomes Project data using LDlink. / GPL-2	noarch
<a href="#">r-ldrtools</a>	0.2_1	Linear dimension reduction subspaces can be uniquely defined using orthogonal projection matrices. This package provides tools to compute distances between such subspaces and to compute the average subspace. For details see Liski, E.Nordhausen K., Oja H., Ruiz-Gazen A. (2016) Combining Linear Dimension Reduction Subspaces <doi:10.1007/978-81-322-3643-6_7>. / GPL-2	noarch

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Table 51 – continued from previous page

Name	Version	Summary/License	Platforms
<a href="#">r-ldtests</a>	1.0	Exact tests for Linkage Disequilibrium (LD) and Hardy-Weinberg Equilibrium (HWE). - 2-sided LD tests based on different measures of LD (Kulinskaya and Lewin 2008) - 1-sided Fisher's exact test for LD - 2-sided Haldane test for HWE (Wigginton 2005) - 1-sided test for inbreeding - conditional p-values proposed in Kulinskaya (2008) to overcome the problems of asymmetric distributions (for both LD and HWE) / GPL-3	noarch
<a href="#">r-leabra</a>	0.1.0	The algorithm Leabra (local error driven and associative biologically realistic algorithm) allows for the construction of artificial neural networks that are biologically realistic and balance supervised and unsupervised learning within a single framework. This package is based on the 'MATLAB' version by Sergio Verduzco-Flores, which in turn was based on the description of the algorithm by Randall O'Reilly (1996) < <a href="ftp://grey.colorado.edu/pub/oreilly/thesis/oreilly_thesis.all.pdf">ftp://grey.colorado.edu/pub/oreilly/thesis/oreilly_thesis.all.pdf</a> >. For more general (not 'R' specific) information on the algorithm Leabra see < <a href="https://grey.colorado.edu/emergent/index.php/Leabra">https://grey.colorado.edu/emergent/index.php/Leabra</a> >. / GPL-2	noarch
<a href="#">r-leafarea</a>	0.1.8	An interface for the image processing program 'ImageJ', which allows a rapid digital image analysis for particle sizes. This package includes function to write an 'ImageJ' macro which is optimized for a leaf area analysis by default. / GPL-2	noarch
<a href="#">r-leaflet</a>	2.0.2	Create and customize interactive maps using the 'Leaflet' JavaScript library and the 'htmlwidgets' package. These maps can be used directly from the R console, from 'RStudio', in Shiny applications and R Markdown documents. / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-leaflet.opacity</a>	0.1.0	Extends the 'leaflet' R package with the 'Leaflet.OpacityControls' JavaScript plugin. Adds controls to the leaflet map for adjusting the opacity of a layer. / GPL-3	noarch
<a href="#">r-leaflet.providers</a>	1.8.0	Contains third-party map tile provider information from 'Leaflet.js', < <a href="https://github.com/leaflet-extras/leaflet-providers">https://github.com/leaflet-extras/leaflet-providers</a> >, to be used with the 'leaflet' R package. Additionally, 'leaflet.providers' enables users to retrieve up-to-date provider information between package updates. / BSD_2_clause	noarch
<a href="#">r-leafletr</a>	0.4.0	Display your spatial data on interactive web-maps using the open-source JavaScript library Leaflet. 'leafletR' provides basic web-mapping functionality to combine vector data and online map tiles from different sources. See < <a href="http://leafletjs.com">http://leafletjs.com</a> > for more information on Leaflet. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-leafstar</a>	1.0	Implementation of trigonometric functions to calculate the exposure of flat, tilted surfaces, such as leaves and slopes, to direct solar radiation. It implements the equations in A.G. Escibano-Rocafort, A. Ventre-Lespiauq, C. Granado-Yela, et al. (2014) <doi:10.1111/2041-210X.12141> in a few user-friendly R functions. All functions handle data obtained with ‘Ahmes’ 1.0 for Android, as well as more traditional data sources (compass, protractor, inclinometer). The main function (star()) calculates the potential exposure of flat, tilted surfaces to direct solar radiation (silhouette to area ratio, STAR). It is equivalent to the ratio of the leaf projected area to total leaf area, but instead of using area data it uses spatial position angles, such as pitch, roll and course, and information on the geographical coordinates, hour, and date. The package includes additional functions to recalculate STAR with custom settings of location and time, to calculate the tilt angle of a surface, and the minimum angle between two non-orthogonal planes. / AGPL-3	noarch
<a href="#">r-leanpubr</a>	0.3.1	Provides access to the ‘Leanpub’ API < <a href="https://leanpub.com/help/api">https://leanpub.com/help/api</a> > for gathering information about publications and submissions to the ‘Leanpub’ platform. / GPL-3	noarch
<a href="#">r-leanr</a>	1.4.9	Implements the method described in Network-based analysis of omics data: The LEAN method [Gwinner Boulday (2016) <DOI:10.1093/bioinformatics/btw676>] Given a protein interaction network and a list of p-values describing a measure of interest (as e.g. differential gene expression) this method computes an enrichment p-value for the protein neighborhood of each gene and compares it to a background distribution of randomly drawn p-values. The resulting scores are corrected for multiple testing and significant hits are returned in tabular format. / GPL-3	noarch
<a href="#">r-leap</a>	0.2	Advances in sequencing technology now allow researchers to capture the expression profiles of individual cells. Several algorithms have been developed to attempt to account for these effects by determining a cell’s so-called ‘pseudotime’, or relative biological state of transition. By applying these algorithms to single-cell sequencing data, we can sort cells into their pseudotemporal ordering based on gene expression. LEAP (Lag-based Expression Association for Pseudotime-series) then applies a time-series inspired lag-based correlation analysis to reveal linearly dependent genetic associations. / GPL-2	noarch
<a href="#">r-leapfrog</a>	1.0.7	Contains LEAPFrOG Gradient Optimisation and Expectation Maximisation functions for inferring parental admixture proportions from an offspring with SNP genotypes. / GPL-3	noarch
<a href="#">r-leaps</a>	3.0	Regression subset selection, including exhaustive search. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-learnbayes</a>	2.15.1	A collection of functions helpful in learning the basic tenets of Bayesian statistical inference. It contains functions for summarizing basic one and two parameter posterior distributions and predictive distributions. It contains MCMC algorithms for summarizing posterior distributions defined by the user. It also contains functions for regression models, hierarchical models, Bayesian tests, and illustrations of Gibbs sampling. / GPL-2	noarch
<a href="#">r-learngeom</a>	1.4	Contains some functions to learn and teach basic plane Geometry at undergraduate level with the aim of being helpful to young students with little programming skills. / GPL-2	noarch
<a href="#">r-learningr</a>	0.29	Crabs in the English channel, deer skulls, English monarchs, half-caste Manga characters, Jamaican cities, Shakespeare's The Tempest, drugged up cyclists and sexually transmitted diseases. / Unlimited	noarch
<a href="#">r-learnn</a>	0.2.0	Implementations of several basic neural network concepts in R, as based on posts on url{ <a href="http://qua.st/">http://qua.st/</a> }. / GPL-3	noarch
<a href="#">r-learnr</a>	0.9.2	Create interactive tutorials using R Markdown. Use a combination of narrative, figures, videos, exercises, and quizzes to create self-paced tutorials for learning about R and R packages. / Apache License 2.0   file LICENSE	noarch
<a href="#">r-learnrbook</a>	0.0.2	Datasets used in the book Learn R ... as you learnt your mother tongue by Pedro J. Aphalo (2017) < <a href="https://leanpub.com/learnr">https://leanpub.com/learnr</a> >. / GPL-2	noarch
<a href="#">r-leersiecyl</a>	1.0.2	Functions to download data from the SIE, which is the Statistical Information System (Sistema de Información Estadística) in the Statistical Portal of the Government of Castilla y León (Spain) < <a href="https://estadistica.jcyl.es">https://estadistica.jcyl.es</a> >. / GPL-2	noarch
<a href="#">r-legocolors</a>	0.2.0	Provides a dataset containing several color naming conventions established by multiple sources, along with associated color metadata. The package also provides related helper functions for mapping among the different Lego color naming conventions and between Lego colors, hex colors, and 'R' color names, making it easy to convert any color palette to one based on existing Lego colors while keeping as close to the original color palette as possible. The functions use nearest color matching based on Euclidean distance in RGB space. Naming conventions for color mapping include those from 'BrickLink' (< <a href="https://www.bricklink.com">https://www.bricklink.com</a> >), 'The Lego Group' (< <a href="https://www.lego.com">https://www.lego.com</a> >), 'LDraw' (< <a href="https://www.ldraw.org/">https://www.ldraw.org/</a> >), and 'Peeon' (< <a href="http://www.peeron.com/">http://www.peeron.com/</a> >). / MIT	noarch
<a href="#">r-leiden</a>	0.3.1	Implements the 'Python leidenalg' module to be called in R. Enables clustering using the leiden algorithm for partition a graph into communities. See the 'Python' repository for more details: < <a href="https://github.com/vtraag/leidenalg">https://github.com/vtraag/leidenalg</a> > Traag et al (2018) From Louvain to Leiden: guaranteeing well-connected communities. <arXiv:1810.08473>. / GPL-3	noarch
<a href="#">r-leiv</a>	2.0_7	Estimate the slope and intercept of a bivariate linear relationship by calculating a posterior density that is invariant to interchange and scaling of the coordinates. / GPL-2	noarch
<a href="#">r-lenses</a>	0.0.3	Provides tools for creating and using lenses to simplify data manipulation. Lenses are composable getter/setter pairs for working with data in a purely functional way. Inspired by the 'Haskell' library 'lens' (Kmett, 2012) < <a href="https://hackage.haskell.org/package/lens">https://hackage.haskell.org/package/lens</a> >. For a fairly comprehensive (and highly technical) history of lenses please see the 'lens' wiki < <a href="https://github.com/ekmett/lens/wiki/History-of-Lenses">https://github.com/ekmett/lens/wiki/History-of-Lenses</a> >. / MIT	noarch
<a href="#">r-lero.lero</a>	0.2	Generates quotes from 'Lero Lero', a database for meaningless sentences filled with corporate buzzwords, intended to be used as corporate lorem ipsum (see < <a href="http://www.lerolero.com/">http://www.lerolero.com/</a> > for more information). Unfortunately, quotes are currently portuguese-only. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-lest	1.0.0	Functions for vectorised conditional recoding of variables. case_when() enables you to vectorise multiple if and else statements (like 'CASE WHEN' in 'SQL'). if_else() is a stricter and more predictable version of ifelse() in 'base' that preserves attributes. These functions are forked from 'dplyr' with all package dependencies removed and behave identically to the originals. / MIT	noarch
r-lestat	1.9	Some simple objects and functions to do statistics using linear models and a Bayesian framework. / GPL-2	noarch
r-lettercase	0.13.1	Utilities for formatting strings and character vectors to for capitalization, word break and white space. Supported formats are: snake_case, spine-case, camel-Case, PascalCase, Title Case, UPPERCASE, lowercase, Sentence case or combinations thereof. 'lettercase' strives to provide a simple, consistent, intuitive and high performing interface. / GPL-2	noarch
r-lexiconpt	0.1.0	Provides easy access for sentiment lexicons for those who want to do text analysis in Portuguese texts. As of now, two Portuguese lexicons are available: 'SentiLex-PT02' and 'OpLexicon' (v2.1 and v3.0). / GPL-2	noarch
r-lfactors	1.0.4	Provides an extension to factors called 'lfactor' that are similar to factors but allows users to refer to 'lfactor' levels by either the level or the label. / GPL-2	noarch
r-lfdr.mle	1.0	Suite of R functions for the estimation of the local false discovery rate (LFDR) using Type II maximum likelihood estimation (MLE). / GPL-3	noarch
r-lfdrempiricalbayes	1.0	New empirical Bayes methods aiming at analyzing the association of single nucleotide polymorphisms (SNPs) to some particular disease are implemented in this package. The package uses local false discovery rate (LFDR) estimates of SNPs within a sample population defined as a reference class and discovers if SNPs are associated with the corresponding disease. Although SNPs are used throughout this document, other biological data such as protein data and other gene data can be used. Karimnezhad, Ali and Bickel, D. R. (2016) < <a href="http://hdl.handle.net/10393/34889">http://hdl.handle.net/10393/34889</a> >. / GPL-3	noarch
r-lga	1.1_1	Tools for linear grouping analysis. Three user-level functions: gap, rlga and lga. / GPL-3	noarch
r-lgr	0.3.2	A flexible, feature-rich yet light-weight logging framework based on 'R6' classes. It supports hierarchical loggers, custom log levels, arbitrary data fields in log events, logging to plaintext, 'JSON', (rotating) files, memory buffers, and databases, as well as email and push notifications. For a full list of features with examples please refer to the package vignette. / MIT	noarch
r-lgrdata	0.1.1	A largish collection of example datasets, including several classics. Many of these datasets are well suited for regression, classification, and visualization. / CC0	noarch
r-lgtldl	1.1.5	A very simple implementation of a class for longitudinal data. / GPL-2	noarch
r-lhmixr	0.1.0	Fits sex-specific life-history models for fish and other taxa where some of the individuals have unknown sex. / GPL-3	noarch
r-libcoin	1.0_4	Basic infrastructure for linear test statistics and permutation inference in the framework of Strasser and Weber (1999) < <a href="http://epub.wu.ac.at/102/">http://epub.wu.ac.at/102/</a> >. This package must not be used by end-users. CRAN package 'coin' implements all user interfaces and is ready to be used by anyone. / GPL-2	linux-64, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
r-librarian	1.7.0	Automatically install, update, and load ‘CRAN’, ‘GitHub’, and ‘Bioconductor’ packages in a single function call. By accepting bare unquoted names for packages, it’s easy to add or remove packages from the list. / GPL-3	noarch
r-librarysnapshot	0.1.2	Generate a local library copy with relevant packages. All packages currently found within the search path - except base packages - will be copied to the directory provided and can be used later on with the .libPaths() function. / MIT	noarch
r-lift	0.0.2	Compute the top decile lift and plot the lift curve. Cumulative lift curves are also supported. / GPL-2	noarch
r-liftr	0.9.2	Persistent reproducible reporting by containerization of R Markdown documents. / GPL-3	noarch
r-lightningr	1.0.2	The purpose of this package is to enable usage of lightningviz server to be accessible from R. The server itself can be found at <a href="http://lightning-viz.org/">http://lightning-viz.org/</a> and is required to work with this package. Package by itself cannot and will not create any visualizations. / MIT	noarch
r-lightsout	0.3	Lights Out is a puzzle game consisting of a grid of lights that are either on or off. Pressing any light will toggle it and its adjacent lights. The goal of the game is to switch all the lights off. This package provides an interface to play the game on different board sizes, both through the command line or with a visual application. Puzzles can also be solved using the automatic solver included. View a demo online at <a href="http://daattali.com/shiny/lightsout/">http://daattali.com/shiny/lightsout/</a> . / MIT	noarch
r-likelihood	1.7	Tools for maximum likelihood estimation of parameters of scientific models. / GPL-2	noarch
r-likelihoodexplore	0.1.0	Provides likelihood functions as defined by Fisher (1922) <doi:10.1098/rsta.1922.0009> and a function that creates likelihood functions from density functions. The functions are meant to aid in education of likelihood based methods. / GPL-2	noarch
r-limitplot	1.2	Values below a specified limit of detection are stacked in rows in order to reduce overplotting and create a clear graphical representation of your data. / GPL-2	noarch
r-linbin	0.1.2	Short for ‘linear binning’, the linbin package provides functions for manipulating, binning, and plotting linearly referenced data. Although developed for data collected on river networks, it can be used with any interval or point data referenced to a 1-dimensional coordinate system. Flexible bin generation and batch processing makes it easy to compute and visualize variables at multiple scales, useful for identifying patterns within and between variables and investigating the influence of scale of observation on data interpretation. / AGPL-3	noarch
r-lincal	1.0	Estimate and confidence/credible intervals for an unknown regressor $x_0$ given an observed $y_0$ . / GPL-2	noarch
r-lindenmayer	0.1.13	L-systems or Lindenmayer systems are parallel rewriting systems which can be used to simulate biological forms and certain kinds of fractals. Briefly, in an L-system a series of symbols in a string are replaced iteratively according to rules to give a more complex string. Eventually, the symbols are translated into turtle graphics for plotting. Wikipedia has a very good introduction: <a href="http://en.wikipedia.org/wiki/L-system">en.wikipedia.org/wiki/L-system</a> This package provides basic functions for exploring L-systems. / GPL-3	noarch
r-linearregressionmde	1.0	Consider linear regression model $Y = Xb + \text{error}$ where the distribution function of errors is unknown, but errors are independent and symmetrically distributed. The package contains a function named LRMDE which takes Y and X as input and returns minimum distance estimator of parameter b in the model. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<code>r-linkedmatrix</code>	1.3.1	A class that links matrix-like objects (nodes) by rows or by columns while behaving similarly to a base R matrix. Very large matrices are supported if the nodes are memory-mapped objects. / MIT	noarch
<code>r-linkim</code>	0.1	A linkage information based method for imputing missing diploid genotypes / GPL-2	noarch
<code>r-linl</code>	0.0.3	A ‘LaTeX’ Letter class for ‘rmarkdown’, using the ‘pandoc-letter’ template adapted for use with ‘markdown’. / GPL-3	noarch
<code>r-linlir</code>	1.1	This package implements the methodology of Likelihood-based Imprecise Regression (LIR) for the case of linear regression with interval data. / GPL-2	noarch
<code>r-linpk</code>	1.0	Generate concentration-time profiles from linear pharmacokinetic (PK) systems, possibly with first-order absorption or zero-order infusion, possibly with one or more peripheral compartments, and possibly under steady-state conditions. Single or multiple doses may be specified. Secondary (derived) PK parameters (e.g. Cmax, Ctrough, AUC, Tmax, half-life, etc.) are computed. / GPL-3	noarch
<code>r-linprog</code>	0.9_2	This package can be used to solve Linear Programming / Linear Optimization problems by using the simplex algorithm. / GPL-2	noarch
<code>r-linreginteractive</code>	0.3_1	Interactive visualization of effects, response functions and marginal effects for different kinds of regression models. In this version linear regression models, generalized linear models, generalized additive models and linear mixed-effects models are supported. Major features are the interactive approach and the handling of the effects of categorical covariates: if two or more factors are used as covariates every combination of the levels of each factor is treated separately. The automatic calculation of marginal effects and a number of possibilities to customize the graphical output are useful features as well. / GPL-2	noarch
<code>r-linselect</code>	1.1.1	Estimate the mean of a Gaussian vector, by choosing among a large collection of estimators. In particular it solves the problem of variable selection by choosing the best predictor among predictors emanating from different methods as lasso, elastic-net, adaptive lasso, pls, randomForest. Moreover, it can be applied for choosing the tuning parameter in a Gauss-lasso procedure. / GPL-3	noarch
<code>r-lintr</code>	1.0.3	Checks adherence to a given style, syntax errors and possible semantic issues. Supports on the fly checking of R code edited with ‘RStudio IDE’, ‘Emacs’, ‘Vim’, ‘Sublime Text’ and ‘Atom’. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<code>r-lisa</code>	0.1.0	Contains 128 palettes from Color Lisa. All palettes are based on masterpieces from the worlds greatest artists. For more information, see < <a href="http://colorlisa.com/">http://colorlisa.com/</a> >. / MIT	noarch
<code>r-lisp</code>	0.1	Though SRFI-1 scopes both list-processing and higher-order programming, we’ll save some list-orthogonal functions for the ‘functional’ package; this is freely a mixture of implementation and API. / GPL-2	noarch
<code>r-lisreitor</code>	0.1.4	This is an unofficial package aimed at automating the import of LISREL output in R. This package or its maintainer is not in any way affiliated with the creators of LISREL and SSI, Inc. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-listarrays</a>	0.2.0	A toolbox for R arrays. Flexibly split, bind, reshape, modify, subset and name arrays. / GPL-3	noarch
<a href="#">r-listenv</a>	0.7.0	List environments are environments that have list-like properties. For instance, the elements of a list environment are ordered and can be accessed and iterated over using index subsetting, e.g. <code>'x &lt;- listenv(a = 1, b = 2); for (i in seq_along(x)) x[[i]] &lt;- x[[i]] ^ 2; y &lt;- as.list(x)'</code> . / LGPL-2.1	noarch
<a href="#">r-listest</a>	2.1	Tests for independence between X and Y computed from a paired sample (x1,y1),... (xn,yn) of (X,Y), using one of the following statistics (a) the Longest Increasing Subsequence (Ln), (b) JLn, a Jackknife version of Ln or (c) JLMn, a Jackknife version of the longest monotonic subsequence. This family of tests can be applied under the assumption of continuity of X and Y. / GPL-2	noarch
<a href="#">r-listviewer</a>	2.1.0	R lists, especially nested lists, can be very difficult to visualize or represent. Sometimes <code>'str()'</code> is not enough, so this suite of <code>htmlwidgets</code> is designed to help see, understand, and maybe even modify your R lists. The function <code>'reactjson()'</code> requires a package <code>'reactR'</code> that can be installed from CRAN or <a href="https://github.com/timelyportfolio/reactR">https://github.com/timelyportfolio/reactR</a> . / MIT	noarch
<a href="#">r-listwithdefaults</a>	1.2.0	Provides a function that, as an alternative to <code>base::list</code> , allows default values to be inherited from another list. / GPL-2	noarch
<a href="#">r-liureg</a>	1.1.2	Linear Liu regression coefficient's estimation and testing with different Liu related measures such as MSE, R-squared etc. REFERENCES i. Akdeniz and Kaciranlar (1995) <doi:10.1080/03610929508831585> ii. Druilhet and Mom (2008) <doi:10.1016/j.jmva.2006.06.011> iii. Imdadullah, Aslam, and Saima (2017) iv. Liu (1993) <doi:10.1080/03610929308831027> v. Liu (2001) <doi:10.1016/j.jspi.2010.05.030>. / GPL-2   GPL-3	noarch
<a href="#">r-lllrcrc</a>	1.2	Applies local log-linear capture-recapture models (LLLMs) for closed populations, as described in the doctoral thesis of Zachary Kurtz. The method is relevant when there are 3-5 capture occasions, with auxiliary covariates available for all capture occasions. As part of estimating the number of missing population units, the method estimates the rate of missingness as it varies over the covariate space. In addition, user-friendly functions are provided to recreate (approximately) the method of Zwane and van der Heijden (2004), which applied the VGAM package in a way that is closely related to LLLMs. / GPL-2	noarch
<a href="#">r-llogistic</a>	1.0.3	Density, distribution function, quantile function and random generation for the L-Logistic distribution with parameters m and phi. The parameter m is the median of the distribution. / GPL-3	noarch
<a href="#">r-lm.beta</a>	1.5_1	Adds standardized regression coefficients to objects created by <code>lm</code> . Also extends the S3 methods <code>print</code> , <code>summary</code> and <code>coef</code> with additional boolean argument <code>standardized</code> . / GPL-2	noarch
<a href="#">r-lme4</a>	1.1_2	Fit linear and generalized linear mixed-effects models. The models and their components are represented using S4 classes and methods. The core computational algorithms are implemented using the 'Eigen' C library for numerical linear algebra and 'RcppEigen' glue. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
r-lmec	1.0	This package includes a function to fit a linear mixed-effects model in the formulation described in Laird and Ware (1982) but allowing for censored normal responses. In this version, the with-in group errors are assumed independent and identically distributed. / GPL-2	noarch
r-lmertest	3.1_0	Provides p-values in type I, II or III anova and summary tables for lmer model fits (cf. lme4) via Satterthwaite's degrees of freedom method. A Kenward-Roger method is also available via the pbkrtest package. Model selection methods include step, drop1 and anova-like tables for random effects (ranova). Methods for Least-Square means (LS-means) and tests of linear contrasts of fixed effects are also available. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-lmesplines	1.1_10	Add smoothing spline modelling capability to nlme. Fit smoothing spline terms in Gaussian linear and nonlinear mixed-effects models / GPL-2	noarch
r-lmf	1.2	This R package provide methods for estimation and statistical inference on directional and fluctuating selection in age-structured populations. / GPL-2	noarch
r-lmfilter	0.1.2	We present a method based on filtering algorithms to estimate the parameters of linear regressions, i.e. the coefficients and the variance of the error term. The proposed algorithms make use of Particle Filters following Ristic, B., Arulampalam, S., Gordon, N. (2004, ISBN: 158053631X) resampling methods. / GPL-2	noarch
r-lmmot	0.1.4	Fit right censored Multiple Ordinal Tobit (MOT) model. / GPL-3	noarch
r-lmodel2	1.7_3	Computes model II simple linear regression using ordinary least squares (OLS), major axis (MA), standard major axis (SMA), and ranged major axis (RMA). / GPL-2	noarch
r-lmreg	1.2	Data files and a few functions used in the book 'Linear Models and Regression with R: An Integrated Approach' by Debasis Sengupta and Sreenivas Rao Jammalamadaka (2019). / GPL-2	noarch
r-lmridge	1.2	Linear ridge regression coefficient's estimation and testing with different ridge related measures such as MSE, R-squared etc. REFERENCES i. Hoerl and Kennard (1970) <doi:10.2307/1267351> ii. Halawa and El-Bassiouni (2000) <doi:10.1080/00949650008812006> iii. Imdadullah, Aslam, and Saima (2017) iv. Marquardt (1970) <doi:10.2307/1267205>. / GPL (>= 2.0)	noarch
r-lmtest	0.9_36	A collection of tests, data sets, and examples for diagnostic checking in linear regression models. Furthermore, some generic tools for inference in parametric models are provided. / GPL-2   GPL-3	linux-32, linux-64, osx-64, win-32, win-64
r-lmviz	0.1.2	Contains three shiny applications. Two are meant to explore linear model inference feature through simulation. The third is a game to learn interpreting diagnostic plots. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-ln0scis</a>	0.1.5	Construct the simultaneous confidence intervals for ratios of means of Log-normal populations with zeros. It also has a Python module that do the same thing, and can be applied to multiple comparisons of parameters of any k mixture distributions. And we provide four methods, the method based on generalized pivotal quantity with order statistics and the quantity based on Wilson by Li et al. (2009) <doi:10.1016/j.spl.2009.03.004> (GPQW), and the methods based on generalized pivotal quantity with order statistics and the quantity based on Hannig (2009) <doi:10.1093/biomet/asp050> (GPQH). The other two methods are based on two-step MOVER intervals by Amany H, Abdel K (2015) <doi:10.1080/03610918.2013.767911>. We deduce Fiducial generalized pivotal two-step MOVER intervals based on Wilson quantity (FMW) and based on Hannig's quantity (FMWH). All these approach you can find in the paper of us which it has been submitted. / GPL-2	noarch
<a href="#">r-lncpath</a>	1.1	Identifies pathways synergistically regulated by the interested lncRNA(long non-coding RNA) sets based on a lncRNA-mRNA(messenger RNA) interaction network. 1) The lncRNA-mRNA interaction network was built from the protein-protein interactions and the lncRNA-mRNA co-expression relationships in 28 RNA-Seq data sets. 2) The interested lncRNAs can be mapped into networks as seed nodes and a random walk strategy will be performed to evaluate the rate of each coding genes influenced by the seed lncRNAs. 3) Pathways regulated by the lncRNA set will be evaluated by a weighted Kolmogorov-Smirnov statistic as an ES Score. 4) The p value and false discovery rate value will also be calculated through a permutation analysis. 5) The running score of each pathway can be plotted and the heat map of each pathway can also be plotted if an expression profile is provided. 6) The rank and scores of the gene list of each pathway can be printed. / GPL-2	noarch
<a href="#">r-lnirt</a>	0.4.0	Allows the simultaneous analysis of responses and response times in an Item Response Theory (IRT) modelling framework. Supports variable person speed functions (intercept, trend, quadratic), and covariates for item and person (random) parameters. Data missing-by-design can be specified. Parameter estimation is done with a MCMC algorithm. LNIRT replaces the package CIRT, which was written by Rinke Klein Entink. For reference, see the paper by Fox, Klein Entink and Van der Linden (2007), Modeling of Responses and Response Times with the Package cirt, Journal of Statistical Software, <doi:10.18637/jss.v020.i07>. / GPL-3	noarch
<a href="#">r-loadr</a>	0.1.2	Provides intuitive functions for loading objects into environments, encouraging less cluttered workspaces and sharing variables with large or reusable data across users and sessions. The user provides named variables which are loaded into the variable environment for later retrieval. / BSD_2_clause	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-localcontrolstrategy</a>	1.3.3	Especially when cross-sectional data are observational, effects of treatment selection bias and confounding are revealed by using the Nonparametric and Unsupervised preprocessing methods central to Local Control (LC) Strategy. The LC objective is to estimate the effect-size distribution that best quantifies a potentially causal relationship between a numeric y-Outcome variable and a t-Treatment variable. This t-variable may be either binary {1 = new vs 0 = control} or a numeric measure of Exposure level. LC Strategy starts by CLUSTERING experimental units (patients) on their pre-exposure X-Covariates, forming mutually exclusive and exhaustive BLOCKS of relatively well-matched units. The implicit statistical model for LC is thus simple one-way ANOVA. The Within-Block measures of effect-size are Local Rank Correlations (LRCs) when Exposure is numeric with more than two levels. Otherwise, Treatment choice is Nested within BLOCKS, and effect-sizes are LOCAL Treatment Differences (LTDs) between within-cluster y-Outcome Means [new minus control]. An Instrumental Variable (IV) method is also provided so that Local Average y-Outcomes (LAOs) within BLOCKS may also contribute information for effect-size inferences ... assuming that X-Covariates influence only Treatment choice or Exposure level and otherwise have no direct effects on y-Outcome. Finally, a Most-Like-Me function provides histograms of effect-size distributions to aid Doctor-Patient communications about Personalized Medicine. / GPL-2	noarch
<a href="#">r-localsolver</a>	2.3	The package converts R data onto input and data for LocalSolver, executes optimization and exposes optimization results as R data. LocalSolver ( <a href="http://www.localsolver.com/">http://www.localsolver.com/</a> ) is an optimization engine developed by Innovation24 ( <a href="http://www.innovation24.fr/">http://www.innovation24.fr/</a> ). It is designed to solve large-scale mixed-variable non-convex optimization problems. The localsolver package is developed and maintained by WLOG Solutions ( <a href="http://www.wlogsolutions.com/en/">http://www.wlogsolutions.com/en/</a> ) in collaboration with Decision Support and Analysis Division at Warsaw School of Economics ( <a href="http://www.sgh.waw.pl/en/">http://www.sgh.waw.pl/en/</a> ). / LGPL-2.1	noarch
<a href="#">r-locfdr</a>	1.1_8	Computation of local false discovery rates. / GPL-2	noarch
<a href="#">r-lock5data</a>	2.8	Datasets for Statistics: Unlocking the Power of Data by Lock^5 Datasets for the first and second editions of the book. Older editions of revised data often have an extra 1e in the name. / GPL-2	noarch
<a href="#">r-lock5withr</a>	1.2.2	Data sets and other utilities for ‘Statistics: Unlocking the Power of Data’ by Lock, Lock, Lock, Lock and Lock (ISBN : 978-0-470-60187-7, <a href="http://lock5stat.com/">http://lock5stat.com/</a> ). / GPL-2	noarch
<a href="#">r-lodi</a>	0.9.1	Impute observed values below the limit of detection (LOD) via censored likelihood multiple imputation (CLMI) in single-pollutant models, developed by Boss et al (2019) <doi:10.1097/EDE.0000000000001052>. CLMI handles exposure detection limits that may change throughout the course of exposure assessment. ‘lodi’ provides functions for imputing and pooling for this method. / GPL-3	noarch
<a href="#">r-logcondiscr</a>	1.0.6	Given independent and identically distributed observations $X(1), \dots, X(n)$ , allows to compute the maximum likelihood estimator (MLE) of probability mass function (pmf) under the assumption that it is log-concave, see Weyermann (2007) and Balabdaoui, Jankowski, Rufibach, and Pavlides (2012). The main functions of the package are ‘logConDiscrMLE’ that allows computation of the log-concave MLE, ‘logConDiscrCI’ that computes pointwise confidence bands for the MLE, and ‘kInflatedLogConDiscr’ that computes a mixture of a log-concave PMF and a point mass at k. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-logger	0.1	Inspired by the the ‘futile.logger’ R package and ‘logging’ Python module, this utility provides a flexible and extensible way of formatting and delivering log messages with low overhead. / AGPL-3	noarch
r-logging	0.9.1	Pure R implementation of the ubiquitous log4j package. It offers hierarchic loggers, multiple handlers per logger, level based filtering, space handling in messages and custom formatting. / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-logicoil	0.99.0	This package contains the functions necessary to run the LOGICOIL algorithm. LOGICOIL can be used to differentiate between antiparallel dimers, parallel dimers, trimers and higher-order coiled-coil sequence. By covering >90 percent of the known coiled-coil structures, LOGICOIL is a net improvement compared with other existing methods, which achieve a predictive coverage of around 31 percent of this population. As such, LOGICOIL is particularly useful for researchers looking to characterize novel coiled-coil sequences or studying coiled-coil containing protein assemblies. It may also be used to assist in the structural characterization of synthetic coiled-coil sequences. / GPL-2	noarch
r-logistic4p	1.5	Error in a binary dependent variable, also known as misclassification, has not drawn much attention in psychology. Ignoring misclassification in logistic regression can result in misleading parameter estimates and statistical inference. This package conducts logistic regression analysis with misspecification in outcome variables. / GPL-3	noarch
r-logisticrr	0.2.0	Adjusted odds ratio conditional on potential confounders can be directly obtained from logistic regression. However, those adjusted odds ratios have been widely incorrectly interpreted as a relative risk. As relative risk is often of interest in public health, we provide a simple code to return adjusted relative risks from logistic regression model under potential confounders. / GPL-3	noarch
r-logitnorm	0.8.37	Density, distribution, quantile and random generation function for the logit-normal distribution. Estimation of the mode and the first two moments. Estimation of distribution parameters. / GPL-2	noarch
r-lognorm	0.1.6	The lognormal distribution (Limpert et al. (2001) <doi:10.1641/0006-3568(2001)051%5B0341:Indats%5D2.0.co;2>) can characterize uncertainty that is bounded by zero. This package provides estimation of distribution parameters, computation of moments and other basic statistics, and an approximation of the distribution of the sum of several correlated lognormally distributed variables (Lo 2013 <doi:10.12988/ams.2013.39511>). / GPL-2	noarch
r-lognormreg	0.2.0	Functions to fits simple linear regression models with log normal errors and identity link (taking the responses on the original scale). See Muggeo (2018) <doi:10.13140/RG.2.2.18118.16965>. / GPL-3	noarch
r-logofgamma	0.0.1	Uses approximations to compute the natural logarithm of the Gamma function for large values. / GPL-3	noarch
r-logranka	1.0	LogrankA provides a logrank test across unlimited groups with the possibility to input aggregated survival data. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-lomb	1.1	Computes the Lomb-Scargle Periodogram for unevenly sampled time series. Includes a randomization procedure to obtain reliable p-values. / GPL-2	noarch
r-longcateda	0.31	Methods for plotting categorical longitudinal and time-series data by mapping individuals to the vertical space (each horizontal line represents a participant), time (or repeated measures) to the horizontal space, categorical (or discrete) states as facets using color or shade, and events to points using plotting characters. Sorting individuals in the vertical space and (or) stratifying them by groups can reveal patterns in the changes over time. / GPL-3	noarch
r-longitudinal	1.1.12	Contains general data structures and functions for longitudinal data with multiple variables, repeated measurements, and irregularly spaced time points. Also implements a shrinkage estimator of dynamical correlation and dynamical covariance. / GPL-3	noarch
r-longmemo	1.1_1	Datasets and Functionality from ‘Jan Beran’ (1994). Statistics for Long-Memory Processes; Chapman & Hall. Estimation of Hurst (and more) parameters for fractional Gaussian noise, ‘fARIMA’ and ‘FEXP’ models. / GPL-2	noarch
r-longpower	1.0_1	Compute power and sample size for linear models of longitudinal data. Supported models include mixed-effects models and models fit by generalized least squares and generalized estimating equations. Relevant formulas are derived by Liu and Liang (1997) <DOI:10.2307/2533554>, Diggle et al (2002) <ISBN:9780199676750>, and Lu, Luo, and Chen (2008) <DOI:10.2202/1557-4679.1098>. / GPL-2	noarch
r-longroc	1.0	Time-dependent Receiver Operating Characteristic curves, Area Under the Curve, and Net Reclassification Indexes for repeated measures. It is based on methods in Barbaty and Farcomeni (2017) <doi:10.1007/s10260-017-0410-2>. / GPL-2	noarch
r-loo	2.1.0	Efficient approximate leave-one-out cross-validation (LOO) for Bayesian models fit using Markov chain Monte Carlo. The approximation uses Pareto smoothed importance sampling (PSIS), a new procedure for regularizing importance weights. As a byproduct of the calculations, we also obtain approximate standard errors for estimated predictive errors and for the comparison of predictive errors between models. The package also provides methods for using stacking and other model weighting techniques to average Bayesian predictive distributions. / GPL (>= 3)	noarch
r-loon.data	0.0.5	Data used as examples in the ‘loon’ package. / GPL-2	noarch
r-loop	1.1	The program can perform loop analysis and plot network structure (especially for food webs), including minimum spanning tree, loop decomposition of weighted directed graphs, and other network properties which may be related to food chain properties in ecology. / GPL-2	noarch
r-loopanalyst	1.2_6	Loop analysis makes qualitative predictions of variable change in a system of causally interdependent variables, where qualitative means sign only (i.e. increases, decreases, non change, and ambiguous). This implementation includes output support for graphs in .dot file format for use with visualization software such as ‘graphviz’ (< <a href="http://graphviz.org">http://graphviz.org</a> >). ‘LoopAnalyst’ provides tools for the construction and output of community matrices, computation and output of community effect matrices, tables of correlations, adjoint, absolute feedback, weighted feedback and weighted prediction matrices, change in life expectancy matrices, and feedback, path and loop enumeration tools. / GPL-2	noarch
r-lotkaslaw	0.0.1	Running Lotka’s Law following Pao (1985)(DOI: 10.1016/0306-4573(85)90055-X). The Law is based around the proof that the number of authors making n contributions is about $1/n^a$ of those making one contribution. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-lotri	0.1.1	Provides a simple mechanism to specify a symmetric block diagonal matrices (often used for covariance matrices). This is based on the domain specific language implemented in ‘nlmixr’ but expanded to create matrices in R generally instead of specifying parts of matrices to estimate. / GPL-2	noarch
r-lpbrim	1.0.0	Optimization of bipartite modularity using LP-BRIM (Label propagation followed by Bipartite Recursively Induced Modularity). / BSD_2_clause	noarch
r-lpc	1.0.2	Implements the LPC method of Witten&Tibshirani(Annals of Applied Statistics 2008) for identification of significant genes in a microarray experiment. / GPL-2	noarch
r-lpcm	0.46	Fitting multivariate data patterns with local principal curves, including tools for data compression (projection) and measuring goodness-of-fit; with some additional functions for mean shift clustering. / GPL-2	noarch
r-lpint	2.0	Estimates the intensity function, or its derivative of a given order, of a multiplicative counting process using the local polynomial method / GPL (>= 2.0)	noarch
r-lpm	2.7	Apply Univariate Long Memory Models, Apply Multivariate Short Memory Models To Hydrological Dataset, Estimate Intensity Duration Frequency curve to rainfall series. / GPL-2	noarch
r-lpmodeler	0.2_1	lpmodeler is a set of user-friendly functions to simplify the modelling of linear programs (LP) and mixed integer programs (MIP). It provides a unified interface compatible with optimization packages: Rsymphony. / GPL-2   BSD_2_clause	noarch
r-lpower	0.1.0	Computes power, or sample size or the detectable difference for a repeated measures model with attrition. It requires the variance covariance matrix of the observations but can compute this matrix for several common random effects models. See Diggle, P, Liang, KY and Zeger, SL (1994, ISBN:9780198522843). / Unlimited	noarch
r-lps	1.0.10	An implementation of the Linear Predictor Score approach, as initiated by Radmacher et al. (J Comput Biol 2001) and enhanced by Wright et al. (PNAS 2003) for gene expression signatures. Several tools for unsupervised clustering of gene expression data are also provided. / GPL-3	noarch
r-lpsolve	5.6.13	Lp_solve is freely available (under LGPL 2) software for solving linear, integer and mixed integer programs. In this implementation we supply a wrapper function in C and some R functions that solve general linear/integer problems, assignment problems, and transportation problems. This version calls lp_solve version 5.5. / LGPL-2	linux-64, osx-64, win-32, win-64
r-lpwc	0.99.5	Computes a time series distance measure for clustering based on weighted correlation and introduction of lags. The lags capture delayed responses in a time series dataset. The timepoints must be specified. T. Chandereeng, A. Gitter (2018) <doi:10.1101/292615>. / MIT	noarch
r-lrequire	0.1.3	In the fashion of ‘node.js’ < <a href="https://nodejs.org/">https://nodejs.org/</a> >, requires a file, sourcing into the current environment only the variables explicitly specified in the module.exports or exports list variable. If the file was already sourced, the result of the earlier sourcing is returned to the caller. / MIT	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-lrgs</a>	0.5.3	Implements a Gibbs sampler to do linear regression with multiple covariates, multiple responses, Gaussian measurement errors on covariates and responses, Gaussian intrinsic scatter, and a covariate prior distribution which is given by either a Gaussian mixture of specified size or a Dirichlet process with a Gaussian base distribution. / MIT	noarch
<a href="#">r-lrmest</a>	3.0	When multicollinearity exists among predictor variables of the linear model, least square estimators does not provide a better solution for estimating parameters. To deal with multicollinearity several estimators are proposed in the literature. Some of these estimators are Ordinary Least Square Estimator (OLSE), Ordinary Generalized Ordinary Least Square Estimator (OGOLSE), Ordinary Ridge Regression Estimator (ORRE), Ordinary Generalized Ridge Regression Estimator (OGRRE), Restricted Least Square Estimator (RLSE), Ordinary Generalized Restricted Least Square Estimator (OGRLE), Ordinary Mixed Regression Estimator (OMRE), Ordinary Generalized Mixed Regression Estimator (OGMRE), Liu Estimator (LE), Ordinary Generalized Liu Estimator (OGLE), Restricted Liu Estimator (RLE), Ordinary Generalized Restricted Liu Estimator (OGRLE), Stochastic Restricted Liu Estimator (SRLE), Ordinary Generalized Stochastic Restricted Liu Estimator (OGSRLE), Type (1),(2),(3) Liu Estimator (Type-1,2,3 LTE), Ordinary Generalized Type (1),(2),(3) Liu Estimator (Type-1,2,3 OGLTE), Type (1),(2),(3) Adjusted Liu Estimator (Type-1,2,3 ALTE), Ordinary Generalized Type (1),(2),(3) Adjusted Liu Estimator (Type-1,2,3 OGALTE), Almost Unbiased Ridge Estimator (AURE), Ordinary Generalized Almost Unbiased Ridge Estimator (OGAURE), Almost Unbiased Liu Estimator (AULE), Ordinary Generalized Almost Unbiased Liu Estimator (OGAULE), Stochastic Restricted Ridge Estimator (SRRE), Ordinary Generalized Stochastic Restricted Ridge Estimator (OGSRRE), Restricted Ridge Regression Estimator (RRRE) and Ordinary Generalized Restricted Ridge Regression Estimator (OGRRE). To select the best estimator in a practical situation the Mean Square Error (MSE) is used. Using this package scalar MSE value of all the above estimators and Prediction Sum of Square (PRESS) values of some of the estimators can be obtained, and the variation of the MSE and PRESS values for the relevant estimators can be shown graphically. / GPL-2   GPL-3	noarch
<a href="#">r-lrth</a>	1.3	R code of a likelihood ratio test for genome-wide association under genetic heterogeneity. / GPL-3	noarch
<a href="#">r-lsa</a>	0.73.1	The basic idea of latent semantic analysis (LSA) is, that text do have a higher order (=latent semantic) structure which, however, is obscured by word usage (e.g. through the use of synonyms or polysemy). By using conceptual indices that are derived statistically via a truncated singular value decomposition (a two-mode factor analysis) over a given document-term matrix, this variability problem can be overcome. / GPL-2	noarch
<a href="#">r-lsasim</a>	1.0.1	Provides functions to simulate data from large-scale educational assessments, including background questionnaire data and cognitive item responses that adhere to a multiple-matrix sampled design. / GPL-3	noarch
<a href="#">r-lsd</a>	4.0_0	Create lots of colorful plots in a plethora of variations. Try the LSD demo-tour(). / Unlimited	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-lsdinterface</a>	0.4.0	Interfaces R with LSD. Reads object-oriented data in results files (.res) produced by LSD and creates appropriate multi-dimensional arrays in R. Supports multiple core parallelization of multi-file data reading for increased performance. Also provides functions to extract basic information and statistics from data files. LSD (Laboratory for Simulation Development) is free software developed by Marco Valente (documentation and downloads available at <a href="http://labsimdev.org">http://labsimdev.org</a> ). / GPL-3	noarch
<a href="#">r-lsdv</a>	1.1	Fit a least square dummy variable regression / Artistic-2.0	noarch
<a href="#">r-lshorth</a>	0.1_6	Calculates the (localised) length of the shorth and supplies corresponding diagnostic plots. / LGPL-3	noarch
<a href="#">r-lsm</a>	0.1.8	When the values of the outcome variable Y are either 0 or 1, the function lsm() calculates the estimation of the log likelihood in the saturated model. This model is characterized by Llinas (2006, ISSN:2389-8976) in section 2.3 through the assumptions 1 and 2. The function LogLik() works (almost perfectly) when the number of independent variables K is high, but for small K it calculates wrong values in some cases. For this reason, when Y is dichotomous and the data are grouped in J populations, it is recommended to use the function lsm() because it works very well for all K. / MIT	noarch
<a href="#">r-lsmeans</a>	2.30_0	Obtain least-squares means for linear, generalized linear, and mixed models. Compute contrasts or linear functions of least-squares means, and comparisons of slopes. Plots and compact letter displays. Least-squares means were proposed in Harvey, W (1960) Least-squares analysis of data with unequal subclass numbers, Tech Report ARS-20-8, USDA National Agricultural Library, and discussed further in Searle, Speed, and Milliken (1980) Population marginal means in the linear model: An alternative to least squares means, The American Statistician 34(4), 216-221 <doi:10.1080/00031305.1980.10483031>. NOTE: lsmeans now relies primarily on code in the 'emmeans' package. 'lsmeans' will be archived in the near future. / GPL-2   GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-lsmontecarlo</a>	1.0	The package compiles functions for calculating prices of American put options with Least Squares Monte Carlo method. The option types are plain vanilla American put, Asian American put, and Quanto American put. The pricing algorithms include variance reduction techniques such as Antithetic Variates and Control Variates. Additional functions are given to derive price surfaces at different volatilities and strikes, create 3-D plots, quickly generate Geometric Brownian motion, and calculate prices of European options with Black & Scholes analytical solution. / GPL-3	noarch
<a href="#">r-lspline</a>	1.0_0	Linear splines with convenient parametrisations such that (1) coefficients are slopes of consecutive segments or (2) coefficients are slope changes at consecutive knots. Knots can be set manually or at break points of equal-frequency or equal-width intervals covering the range of 'x'. The implementation follows Greene (2003), chapter 7.2.5. / MIT	noarch
<a href="#">r-lsplsls</a>	0.2_2	Implements the LS-PLS (least squares - partial least squares) method described in for instance Jørgensen, K., Segtnan, V. H., Thyholt, K., Næs, T. (2004) A Comparison of Methods for Analysing Regression Models with Both Spectral and Designed Variables Journal of Chemometrics, 18(10), 451–464, <doi:10.1002/cem.890>. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-lsplsglm</a>	1.0	Fit logistic regression models using LS-PLS approaches to analyse both clinical and genomic data. (C. Bazzoli and S. Lambert-Lacroix. (2017) Classification using LS-PLS with logistic regression based on both clinical and gene expression variables < <a href="https://hal.archives-ouvertes.fr/hal-01405101">https://hal.archives-ouvertes.fr/hal-01405101</a> >). / GPL-2	noarch
<a href="#">r-lsr</a>	0.5	A collection of tools intended to make introductory statistics easier to teach, including wrappers for common hypothesis tests and basic data manipulation. It accompanies Navarro, D. J. (2015). Learning Statistics with R: A Tutorial for Psychology Students and Other Beginners, Version 0.5. [Lecture notes] School of Psychology, University of Adelaide, Adelaide, Australia. ISBN: 978-1-326-18972-3. URL: <a href="http://health.adelaide.edu.au/psychology/ccs/teaching/lsr/">http://health.adelaide.edu.au/psychology/ccs/teaching/lsr/</a> . / GPL-3	noarch
<a href="#">r-lsrs</a>	0.2.0	Rapid satellite data streams in operational applications have clear benefits for monitoring land cover, especially when information can be delivered as fast as changing surface conditions. Over the past decade, remote sensing has become a key tool for monitoring and predicting environmental variables by using satellite data. This package presents the main applications in remote sensing for land surface monitoring and land cover mapping (soil, vegetation, water...). Tomlinson, C.J., Chapman, L., Thornes, E., Baker, C (2011) <doi:10.1002/met.287>. / GPL-3	noarch
<a href="#">r-ltable</a>	1.0	Constructs tables of counts and proportions out of data sets. It has simplified syntax appealing for novice and even for advanced user under time pressure. It is particularly suitable for exploratory data analysis or presentation to single out most appropriate pieces of tabulated information. The other important feature is possibility to insert tables to Excel and Word documents. / GPL-2	noarch
<a href="#">r-ltpdvar</a>	1.2	Calculation of rectifying LTPD and AOQL plans for sampling inspection by variables which minimize mean inspection cost per lot of process average quality. / GPL-2	noarch
<a href="#">r-ltr</a>	1.0.0	A set of functions to execute the linear-transformation of replicate (LTR) algorithm for preprocessing of microarray data / GPL-2	noarch
<a href="#">r-ltsbase</a>	1.0.1	This is a new tool to estimate Ridge and Liu estimators based on LTS method in multiple linear regression analysis. / GPL-3	noarch
<a href="#">r-ltxsparklines</a>	1.1.2	Sparklines are small plots (about one line of text high), made popular by Edward Tufte. This package is the interface from R to the LaTeX package sparklines by Andreas Loeffler and Dan Luecking (< <a href="http://www.ctan.org/pkg/sparklines">http://www.ctan.org/pkg/sparklines</a> >). It can work with Sweave or knitr or other engines that produce TeX. The package can be used to plot vectors, matrices, data frames, time series (in ts or zoo format). / GPL-2   GPL-3	noarch
<a href="#">r-lubridate</a>	1.7.4	Functions to work with date-times and time-spans: fast and user friendly parsing of date-time data, extraction and updating of components of a date-time (years, months, days, hours, minutes, and seconds), algebraic manipulation on date-time and time-span objects. The ‘lubridate’ package has a consistent and memorable syntax that makes working with dates easy and fun. Parts of the ‘CCTZ’ source code, released under the Apache 2.0 License, are included in this package. See < <a href="https://github.com/google/cctz">https://github.com/google/cctz</a> > for more details. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
r-lucid	1.7	Print vectors (and data frames) of floating point numbers using a non-scientific format optimized for human readers. Vectors of numbers are rounded using significant digits, aligned at the decimal point, and all zeros trailing the decimal point are dropped. See: Wright (2016). Lucid: An R Package for Pretty-Printing Floating Point Numbers. In JSM Proceedings, Statistical Computing Section. Alexandria, VA: American Statistical Association. 2270-2279. / GPL-3	noarch
r-lumberjack	1.0.3	A framework that allows for easy logging of changes in data. Main features: start tracking changes by adding a single line of code to an existing script. Track changes in multiple datasets, using multiple loggers. Add custom-built loggers or use loggers offered by other packages. / GPL-3	noarch
r-lunar	0.1_04	Provides functions to calculate lunar and other environmental covariates. / MIT	noarch
r-luzlogr	0.2.0	Provides flexible but lightweight logging facilities for R scripts. Supports priority levels for logs and messages, flagging messages, capturing script output, switching logs, and logging to files or connections. / MIT	noarch
r-lzerospikeinference	1.0.3	An implementation of algorithms described in Jewell and Witten (2017) <arXiv:1703.08644>. / GPL-3	noarch
r-mac	1.1.1	This is an integrated meta-analysis package for conducting a correlational research synthesis. One of the unique features of this package is in its integration of user-friendly functions to facilitate statistical analyses at each stage in a meta-analysis with correlations. It uses recommended procedures as described in The Handbook of Research Synthesis and Meta-Analysis (Cooper, Hedges, & Valentine, 2009). / GPL-2	noarch
r-mad	0.8_2	A collection of functions for conducting a meta-analysis with mean differences data. It uses recommended procedures as described in The Handbook of Research Synthesis and Meta-Analysis (Cooper, Hedges, & Valentine, 2009). / GPL-2	noarch
r-maddison	0.1	Contains the Maddison Project database, which provides estimates of GDP per capita for all countries in the world between AD 1 and 2010. See <a href="http://www.ggdc.net/maddison">http://www.ggdc.net/maddison</a> for more information. / CC0	noarch
r-maditr	0.6.2	Package provides pipe-style interface for 'data.table'. It preserves all 'data.table' features without significant impact on performance. 'let' and 'take' functions are simplified interfaces for most common data manipulation tasks. For example, you can write 'mtcars %>% take(mean(mpg), by = am)' for aggregation or 'mtcars %>% let(hp_wt = hp/wt, hp_wt_mpg = hp_wt/mpg)' for modification. Use 'take_if/let_if' for conditional aggregation/modification. 'query_if' function translates its arguments one-to-one to '[.data.table]' method. Additionally there are some conveniences such as automatic 'data.frame' conversion to 'data.table'. / GPL-2	noarch
r-madr	1.0.0	Estimates average treatment effects using model average double robust (MA-DR) estimation. The MA-DR estimator is defined as weighted average of double robust estimators, where each double robust estimator corresponds to a specific choice of the outcome model and the propensity score model. The MA-DR estimator extend the desirable double robustness property by achieving consistency under the much weaker assumption that either the true propensity score model or the true outcome model be within a specified, possibly large, class of models. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-madsim	1.2.1	This function allows to generate two biological conditions synthetic microarray dataset which has similar behavior to those currently observed with common platforms. User provides a subset of parameters. Available default parameters settings can be modified. / GPL ( $\geq 2.0$ )	noarch
r-magclass	4.107	Data class for increased interoperability working with spatial- temporal data together with corresponding functions and methods (conversions, basic calculations and basic data manipulation). The class distinguishes between spatial, temporal and other dimensions to facilitate the development and interoperability of tools build for it. Additional features are name-based addressing of data and internal consistency checks (e.g. checking for the right data order in calculations). / LGPL-3	noarch
r-magic	1.5_9	A collection of efficient, vectorized algorithms for the creation and investigation of magic squares and hypercubes, including a variety of functions for the manipulation and analysis of arbitrarily dimensioned arrays. The package includes methods for creating normal magic squares of any order greater than 2. The ultimate intention is for the package to be a computerized embodiment all magic square knowledge, including direct numerical verification of properties of magic squares (such as recent results on the determinant of odd-ordered semimagic squares). Some antimagic functionality is included. The package also serves as a rebuttal to the often-heard comment I thought R was just for statistics. / GPL-2	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-magicfor	0.1.0	Magic functions to obtain results from for loops. / MIT	noarch
r-magrittr	1.5	Provides a mechanism for chaining commands with a new forward-pipe operator, <code>%&gt;%</code> . This operator will forward a value, or the result of an expression, into the next function call/expression. There is flexible support for the type of right-hand side expressions. For more information, see package vignette. To quote Rene Magritte, Ceci n'est pas un pipe. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-mail	1.0	Easy to use package for sending email notifications with status information from R / GPL-2	noarch
r-mailr	0.4.1	Interface to Apache Commons Email to send emails from R. / GPL-3	noarch
r-makefiler	1.0	A user-friendly interface for the construction of 'Makefiles'. / GPL-3	noarch
r-makeproject	1.0	This package creates an empty framework of files and directories for the Load, Clean, Func, Do structure described by Josh Reich. / GPL-3	noarch
r-malani	1.0	Find dark genes. These genes are often disregarded due to no detected mutation or differential expression, but are important in coordinating the functionality in cancer networks. / GPL-3	noarch
r-mallet	1.0	This package allows you to train topic models in mallet and load results directly into R. / MIT	noarch
r-mams	1.3	Designing multi-arm multi-stage studies with (asymptotically) normal endpoints and known variance. / GPL-2	noarch
r-managelocalrepo	0.1.5	This will allow easier management of a CRAN-style repository on local networks (i.e. not on CRAN). This might be necessary where hosted packages contain intellectual property owned by a corporation. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-mancie</a>	1.4	High-dimensional data integration is a critical but difficult problem in genomics research because of potential biases from high-throughput experiments. We present MANCIE, a computational method for integrating two genomic data sets with homogenous dimensions from different sources based on a PCA procedure as an approximation to a Bayesian approach. / GPL-2	noarch
<a href="#">r-mangotraining</a>	1.0.7	Datasets designed to be used in conjunction with Mango Solutions training materials and the book SAMS Teach Yourself R in 24 Hours (ISBN: 978-0-672-33848-9). / GPL-2	noarch
<a href="#">r-mangrove</a>	1.21	Methods for performing genetic risk prediction from genotype data. You can use it to perform risk prediction for individuals, or for families with missing data. / GPL-2	noarch
<a href="#">r-manipulate</a>	1.0.1	Interactive plotting functions for use within RStudio. The manipulate function accepts a plotting expression and a set of controls (e.g. slider, picker, checkbox, or button) which are used to dynamically change values within the expression. When a value is changed using its corresponding control the expression is automatically re-executed and the plot is redrawn. / GPL-2	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-manipulatewidget</a>	0.10.0	Like package ‘manipulate’ does for static graphics, this package helps to easily add controls like sliders, pickers, checkboxes, etc. that can be used to modify the input data or the parameters of an interactive chart created with package ‘htmlwidgets’. / GPL (>= 2)   file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-manytests</a>	1.2	Performs the multiple testing procedures of Cox (2011) <doi:10.5170/CERN-2011-006> and Wong and Cox (2007) <doi:10.1080/02664760701240014>. / GPL-2	noarch
<a href="#">r-maples</a>	1.0	MAPLES is a general method for the estimation of age profiles that uses standard micro-level demographic survey data. The aim is to estimate smoothed age profiles and relative risks for time-fixed and time-varying covariates. / GPL-2	noarch
<a href="#">r-mapmisc</a>	1.7.2	A minimal, light-weight set of tools for producing nice looking maps in R, with support for map projections. / GPL-3	noarch
<a href="#">r-mapplots</a>	1.5.1	Create simple maps; add sub-plots like pie plots to a map or any other plot; format, plot and export gridded data. The package was developed for displaying fisheries data but most functions can be used for more generic data visualisation. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-mapproj	1.2.6	Converts latitude/longitude into projected coordinates. / Lucent Public License	linux-32, linux-64, osx-64, win-32, win-64
r-maps	3.3.0	Display of maps. Projection code and larger maps are in separate packages ('mapproj' and 'mapdata'). / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
r-maptools	0.9_5	Set of tools for manipulating and reading geographic data, in particular 'ESRI Shapefiles'; C code used from 'shapelib'. It includes binary access to 'GSHHG' shoreline files. The package also provides interface wrappers for exchanging spatial objects with packages such as 'PBSmapping', 'spatstat', 'maps', 'RArcInfo', 'Stata tmap', 'WinBUGS', 'Mondrian', and others. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
r-maptree	1.4_7	Functions with example data for graphing, pruning, and mapping models from hierarchical clustering, and classification and regression trees. / Unlimited	noarch
r-mar	1.1_2	R functions for multivariate autoregressive analysis / GPL-2	noarch
r-march	3.1	Computation of various Markovian models for categorical data including homogeneous Markov chains of any order, MTD models, Hidden Markov models, and Double Chain Markov Models. / GPL-2	noarch
r-mareymap	1.3.4	Local recombination rates are graphically estimated across a genome using Marey maps. / GPL-2	noarch
r-marima	2.2	Multivariate ARIMA and ARIMA-X estimation using Spliid's algorithm (marima()) and simulation (marima.sim()). / GPL-2	noarch
r-markdown	0.9	Provides R bindings to the 'Sundown' 'Markdown' rendering library ( <a href="https://github.com/vmg/sundown">https://github.com/vmg/sundown</a> ). 'Markdown' is a plain-text formatting syntax that can be converted to 'XHTML' or other formats. See <a href="http://en.wikipedia.org/wiki/Markdown">http://en.wikipedia.org/wiki/Markdown</a> for more information about 'Markdown'. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-markmyassignment</a>	0.8.2	Automatic marking of R assignments for students and teachers based on ‘test-that’ test suites. / BSD_2_clause	noarch
<a href="#">r-mar1</a>	1.0	Functions provided allow data simulation; construction of weighted relative likelihood functions; clustering and principal component analysis based on weighted relative likelihood functions. / GPL-2	noarch
<a href="#">r-masae</a>	0.1_5	An S4 implementation of the unbiased extension of the model-assisted synthetic-regression estimator proposed by Mandallaz (2013) <DOI:10.1139/cjfr-2012-0381>, Mandallaz et al. (2013) <DOI:10.1139/cjfr-2013-0181> and Mandallaz (2014) <DOI:10.1139/cjfr-2013-0449>. It yields smaller variances than the standard bias correction, the generalised regression estimator. / GPL-2	noarch
<a href="#">r-mass</a>	7.3_5	Functions and datasets to support Venables and Ripley, Modern Applied Statistics with S (4th edition, 2002). / GPL-2   GPL-3	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-massign</a>	1.1.0	Constructing matrices for quick prototyping can be a nuisance, requiring the user to think about how to fill the matrix with values using the matrix() function. The %<-% operator solves that issue by allowing the user to construct matrices using code that shows the actual matrices. / MIT	noarch
<a href="#">r-masstimate</a>	1.3	Estimation equations are from a variety of sources but are, in general, based on regressions between skeletal measurements (e.g., femoral circumference) and body mass in living taxa. / GPL-2	noarch
<a href="#">r-mata</a>	0.4	Calculates Model-Averaged Tail Area Wald (MATA-Wald) confidence intervals, which are constructed using single-model estimators and model weights. See Turek and Fletcher (2012) <doi:10.1016/j.csda.2012.03.002> for details. / GPL-2	noarch
<a href="#">r-matchbook</a>	1.0.7	Provides a wrapper for the some basic functionality around the ‘Matchbook’ < <a href="http://www.matchbook.com">http://www.matchbook.com</a> > REST API. It features calls to get events, markets and runners in data frame format. It features functions for bet placement and position management and also allows reporting of settled bet transactions. Note: this package uses the back-lay format. The default for odds type, currency and language are set according to those of the registered user account. / MIT	noarch
<a href="#">r-matconv</a>	0.4.0	Transferring over a code base from Matlab to R is often a repetitive and inefficient use of time. This package provides a translator for Matlab / Octave code into R code. It does some syntax changes, but most of the heavy lifting is in the function changes since the languages are so similar. Options for different data structures and the functions that can be changed are given. The Matlab code should be mostly in adherence to the standard style guide but some effort has been made to accommodate different number of spaces and other small syntax issues. This will not make the code more R friendly and may not even run afterwards. However, the rudimentary syntax, base function and data structure conversion is done quickly so that the maintainer can focus on changes to the design structure. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-mathgraph</a>	0.9_1	Simple tools for constructing and manipulating objects of class mathgraph from the book S Poetry, available at <a href="http://www.burns-stat.com/pages/spoetry.html">http://www.burns-stat.com/pages/spoetry.html</a> . / GPL-2	noarch
<a href="#">r-matlab</a>	1.0.2	Emulate MATLAB code using R / Artistic-2.0	noarch
<a href="#">r-matlabr</a>	1.5.2	Provides users to call MATLAB from using the system command. Allows users to submit lines of code or MATLAB m files. This is in comparison to 'R.matlab', which creates a MATLAB server. / GPL-2	noarch
<a href="#">r-matpow</a>	0.1.1	A general framework for computing powers of matrices. A key feature is the capability for users to write callback functions, called after each iteration, thus enabling customization for specific applications. Diverse types of matrix classes/matrix multiplication are accommodated. If the multiplication type computes in parallel, then the package computation is also parallel. / GPL-2	noarch
<a href="#">r-matrix</a>	1.2_1	A rich hierarchy of matrix classes, including triangular, symmetric, and diagonal matrices, both dense and sparse and with pattern, logical and numeric entries. Numerous methods for and operations on these matrices, using 'LAPACK' and 'SuiteSparse' libraries. / GPL (>= 2)   file LICENCE	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-matrixcalc</a>	1.0_3	A collection of functions to support matrix calculations for probability, econometric and numerical analysis. There are additional functions that are comparable to APL functions which are useful for actuarial models such as pension mathematics. This package is used for teaching and research purposes at the Department of Finance and Risk Engineering, New York University, Polytechnic Institute, Brooklyn, NY 11201. / GPL (>= 2)	linux-64, noarch, win-64
<a href="#">r-matrixeqtl</a>	2.2	Matrix eQTL is designed for fast eQTL analysis on large datasets. Matrix eQTL can test for association between genotype and gene expression using linear regression with either additive or ANOVA genotype effects. The models can include covariates to account for factors as population stratification, gender, and clinical variables. It also supports models with heteroscedastic and/or correlated errors, false discovery rate estimation and separate treatment of local (cis) and distant (trans) eQTLs. / LGPL-3	noarch
<a href="#">r-matrixmodels</a>	0.4_1	Modelling with sparse and dense 'Matrix' matrices, using modular prediction and response module classes. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-matrixnormal</a>	0.0.1	Computes densities, probabilities, and random deviates of the Matrix Normal (Iranmanesh et al. (2010) <doi:10.7508/ijmsi.2010.02.004>). Also includes simple but useful matrix functions. See the vignette for more information. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-matrixstats</a>	0.54.0	High-performing functions operating on rows and columns of matrices, e.g. <code>col / rowMedians()</code> , <code>col / rowRanks()</code> , and <code>col / rowSds()</code> . Functions optimized per data type and for subsetting calculations such that both memory usage and processing time is minimized. There are also optimized vector-based methods, e.g. <code>binMeans()</code> , <code>madDiff()</code> and <code>weightedMedian()</code> . / Artistic-2.0	linux-64, osx-64, win-32, win-64
<a href="#">r-matrixstructest</a>	1.0.0	Tests for block-diagonal structure in symmetric matrices (e.g. correlation matrices) under the null hypothesis of exchangeable off-diagonal elements. As described in Segal et al. (2019), these tests can be useful for construct validation either by themselves or as a complement to confirmatory factor analysis. Monte Carlo methods are used to approximate the permutation p-value with Hubert's Gamma (Hubert, 1976) and a t-statistic. This package also implements the chi-squared statistic described by Steiger (1980). Please see Segal, et al. (2019) <doi:10.1007/s11336-018-9647-4> for more information. / GPL-3	noarch
<a href="#">r-matrixtests</a>	0.1.5	Functions to perform fast statistical hypothesis tests on rows/columns of matrices. The main goals are: 1) speed via vectorization, 2) output that is detailed and easy to use, 3) compatibility with tests implemented in R (like those available in the 'stats' package). / GPL-2	noarch
<a href="#">r-matskew</a>	0.1.5	Performs matrix skew-t parameter estimation, Gallagher and McNicholas (2017) <doi: 10.1002/sta4.143>. / GPL-2	noarch
<a href="#">r-mattools</a>	1.1	This package includes functions for receiver operating characteristic (ROC) analyses as well as Monte Carlo simulation. It includes specific graphical functions for interpreting the output of these techniques. / GPL-2	noarch
<a href="#">r-mavtgsa</a>	1.3	This package is a gene set analysis function for one-sided test (OLS), two-sided test (multivariate analysis of variance). If the experimental conditions are equal to 2, the p-value for Hotelling's $t^2$ test is calculated. If the experimental conditions are greater than 2, the p-value for Wilks' Lambda is determined and post-hoc test is reported too. Three multiple comparison procedures, Dunnett, Tukey, and sequential pairwise comparison, are implemented. The program computes the p-values and FDR (false discovery rate) q-values for all gene sets. The p-values for individual genes in a significant gene set are also listed. MAVTgsa generates two visualization output: a p-value plot of gene sets (GSA plot) and a GST-plot of the empirical distribution function of the ranked test statistics of a given gene set. A Random Forests-based procedure is to identify gene sets that can accurately predict samples from different experimental conditions or are associated with the continuous phenotypes. / GPL-2	noarch
<a href="#">r-maxlik</a>	1.3.4	Functions for Maximum Likelihood (ML) estimation and non-linear optimization, and related tools. It includes a unified way to call different optimizers, and classes and methods to handle the results from the ML viewpoint. It also includes a number of convenience tools for testing and developing your own models. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-maxlike</a>	0.1.7	Provides a likelihood-based approach to modeling species distributions using presence-only data. In contrast to the popular software program MAXENT, this approach yields estimates of the probability of occurrence, which is a natural descriptor of a species' distribution. / GPL-3	noarch
<a href="#">r-maxmatching</a>	0.1.0	Computes the maximum matching for unweighted graph and maximum matching for (un)weighted bipartite graph efficiently. / CC0	noarch
<a href="#">r-maxnet</a>	0.1.2	Procedures to fit species distributions models from occurrence records and environmental variables, using 'glmnet' for model fitting. Model structure is the same as for the 'Maxent' Java package, version 3.4.0, with the same feature types and regularization options. See the 'Maxent' website < <a href="http://biodiversityinformatics.amnh.org/open_source/maxent">http://biodiversityinformatics.amnh.org/open_source/maxent</a> > for more details. / MIT	noarch
<a href="#">r-maxskew</a>	1.1	It finds Orthogonal Data Projections with Maximal Skewness. The first data projection in the output is the most skewed among all linear data projections. The second data projection in the output is the most skewed among all data projections orthogonal to the first one, and so on. / GPL-2	noarch
<a href="#">r-mazegen</a>	0.1.3	A maze generator that creates the Elithorn Maze (HTML file) and the functions to calculate the associated maze parameters (i.e. Difficulty and Ability). / GPL-3	noarch
<a href="#">r-mazeinda</a>	0.0.1	Methods for calculating and testing the significance of pairwise monotonic association from and based on the work of Pimentel (2009) <doi:10.4135/9781412985291.n2>. Computation of association of vectors from one or multiple sets can be performed in parallel thanks to the packages 'foreach' and 'doMC'. / GPL-3	noarch
<a href="#">r-mbc</a>	0.10.4	Calibrate and apply multivariate bias correction algorithms for climate model simulations of multiple climate variables. Three methods described by Cannon (2016) <doi:10.1175/JCLI-D-15-0679.1> and Cannon (2018) <doi:10.1007/s00382-017-3580-6> are implemented: (i) MBC Pearson correlation (MBCp), (ii) MBC rank correlation (MBCr), and (iii) MBC N-dimensional PDF transform (MBCn). / GPL-2	noarch
<a href="#">r-mbcluster.seq</a>	1.0	Cluster genes based on Poisson or Negative-Binomial model for RNA-Seq or other digital gene expression (DGE) data / GPL-3	noarch
<a href="#">r-mbi</a>	1.0	Over 20 multiple-site diversity indices can be calculated. Later versions will include phylogenetic diversity / GPL-2	noarch
<a href="#">r-mbir</a>	1.3.5	Allows practitioners and researchers a wholesale approach for deriving magnitude-based inferences from raw data. A major goal of 'mbir' is to programmatically detect appropriate statistical tests to run in lieu of relying on practitioners to determine correct stepwise procedures independently. / GPL-2	noarch
<a href="#">r-mblm</a>	0.12.1	Provides linear models based on Theil-Sen single median and Siegel repeated medians. They are very robust (29 or 50 percent breakdown point, respectively), and if no outliers are present, the estimators are very similar to OLS. / GPL-2	noarch
<a href="#">r-mc2d</a>	0.1.18	A complete framework to build and study Two-Dimensional Monte-Carlo simulations, aka Second-Order Monte-Carlo simulations. Also includes various distributions (pert, triangular, Bernoulli, empirical discrete and continuous). / GPL-2	noarch
<a href="#">r-mcbftest</a>	0.1.0	Monte Carol based tests for the Behrens Fisher Problem enhance the statistical power and performs better than Welch's t-approximation, see Ullah et al. (2019). / GPL (>= 2.0)	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-mcbiopi</a>	1.1.6	Computes the prime implicants or a minimal disjunctive normal form for a logic expression presented by a truth table or a logic tree. Has been particularly developed for logic expressions resulting from a logic regression analysis, i.e. logic expressions typically consisting of up to 16 literals, where the prime implicants are typically composed of a maximum of 4 or 5 literals. / LGPL-2	noarch
<a href="#">r-mcc</a>	1.0	A number of biomedical problems involve performing many hypothesis tests, with an attendant need to apply stringent thresholds. Often the data take the form of a series of predictor vectors, each of which must be compared with a single response vector, perhaps with nuisance covariates. Parametric tests of association are often used, but can result in inaccurate type I error at the extreme thresholds, even for large sample sizes. Furthermore, standard two-sided testing can reduce power compared to the doubled p-value, due to asymmetry in the null distribution. Exact (permutation) testing approaches are attractive, but can be computationally intensive and cumbersome. MCC is an approximation to exact association testing of two vectors that is accurate and fast enough for standard use in high-throughput settings, and can easily provide standard two-sided or doubled p-values. / GPL-2	noarch
<a href="#">r-mccmeiv</a>	2.1	Applying the methodology from Manuel et al. to estimate parameters using a matched case control data with a mismeasured exposure variable that is accompanied by instrumental variables (Submitted). / GPL-2	noarch
<a href="#">r-mccr</a>	0.4.4	The Matthews correlation coefficient (MCC) score is calculated (Matthews BW (1975) <DOI:10.1016/0005-2795(75)90109-9>). / MIT	noarch
<a href="#">r-mcgibbsit</a>	1.1.0	'mcgibbsit' provides an implementation of Warnes & Raftery's MCGibbsit run-length diagnostic for a set of (not-necessarily independent) MCMC samplers. It combines the estimate error-bounding approach of the Raftery and Lewis MCMC run length diagnostic with the between verses within chain approach of the Gelman and Rubin MCMC convergence diagnostic. / GPL-3	noarch
<a href="#">r-mcheatmaps</a>	1.0.0	mcheatmaps serves to visualize multiple different symmetric matrices and matrix clusters in a single figure using a dendrogram, two half matrices and various color labels. / GPL-3	noarch
<a href="#">r-mchtest</a>	1.0.3	Performs Monte Carlo hypothesis tests, allowing a couple of different sequential stopping boundaries. For example, a truncated sequential probability ratio test boundary (Fay, Kim and Hachey, 2007 <DOI:10.1198/106186007X257025>) and a boundary proposed by Besag and Clifford, 1991 <DOI:10.1093/biomet/78.2.301>. Gives valid p-values and confidence intervals on p-values. / GPL-3	noarch
<a href="#">r-mci</a>	1.3.3	Market area models are used to analyze and predict store choices and market areas concerning retail and service locations. This package implements two market area models (Huff Model, Multiplicative Competitive Interaction Model) into R, while the emphases lie on 1.) fitting these models based on empirical data via OLS regression and nonlinear techniques and 2.) data preparation and processing (esp. interaction matrices and data preparation for the MCI Model). / GPL-2	noarch
<a href="#">r-mcmcplots</a>	0.4.3	Functions for convenient plotting and viewing of MCMC output. / GPL-2	noarch
<a href="#">r-mconjoint</a>	0.1	The package aids in creating a Conjoint Analysis design with extra cards. Unlike traditional holdout cards these cards are used to create a set of good (balanced and low correlation) designs. Each of these designs is analyzed and the average calculated. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<code>r-mcparallel</code>	1.1.0	Provides a function that wraps <code>mcparallel()</code> and <code>mccollect()</code> from ‘parallel’ with temporary variables and a task handler. Wrapped in this way the results of an <code>mcparallel()</code> call can be returned to the R session when the fork is complete without explicitly issuing a specific <code>mccollect()</code> to retrieve the value. Outside of top-level tasks, multiple <code>mcparallel()</code> jobs can be retrieved with a single call to <code>mcparallelDoCheck()</code> . / GPL-2	noarch
<code>r-mcpmod</code>	1.0_1	Implements a methodology for the design and analysis of dose-response studies that combines aspects of multiple comparison procedures and modeling approaches (Bretz, Pinheiro and Branson, 2005, Biometrics 61, 738-748, <doi:10.1111/j.1541-0420.2005.00344.x>). The package provides tools for the analysis of dose finding trials as well as a variety of tools necessary to plan a trial to be conducted with the MCP-Mod methodology. Please note: The ‘MCPMod’ package will not be further developed, all future development of the MCP-Mod methodology will be done in the ‘DoseFinding’ R-package. / GPL-3	noarch
<code>r-mcpmodgeneral</code>	0.1_0	Analyzes non-normal data via the Multiple Comparison Procedures and Modeling approach (MCP-Mod). Many functions rely on the ‘DoseFinding’ package. This package makes it so the user does not need to provide or calculate the mu vector and S matrix. Instead, the user typically supplies the data in its raw form, and this package will calculate the needed objects and passes them into the ‘DoseFinding’ functions. If the user wishes to primarily use the functions provided in the ‘DoseFinding’ package, a singular function ( <code>prepareGen()</code> ) will provide mu and S. The package currently handles power analysis and the MCP-Mod procedure for negative binomial, Poisson, and binomial data. The MCP-Mod procedure can also be applied to survival data, but power analysis is not available. Bretz, F., Pinheiro, J. C., and Branson, M. (2005) <doi:10.1111/j.1541-0420.2005.00344.x>. Buckland, S. T., Burnham, K. P. and Augustin, N. H. (1997) <doi:10.2307/2533961>. Pinheiro, J. C., Bornkamp, B., Glimm, E. and Bretz, F. (2014) <doi:10.1002/sim.6052>. / GPL-3	noarch
<code>r-mcs</code>	0.1.3	Perform the model confidence set procedure of Hansen et al (2011) <doi:10.3982/ECTA5771>. / GPL-2	noarch
<code>r-mcsim</code>	1.0	Identifies the optimal number of clusters by calculating the similarity between two clustering methods at the same number of clusters using the corrected indices of Rand and Jaccard as described in Albatineh and Niewiadomska-Bugaj (2011). The number of clusters at which the index attain its maximum more frequently is a candidate for being the optimal number of clusters. / GPL-2	noarch
<code>r-mcsm</code>	1.0	<code>mcsm</code> contains a collection of functions that allows the reenactment of the R programs used in the book <i>EnteR Monte Carlo Methods</i> without further programming. Programs being available as well, they can be modified by the user to conduct one’s own simulations. / GPL-2	noarch
<code>r-mctest</code>	1.2	Package computes popular and widely used multicollinearity diagnostic measures. Package also indicates which regressors may be the reason of collinearity among regressors. / GPL-2	noarch
<code>r-mctm</code>	1.0	Transition matrices (probabilities or counts) estimation for discrete Markov Chains of order n ( $1 \leq n \leq 5$ ). / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-md	1.0.4	Selects bandwidth for the kernel density estimator with minimum distance method as proposed by Devroye and Lugosi (1996). The minimum distance method directly selects the optimal kernel density estimator from countably infinite kernel density estimators and indirectly selects the optimal bandwidth. This package selects the optimal bandwidth from finite kernel density estimators. / GPL-2   GPL-3	noarch
r-mdatools	0.9.4	Package implements projection based methods for preprocessing, exploring and analysis of multivariate data used in chemometrics. / MIT	noarch
r-mded	0.1_2	Provides a function for measuring the difference between two independent or non-independent empirical distributions and returning a significance level of the difference. / CC0	noarch
r-mdendro	1.0.1	A collection of methods for agglomerative hierarchical clustering strategies on a matrix of distances, implemented using the variable-group approach introduced in Fernandez and Gomez (2008) <doi:10.1007/s00357-008-9004-x>. Descriptive measures to analyze the resulting hierarchical trees are also provided. In addition to the usual clustering methods, two parameterized methods are provided to explore an infinite family of hierarchical clustering strategies. When there are ties in proximity values, the hierarchical trees obtained are unique and independent of the order of the elements in the input matrix. / LGPL-2.1	noarch
r-mdhglm	1.8	Allows various models for multivariate response variables where each response is assumed to follow double hierarchical generalized linear models. In double hierarchical generalized linear models, the mean, dispersion parameters for variance of random effects, and residual variance can be further modeled as random-effect models. / Unlimited	noarch
r-mdimnormn	0.8.0	Normalize data to minimize the difference between sample plates (batch effects). For given data in a matrix and grouping variable (or plate), the function 'normn_MA' normalizes the data on MA coordinates. More details are in the citation. The primary method is 'Multi-MA'. Other fitting functions on MA coordinates can also be employed e.g. loess. / GPL-3	noarch
r-mdir.logrank	0.0.4	Implemented are the one-sided and two-sided multiple-direction logrank test for two-sample right censored data. In addition to the statistics p-values are calculated: 1. For the one-sided testing problem one p-value based on a wild bootstrap approach is determined. 2. In the two-sided case one p-value based on a chi-squared approximation and a second p-values based on a permutation approach are calculated. Ditzhaus, M. and Friedrich, S. (2018) <arXiv:1807.05504>. Ditzhaus, M. and Pauly, M. (2018) <arXiv:1808.05627>. / GPL-2   GPL-3	noarch
r-mdplot	1.0.1	Provides automatization for plot generation succeeding common molecular dynamics analyses. This includes straightforward plots, such as RMSD (Root-Mean-Square-Deviation) and RMSF (Root-Mean-Square-Fluctuation) but also more sophisticated ones such as dihedral angle maps, hydrogen bonds, cluster bar plots and DSSP (Definition of Secondary Structure of Proteins) analysis. Currently able to load GROMOS, GROMACS and AMBER formats, respectively. / GPL-3	noarch
r-mdscore	0.1_3	A set of functions to obtain modified score test for generalized linear models. / GPL-2	noarch
r-mdw	2017.12.03	Dimension-reduction methods aim at defining a score that maximizes signal diversity. Two approaches, namely maximum entropy weights and maximum variance weights, are provided. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-measurements	1.4.0	Collection of tools to make working with physical measurements easier. Convert between metric and imperial units, or calculate a dimension's unknown value from other dimensions' measurements. / GPL-3	noarch
r-measures	0.2	Provides the biggest amount of statistical measures in the whole R world. Includes measures of regression, (multiclass) classification and multilabel classification. The measures come mainly from the 'mlr' package and were programmed by several 'mlr' developers. / GPL-3	noarch
r-med	0.1.0	Nonparametric estimation and inference for natural direct and indirect effects by Chan, Imai, Yam and Zhang (2016) <arXiv:1601.03501>. / GPL-2	noarch
r-meddietcalc	0.1.1	Multi Calculator of different scores to measure adherence to Mediterranean Diet, to compute them in nutrieidemiological data. Additionally, a sample dataset of this kind of data is provided, and some other minor tools useful in epidemiological studies. / GPL-3	noarch
r-mederrrank	0.0.8	Two distinct but related statistical approaches to the problem of identifying the combinations of medication error characteristics that are more likely to result in harm are implemented in this package: 1) a Bayesian hierarchical model with optimal Bayesian ranking on the log odds of harm, and 2) an empirical Bayes model that estimates the ratio of the observed count of harm to the count that would be expected if error characteristics and harm were independent. In addition, for the Bayesian hierarchical model, the package provides functions to assess the sensitivity of results to different specifications of the random effects distributions. / GPL-2	noarch
r-medextractr	0.1	Function and support for medication and dosing information extraction from free-text clinical notes. Medication entities that can be extracted include drug name, strength, dose amount, dose, frequency, intake time, and time of last dose. / GPL-2	noarch
r-mediadcloudr	0.1.0	API wrapper to gather news stories, media information and tags from the 'mediadcloud.org' API, based on a multilevel query < <a href="https://mediadcloud.org/">https://mediadcloud.org/</a> >. A personal API key is required. / MIT	noarch
r-mediak	1.0	Calculates MeDiA_K (means Mean Distance Association by K-nearest neighbor) in order to detect nonlinear associations. / GPL-3	linux-64, osx-64, win-64
r-mediana	1.0.8	Provides a general framework for clinical trial simulations based on the Clinical Scenario Evaluation (CSE) approach. The package supports a broad class of data models (including clinical trials with continuous, binary, survival-type and count-type endpoints as well as multivariate outcomes that are based on combinations of different endpoints), analysis strategies and commonly used evaluation criteria. / GPL-2	noarch
r-medicare	0.2.1	Publicly available data from Medicare frequently requires extensive initial effort to extract desired variables and merge them; this package formalizes the techniques I've found work best. More information on the Medicare program, as well as guidance for the publicly available data this package targets, can be found on CMS's website covering publicly available data. See < <a href="https://www.cms.gov/Research-Statistics-Data-and-Systems/Research-Statistics-Data-and-Systems.html">https://www.cms.gov/Research-Statistics-Data-and-Systems/Research-Statistics-Data-and-Systems.html</a> >. / MIT	noarch
r-meditations	1.0.1	Prints a random quote from Marcus Aurelius' book Meditations. / GPL-3	noarch
r-medor	0.1	This package contains the functions used to perform some confidence statistics based in population median. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-mefa	3.2.7	A framework package aimed to provide standardized computational environment for specialist work via object classes to represent the data coded by samples, taxa and segments (i.e. subpopulations, repeated measures). It supports easy processing of the data along with cross tabulation and relational data tables for samples and taxa. An object of class ‘mefa’ is a project specific compendium of the data and can be easily used in further analyses. Methods are provided for extraction, aggregation, conversion, plotting, summary and reporting of ‘mefa’ objects. Reports can be generated in plain text or LaTeX format. Vignette contains worked examples. / GPL-2	noarch
r-mefa4	0.3.6	An S4 update of the ‘mefa’ package using sparse matrices for enhanced efficiency. Sparse array-like objects are supported via lists of sparse matrices. / GPL-2	noarch
r-meifly	0.3	Exploratory model analysis. Fit and graphical explore ensembles of linear models. / MIT	noarch
r-memnet	0.1.0	Efficient implementations of network science tools to facilitate research into human (semantic) memory. In its current version, the package contains several methods to infer networks from verbal fluency data, various network growth models, diverse (switcher-) random walk processes, and tools to analyze and visualize networks. To deliver maximum performance the majority of the code is written in C. For an application see: Wulff, D. U., Hills, T., & Mata, R. (2018) <doi:10.31234/osf.io/s73dp>. / GPL-3	linux-64, osx-64, win-64
r-memo	1.0.1	A simple in-memory, LRU cache that can be wrapped around any function to memoize it. The cache can be keyed on a hash of the input data (using ‘digest’) or on pointer equivalence. / MIT	linux-64, osx-64, win-64
r-memoise	1.1.0	Cache the results of a function so that when you call it again with the same arguments it returns the pre-computed value. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-memor	0.2	A ‘rmarkdown’ template that supports company logo, contact info, watermarks and more. Currently restricted to ‘Latex’/‘Markdown’; a similar ‘HTML’ theme will be added in the future. / GPL-3	noarch
r-memss	0.9.3	Data sets and sample analyses from Pinheiro and Bates, Mixed-effects Models in S and S-PLUS (Springer, 2000). / GPL-2	noarch
r-memuse	4.0.0	How much ram do you need to store a 100,000 by 100,000 matrix? How much ram is your current R session using? How much ram do you even have? Learn the scintillating answer to these and many more such questions with the ‘memuse’ package. / BSD_2_clause	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-mergetrees	0.1.3	Aggregates a set of trees with the same leaves to create a consensus tree. The trees are typically obtained via hierarchical clustering, hence the hclust format is used to encode both the aggregated trees and the final consensus tree. The method is exact and proven to be $O(nq\log(n))$ , $n$ being the individuals and $q$ being the number of trees to aggregate. / GPL-2	linux-64, osx-64, win-64
r-merror	2.0.2	$N \geq 3$ methods are used to measure each of $n$ items. The data are used to estimate simultaneously systematic error (bias) and random error (imprecision). Observed measurements for each method or device are assumed to be linear functions of the unknown true values and the errors are assumed normally distributed. Maximum likelihood estimation is used for the imprecision standard deviation estimates. Pairwise calibration curves and plots can be easily generated. / GPL-2	noarch
r-meta4diag	2.0.8	Bayesian inference analysis for bivariate meta-analysis of diagnostic test studies using integrated nested Laplace approximation with INLA. A purpose built graphic user interface is available. The installation of R package INLA is compulsory for successful usage. The INLA package can be obtained from <a href="http://www.r-inla.org">http://www.r-inla.org</a> . We recommend the testing version, which can be downloaded by running: <code>install.packages(INLA, repos=c(getOption(repos), INLA=https://inla.r-inla-download.org/R/testing), dep=TRUE)</code> . / GPL-3	noarch
r-metabel	0.2.0	A package for meta-analysis of genome-wide association scans between quantitative or binary traits and SNPs / GPL-2	noarch
r-metablue	1.0.0	The sample mean and standard deviation are two commonly used statistics in meta-analyses, but some trials use other summary statistics such as the median and quartiles to report the results. Therefore, researchers need to transform those information back to the sample mean and standard deviation. This package implemented sample mean estimators by Luo et al. (2016) <arXiv:1505.05687>, sample standard deviation estimators by Wan et al. (2014) <arXiv:1407.8038>, and the best linear unbiased estimators (BLUEs) of location and scale parameters by Yang et al. (2018, submitted) based on sample quantiles derived summaries in a meta-analysis. / GPL-2	noarch
r-metabolouise	1.0.0	Simulating dynamic (longitudinal, time-resolved) metabolomics data based on an underlying biological network. The network is initiating with certain concentrations and evolves over a simulated time period. Optionally external influxes (concentration drivers) can be added. / GPL-3	noarch
r-metaboqc	1.0	Takes QC signal for each day and normalize metabolomic data that has been acquired in a certain period of time. At least three QC per day are required. / GPL-2	noarch
r-metadynminer	0.1.6	Metadynamics is a state of the art biomolecular simulation technique. ‘Plumed’ Tribello, G.A. et al. (2014) <doi:10.1016/j.cpc.2013.09.018> program makes it possible to perform metadynamics using various simulation codes. The results of metadynamics done in ‘Plumed’ can be analyzed by ‘metadynminer’. The package ‘metadynminer’ reads 1D and 2D metadynamics hills files from ‘Plumed’ package. It uses a fast algorithm by Hosek, P. and Spiwok, V. (2016) <doi:10.1016/j.cpc.2015.08.037> to calculate a free energy surface from hills. Minima can be located and plotted on the free energy surface. Transition states can be analyzed by Nudged Elastic Band method by Henkelman, G. and Jonsson, H. (2000) <doi:10.1063/1.1323224>. Free energy surfaces, minima and transition paths can be plotted to produce publication quality images. / GPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-metafolio	0.1.0	The metafolio R package is a tool to simulate salmon metapopulations and apply financial portfolio optimization concepts. The package accompanies the paper ‘Portfolio conservation of metapopulations under climate change’. See citation(metafolio). / GPL-2	linux-64, osx-64, win-64
r-metafor	2.1_0	A comprehensive collection of functions for conducting meta-analyses in R. The package includes functions to calculate various effect sizes or outcome measures, fit fixed-, random-, and mixed-effects models to such data, carry out moderator and meta-regression analyses, and create various types of meta-analytical plots (e.g., forest, funnel, radial, L’Abbe, Baujat, GOSH plots). For meta-analyses of binomial and person-time data, the package also provides functions that implement specialized methods, including the Mantel-Haenszel method, Peto’s method, and a variety of suitable generalized linear (mixed-effects) models (i.e., mixed-effects logistic and Poisson regression models). Finally, the package provides functionality for fitting meta-analytic multivariate/multilevel models that account for non-independent sampling errors and/or true effects (e.g., due to the inclusion of multiple treatment studies, multiple endpoints, or other forms of clustering). Network meta-analyses and meta-analyses accounting for known correlation structures (e.g., due to phylogenetic relatedness) can also be conducted. / GPL-2	noarch
r-metaheuristicfpa	1.0	A nature-inspired metaheuristics algorithm based on the pollination process of flowers. This R package makes it easy to implement the standard flower pollination algorithm for every user. The algorithm was first developed by Xin-She Yang in 2012 (<DOI:10.1007/978-3-642-32894-7_27>). / GPL-2	linux-64, osx-64, win-64
r-metaheuristicopt	2.0.0	An implementation of metaheuristic algorithms for continuous optimization. Currently, the package contains the implementations of 21 algorithms, as follows: particle swarm optimization (Kennedy and Eberhart, 1995), ant lion optimizer (Mirjalili, 2015 <doi:10.1016/j.advengsoft.2015.01.010>), grey wolf optimizer (Mirjalili et al., 2014 <doi:10.1016/j.advengsoft.2013.12.007>), dragonfly algorithm (Mirjalili, 2015 <doi:10.1007/s00521-015-1920-1>), firefly algorithm (Yang, 2009 <doi:10.1007/978-3-642-04944-6_14>), genetic algorithm (Holland, 1992, ISBN:978-0262581110), grasshopper optimisation algorithm (Saremi et al., 2017 <doi:10.1016/j.advengsoft.2017.01.004>), harmony search algorithm (Mahdavi et al., 2007 <doi:10.1016/j.amc.2006.11.033>), moth flame optimizer (Mirjalili, 2015 <doi:10.1016/j.knosys.2015.07.006>), sine cosine algorithm (Mirjalili, 2016 <doi:10.1016/j.knosys.2015.12.022>), whale optimization algorithm (Mirjalili and Lewis, 2016 <doi:10.1016/j.advengsoft.2016.01.008>), clonal selection algorithm (Castro, 2002 <doi:10.1109/TEVC.2002.1011539>), differential evolution (Das & Suganthan, 2011), shuffled frog leaping (Eusuff, Landsey & Pasha, 2006), cat swarm optimization (Chu et al., 2006), artificial bee colony algorithm (Karaboga & Akay, 2009), krill-herd algorithm (Gandomi & Alavi, 2012), cuckoo search (Yang & Deb, 2009), bat algorithm (Yang, 2012), gravitational based search (Rashedi et al., 2009) and black hole optimization (Hatamlou, 2013). / GPL-2	noarch
r-metalik	0.43.0	First- and higher-order likelihood inference in meta-analysis and meta-regression models. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-metansue</a>	2.3	Novel method to unbiasedly include studies with Non-statistically Significant Unreported Effects (NSUEs) in a meta-analysis <a href="https://doi.org/10.1001/jamapsychiatry.2015.2196">doi:10.1001/jamapsychiatry.2015.2196</a> and <a href="https://doi.org/10.1177/0962280218811349">doi:10.1177/0962280218811349</a> . Briefly, the method first calculates the interval where the unreported effects (e.g. t-values) should be according to the threshold of statistical significance used in each study. Afterwards, maximum likelihood techniques are used to impute the expected effect size of each study with NSUEs, accounting for between-study heterogeneity and potential covariates. Multiple imputations of the NSUEs are then randomly created based on the expected value, variance and statistical significance bounds. Finally, a restricted-maximum likelihood random-effects meta-analysis is separately conducted for each set of imputations, and estimations from these meta-analyses are pooled. Please read the reference in ‘metansue’ for details of the procedure. / GPL-3	noarch
<a href="#">r-metapca</a>	0.1.4	MetaPCA implements simultaneous dimension reduction using PCA when multiple studies are combined. We propose two basic ideas to find a common PC subspace by eigenvalue maximization approach and angle minimization approach, and we extend the concept to incorporate Robust PCA and Sparse PCA in the meta-analysis realm. / GPL-2	noarch
<a href="#">r-metarnaseq</a>	1.0.2	Implementation of two p-value combination techniques (inverse normal and Fisher methods). A vignette is provided to explain how to perform a meta-analysis from two independent RNA-seq experiments. / GPL-3	noarch
<a href="#">r-metasubtract</a>	1.50	If results from a meta-GWAS are used for validation in one of the cohorts that was included in the meta-analysis, this will yield biased (i.e. too optimistic) results. The validation cohort needs to be independent from the meta-Genome-Wide-Association-Study (meta-GWAS) results. ‘MetaSubtract’ will subtract the results of the respective cohort from the meta-GWAS results analytically without having to redo the meta-GWAS analysis using the leave-one-out methodology. It can handle different meta-analyses methods and takes into account if single or double genomic control correction was applied to the original meta-analysis. It can also handle different meta-analysis methods. It can be used for whole GWAS, but also for a limited set of genetic markers. / GPL-3	noarch
<a href="#">r-metatest</a>	1.0_5	Fits and tests meta regression models and generates a number of useful test statistics: next to t- and z-tests, the likelihood ratio, bartlett corrected likelihood ratio and permutation tests are performed on the model coefficients. / GPL-3	noarch
<a href="#">r-metavcov</a>	1.1	Compute variance-covariance matrix for multivariate meta-analysis. Effect sizes include correlation (r), mean difference (MD), standardized mean difference (SMD), log odds ratio (logOR), log risk ratio (logRR), and risk difference (RD). / GPL-2	noarch
<a href="#">r-meteor</a>	0.3_4	A set of functions for weather and climate data manipulation, and other helper functions, to support dynamic ecological modelling, particularly crop and crop disease modeling. / GPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-meth27qc</a>	1.1	Meth27QC is a tool for analyzing Illumina Infinium HumanMethylation27 BeadChip Data and generating QC reports. This package allows users quickly assess data quality of the Assay. Users can evaluate the data quality in the way that Illumina GenomeStudio/BeadStudio recommended based on the control probes. The package reads files exported from GenomeStudio/BeadStudio software, generating intensity and standard deviation plots grouped by the types of the control probes. Meth27 carries 40 control probes for staining, hybridization, target removal, extension, bisulfite conversion, specificity, negative and non-polymorphic controls. Details of those control probes can be found in the Infinium Assay for Methylation Protocol Guide from Illumina. We also used the other non-control probes to plot intensity of detected genes, signal average for green and red. Outliers can be identified. / GPL-2	noarch
<a href="#">r-methodcompare</a>	0.1.0	Implementation of the methodology from the paper titled Effective plots to assess bias and precision in method comparison studies published in Statistical Methods in Medical Research, P. Taffe (2016) <doi:10.1177/0962280216666667>. / GPL-3	noarch
<a href="#">r-metnorm</a>	0.1	Metabolomics data are inevitably subject to a component of unwanted variation, due to factors such as batch effects, matrix effects, and confounding biological variation. This package contains a collection of R functions which can be used to remove unwanted variation and obtain normalized metabolomics data. / GPL-2   GPL-3	noarch
<a href="#">r-meto</a>	0.1.0	Meteorological Tools following the FAO56 irrigation paper of Allen et al. (1998) [1]. Functions for calculating: reference evapotranspiration (ETref), extraterrestrial radiation (Ra), net radiation (Rn), saturation vapor pressure (satVP), global radiation (Rs), soil heat flux (G), daylight hours, and more. [1] Allen, R. G., Pereira, L. S., Raes, D., & Smith, M. (1998). Crop evapotranspiration-Guidelines for computing crop water requirements-FAO Irrigation and drainage paper 56. FAO, Rome, 300(9). / GPL-2	noarch
<a href="#">r-metrics</a>	0.1.4	An implementation of evaluation metrics in R that are commonly used in supervised machine learning. It implements metrics for regression, time series, binary classification, classification, and information retrieval problems. It has zero dependencies and a consistent, simple interface for all functions. / BSD_3_clause	noarch
<a href="#">r-metricsgraphics</a>	0.9.0	Provides an 'htmlwidgets' interface to the 'MetricsGraphics.js' ('D3'-based) charting library which is geared towards displaying time-series data. Chart types include line charts, scatterplots, histograms and rudimentary bar charts. Support for laying out multiple charts into a grid layout is also provided. All charts are interactive and many have an option for line, label and region annotations. / MIT	noarch
<a href="#">r-metricsweighted</a>	0.2.0	Provides weighted versions of several metrics, scoring functions and performance measures used in machine learning, including average unit deviances of the Bernoulli, Tweedie, Poisson, and Gamma distributions, see Jorgensen B. (1997, ISBN: 978-0412997112). The package also contains a weighted version of generalized R-squared, see e.g. Cohen, J. et al. (2002, ISBN: 978-0805822236). Furthermore, 'dplyr' chains are supported. / GPL-2	noarch
<a href="#">r-metrology</a>	0.9_28	Provides classes and calculation and plotting functions for metrology applications, including measurement uncertainty estimation and inter-laboratory metrology comparison studies. / GPL-2	noarch
<a href="#">r-metstat</a>	1.0	A diverse collection of metabolomics related statistical tools. / Apache License (== 2.0)	noarch

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Name	Version	Summary/License	Platforms
r-mewavg	0.3.0	Computes the average of a sequence of random vectors in a moving expanding window using a fixed amount of storage / GPL (>= 2.0)	linux-64, osx-64, win-64
r-mf	4.3.2	Calculate MF (mitigated fraction) with clustering and bootstrap options. See <a href="http://goo.gl/pcXYVr">http://goo.gl/pcXYVr</a> for definition of MF. / MIT	noarch
r-mfag	1.5	Performs Multiple Factor Analysis method for quantitative, categorical, frequency and mixed data, in addition to generating a lot of graphics, also has other useful functions. / GPL-2	noarch
r-mfgarch	0.1.8	Estimating GARCH-MIDAS (MIXed-DAta-Sampling) models (Engle, Ghysels, Sohn, 2013, <doi:10.1162/REST_a_00300>) and related statistical inference, accompanying the paper Two are better than one: volatility forecasting using multiplicative component GARCH models by Conrad and Kleen (2018, <doi:10.2139/ssrn.2752354>). The GARCH-MIDAS model decomposes the conditional variance of (daily) stock returns into a short- and long-term component, where the latter may depend on an exogenous covariate sampled at a lower frequency. / MIT	linux-64, osx-64, win-64
r-mfilter	0.1.5	The mFilter package implements several time series filters useful for smoothing and extracting trend and cyclical components of a time series. The routines are commonly used in economics and finance, however they should also be interest to other areas. Currently, Christiano-Fitzgerald, Baxter-King, Hodrick-Prescott, Butterworth, and trigonometric regression filters are included in the package. / GPL-2	noarch
r-mfp	1.5.2	Fractional polynomials are used to represent curvature in regression models. A key reference is Royston and Altman, 1994. / GPL-2	noarch
r-mft	2.0	Provides statistical tests and algorithms for the detection of change points in time series and point processes - particularly for changes in the mean in time series and for changes in the rate and in the variance in point processes. References - Michael Messer, Marietta Kirchner, Julia Schiemann, Jochen Roeper, Ralph Neiningen and Gaby Schneider (2014), A multiple filter test for the detection of rate changes in renewal processes with varying variance <doi:10.1214/14-AOAS782>. Stefan Albert, Michael Messer, Julia Schiemann, Jochen Roeper, Gaby Schneider (2017), Multi-scale detection of variance changes in renewal processes in the presence of rate change points <doi:10.1111/jtsa.12254>. Michael Messer, Kaue M. Costa, Jochen Roeper and Gaby Schneider (2017), Multi-scale detection of rate changes in spike trains with weak dependencies <doi:10.1007/s10827-016-0635-3>. Michael Messer, Stefan Albert and Gaby Schneider (2018), The multiple filter test for change point detection in time series <doi:10.1007/s00184-018-0672-1>. Michael Messer, Hendrik Backhaus, Albrecht Stroh and Gaby Schneider (2019) Peak detection in time series. / GPL-3	noarch
r-mgarchbekk	0.0.2	Procedures to simulate, estimate and diagnose MGARCH processes of BEKK and multivariate GJR (bivariate asymmetric GARCH model) specification. / GPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-mgcv	1.8.28	Generalized additive (mixed) models, some of their extensions and other generalized ridge regression with multiple smoothing parameter estimation by (Restricted) Marginal Likelihood, Generalized Cross Validation and similar. Includes a gam() function, a wide variety of smoothers, JAGS support and distributions beyond the exponential family. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
r-mgl	1.1	An aggressive dimensionality reduction and network estimation technique for a high-dimensional Gaussian graphical model (GGM). Please refer to: Efficient Dimensionality Reduction for High-Dimensional Network Estimation, Safiye Celik, Benjamin A. Logsdon, Su-In Lee, Proceedings of The 31st International Conference on Machine Learning, 2014, p. 1953–1961. / GPL-2	linux-64, osx-64, win-64
r-mglm	0.2.0	Provides functions that (1) fit multivariate discrete distributions, (2) generate random numbers from multivariate discrete distributions, and (3) run regression and penalized regression on the multivariate categorical response data. Implemented models include: multinomial logit model, Dirichlet multinomial model, generalized Dirichlet multinomial model, and negative multinomial model. Making the best of the minorization-maximization (MM) algorithm and Newton-Raphson method, we derive and implement stable and efficient algorithms to find the maximum likelihood estimates. On a multi-core machine, multi-threading is supported. / GPL-2	noarch
r-mgraster	0.9	Convenience Functions for R Language Access to the v.1 API of the MG-RAST Metagenome Annotation Server, part of the US Department of Energy (DOE) Systems Biology Knowledge Base (KBase). / BSD_2_clause	noarch
r-mgsda	1.4	Implements Multi-Group Sparse Discriminant Analysis proposal of I.Gaynanova, J.Booth and M.Wells (2015), Simultaneous sparse estimation of canonical vectors in the $p \gg N$ setting, JASA, to appear,[DOI:10.1080/01621459.2015.1034318]. / GPL-2	linux-64, osx-64, win-64
r-mgsub	1.7.1	Designed to enable simultaneous substitution in strings in a safe fashion. Safe means it does not rely on placeholders (which can cause errors in same length matches). / MIT	noarch
r-mhadaptive	1.1.8	Performs general Metropolis-Hastings Markov Chain Monte Carlo sampling of a user defined function which returns the un-normalized value (likelihood times prior) of a Bayesian model. The proposal variance-covariance structure is updated adaptively for efficient mixing when the structure of the target distribution is unknown. The package also provides some functions for Bayesian inference including Bayesian Credible Intervals (BCI) and Deviance Information Criterion (DIC) calculation. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-mhctools</a>	1.2.1	Ten tools for analysis of major histocompatibility complex (MHC) data in non- model species. The functions are tailored for amplicon data sets that have been filtered using the ‘dada2’ method (for more information visit < <a href="https://benjjneb.github.io/dada2">https://benjjneb.github.io/dada2</a> >), but even other data sets can be analyzed, if the data tables are formatted according to the description in each function. The ReplMatch() function matches replicates in data sets in order to evaluate genotyping success. The GetReplTable() and GetReplStats() functions perform such an evaluation. The HpltFind() function infers putative haplotypes from families in the data set. The GetHpltTable() and GetHpltStats() functions evaluate the accuracy of the haplotype inference. The PapaDiv() function compares parent pairs in the data set and calculate their joint MHC diversity, taking into account sequence variants that occur in both parents. The CalcPdist() function calculates the p-distances from pairwise comparisons of all sequences in a data set, and mean p-distances of all pairwise comparisons within each sample in a data set. The function includes the options to specify which codons to compare and to calculate amino acid p-distances. The CreateFas() function creates a fasta file with all the sequences in the data set. The CreateSamplesFas() function creates a fasta file for each sample in the data set. / MIT	noarch
<a href="#">r-mhg</a>	1.1	Runs a minimum-hypergeometric (mHG) test as described in: Eden, E. (2007). Discovering Motifs in Ranked Lists of DNA Sequences. Haifa. / GPL-2	noarch
<a href="#">r-mhsmm</a>	0.4.16	Parameter estimation and prediction for hidden Markov and semi-Markov models for data with multiple observation sequences. Suitable for equidistant time series data, with multivariate and/or missing data. Allows user defined emission distributions. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-mht</a>	3.1.2	Multiple Hypothesis Testing For Variable Selection in high dimensional linear models. This package performs variable selection with multiple hypothesis testing, either for ordered variable selection or non-ordered variable selection. In both cases, a sequential procedure is performed. It starts to test the null hypothesis no variable is relevant; if this hypothesis is rejected, it then tests only the first variable is relevant, and so on until the null hypothesis is accepted. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-mhtdiscrete</a>	1.0.1	A comprehensive tool for almost all existing multiple testing methods for discrete data. The package also provides some novel multiple testing procedures controlling FWER/FDR for discrete data. Given discrete p-values and their domains, the [method].p.adjust function returns adjusted p-values, which can be used to compare with the nominal significant level alpha and make decisions. For users’ convenience, the functions also provide the output option for printing decision rules. / GPL-2	noarch
<a href="#">r-mhtmult</a>	0.1.0	A Comprehensive tool for almost all existing multiple testing methods for multiple families. The package summarizes the existing methods for multiple families multiple testing procedures (MTPs) such as double FDR, group Benjamini-Hochberg (GBH) procedure and average FDR controlling procedure. The package also provides some novel multiple testing procedures using selective inference idea. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-mhtrajectoryr</a>	1.0.1	Spontaneous adverse event reports have a high potential for detecting adverse drug reactions. However, due to their dimension, the analysis of such databases requires statistical methods. We propose to use a logistic regression whose sparsity is viewed as a model selection challenge. Since the model space is huge, a Metropolis-Hastings algorithm carries out the model selection by maximizing the BIC criterion. / GPL-2	noarch
<a href="#">r-mi</a>	1.0	The mi package provides functions for data manipulation, imputing missing values in an approximate Bayesian framework, diagnostics of the models used to generate the imputations, confidence-building mechanisms to validate some of the assumptions of the imputation algorithm, and functions to analyze multiply imputed data sets with the appropriate degree of sampling uncertainty. / GPL-2	noarch
<a href="#">r-micar</a>	1.1.1	‘Mica’ is a server application used to create data web portals for large-scale epidemiological studies or multiple-study consortia. ‘Mica’ helps studies to provide scientifically robust data visibility and web presence without significant information technology effort. ‘Mica’ provides a structured description of consortia, studies, annotated and searchable data dictionaries, and data access request management. This ‘Mica’ client allows to perform data extraction for reporting purposes. / GPL-3	noarch
<a href="#">r-miceconindex</a>	0.1_6	Tools for calculating Laspeyres, Paasche, and Fisher price and quantity indices. / GPL-2	noarch
<a href="#">r-micefast</a>	0.5.1	Fast imputations under the object-oriented programming paradigm. There was used quantitative models with a closed-form solution. Thus package is based on linear algebra operations. The biggest improvement in time performance could be achieve for a calculation where a grouping variable have to be used. A single evaluation of a quantitative model for the multiple imputations is another major enhancement. Moreover there are offered a few functions built to work with popular R packages such as ‘data.table’ or ‘dplyr’. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-michelrodange</a>	1.0.0	Michel Rodange was a Luxembourgish writer and poet who lived in the 19th century. His most notable work is Rodange (1872, ISBN:1166177424), (Renert oder de Fuuß am Frack an a Ma’nsgrëßt), but he also wrote many more works, including Rodange, Tockert (1928) < <a href="https://www.autorenlexikon.lu/page/document/361/3614/1/FRE/index.html">https://www.autorenlexikon.lu/page/document/361/3614/1/FRE/index.html</a> > (D’Léierchen - Dem Léiweckerche säi Lidd) and Rodange, Welter (1929) < <a href="https://www.autorenlexikon.lu/page/document/361/3615/1/FRE/index.html">https://www.autorenlexikon.lu/page/document/361/3615/1/FRE/index.html</a> > (Dem Grow Sigfrid seng Goldkuommer). This package contains three datasets, each made from the plain text versions of his works available on < <a href="https://data.public.lu/fr/datasets/the-works-in-luxembourgish-of-michel-rodange/">https://data.public.lu/fr/datasets/the-works-in-luxembourgish-of-michel-rodange/</a> >. / CC0	noarch
<a href="#">r-micompr</a>	1.1.0	A procedure for comparing multivariate samples associated with different groups. It uses principal component analysis to convert multivariate observations into a set of linearly uncorrelated statistical measures, which are then compared using a number of statistical methods. The procedure is independent of the distributional properties of samples and automatically selects features that best explain their differences, avoiding manual selection of specific points or summary statistics. It is appropriate for comparing samples of time series, images, spectrometric measures or similar multivariate observations. / MIT	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-microbats</a>	0.1_1	A nature-inspired metaheuristic algorithm based on the echolocation behavior of microbats that uses frequency tuning to optimize problems in both continuous and discrete dimensions. This R package makes it easy to implement the standard bat algorithm on any user-supplied function. The algorithm was first developed by Xin-She Yang in 2010 (<DOI:10.1007/978-3-642-12538-6_6>, <DOI:10.1109/CINTI.2014.7028669>). / GPL-2	noarch
<a href="#">r-microbenchmark</a>	1.4_6	Provides infrastructure to accurately measure and compare the execution time of R expressions. / BSD_2_clause file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-micromacromultilevel</a>	0.4.0	Most multilevel methodologies can only model macro-micro multilevel situations in an unbiased way, wherein group-level predictors (e.g., city temperature) are used to predict an individual-level outcome variable (e.g., citizen personality). In contrast, this R package enables researchers to model micro-macro situations, wherein individual-level (micro) predictors (and other group-level predictors) are used to predict a group-level (macro) outcome variable in an unbiased way. / GPL-2	noarch
<a href="#">r-micromapst</a>	1.1.1	Provides the users with the ability to quickly create Linked Micromap plots for a collection of geographic areas. Linked Micromaps are visualizations of georeferenced data that link statistical graphics to an organized series of small maps or graphic images. The Help description contains examples of how to use the micromapST function. Contained in this package are border group datasets to support creating micromaps for the 50 U.S. states and District of Columbia (51 areas), the U. S. 20 Seer Registries, the 105 counties in the state of Kansas, the 62 counties of New York, the 24 counties of Maryland, the 29 counties of Utah, the 32 administrative areas in China, the 218 administrative areas in the UK and Ireland (for testing only), the 25 districts in the city of Seoul South Korea, and the 52 counties on the Africa continent. A border group dataset contains the boundaries related to the data level areas, a second layer boundaries, a top or third layer boundary, a parameter list of run options, and a cross indexing table between area names, abbreviations, numeric identification and alias matching strings for the specific geographic area. By specifying a border group, the package create micromaps for any geographic region. The user can create and provide their own border group dataset for any area beyond the areas contained within the package. Copyrighted 2013, 2014, 2015 and 2016 by Carr, Pearson and Pickle. / GPL-2	noarch
<a href="#">r-micropop</a>	1.5	Modelling interacting microbial populations - example applications include human gut microbiota, rumen microbiota and phytoplankton. Solves a system of ordinary differential equations to simulate microbial growth and resource uptake over time. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-microseq	1.2.3	Basic functions for microbial sequence data analysis. The idea is to use the basic R data structures as much as possible, without building complex data types. / GPL-2	linux-64, osx-64, win-64
r-microsoftr	3.5.0.108	Umbrella package with licenses and notices for all Microsoft R packages / file LICENSE	linux-64, osx-64, win-64
r-midas	1.0.1	Contains functions for converting existing HTML/JavaScript source into equivalent ‘shiny’ functions. Bootstraps the process of making new ‘shiny’ functions by allowing us to turn HTML snippets directly into R functions. / GPL-3	noarch
r-midastouch	1.3	Contains the function mice.impute.midastouch(). Technically this function is to be run from within the ‘mice’ package (van Buuren et al. 2011), type ??mice. It substitutes the method ‘pmm’ within mice by ‘midastouch’. The authors have shown that ‘midastouch’ is superior to default ‘pmm’. Many ideas are based on Siddique / Belin 2008’s MIDAS. / GPL-2   GPL-3	noarch
r-midn	1.0	Implementation of the mid-n algorithms presented in Wellek S (2015) <DOI:10.1111/stan.12063> Statistica Neerlandica 69, 358-373 for exact sample size calculation for superiority trials with binary outcome. / CC0	noarch
r-migest	1.8.0	Indirect methods for estimating bilateral migration flows in the presence of partial or missing data, including the estimation of bilateral migration flows from changes in bilateral migrant stock tables (e.g. Abel (2013) <doi:10.4054/DemRes.2013.28.18>). / GPL-3	noarch
r-migration.indices	0.3.0	This package provides various indices, like Crude Migration Rate, different Gini indices or the Coefficient of Variation among others, to show the (un)equality of migration. / AGPL-3	noarch
r-milc	1.0	The MILC package is designed to predict individual trajectories using the continuous time microsimulation model MILC, that describes the natural history of lung cancer. / GPL-2	noarch
r-mime	0.6	Guesses the MIME type from a filename extension using the data derived from /etc/mime.types in UNIX-type systems. / GPL	linux-32, linux-64, osx-64, win-32, win-64
r-mimix	1.0	Tools to combine results for multiply-imputed data using mixture approximations / GPL-2	noarch
r-mindonstats	0.11	66 data sets that were imported using read.table() where appropriate but more commonly after converting to a csv file for importing via read.csv(). / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-mined	1.0.2	This is a method (MinED) for mining probability distributions using deterministic sampling which is proposed by Joseph, Wang, Gu, Lv, and Tuo (2018). The MinED samples can be used for approximating the target distribution. They can be generated from a density function that is known only up to a proportionality constant and thus, it might find applications in Bayesian computation. Moreover, the MinED samples are generated with much fewer evaluations of the density function compared to random sampling-based methods such as MCMC and therefore, this method will be especially useful when the unnormalized posterior is expensive or time consuming to evaluate. / LGPL-2.1	linux-64, osx-64, win-64
r-minerva	1.5.8	Wrapper for ‘minepy’ implementation of Maximal Information-based Non-parametric Exploration statistics (MIC and MINE family). Detailed information of the ANSI C implementation of ‘minepy’ can be found at < <a href="http://minepy.readthedocs.io/en/latest">http://minepy.readthedocs.io/en/latest</a> >. / GPL-3	linux-64, osx-64, win-64
r-miney	0.1	This package implements the core idea of games known as ‘Minesweeper’ on Microsoft Windows or ‘KMines’ for KDE on Unix-like operating systems. / GPL-2	noarch
r-minicran	0.2.12	Makes it possible to create an internally consistent repository consisting of selected packages from CRAN-like repositories. The user specifies a set of desired packages, and ‘miniCRAN’ recursively reads the dependency tree for these packages, then downloads only this subset. The user can then install packages from this repository directly, rather than from CRAN. This is useful in production settings, e.g. server behind a firewall, or remote locations with slow (or zero) Internet access. / GPL-2	noarch
r-minigui	0.8.1	Quick and simple Tcl/Tk Graphical User Interface to call functions. Also comprises a very simple experimental GUI framework. / GPL (<= 2.0)	noarch
r-minimalrsd	1.0.0	Generate central composite designs (CCD) with full as well as fractional factorial points (half replicate) and Box Behnken designs (BBD) with minimally changed run sequence. / GPL-2	noarch
r-minimap	0.1.0	Create tile grid maps, which are like choropleth maps except each region is represented with equal visual space. / MIT	noarch
r-minimax	1.0	The minimax family of distributions is a two-parameter family like the beta family, but computationally a lot more tractable. / GPL-2   GPL-3	noarch
r-minirand	0.1.0	Randomization schedules are generated in the schemes with k (k>=2) treatment groups and any allocation ratios by minimization algorithms. / GPL-2	noarch
r-miniui	0.1.1	Provides UI widget and layout functions for writing Shiny apps that work well on small screens. / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-minpack.lm</a>	1.2_1	The nls.lm function provides an R interface to lmdcr and lmdif from the MINPACK library, for solving nonlinear least-squares problems by a modification of the Levenberg-Marquardt algorithm, with support for lower and upper parameter bounds. The implementation can be used via nls-like calls using the nlsLM function. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-minqa</a>	1.2.4	Derivative-free optimization by quadratic approximation based on an interface to Fortran implementations by M. J. D. Powell. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-minval</a>	0.8_1	For a given set of stoichiometric reactions, this package evaluates the mass and charge balance, extracts all reactants, products, orphan metabolites, metabolite names and compartments. Also are included some options to characterize and write models in TSV and SBML formats. / GPL-2	noarch
<a href="#">r-minxent</a>	0.01	This package implements entropy optimization distribution under specified constraints. It also offers an R interface to the MinxEnt and MaxEnt distributions. / GPL-2	noarch
<a href="#">r-mirada</a>	1.13.8	This package collects algorithms/functions developed for microRNA profiling data analyses. Analytical platforms include traditional hybridization microarray, CGH, beads-based microarray, and qRT-PCR array. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-mirsea</a>	1.1	The tools for ‘MicroRNA Set Enrichment Analysis’ can identify risk pathways(or prior gene sets) regulated by microRNA set in the context of microRNA expression data. (1) This package constructs a correlation profile of microRNA and pathways by the hypergeometric statistic test. The gene sets of pathways derived from the three public databases (Kyoto Encyclopedia of Genes and Genomes (‘KEGG’); ‘Reactome’; ‘Biocarta’) and the target gene sets of microRNA are provided by four databases(‘TarBaseV6.0’; ‘mir2Disease’; ‘miRecords’; ‘miRTarBase’;). (2) This package can quantify the change of correlation between microRNA for each pathway(or prior gene set) based on a microRNA expression data with cases and controls. (3) This package uses the weighted Kolmogorov-Smirnov statistic to calculate an enrichment score (ES) of a microRNA set that co-regulate to a pathway , which reflects the degree to which a given pathway is associated with the specific phenotype. (4) This package can provide the visualization of the results. / GPL-2	noarch
<a href="#">r-misaem</a>	0.9.1	Estimate parameters of logistic regression with missing data and perform model selection, using algorithm Stochastic Approximation EM. / GPL-3	noarch
<a href="#">r-misc3d</a>	0.8_4	A collection of miscellaneous 3d plots, including isosurfaces. / GPL-3	noarch
<a href="#">r-miscfuncs</a>	1.2_10	Implementing various things including functions for LaTeX tables, the Kalman filter, web scraping, development tools, relative risk and odds ratio. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-miscor	0.1_1	Statistical test for the product-moment correlation coefficient based on $H_0: \rho = \rho_0$ including sample size computation, statistical test for comparing the product-moment correlation coefficient in independent and dependent samples, sequential triangular test for the product-moment correlation coefficient, partial and semipartial correlation, simulation of bivariate normal and non-normal distribution with a specified correlation. / GPL-3	noarch
r-misctools	0.6_2	Miscellaneous small tools and utilities. Many of them facilitate the work with matrices, e.g. inserting rows or columns, creating symmetric matrices, or checking for semidefiniteness. Other tools facilitate the work with regression models, e.g. extracting the standard errors, obtaining the number of (estimated) parameters, or calculating R-squared values. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-mise	0.1.0	Clears the workspace. Useful for the beginnings of R scripts, to avoid potential problems with accidentally using information from variables or functions from previous script evaluations, too many figure windows open at the same time, packages that you don't need any more, or a cluttered console. Uses code from various StackOverflow users. See help(mise) for pointers to the relevant StackOverflow pages. / MIT	noarch
r-misreport	0.1.1	Enables investigation of the predictors of misreporting on sensitive survey questions through a multivariate list experiment regression method. The method permits researchers to model whether a survey respondent's answer to the sensitive item in a list experiment is different from his or her answer to an analogous direct question. / GPL-3	noarch
r-missmech	1.0.2	To test whether the missing data mechanism, in a set of incompletely observed data, is one of missing completely at random (MCAR). For detailed description see Jamshidian, M. Jalal, S., and Jansen, C. (2014). MissMech: An R Package for Testing Homoscedasticity, Multivariate Normality, and Missing Completely at Random (MCAR), Journal of Statistical Software, 56(6), 1-31. URL <a href="http://www.jstatsoft.org/v56/i06/">http://www.jstatsoft.org/v56/i06/</a> . / GPL-2	noarch
r-misssbm	0.2.0	When a network is partially observed (here, NAs in the adjacency matrix rather than 1 or 0 due to missing information between node pairs), it is possible to account for the underlying process that generates those NAs. 'missSBM' adjusts the popular stochastic block model from network data sampled under various missing data conditions, as described in Tabouy, Barbillon and Chiquet (2019) <doi:10.1080/01621459.2018.1562934>. / GPL-3	linux-64, osx-64, win-64
r-mist	1.0	Test for association between a set of SNPS/genes and continuous or binary outcomes by including variant characteristic information and using (weighted) score statistics. / LGPL (>= 2.0)	noarch
r-mistat	1.0_5	Provide all the data sets and statistical analysis applications used in Modern Industrial Statistics: with applications in R, MINITAB and JMP by R.S. Kenett and S. Zacks with contributions by D. Amberti, John Wiley and Sons, 2013, which is a second revised and expanded revision of Modern Industrial Statistics: Design and Control of Quality and Reliability, R. Kenett and S. Zacks, Duxbury/Wadsworth Publishing, 1998. / GPL-2	noarch
r-mistr	0.0.2	A flexible computational framework for mixture distributions with the focus on the composite models. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<code>r-mitisem</code>	1.2	Flexible multivariate function approximation using adapted Mixture of Student t Distributions. Mixture of t distribution is obtained using Importance Sampling weighted Expectation Maximization algorithm. / GPL-3	noarch
<code>r-mitools</code>	2.4	Tools to perform analyses and combine results from multiple-imputation datasets. / GPL-2	noarch
<code>r-mittagleffler</code>	0.3.0	Implements the Mittag-Leffler function, distribution, random variate generation, and estimation. Based on the Laplace-Inversion algorithm by Garrappa, R. (2015) <doi:10.1137/140971191>. / GPL-2	noarch
<code>r-mix</code>	1.0_1	Estimation/multiple imputation programs for mixed categorical and continuous data. / Unlimited	linux-64, osx-64, win-64
<code>r-mixdist</code>	0.5_5	Fit finite mixture distribution models to grouped data and conditional data by maximum likelihood using a combination of a Newton-type algorithm and the EM algorithm. / GPL-2	noarch
<code>r-mixeddataimpute</code>	0.1	Missing data imputation for continuous and categorical data, using nonparametric Bayesian joint models (specifically the hierarchically coupled mixture model with local dependence described in Murray and Reiter (2015); see ‘citation(MixedDataImpute)’ or <a href="http://arxiv.org/abs/1410.0438">http://arxiv.org/abs/1410.0438</a> ). See ‘?hmm_impute’ for example usage. / GPL-3	linux-64, osx-64, win-64
<code>r-mixedmem</code>	1.1.0	Fits mixed membership models with discrete multivariate data (with or without repeated measures) following the general framework of Erosheva et al (2004). This package uses a Variational EM approach by approximating the posterior distribution of latent memberships and selecting hyperparameters through a pseudo-MLE procedure. Currently supported data types are Bernoulli, multinomial and rank (Plackett-Luce). The extended GoM model with fixed stayers from Erosheva et al (2007) is now also supported. See Airolidi et al (2014) for other examples of mixed membership models. / GPL-2	linux-64, osx-64, win-64
<code>r-mixedpsy</code>	1.0.0	Tools for the analysis of psychophysical data. This package allows to estimate the Point of Subjective Equivalence (PSE) and the Just Noticeable Difference (JND), either from a psychometric function or from a Generalized Linear Mixed Model (GLMM). Additionally, the package allows plotting the fitted models and the response data, simulating psychometric functions of different shapes, and simulating data sets. For a description of the use of GLMMs applied to psychophysical data, refer to Moscatelli et al. (2012), <doi:10.1167/12.11.26>. / GPL-2	noarch
<code>r-mixedts</code>	1.0.4	We provide detailed functions for univariate Mixed Tempered Stable distribution. / GPL-2	noarch
<code>r-mixemm</code>	1.0	Contains functions for estimating a mixed-effects model for clustered data (or batch-processed data) with cluster-level (or batch-level) missing values in the outcome, i.e., the outcomes of some clusters are either all observed or missing altogether. The model is developed for analyzing incomplete data from labeling-based quantitative proteomics experiments but is not limited to this type of data. We used an expectation conditional maximization (ECM) algorithm for model estimation. The cluster-level missingness may depend on the average value of the outcome in the cluster (missing not at random). / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-mixmap</a>	1.3.4	A collection of functions to implement the MixMAP algorithm, which performs gene level tests of association using data from a previous GWAS or data from a meta-analysis of several GWAS. Conceptually, genes are detected as significant if the collection of p-values within a gene are determined to be collectively smaller than would be observed by chance. / GPL-3	noarch
<a href="#">r-mixmap</a>	0.2.4	Provides sampling and density functions for matrix variate normal, t, and inverted t distributions; ML estimation for matrix variate normal and t distributions using the EM algorithm, including some restrictions on the parameters; and classification by linear and quadratic discriminant analysis for matrix variate normal and t distributions described in Thompson et al. (2019) <arXiv:1907.09565>. Performs clustering with matrix variate normal and t mixture models. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-mixmeta</a>	1.0.3	A collection of functions to perform various meta-analytical models through a unified mixed-effects framework, including standard univariate fixed and random-effects meta-analysis and meta-regression, and non-standard extensions such as multivariate, multilevel, longitudinal, and dose-response models. / GPL-2	noarch
<a href="#">r-mixor</a>	1.0.4	Provides the function ‘mixor’ for fitting a mixed-effects ordinal and binary response models and associated methods for printing, summarizing, extracting estimated coefficients and variance-covariance matrix, and estimating contrasts for the fitted models. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-mixphm</a>	0.7_2	Fits multiple variable mixtures of various parametric proportional hazard models using the EM-Algorithm. Proportionality restrictions can be imposed on the latent groups and/or on the variables. Several survival distributions can be specified. Missing values and censored values are allowed. Independence is assumed over the single variables. / GPL-2	noarch
<a href="#">r-mixrasch</a>	1.1	Estimates Rasch models and mixture Rasch models, including the dichotomous Rasch model, the rating scale model, and the partial credit model. / GPL-2	noarch
<a href="#">r-mixraschtools</a>	1.1	Provides supplemental functions for the ‘mixRasch’ package (Willse, 2014), < <a href="https://cran.r-project.org/package=mixRasch/mixRasch.pdf">https://cran.r-project.org/package=mixRasch/mixRasch.pdf</a> > including a plotting function to compare item parameters for multiple class models and a function that provides average theta values for each class in a mixture model. / GPL-3	noarch
<a href="#">r-mixreg</a>	0.0_6	Fits mixtures of (possibly multivariate) regressions (which has been described as doing ANCOVA when you don’t know the levels). / GPL-2	noarch
<a href="#">r-mixrf</a>	1.0	It offers random-forest-based functions to impute clustered incomplete data. The package is tailored for but not limited to imputing multitissue expression data, in which a gene’s expression is measured on the collected tissues of an individual but missing on the uncollected tissues. / GPL-3	noarch
<a href="#">r-mixsal</a>	1.0	The current version of the ‘MixSAL’ package allows users to generate data from a multivariate SAL distribution or a mixture of multivariate SAL distributions, evaluate the probability density function of a multivariate SAL distribution or a mixture of multivariate SAL distributions, and fit a mixture of multivariate SAL distributions using the Expectation-Maximization (EM) algorithm (see Franczak et. al, 2014, <doi:10.1109/TPAMI.2013.216>, for details). / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-mixsim</a>	1.1_3	The utility of this package is in simulating mixtures of Gaussian distributions with different levels of overlap between mixture components. Pairwise overlap, defined as a sum of two misclassification probabilities, measures the degree of interaction between components and can be readily employed to control the clustering complexity of datasets simulated from mixtures. These datasets can then be used for systematic performance investigation of clustering and finite mixture modeling algorithms. Among other capabilities of ‘MixSim’, there are computing the exact overlap for Gaussian mixtures, simulating Gaussian and non-Gaussian data, simulating outliers and noise variables, calculating various measures of agreement between two partitionings, and constructing parallel distribution plots for the graphical display of finite mixture models. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-mixsmn</a>	1.1_5	Functions to fit finite mixture of scale mixture of skew-normal (FM-SMSN) distributions. / GPL (>= 2.0)	noarch
<a href="#">r-mixspe</a>	0.1.1	Mixtures of skewed and elliptical distributions are implemented using mixtures of multivariate skew power exponential and power exponential distributions, respectively. A generalized expectation-maximization framework is used for parameter estimation. Methodology for mixtures of power exponential distributions is from Dang et al. (2015) <doi: 10.1111/biom.12351>. / GPL-2	noarch
<a href="#">r-mixsqp</a>	0.2_2	Provides optimization algorithms based on sequential quadratic programming (SQP) for maximum likelihood estimation of the mixture proportions in a finite mixture model where the component densities are known. The algorithms are expected to obtain solutions that are at least as accurate as the state-of-the-art MOSEK interior-point solver (called by function KWDual in the ‘REBayes’ package), and they are expected to arrive at solutions more quickly in large data sets. The algorithms are described in Y. Kim, P. Carbonetto, M. Stephens & M. Anitescu (2018) <arXiv:1806.01412>. / MIT	linux-64, osx-64, win-64
<a href="#">r-mixtnb</a>	1.0	Differential expression analysis of RNA-Seq data when replicates under two conditions are available is performed. First, mixtures of Negative Binomial distributions are fitted on the data in order to estimate the dispersions, then the Wald test is computed. / GPL-3	noarch
<a href="#">r-mixture</a>	1.5	An implementation of all 14 Gaussian parsimonious clustering models (GPCMs) for model-based clustering and model-based classification. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-mixtureinf</a>	1.1	Functions for computing the penalized maximum likelihood estimate (PMLE) or maximum likelihood estimate (MLE), testing the order of a finite mixture model using EM-test, drawing histogram of observations and the fitted density or probability mass function of the mixture model. / AGPL-3	noarch
<a href="#">r-mixtureregtic</a>	1.0.0	Fit mixture regression models with nonsusceptibility/cure for left-truncated and interval-censored (LTIC) data (see Chen et al. (2013) <doi:10.1002/sim.5845>). This package also provides the nonparametric maximum likelihood estimator (NPMLE) for the survival/event curves with LTIC data. / GPL-2   GPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-mize	0.2.2	Optimization algorithms implemented in R, including conjugate gradient (CG), Broyden-Fletcher-Goldfarb-Shanno (BFGS) and the limited memory BFGS (L-BFGS) methods. Most internal parameters can be set through the call interface. The solvers hold up quite well for higher-dimensional problems. / BSD_2_clause	noarch
r-mkde	0.1	Provides functions to compute and visualize movement-based kernel density estimates (MKDEs) for animal utilization distributions in 2 or 3 spatial dimensions. / GPL-3	linux-64, osx-64, win-64
r-mkin	0.9.4	Calculation routines based on the FOCUS Kinetics Report (2006, 2014). Includes a function for conveniently defining differential equation models, model solution based on eigenvalues if possible or using numerical solvers and a choice of the optimisation methods made available by the 'FME' package. If a C compiler (on windows: 'Rtools') is installed, differential equation models are solved using compiled C functions. Please note that no warranty is implied for correctness of results or fitness for a particular purpose. / GPL-3	noarch
r-mkle	0.05	Package for fast computation of the maximum kernel likelihood estimator (mkle) / GPL-3	noarch
r-mknapsack	0.1.0	Package solves multiple knapsack optimisation problem. Given a set of items, each with volume and value, it will allocate them to knapsacks of a given size in a way that value of top N knapsacks is as large as possible. / GPL-2	noarch
r-mkssd	1.1	mkssd is a package that generates efficient balanced non-aliased multi-level k-circulant supersaturated designs by interchanging the elements of the generator vector. The package tries to generate a supersaturated design that has chisquare efficiency more than user specified efficiency level (mef). The package also displays the progress of generation of an efficient multi-level k-circulant design through a progress bar. The progress of 100% means that one full round of interchange is completed. More than one full round (typically 4-5 rounds) of interchange may be required for larger designs. / GPL-2	noarch
r-ml.msbd	1.1.1	Inference of a multi-states birth-death model from a phylogeny, comprising a number of states N, birth and death rates for each state and on which edges each state appears. Inference is done using a hybrid approach: states are progressively added in a greedy approach. For a fixed number of states N the best model is selected via maximum likelihood. Reference: J. Barido-Sottani and T. Stadler (2017) <doi:10.1101/215491>. / GPL-3	noarch
r-mlapi	0.1.0	Provides 'R6' abstract classes for building machine learning models with 'scikit-learn' like API. < <a href="http://scikit-learn.org/">http://scikit-learn.org/</a> > is a popular module for 'Python' programming language which design became de facto a standard in industry for machine learning tasks. / MIT	noarch
r-mlbench	2.1.1	A collection of artificial and real-world machine learning benchmark problems, including, e.g., several data sets from the UCI repository. / GPL-2	linux-64, osx-64, win-64
r-mlbstats	0.1.0	Computational functions for player metrics in major league baseball including batting, pitching, fielding, base-running, and overall player statistics. This package is actively maintained with new metrics being added as they are developed. / MIT	noarch

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Name	Version	Summary/License	Platforms
r-mlcm	0.4.2	Conjoint measurement is a psychophysical procedure in which stimulus pairs are presented that vary along 2 or more dimensions and the observer is required to compare the stimuli along one of them. This package contains functions to estimate the contribution of the n scales to the judgment by a maximum likelihood method under several hypotheses of how the perceptual dimensions interact. Reference: Knoblauch & Maloney (2012) Modeling Psychophysical Data in R. <doi:10.1007/978-1-4614-4475-6>. / GPL-2	noarch
r-mlr.datasets	0.4.2	Large collection of multilabel datasets along with the functions needed to export them to several formats, to make partitions, and to obtain bibliographic information. / LGPL-3	noarch
r-mls	0.4.5	Difference scaling is a method for scaling perceived supra-threshold differences. The package contains functions that allow the user to design and run a difference scaling experiment, to fit the resulting data by maximum likelihood and test the internal validity of the estimated scale. / GPL-2	noarch
r-mle.tools	1.0.0	Calculates the expected/observed Fisher information and the bias-corrected maximum likelihood estimate(s) via Cox-Snell Methodology. / GPL-2	noarch
r-mlearning	1.0_0	This package provides a unified interface to various machine learning algorithms. Confusion matrices are provided too. / GPL-2	noarch
r-mlecons	0.1_4	This package contains functions to compute the nonparametric maximum likelihood estimator (MLE) for the bivariate distribution of (X,Y), when realizations of (X,Y) cannot be observed directly. To be more precise, we consider the situation where we observe a set of rectangles that are known to contain the unobservable realizations of (X,Y). We compute the MLE based on such a set of rectangles. The methods can also be used for univariate censored data (see data set 'cosmesis'), and for censored data with competing risks (see data set 'menopause'). We also provide functions to visualize the observed data and the MLE. / GPL-2	linux-64, osx-64, win-64
r-mlegp	3.1.7	Maximum likelihood Gaussian process modeling for univariate and multi-dimensional outputs with diagnostic plots following Santner et al (2003) <doi:10.1007/978-1-4757-3799-8>. Contact the maintainer for a package version that includes sensitivity analysis. / GPL-2	linux-64, osx-64, win-64
r-mleur	1.0_6	Provides functions for unit root testing using MLE method / GPL-2	noarch
r-mlf	1.2.1	Offers a gentle introduction to machine learning concepts for practitioners with a statistical pedigree: decomposition of model error (bias-variance trade-off), nonlinear correlations, information theory and functional permutation/bootstrap simulations. Székely GJ, Rizzo ML, Bakirov NK. (2007). <doi:10.1214/009053607000000505>. Reshef DN, Reshef YA, Finucane HK, Grossman SR, McVean G, Turnbaugh PJ, Lander ES, Mitzenmacher M, Sabeti PC. (2011). <doi:10.1126/science.1205438>. / GPL-2	noarch
r-mlca2	2.1	An R code implementation of the maximum likelihood (fixed point) algorithm of Hyvärinen, Karhuna, and Oja for independent component analysis. / GPL-2	noarch
r-mlid	1.0.1	Tools and functions to fit a multilevel index of dissimilarity. / GPL-3	noarch
r-mlmetrics	1.1.1	A collection of evaluation metrics, including loss, score and utility functions, that measure regression, classification and ranking performance. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-mlml2r</a>	0.3.2	Maximum likelihood estimates (MLE) of the proportions of 5-mC and 5-hmC in the DNA using information from BS-conversion, TAB-conversion, and oxBS-conversion methods. One can use information from all three methods or any combination of two of them. Estimates are based on Binomial model by Qu et al. (2013) <doi:10.1093/bioinformatics/btt459> and Kiihl et al. (2019) <doi:10.1515/sagmb-2018-0031>. / MIT	noarch
<a href="#">r-mlmmm</a>	0.3_1	Computational strategies for multivariate linear mixed-effects models with missing values, Schafer and Yucel (2002), Journal of Computational and Graphical Statistics, 11, 421-442. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-mlmrev</a>	1.0_7	Data and examples from a multilevel modelling software review as well as other well-known data sets from the multilevel modelling literature. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-mlphaser</a>	0.01	Phase haplotypes from genotypes based on a list of known haplotypes. Suited to highly diverse loci such as HLA. / GPL-2	noarch
<a href="#">r-mlpugs</a>	0.2.0	An implementation of classifier chains (CC's) for multi-label prediction. Users can employ an external package (e.g. 'randomForest', 'C50'), or supply their own. The package can train a single set of CC's or train an ensemble of CC's – in parallel if running in a multi-core environment. New observations are classified using a Gibbs sampler since each unobserved label is conditioned on the others. The package includes methods for evaluating the predictions for accuracy and aggregating across iterations and models to produce binary or probabilistic classifications. / MIT	noarch
<a href="#">r-mlr3misc</a>	0.1.3	Frequently used helper functions and assertions used in 'mlr3' and its companion packages. Comes with helper functions for functional programming, for printing, to work with 'data.table', as well as some generally useful 'R6' classes. This package also supersedes the package 'BBmisc'. / LGPL-3	linux-64, osx-64, win-64
<a href="#">r-mlsjunkgen</a>	0.1.1	Generate a stream of pseudo-random numbers generated using the MLS Junk Generator algorithm. Functions exist to generate single pseudo-random numbers as well as a vector, data frame, or matrix of pseudo-random numbers. / MIT	noarch
<a href="#">r-mltest</a>	1.0.1	A fast, robust and easy-to-use calculation of multi-class classification evaluation metrics based on confusion matrix. / GPL-2	noarch
<a href="#">r-mltools</a>	0.3.5	A collection of machine learning helper functions, particularly assisting in the Exploratory Data Analysis phase. Makes heavy use of the 'data.table' package for optimal speed and memory efficiency. Highlights include a versatile bin_data() function, sparsify() for converting a data.table to sparse matrix format with one-hot encoding, fast evaluation metrics, and empirical_cdf() for calculating empirical Multivariate Cumulative Distribution Functions. / MIT	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-mm4lmm</a>	1.1.5	The main function MMEst() performs (Restricted) Maximum Likelihood in a variance component mixed models using a Min-Max (MM) algorithm (Hunter, D. R., & Lange, K. (2004) <doi:10.1198/0003130042836>). / GPL-2	linux-64, osx-64, win-64
<a href="#">r-mmacc</a>	0.1.2	Contains the data sets for the textbook Mathematical Modeling and Applied Calculus by Joel Kilty and Alex M. McAllister. The book will be published by Oxford University Press in 2018 with ISBN-13: 978-019882472. / GPL-2	noarch
<a href="#">r-mmand</a>	1.5.4	Provides tools for performing mathematical morphology operations, such as erosion and dilation, on data of arbitrary dimensionality. Can also be used for finding connected components, resampling, filtering, smoothing and other image processing-style operations. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-mmmap</a>	0.6.1	R interface to POSIX mmap and Window's MapViewOfFile. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-mmcc</a>	0.0.3	Provides routines for multivariate measurement error correction. Includes procedures for linear, logistic and Cox regression models. Bootstrapped standard errors and confidence intervals can be obtained for corrected estimates. / GPL-3	noarch
<a href="#">r-mmmds</a>	1.1	This library implements mixture model distance sampling methods. See Miller and Thomas (in prep.). / GPL-2	noarch
<a href="#">r-mme</a>	0.1.6	Fit Gaussian Multinomial mixed-effects models for small area estimation: Model 1, with one random effect in each category of the response variable (Lopez-Vizcaino, E. et al., 2013) <doi:10.1177/1471082X13478873>; Model 2, introducing independent time effect; Model 3, introducing correlated time effect. mme calculates direct and parametric bootstrap MSE estimators (Lopez-Vizcaino, E et al., 2014) <doi:10.1111/rssa.12085>. / GPL-2	noarch
<a href="#">r-mmeln</a>	1.3	Fit multivariate mixture of normal distribution using covariance structure. / GPL-3	noarch
<a href="#">r-mmmeta</a>	2.3	A novel multivariate meta-analysis. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-mmgee</a>	1.20	Provides global hypothesis tests, multiple testing procedures and simultaneous confidence intervals for multiple linear contrasts of regression coefficients in a single generalized estimating equation (GEE) model or across multiple GEE models. GEE models are fit by a modified version of the 'geeM' package. / GPL-3	noarch
<a href="#">r-mmms</a>	0.1	The package implements a multi-marker molecular signature (MMMS) approach for treatment-specific subgroup identification. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-mmpa	1.2.0	To determine the number of quantitative assays needed for a sample of data using pooled testing methods, which include mini-pooling (MP), MP with algorithm (MPA), and marker-assisted MPA (mMPA). To estimate the number of assays needed, the package also provides a tool to conduct Monte Carlo (MC) to simulate different orders in which the sample would be collected to form pools. Using MC avoids the dependence of the estimated number of assays on any specific ordering of the samples to form pools. / MIT	noarch
r-mmpf	0.0.5	Marginalizes prediction functions using Monte-Carlo integration and computes permutation importance. / MIT	noarch
r-mmpp	0.6	Compute similarities and distances between marked point processes. / GPL-2	noarch
r-mmsample	0.1	Subset a control group to match an intervention group on a set of features using multivariate matching and propensity score calipers. Based on methods in Rosenbaum and Rubin (1985). / GPL-3	linux-64, osx-64, win-64
r-mmtsne	0.1.0	An implementation of multiple maps t-distributed stochastic neighbor embedding (t-SNE). Multiple maps t-SNE is a method for projecting high-dimensional data into several low-dimensional maps such that non-metric space properties are better preserved than they would be by a single map. Multiple maps t-SNE with only one map is equivalent to standard t-SNE. When projecting onto more than one map, multiple maps t-SNE estimates a set of latent weights that allow each point to contribute to one or more maps depending on similarity relationships in the original data. This implementation is a port of the original 'Matlab' library by Laurens van der Maaten. See Van der Maaten and Hinton (2012) <doi:10.1007/s10994-011-5273-4>. This material is based upon work supported by the United States Air Force and Defense Advanced Research Project Agency (DARPA) under Contract No. FA8750-17-C-0020. Any opinions, findings and conclusions or recommendations expressed in this material are those of the author(s) and do not necessarily reflect the views of the United States Air Force and Defense Advanced Research Projects Agency. Distribution Statement A: Approved for Public Release; Distribution Unlimited. / FreeBSD   file LICENSE	noarch
r-mmwrweek	0.1.1	The first day of any MMWR week is Sunday. MMWR week numbering is sequential beginning with 1 and incrementing with each week to a maximum of 52 or 53. MMWR week #1 of an MMWR year is the first week of the year that has at least four days in the calendar year. This package provides functionality to convert Dates to MMWR day, week, and year and the reverse. / GPL-2	noarch
r-mnormpow	0.1.1	Computes integral of $f(x) \cdot x_i^k$ on a product of intervals, where $f$ is the density of a gaussian law. This is a small alteration of the mnormt code from A. Genz and A. Azzalini. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-mnormt</a>	1.5_5	Functions are provided for computing the density and the distribution function of multivariate normal and t random variables, and for generating random vectors sampled from these distributions. Probabilities are computed via non-Monte Carlo methods; different routines are used in the case $d=1$ , $d=2$ , $d>2$ , if $d$ denotes the number of dimensions. / GPL-2   GPL-3	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-mnp</a>	3.1_0	Fits the Bayesian multinomial probit model via Markov chain Monte Carlo. The multinomial probit model is often used to analyze the discrete choices made by individuals recorded in survey data. Examples where the multinomial probit model may be useful include the analysis of product choice by consumers in market research and the analysis of candidate or party choice by voters in electoral studies. The MNP package can also fit the model with different choice sets for each individual, and complete or partial individual choice orderings of the available alternatives from the choice set. The estimation is based on the efficient marginal data augmentation algorithm that is developed by Imai and van Dyk (2005). “A Bayesian Analysis of the Multinomial Probit Model Using the Data Augmentation,” Journal of Econometrics, Vol. 124, No. 2 (February), pp. 311-334. <DOI:10.1016/j.jeconom.2004.02.002> Detailed examples are given in Imai and van Dyk (2005). “MNP: R Package for Fitting the Multinomial Probit Model.” Journal of Statistical Software, Vol. 14, No. 3 (May), pp. 1-32. <DOI:10.18637/jss.v014.i03>. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-mns</a>	1.0	An implementation of the mixed neighbourhood selection (MNS) algorithm. The MNS algorithm can be used to estimate multiple related precision matrices. In particular, the motivation behind this work was driven by the need to understand functional connectivity networks across multiple subjects. This package also contains an implementation of a novel algorithm through which to simulate multiple related precision matrices which exhibit properties frequently reported in neuroimaging analysis. / GPL-2	noarch
<a href="#">r-moc</a>	2.0	Fits and visualize user defined finite mixture models for multivariate observations using maximum likelihood. (McLachlan, G., Peel, D. (2000) Finite Mixture Models. Wiley-Interscience.) / GPL-2	linux-64, osx-64, win-64
<a href="#">r-mocca</a>	1.3	Provides methods to analyze cluster alternatives based on multi-objective optimization of cluster validation indices. For details see Kraus et al. (2011) <doi:10.1007/s00180-011-0244-6>. / Artistic-2.0	noarch
<a href="#">r-mockery</a>	0.4.2	The two main functionalities of this package are creating mock objects (functions) and selectively intercepting calls to a given function that originate in some other function. It can be used with any testing framework available for R. Mock objects can be injected with either this package’s own stub() function or a similar with_mock() facility present in the ‘testthat’ package. / MIT	noarch
<a href="#">r-mockr</a>	0.1	Provides a means to mock a package function, i.e., temporarily substitute it for testing. Designed as a drop-in replacement for ‘testthat::with_mock()’, which may break in R 3.4.0 and later. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-mod</a>	0.1.3	Creates modules inline or from a file. Modules can contain any R object and be nested. Each module have their own scope and package search path that does not interfere with one another or the user's working environment. / GPL-3	noarch
<a href="#">r-mod09nrt</a>	0.14	Package for processing downloaded MODIS Surface reflectance Product HDF files. Specifically, MOD09 surface reflectance product files, and the associated MOD03 geolocation files (for MODIS-TERRA). The package will be most effective if the user installs MRTSwath (MODIS Reprojection Tool for swath products; < <a href="https://lpdaac.usgs.gov/tools/modis_reprojection_tool_swath">https://lpdaac.usgs.gov/tools/modis_reprojection_tool_swath</a> >, and adds the directory with the MRTSwath executable to the default R PATH by editing ~/.Rprofile. / GPL-2	noarch
<a href="#">r-modalclust</a>	0.7	Performs Modal Clustering (MAC) including Hierarchical Modal Clustering (HMAC) along with their parallel implementation (PHMAC) over several processors. These model-based non-parametric clustering techniques can extract clusters in very high dimensions with arbitrary density shapes. By default clustering is performed over several resolutions and the results are summarised as a hierarchical tree. Associated plot functions are also provided. There is a package vignette that provides many examples. This version adheres to CRAN policy of not spanning more than two child processes by default. / GPL-2	noarch
<a href="#">r-modcmftr</a>	0.1.0	Fits a modified version of the Connor-Mosimann distribution (Connor & Mosimann (1969)<doi:10.2307/2283728>), a Connor-Mosimann distribution or Dirichlet distribution (e.g. Gelman, Carlin, Stern & Rubin Chapter 3.5 (2004, <ISBN:1-58488-388-X>) to elicited quantiles of a multinomial distribution. Code is also provided to sample from the distributions, generating inputs suitable for a probabilistic sensitivity analysis / Monte Carlo simulation in a decision model. / GPL-2	noarch
<a href="#">r-modehunt</a>	1.0.7	Given independent and identically distributed observations $X(1), \dots, X(n)$ from a density $f$ , provides five methods to perform a multiscale analysis about $f$ as well as the necessary critical values. The first method, introduced in Duembgen and Walther (2008), provides simultaneous confidence statements for the existence and location of local increases (or decreases) of $f$ , based on all intervals $I(\text{all})$ spanned by any two observations $X(j), X(k)$ . The second method approximates the latter approach by using only a subset of $I(\text{all})$ and is therefore computationally much more efficient, but asymptotically equivalent. Omitting the additive correction term $\Gamma$ in either method offers another two approaches which are more powerful on small scales and less powerful on large scales, however, not asymptotically minimax optimal anymore. Finally, the block procedure is a compromise between adding $\Gamma$ or not, having intermediate power properties. The latter is again asymptotically equivalent to the first and was introduced in Rufibach and Walther (2010). / GPL-2	noarch
<a href="#">r-modelgood</a>	1.0.9	Bootstrap cross-validation for ROC, AUC and Brier score to assess and compare predictions of binary status responses. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-modeltest</a>	1.0.0	An implementation of the cross-validated difference in means (CVDm) test by Desmarais and Harden (2014) <doi:10.1007/s11135-013-9884-7> (see also Harden and Desmarais, 2011 <doi:10.1177/1532440011408929>) and the cross-validated median fit (CVMF) test by Desmarais and Harden (2012) <doi:10.1093/pan/mpr042>. These tests use leave-one-out cross-validated log-likelihoods to assist in selecting among model estimations. You can also utilize data from Golder (2010) <doi:10.1177/0010414009341714> and Joshi & Mason (2008) <doi:10.1177/0022343308096155> that are included to facilitate examples from real-world analysis. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-modelmetrics</a>	1.2.2	Collection of metrics for evaluating models written in C using ‘Rcpp’. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-modelobj</a>	4.0	A utility library to facilitate the generalization of statistical methods built on a regression framework. Package developers can use ‘modelObj’ methods to initiate a regression analysis without concern for the details of the regression model and the method to be used to obtain parameter estimates. The specifics of the regression step are left to the user to define when calling the function. The user of a function developed within the ‘modelObj’ framework creates as input a ‘modelObj’ that contains the model and the R methods to be used to obtain parameter estimates and to obtain predictions. In this way, a user can easily go from linear to non-linear models within the same package. / GPL-2	noarch
<a href="#">r-modelr</a>	0.1.4	Functions for modelling that help you seamlessly integrate modelling into a pipeline of data manipulation and visualisation. / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-modeltools</a>	0.2_22	A collection of tools to deal with statistical models. The functionality is experimental and the user interface is likely to change in the future. The documentation is rather terse, but packages ‘coin’ and ‘party’ have some working examples. However, if you find the implemented ideas interesting we would be very interested in a discussion of this proposal. Contributions are more than welcome! / GPL-2	linux-32, linux-64, noarch, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
r-modelwordcloud	0.1	Makes a word cloud of text, sized by the frequency of the word, and colored either by user-specified colors or colored by the strength of the coefficient of that text derived from a regression model. / LGPL-2.1	noarch
r-modes	0.7.0	Designed with a dual purpose of accurately estimating the mode (or modes) as well as characterizing the modality of data. The specific application area includes complex or mixture distributions particularly in a big data environment. The heterogeneous nature of (big) data may require deep introspective statistical and machine learning techniques, but these statistical tools often fail when applied without first understanding the data. In small datasets, this often isn't a big issue, but when dealing with large scale data analysis or big data thoroughly inspecting each dimension typically yields an $O(n^{n-1})$ problem. As such, dealing with big data require an alternative toolkit. This package not only identifies the mode or modes for various data types, it also provides a programmatic way of understanding the modality (i.e. uni-modal, bimodal, etc.) of a dataset (whether it's big data or not). See <a href="http://www.sdeevi.com/modes_package">http://www.sdeevi.com/modes_package</a> for examples and discussion. / CC BY-NC-SA 4.0	noarch
r-modeva	1.3.2	Analyses species distribution models and evaluates their performance. It includes functions for performing variation partitioning, calculating several measures of model discrimination and calibration, optimizing prediction thresholds based on a number of criteria, performing multivariate environmental similarity surface (MESS) analysis, and displaying various analytical plots. / GPL-3	noarch
r-modifiedmk	1.4.0	Power of non-parametric Mann-Kendall test and Spearman's Rho test is highly influenced by serially correlated data. To address this issue, trend tests may be applied on the modified versions of the time series data by Block Bootstrapping (BBS), Prewhitening (PW), Trend Free Prewhitening (TFPW), Bias Corrected Prewhitening and Variance Correction Approach by calculating effective sample size. Mann, H. B. (1945).<doi:10.1017/CBO9781107415324.004>. Kendall, M. (1975). Multivariate analysis. Charles Griffin&Company Ltd., sen, P. K. (1968).<doi:10.2307/2285891>. Önöz, B., & Bayazit, M. (2012) <doi:10.1002/hyp.8438>. Hamed, K. H. (2009).<doi:10.1016/j.jhydrol.2009.01.040>. Yue, S., & Wang, C. Y. (2002) <doi:10.1029/2001WR000861>. Yue, S., Pilon, P., Phinney, B., & Cavadias, G. (2002) <doi:10.1002/hyp.1095>. Hamed, K. H., & Ramachandra Rao, A. (1998) <doi:10.1016/S0022-1694(97)00125-X>. Yue, S., & Wang, C. Y. (2004) <doi:10.1023/B:WARM.0000043140.61082.60>. / AGPL-3	noarch
r-modmarg	0.9.2	Calculate predicted levels and marginal effects, using the delta method to calculate standard errors. This is an R-based version of the 'margins' command from Stata. / GPL-3	noarch
r-modmax	1.1	The algorithms implemented here are used to detect the community structure of a network. These algorithms follow different approaches, but are all based on the concept of modularity maximization. / GPL-2	noarch
r-modtempeff	1.5.2	Fits a Constrained Segmented Distributed Lag regression model to epidemiological time series of mortality, temperature, and other confounders. / GPL-3	noarch
r-modturpoint	0.1.0	Turning point method is a method proposed by Choi (1990) <doi:10.2307/2531453> to estimate 50 percent effective dose (ED50) in the study of drug sensitivity. The method has its own advantages for that it can provide robust ED50 estimation. This package contains the modified function of Choi's turning point method. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-modules</a>	0.8.0	Provides modules as an organizational unit for source code. Modules enforce to be more rigorous when defining dependencies and have a local search path. They can be used as a sub unit within packages or in scripts. / MIT	noarch
<a href="#">r-modygliani</a>	1.0	RMSD and Internal Energy analysis of NAMD and YASARA Molecular Dynamics output files. Allows to comparison of different dynamics per different complexes. Input files have to be ASCII files tab separated. / MIT	noarch
<a href="#">r-mogavs</a>	1.1.0	Functions for exploring the best subsets in regression with a genetic algorithm. The package is much faster than methods relying on complete enumeration, and is suitable for data sets with large number of variables. For more information, see Sinha, Malo & Kuosmanen (2015) <doi:10.1080/10618600.2014.899236>. / GPL-2	noarch
<a href="#">r-mole</a>	1.0.1	Model for simulating language evolution in terms of cultural evolution (Smith & Kirby (2008) <DOI:10.1098/rstb.2008.0145>; Deacon 1997). The focus is on the emergence of argument-marking systems (Dowty (1991) <DOI:10.1353/lan.1991.0021>, Van Valin 1999, Dryer 2002, Lestrade 2015a), i.e. noun marking (Aristar (1997) <DOI:10.1075/sl.21.2.04ari>, Lestrade (2010) <DOI:10.7282/T3ZG6R4S>), person indexing (Ariel 1999, Dahl (2000) <DOI:10.1075/fol.7.1.03dah>, Bhat 2004), and word order (Dryer 2013), but extensions are foreseen. Agents start out with a protolanguage (a language without grammar; Bickerton (1981) <DOI:10.17169/langsci.b91.109>, Jackendoff 2002, Arbib (2015) <DOI:10.1002/9781118346136.ch27>) and interact through language games (Steels 1997). Over time, grammatical constructions emerge that may or may not become obligatory (for which the tolerance principle is assumed; Yang 2016). Throughout the simulation, uniformitarianism of principles is assumed (Hopper (1987) <DOI:10.3765/bls.v13i0.1834>, Givon (1995) <DOI:10.1075/z.74>, Croft (2000), Saffran (2001) <DOI:10.1111/1467-8721.01243>, Heine & Kuteva 2007), in which maximal psychological validity is aimed at (Grice (1975) <DOI:10.1057/9780230005853_5>, Levelt 1989, Gaerdenfors 2000) and language representation is usage based (Tomasello 2003, Bybee 2010). In Lestrade (2015b) <DOI:10.15496/publikation-8640>, Lestrade (2015c) <DOI:10.1075/avt.32.08les>, and Lestrade (2016) <DOI:10.17617/2.2248195>), which reported on the results of preliminary versions, this package was announced as WDWTW (for who does what to whom), but for reasons of pronunciation and generalization the title was changed. / GPL-2	noarch
<a href="#">r-momentchi2</a>	0.1.5	A collection of moment-matching methods for computing the cumulative distribution function of a positively-weighted sum of chi-squared random variables. Methods include the Satterthwaite-Welch method, Hall-Buckley-Eagleson method, Wood's F method, and the Lindsay-Pilla-Basak method. / GPL-2   GPL-3	noarch
<a href="#">r-moments</a>	0.14	Functions to calculate: moments, Pearson's kurtosis, Geary's kurtosis and skewness; tests related to them (Anscombe-Glynn, D'Agostino, Bonett-Seier). / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-momtrunc</a>	4.51	It computes the raw moments for the truncated and folded multivariate normal, Skew-normal (SN), Extended skew normal (ESN) and Student's t-distribution. It also offers specific functions to compute the mean and variance-covariance matrix as well as the cumulative distribution function (cdf) for the folded normal, SN, ESN, and folded t-distribution. Density and random deviates are offered for the ESN (SN as particular case) distribution. Most algorithms are extensions based on Kan, R., & Robotti, C. (2017) <doi:10.1080/10618600.2017.1322092>. / GPL-2	noarch
<a href="#">r-mondate</a>	0.10.0	Keep track of dates in terms of months. Model dates as at close of business. Perform date arithmetic in units of months and years (multiples of months). Allow infinite dates to model ultimate time spans. / GPL-2	noarch
<a href="#">r-mondrian</a>	1.0_0	The unique function of this package allows representing in a single graph the relative occurrence and co-occurrence of events measured in a sample. As examples, the package was applied to describe the occurrence and co-occurrence of different species of bacterial or viral symbionts infecting arthropods at the individual level. The graphics allows determining the prevalence of each symbiont and the patterns of multiple infections (i.e. how different symbionts share or not the same individual hosts). We named the package after the famous painter as the graphical output recalls Mondrian's paintings. / GPL (>= 2.0)	noarch
<a href="#">r-monetdb.r</a>	1.0.1	Allows to pull data from MonetDB into R. Includes a DBI implementation and a dplyr backend. / MPL (== 2.0)	linux-64, osx-64, win-64
<a href="#">r-mongolite</a>	2.0.1	High-performance 'MongoDB' client based on 'libmongoc' and 'jsonlite'. Includes support for aggregation, indexing, map-reduce, streaming, encryption, enterprise authentication. The online user manual provides an overview of the available methods in the package: < <a href="https://jeroen.github.io/mongolite/">https://jeroen.github.io/mongolite/</a> >. / Apache License 2.0	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-monographar</a>	1.2.0	Contains functions intended to facilitate the production of plant taxonomic monographs. The package includes functions to convert tables into taxonomic descriptions, lists of collectors, examined specimens, and can generate a monograph skeleton. Additionally, wrapper functions to batch the production of phenology charts and distributional and diversity maps are also available. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-monomvn</a>	1.9_1	Estimation of multivariate normal and student-t data of arbitrary dimension where the pattern of missing data is monotone. Through the use of parsimonious/shrinkage regressions (plsr, pcr, lasso, ridge, etc.), where standard regressions fail, the package can handle a nearly arbitrary amount of missing data. The current version supports maximum likelihood inference and a full Bayesian approach employing scale-mixtures for Gibbs sampling. Monotone data augmentation extends this Bayesian approach to arbitrary missingness patterns. A fully functional standalone interface to the Bayesian lasso (from Park & Casella), Normal-Gamma (from Griffin & Brown), Horseshoe (from Carvalho, Polson, & Scott), and ridge regression with model selection via Reversible Jump, and student-t errors (from Geweke) is also provided. / LGPL-3	linux-64, osx-64, win-64
<a href="#">r-monopoly</a>	0.3_1	Functions for fitting monotone polynomials to data. Detailed discussion of the methodologies used can be found in Murray, Mueller and Turlach (2013) <doi:10.1007/s00180-012-0390-5> and Murray, Mueller and Turlach (2016) <doi:10.1080/00949655.2016.1139582>. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-monotonicity</a>	1.3	Test for monotonicity in financial variables sorted by portfolios. It is conventional practice in empirical research to form portfolios of assets ranked by a certain sort variable. A t-test is then used to consider the mean return spread between the portfolios with the highest and lowest values of the sort variable. Yet comparing only the average returns on the top and bottom portfolios does not provide a sufficient way to test for a monotonic relation between expected returns and the sort variable. This package provides nonparametric tests for the full set of monotonic patterns by Patton, A. and Timmermann, A. (2010) <doi:10.1016/j.jfineco.2010.06.006> and compares the proposed results with extant alternatives such as t-tests, Bonferroni bounds, and multivariate inequality tests through empirical applications and simulations. / BSD_3_clause	noarch
<a href="#">r-monreg</a>	0.1.3	Estimates monotone regression and variance functions in a nonparametric model. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-monte.carlo.se</a>	0.1.0	Computes Monte Carlo standard errors for summaries of Monte Carlo output. Summaries and their standard errors are based on columns of Monte Carlo simulation output. Dennis D. Boos and Jason A. Osborne (2015) <doi:10.1111/insr.12087>. / GPL-3	noarch
<a href="#">r-mopsocd</a>	0.5.1	A multi-objective optimization solver based on particle swarm optimization with crowding distance. / GPL-2	noarch
<a href="#">r-morder</a>	0.1	MOrder provide functions to check time homogeneity and order of markov chain by using chi-squared test, AIC value and BIC value. / GPL-2	noarch
<a href="#">r-morgenstemning</a>	1.0	This package is a port of the MATLAB colourmap functions accompanying the paper M. Geissbuehler and T. Lasser, How to display data by color schemes compatible with red-green color perception deficiencies, Opt. Express 21, 9862-9874 (2013) to R. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-morsegen</a>	1.2	MorseGen is a program for generating raw data based on user-specified summary (descriptive) statistics. Samples based on the supplied statistics are drawn from a normal distribution (or, in some cases, an exponential distribution) and scaled to match the desired descriptive statistics. Intended uses include creating raw data that fits desired characteristics or to replicate the results in a published study. / GPL-2	noarch
<a href="#">r-mosaicdata</a>	0.17.0	Data sets from Project MOSAIC (< <a href="http://mosaic-web.org">http://mosaic-web.org</a> >) used to teach mathematics, statistics, computation and modeling. Funded by the NSF, Project MOSAIC is a community of educators working to tie together aspects of quantitative work that students in science, technology, engineering and mathematics will need in their professional lives, but which are usually taught in isolation, if at all. / GPL-2	noarch
<a href="#">r-most</a>	0.1.0	Provides functions similar to the ‘SAS’ macros previously provided to accompany Collins, Dziak, and Li (2009) <DOI:10.1037/a0015826> and Dziak, Nahum-Shani, and Collins (2012) <DOI:10.1037/a0026972>, papers which outline practical benefits and challenges of factorial and fractional factorial experiments for scientists interested in developing biological and/or behavioral interventions, especially in the context of the multiphase optimization strategy (see Collins, Kugler & Gwadz 2016) <DOI:10.1007/s10461-015-1145-4>. The package currently contains three functions. First, RelativeCosts1() draws a graph of the relative cost of complete and reduced factorial designs versus other alternatives. Second, RandomAssignmentGenerator() returns a dataframe which contains a list of random numbers that can be used to conveniently assign participants to conditions in an experiment with many conditions. Third, FactorialPowerPlan() estimates the power, detectable effect size, or required sample size of a factorial or fractional factorial experiment, for main effects or interactions, given several possible choices of effect size metric, and allowing pretests and clustering. / GPL-2	noarch
<a href="#">r-motilitylab</a>	0.2.5	Statistics to quantify tracks of moving things (x-y-z-t data), such as cells, bacteria or animals. Available measures include mean square displacement, confinement ratio, autocorrelation, straightness, turning angle, and fractal dimension. / GPL-2	noarch
<a href="#">r-moult</a>	2.1.0	Functions to estimate start and duration of moult from moult data, based on models developed in Underhill and Zucchini (1988, 1990). / GPL-2	noarch
<a href="#">r-mountainplot</a>	1.2	Lattice functions for drawing folded empirical cumulative distribution plots, or mountain plots. A mountain plot is similar to an empirical CDF plot, except that the curve increases from 0 to 0.5, then decreases from 0.5 to 1 using an inverted scale at the right side. / GPL-3	noarch
<a href="#">r-mozzie</a>	0.1.0	Weekly notified dengue cases in 25 districts of Sri Lanka from 2008/ week-52 to 2014/ week-21. / CC0	noarch
<a href="#">r-mp</a>	0.4.1	Multidimensional projection techniques are used to create two dimensional representations of multidimensional data sets. / GPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-mpci	1.0.7	It performs the followings Multivariate Process Capability Indices: Shahriari et al. (1995) Multivariate Capability Vector, Taam et al. (1993) Multivariate Capability Index (MCpm), Pan and Lee (2010) proposal (NMCpm) and the followings based on Principal Component Analysis (PCA): Wang and Chen (1998), Xekalaki and Perakis (2002) and Wang (2005). Two datasets are included. / GPL-2	noarch
r-mpcmp	0.1.3	A collection of functions for estimation, testing and diagnostic checking for the mean-parametrized Conway-Maxwell Poisson (COM-Poisson) regression model of Huang (2017) <doi:10.1177/1471082X17697749>. / GPL-2	noarch
r-mpcv	1.1	Multivariate process capability analysis using the multivariate process capability vector. Allows to analyze a multivariate process with both normally and non-normally distributed and also with dependent and independent quality characteristics. / GPL (>= 2.0)	noarch
r-mpdir	0.1_1	Data sets and scripts for Modeling Psychophysical Data in R (Springer). / GPL-2	noarch
r-mpe	1.0	Functions for calculating sample size and power for clinical trials with multiple (co-)primary endpoints. / LGPL-3	noarch
r-mpinet	1.0	(1) Our system provides a network-based strategies for metabolite pathway identification.(2) The MPINet can support the identification of pathways using Hypergeometric test based on metabolite set. (3)MPINet can support pathways from multiple databases. / GPL-2	noarch
r-mpkn	0.1.0	A matrix discrete model having the form ' $M[i1] = (I - Q)^{-1} * M[i]$ '. The calculation of the values of ' $M[i]$ ' only for pre-selected values of ' $i$ '. The method of calculation is presented in the vignette 'Fundament' ('Base'). Maybe it's own idea of the author of the package. A weakness is that the method gives information only in selected steps of the process. It mainly refers to cases with matrices that are not Markov chain. If ' $Q$ ' is Markov transition matrix, then MUPkL() may be used to calculate the steady-state distribution ' $p$ ' for ' $p = Q * p$ '. Matrix power of non integer (matrix.powerni()) gives the same results as a mpower() from package 'matlib'. References: Markov chains, (< <a href="https://en.wikipedia.org/wiki/Markov_chain#Expected_number_of_visits">https://en.wikipedia.org/wiki/Markov_chain#Expected_number_of_visits</a> >). Donald R. Burleson, Ph.D. (2005), ON NON-INTEGGER POWERS OF A SQUARE MATRIX, (< <a href="http://www.blackmesapress.com/Eigenvalues.htm">http://www.blackmesapress.com/Eigenvalues.htm</a> >). / GPL-3	noarch
r-mplikelihoodwb	1.1	Computing modified profile likelihood estimates for Weibull Shape and Regression Parameters. Modified likelihood estimates are provided. / GPL-2	noarch
r-mpm	1.0_2	Exploratory graphical analysis of multivariate data, specifically gene expression data with different projection methods: principal component analysis, correspondence analysis, spectral map analysis. / GPL-2	noarch
r-mpmi	0.43	Uses a kernel smoothing approach to calculate Mutual Information for comparisons between all types of variables including continuous vs continuous, continuous vs discrete and discrete vs discrete. Uses a nonparametric bias correction giving Bias Corrected Mutual Information (BCMI). Implemented efficiently in Fortran 95 with OpenMP and suited to large genomic datasets. / GPL-3	linux-64, osx-64, win-64
r-mpn	0.3.0	Calculates the Most Probable Number (MPN) to quantify the concentration (density) of microbes in serial dilutions of a laboratory sample (described in Jarvis, 2010 <doi:10.1111/j.1365-2672.2010.04792.x>). Also calculates the Aerobic Plate Count (APC) for similar microbial enumeration experiments. / Unlimited	noarch

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Name	Version	Summary/License	Platforms
r-mppa	1.0	A procedure to test for dependence between point processes on the real line, e.g. causal dependence, correlation, inhibition or anti-correlation. The package also provides a number of utilities for plotting simultaneous point processes, and combining p-values. / GPL-2	noarch
r-mpr	1.0.4	Package for fitting Multi-Parameter Regression (MPR) models to right-censored survival data. These are flexible parametric regression models which extend standard models, for example, proportional hazards. / GPL-3	noarch
r-mps	2.3.0	Developed for computing the probability density function, computing the cumulative distribution function, computing the quantile function, random generation, and estimating the parameters of 24 G-family of statistical distributions via the maximum product spacing approach introduced in < <a href="https://www.jstor.org/stable/2345411">https://www.jstor.org/stable/2345411</a> >. The set of families contains: beta G distribution, beta exponential G distribution, beta extended G distribution, exponentiated G distribution, exponentiated exponential Poisson G distribution, exponentiated generalized G distribution, exponentiated Kumaraswamy G distribution, gamma type I G distribution, gamma type II G distribution, gamma uniform G distribution, gamma-X generated of log-logistic family of G distribution, gamma-X family of modified beta exponential G distribution, geometric exponential Poisson G distribution, generalized beta G distribution, generalized transmuted G distribution, Kumaraswamy G distribution, log gamma type I G distribution, log gamma type II G distribution, Marshall Olkin G distribution, Marshall Olkin Kumaraswamy G distribution, modified beta G distribution, odd log-logistic G distribution, truncated-exponential skew-symmetric G distribution, and Weibull G distribution. / GPL-2	noarch
r-mpsem	0.3_6	Computational tools to represent phylogenetic signals using adapted eigenvector maps. / GPL-2	linux-64, osx-64, win-64
r-mpsychor	0.10_1	Supplementary materials and datasets for the book Modern Psychometrics With R (Mair, 2018, Springer user! series). / GPL-2	noarch
r-mpt	0.6_0	Fitting and testing multinomial processing tree (MPT) models, a class of nonlinear models for categorical data. The parameters are the link probabilities of a tree-like graph and represent the latent cognitive processing steps executed to arrive at observable response categories (Batchelder & Riefer, 1999 <doi:10.3758/bf03210812>; Erdfelder et al., 2009 <doi:10.1027/0044-3409.217.3.108>; Riefer & Batchelder, 1988 <doi:10.1037/0033-295x.95.3.318>). / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-mptnr</a>	1.11.0	Provides a user-friendly way for the analysis of multinomial processing tree (MPT) models (e.g., Riefer, D. M., and Batchelder, W. H. [1988]. Multinomial modeling and the measurement of cognitive processes. Psychological Review, 95, 318-339) for single and multiple datasets. The main functions perform model fitting and model selection. Model selection can be done using AIC, BIC, or the Fisher Information Approximation (FIA) a measure based on the Minimum Description Length (MDL) framework. The model and restrictions can be specified in external files or within an R script in an intuitive syntax or using the context-free language for MPTs. The 'classical' .EQN file format for model files is also supported. Besides MPTs, this package can fit a wide variety of other cognitive models such as SDT models (see fit.model). It also supports multicore fitting and FIA calculation (using the snowfall package), can generate or bootstrap data for simulations, and plot predicted versus observed data. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-mpv</a>	1.55	Most of this package consists of data sets from the textbook Introduction to Linear Regression Analysis (3rd ed), by Montgomery, Peck and Vining. Some additional data sets and functions related to visualization of linear and non-parametric regression results are included. / Unlimited	noarch
<a href="#">r-mra</a>	2.16.1	Accomplishes mark-recapture analysis with covariates. Models available include the Cormack-Jolly-Seber open population (Cormack (1972) <doi:10.2307/2556151>; Jolly (1965) <doi:10.2307/2333826>; Seber (1965) <doi:10.2307/2333827>) and Huggin's (1989) <doi:10.2307/2336377> closed population. Link functions include logit, sine, and hazard. Model selection, model averaging, plot, and simulation routines included. Open population size by the Horvitz-Thompson (1959) <doi:10.2307/2280784> estimator. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-mratios</a>	1.4.0	Performs (simultaneous) inferences for ratios of linear combinations of coefficients in the general linear model. Multiple comparisons and simultaneous confidence interval estimations can be performed for ratios of treatment means in the normal one-way layout with homogeneous and heterogeneous treatment variances, according to Dilba et al. (2007) < <a href="https://cran.r-project.org/doc/Rnews/Rnews_2007-1.pdf">https://cran.r-project.org/doc/Rnews/Rnews_2007-1.pdf</a> > and Hasler and Hothorn (2008) <doi:10.1002/bimj.200710466>. Confidence interval estimations for ratios of linear combinations of linear model parameters like in (multiple) slope ratio and parallel line assays can be carried out. Moreover, it is possible to calculate the sample sizes required in comparisons with a control based on relative margins. For the simple two-sample problem, functions for a t-test for ratio-formatted hypotheses and the corresponding confidence interval are provided assuming homogeneous or heterogeneous group variances. / GPL-2	noarch
<a href="#">r-mrbayes</a>	0.1.0	Bayesian estimation of inverse variance weighted (IVW), Burgess et al. (2013) <doi:10.1002/gepi.21758>, and MR-Egger, Bowden et al. (2015) <doi:10.1093/ije/dyv080>, summary data models for Mendelian randomization analyses. / GPL-3	noarch
<a href="#">r-mrclient</a>	3.4.3	A free, community-supported, data science tool for high performance analytics / Proprietary	linux-64, win-64
<a href="#">r-mrclient-mlm</a>	3.4.3	Pre-trained machine learning models for sentiment analysis and image detection / Proprietary	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-mrclient-mml</a>	3.4.3	Provides state-of-the-art fast, scalable machine learning algorithms and transforms for R / Proprietary	linux-64, win-64
<a href="#">r-mreg</a>	1.1	Implements the methods described in Bond S, Farewell V, 2006, Exact Likelihood Estimation for a Negative Binomial Regression Model with Missing Outcomes, Biometrics / GPL-3	noarch
<a href="#">r-mrfse</a>	0.1	A Markov random field structure estimator that uses a penalized maximum conditional likelihood method similar to the Bayesian Information Criterion (Fronzana, 2016) <doi:10.11606/T.45.2018.tde-02022018-151123>. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-mri</a>	1.0.1	It provides functions to compute the values of different modifications of the Rand and Wallace indices. The indices are used to measure the stability or similarity of two partitions obtained on two different sets of units with a non-empty intercept. Splitting and merging of clusters can (depends on the selected index) have a different effect on the value of the indices. The indices are proposed in Cugmas and Ferligoj (2018) < <a href="http://ibmi.mf.uni-lj.si/mz/2018/no-1/Cugmas2018.pdf">http://ibmi.mf.uni-lj.si/mz/2018/no-1/Cugmas2018.pdf</a> >. / GPL-2	noarch
<a href="#">r-mrm</a>	1.1.6	Conditional maximum likelihood estimation via the EM algorithm and information-criterion-based model selection in binary mixed Rasch models. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-mrmre</a>	2.0.9	Computes mutual information matrices from continuous, categorical and survival variables, as well as feature selection with minimum redundancy, maximum relevance (mRMR) and a new ensemble mRMR technique with DOI: N De Jay et al. (2013) <doi:10.1093/bioinformatics/btt383>. / Artistic-2.0	linux-64, osx-64, win-64
<a href="#">r-mro</a>	0.1.1	Computes multiple correlation coefficient when the data matrix is given and tests its significance. / GPL-2	linux-64, win-64
<a href="#">r-mrpostman</a>	0.2.0	Multiple IMAP (Internet Message Access Protocol) commands based on the RFC 3501 manual (Crispin, 2003, <doi:10.17487/RFC3501>), its updates, and other related documents. Besides other features, 'mRpostman' provides functions for listing, selecting and renaming mailboxes, as well as moving, fetching, and searching for messages using several criteria. / GPL-3	noarch
<a href="#">r-mrqol</a>	1.0	We can calculate directly using this package the Minimal Clinically Important Difference by applying the Anchor-based method and the Response shift effect by applying the Then-Test method. / GPL (>= 2.0)	noarch
<a href="#">r-mrs</a>	1.2.4	An implementation of the MRS algorithm for comparison across distributions, as described in Jacopo Soriano, Li Ma (2016) <doi:10.1111/rssb.12180>. The model is based on a nonparametric process taking the form of a Markov model that transitions between a null and an alternative state on a multi-resolution partition tree of the sample space. MRS effectively detects and characterizes a variety of underlying differences. These differences can be visualized using several plotting functions. / GPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-mrsurv</a>	0.2	This package contains functions, data and examples to compute a multiplicative-regression model for relative survival. / GPL-2	noarch
<a href="#">r-mrtsamplesize</a>	0.1.0	Provide a sample size calculator for micro-randomized trials (MRTs) based on methodology developed in Sample Size Calculations for Micro-randomized Trials in mHealth by Liao et al. (2016) <DOI:10.1002/sim.6847>. / GPL-2	noarch
<a href="#">r-ms.sev</a>	1.0.4	Calculates ARMSS (age related multiple sclerosis severity), and both local and global MSSS (multiple sclerosis severity score). / GPL-2	noarch
<a href="#">r-msaface</a>	0.1.0	The new methodology moving subset analysis provides functions to investigate the effect of environmental conditions on the CO2 fertilization effect within longterm free air carbon enrichment (FACE) experiments. In general, the functionality is applicable to derive the influence of a third variable (forcing experiment-support variable) on the relation between a dependent and an independent variable. / GPL-3	noarch
<a href="#">r-msap</a>	1.1.8	Statistical Analyses of Methylation-sensitive Amplification Polymorphism (MSAP) assays. / GPL-2	noarch
<a href="#">r-msar</a>	0.3.0	Visualises multiple sequence alignments dynamically within the Shiny web application framework. / BSL-1.0	noarch
<a href="#">r-msbox</a>	1.2.1	Common mass spectrometry tools described in John Roboz (2013) <doi:10.1201/b15436>. It allows checking element isotopes, calculating (isotope labelled) exact monoisotopic mass, m/z values and mass accuracy, and inspecting possible contaminant mass peaks, examining possible adducts in electrospray ionization (ESI) and matrix-assisted laser desorption ionization (MALDI) ion sources. / GPL-2	noarch
<a href="#">r-msbp</a>	1.4	Performs Bayesian nonparametric multiscale density estimation and multiscale testing of group differences with multiscale Bernstein polynomials (msBP) mixtures as in Canale and Dunson (2016). / GPL-2	linux-64, osx-64, win-64
<a href="#">r-mscombine</a>	1.4	Find common entities detected in both positive and negative ionization mode, delete this entity in the less sensible mode and combine both matrices. / GPL-2	noarch
<a href="#">r-msda</a>	1.0.2	Efficient procedures for computing a new Multi-Class Sparse Discriminant Analysis method that estimates all discriminant directions simultaneously. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-msde</a>	1.0.4	Implements an MCMC sampler for the posterior distribution of arbitrary time-homogeneous multivariate stochastic differential equation (SDE) models with possibly latent components. The package provides a simple entry point to integrate user-defined models directly with the sampler's C code, and parallelizes large portions of the calculations when compiled with 'OpenMP'. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-mseapca</a>	1.0	This package provides functions for metabolite set enrichment analysis (MSEA) and principal component analysis (PCA), and converting metabolite set list from your own csv files or KEGG's tar.gz files to XML documents. This package is suitable for computation of MSEA for factor loading in PCA. / BSD	noarch
<a href="#">r-msg</a>	0.4	A companion to the Chinese book “Modern Statistical Graphics”. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-msglasso	2.1	For fitting multivariate response and multiple predictor linear regressions with an arbitrary group structure assigned on the regression coefficient matrix, using the multivariate sparse group lasso and the mixed coordinate descent algorithm. / GPL-2	linux-64, osx-64, win-64
r-msgpackr	1.1	This is the library that can serialize or unserialize MessagePack format data. / BSD_2_clause	noarch
r-msgps	1.3.1	Computes the degrees of freedom of the lasso, elastic net, generalized elastic net and adaptive lasso based on the generalized path seeking algorithm. The optimal model can be selected by model selection criteria including Mallows' Cp, bias-corrected AIC (AICc), generalized cross validation (GCV) and BIC. / GPL-2	linux-64, osx-64, win-64
r-msimcc	0.0.1	Micro simulation model to reproduce natural history of cervical cancer and cost-effectiveness evaluation of prevention strategies. See Georgalis L, de Sanjose S, Esnaola M, Bosch F X, Diaz M (2016) <doi:10.1097/CEJ.0000000000000202> for more details. / GPL-2	linux-64, osx-64, win-64
r-msma	2.0	Several functions can be used to analyze multiblock multivariable data. If the input is a single matrix, then principal components analysis (PCA) is implemented. If the input is a list of matrices, then multiblock PCA is implemented. If the input is two matrices, for exploratory and objective variables, then partial least squares (PLS) analysis is implemented. If the input is two lists of matrices, for exploratory and objective variables, then multiblock PLS analysis is implemented. Additionally, if an extra outcome variable is specified, then a supervised version of the methods above is implemented. For each method, sparse modeling is also incorporated. Functions for selecting the number of components and regularized parameters are also provided. / GPL-2	noarch
r-msme	0.5.3	Functions and datasets from Hilbe, J.M., and Robinson, A.P. 2013. Methods of Statistical Model Estimation. Chapman & Hall / CRC. / GPL-3	noarch
r-msmwra	1.3	Data sets in the book entitled Multivariate Statistical Methods with R Applications, H.Bulut (2018). The book will be published in Turkish and the original name of this book will be R Uygulamaları ile Çok Degiskenli Istatistiksel Yontemler. / GPL-3	noarch
r-mssm	0.1.2	Provides methods to perform parameter estimation and make analysis of multivariate observed outcomes through time which depends on a latent state variable. All methods scale well in the dimension of the observed outcomes at each time point. The package contains an implementation of a Laplace approximation, particle filters like suggested by Lin, Zhang, Cheng, & Chen (2005) <doi:10.1198/016214505000000349>, and the gradient and observed information matrix approximation suggested by Poyiadjis, Doucet, & Singh (2011) <doi:10.1093/biomet/asq062>. / GPL-2	linux-64, osx-64, win-64
r-mssqlr	1.0.0	Can be used to query data from data from Microsoft SQL Server (MSSQL, see < <a href="http://www.microsoft.com/sqlserver/">http://www.microsoft.com/sqlserver/</a> > for more information). Based on the concepts of Entity Framework, the package allows querying data from MSSQL Database. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-mstate</a>	0.2.11	Contains functions for data preparation, descriptives, hazard estimation and prediction with Aalen-Johansen or simulation in competing risks and multi-state models, see Putter, Fiocco, Geskus (2007) <doi:10.1002/sim.2712>. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-mstknncust</a>	0.1.0	Implements the MST-kNN clustering algorithm which was proposed by Inostroza-Ponta, M. (2008) < <a href="https://trove.nla.gov.au/work/28729389?selectedversion=NBD44634158">https://trove.nla.gov.au/work/28729389?selectedversion=NBD44634158</a> >. / GPL-2	noarch
<a href="#">r-mstr</a>	1.2	Generation of response patterns under dichotomous and polytomous computerized multistage testing (MST) framework. It holds various item response theory (IRT) and score-based methods to select the next module and estimate ability levels (Magis, Yan and von Davier (2017, ISBN:978-3-319-69218-0)). / GPL-2	noarch
<a href="#">r-mstrio</a>	10.11	Interface for creating data sets and extracting data through the ‘MicroStrategy’ REST API. Access the demo API at < <a href="https://demo.microstrategy.com/MicroStrategyLibrary/api-docs/index.html">https://demo.microstrategy.com/MicroStrategyLibrary/api-docs/index.html</a> >. / Apache License 2.0   file LICENSE	noarch
<a href="#">r-msu</a>	0.0.1	Estimators for multivariate symmetrical uncertainty based on the work of Gustavo Sosa et al. (2016) <arXiv:1709.08730>, total correlation, information gain and symmetrical uncertainty of categorical variables. / GPL-3	noarch
<a href="#">r-mswm</a>	1.4	Estimation, inference and diagnostics for Univariate Autoregressive Markov Switching Models for Linear and Generalized Models. Distributions for the series include gaussian, Poisson, binomial and gamma cases. The EM algorithm is used for estimation (see Perlin (2012) <doi:10.2139/ssrn.1714016>). / GPL (>= 2.0)	noarch
<a href="#">r-mtdrh</a>	0.1.0	The Mass Transportation Distance rank histogram was developed to assess the reliability of scenarios with equal or different probabilities of occurrence <doi:10.1002/we.1872>. / GPL-2	noarch
<a href="#">r-mthapower</a>	0.1.1	Calculate Sample Size and Power for Association Studies Involving Mitochondrial DNA Haplogroups. Based on formulae by Samuels et al. AJHG, 2006. 78(4):713-720. <DOI:10.1086/502682>. / GPL-3	noarch
<a href="#">r-mtlr</a>	0.2.1	An implementation of Multi-Task Logistic Regression (MTLR) for R. This package is based on the method proposed by Yu et al. (2011) which utilized MTLR for generating individual survival curves by learning feature weights which vary across time. This model was further extended to account for left and interval censored data. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-mts</a>	1.0	Multivariate Time Series (MTS) is a general package for analyzing multivariate linear time series and estimating multivariate volatility models. It also handles factor models, constrained factor models, asymptotic principal component analysis commonly used in finance and econometrics, and principal volatility component analysis. (a) For the multivariate linear time series analysis, the package performs model specification, estimation, model checking, and prediction for many widely used models, including vector AR models, vector MA models, vector ARMA models, seasonal vector ARMA models, VAR models with exogenous variables, multivariate regression models with time series errors, augmented VAR models, and Error-correction VAR models for co-integrated time series. For model specification, the package performs structural specification to overcome the difficulties of identifiability of VARMA models. The methods used for structural specification include Kronecker indices and Scalar Component Models. (b) For multivariate volatility modeling, the MTS package handles several commonly used models, including multivariate exponentially weighted moving-average volatility, Cholesky decomposition volatility models, dynamic conditional correlation (DCC) models, copula-based volatility models, and low-dimensional BEKK models. The package also considers multiple tests for conditional heteroscedasticity, including rank-based statistics. (c) Finally, the MTS package also performs forecasting using diffusion index, transfer function analysis, Bayesian estimation of VAR models, and multivariate time series analysis with missing values. Users can also use the package to simulate VARMA models, to compute impulse response functions of a fitted VARMA model, and to calculate theoretical cross-covariance matrices of a given VARMA model. / Artistic-2.0	linux-64, osx-64, win-64
<a href="#">r-mtsys</a>	1.2.0	Mahalanobis-Taguchi (MT) system is a collection of multivariate analysis methods developed for the field of quality engineering. MT system consists of two families depending on their purpose. One is a family of Mahalanobis-Taguchi (MT) methods (in the broad sense) for diagnosis (see Woodall, W. H., Koudelik, R., Tsui, K. L., Kim, S. B., Stoumbos, Z. G., and Carvounis, C. P. (2003) <doi:10.1198/004017002188618626>) and the other is a family of Taguchi (T) methods for forecasting (see Kawada, H., and Nagata, Y. (2015) <doi:10.17929/tqs.1.12>). The MT package contains three basic methods for the family of MT methods and one basic method for the family of T methods. The MT method (in the narrow sense), the Mahalanobis-Taguchi Adjoint (MTA) methods, and the Recognition-Taguchi (RT) method are for the MT method and the two-sided Taguchi (T1) method is for the family of T methods. In addition, the Ta and Tb methods, which are the improved versions of the T1 method, are included. / MIT	noarch
<a href="#">r-muchpoint</a>	0.6.1	Nonparametric approach to estimate the location of block boundaries (change-points) of non-overlapping blocks in a random symmetric matrix which consists of random variables whose distribution changes from block to block. BRAULT Vincent, OUADAH Sarah, SANSONNET Laure and LEVY-LEDUC Celine (2017) <doi:10.1016/j.jmva.2017.12.005>. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-muckrock</a>	0.1.0	A data package containing public domain information on requests made by the 'MuckRock' ( <a href="https://www.muckrock.com/">https://www.muckrock.com/</a> ) project under the United States Freedom of Information Act. / Unlimited	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-mudens</a>	1.3.2	Compute a density estimate from a vector of right-censored survival time using kernel functions. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-muellerplot</a>	0.1.1	Implements an estimator for relative risk based on the median unbiased estimator. The relative risk estimator is well defined and performs satisfactorily for a wide range of data configurations. The details of the method are available in Carter et al (2010) <doi:10.1111/j.1467-9876.2010.00711.x>. / GPL-3	noarch
<a href="#">r-muficokriging</a>	1.2	This package builds multi-fidelity cokriging models from responses with different levels of fidelity. Important functions : MuFicokm, predict.MuFicokm, summary.MuFicokm. / GPL-3	noarch
<a href="#">r-muhaz</a>	1.2.6	Produces a smooth estimate of the hazard function for censored data. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-mulset</a>	1.0.0	Generates Muller plot from parental/genealogy/phylogeny information and population/abundance/frequency dynamics data. Muller plots are plots which combine information about succession of different OTUs (genotypes, phenotypes, species, ...) and information about dynamics of their abundances (populations or frequencies) over time. They are powerful and fascinating tools to visualize evolutionary dynamics. They may be employed also in study of diversity and its dynamics, i.e. how diversity emerges and how changes over time. They are called Muller plots in honor of Hermann Joseph Muller which used them to explain his idea of Muller's ratchet (Muller, 1932, American Naturalist). A big difference between Muller plots and normal box plots of abundances is that a Muller plot depicts not only the relative abundances but also succession of OTUs based on their genealogy/phylogeny/parental relation. In a Muller plot, horizontal axis is time/generations and vertical axis represents relative abundances of OTUs at the corresponding times/generations. Different OTUs are usually shown with polygons with different colors and each OTU originates somewhere in the middle of its parent area in order to illustrate their succession in evolutionary process. To generate a Muller plot one needs the genealogy/phylogeny/parental relation of OTUs and their abundances over time. MullerPlot package has the tools to generate Muller plots which clearly depict the origin of successors of OTUs. / GPL-3	noarch
<a href="#">r-mulset</a>	1.0.0	Computes efficient data distributions from highly inconsistent datasets with many missing values using multi-set intersections. Based upon hash functions, 'mulset' can quickly identify intersections from very large matrices of input vectors across columns and rows and thus provides scalable solution for dealing with missing values. Tomic et al. (2019) <doi:10.1101/545186>. / EUPL (>= 1.2)	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-multcomp</a>	1.4.1	Simultaneous tests and confidence intervals for general linear hypotheses in parametric models, including linear, generalized linear, linear mixed effects, and survival models. The package includes demos reproducing analyzes presented in the book Multiple Comparisons Using R (Bretz, Hothorn, Westfall, 2010, CRC Press). / GPL-2	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-multcompview</a>	0.1.7	Convert a logical vector or a vector of p-values or a correlation, difference, or distance matrix into a display identifying the pairs for which the differences were not significantly different. Designed for use in conjunction with the output of functions like TukeyHSD, dist{stats}, simint, simtest, csimint, csimtest{multcomp}, friedmanmc, kruskalmc{pgirmess}. / GPL-3	noarch
<a href="#">r-multdm</a>	1.0	Allows to perform the multivariate version of the Diebold-Mariano test for equal predictive ability of multiple forecast comparison. Main reference: Mariano, R.S., Preve, D. (2012) <doi:10.1016/j.jeconom.2012.01.014>. / GPL-3	noarch
<a href="#">r-multeq</a>	2.3	Equivalence tests and related confidence intervals for the comparison of two treatments, simultaneously for one or many normally distributed, primary response variables (endpoints). The step-up procedure of Quan et al. (2001) is both applied for differences and extended to ratios of means. A related single-step procedure is also available. / GPL-3	noarch
<a href="#">r-multfisher</a>	1.1	Calculates exact hypothesis tests to compare a treatment and a reference group with respect to multiple binary endpoints. The tested null hypothesis is an identical multidimensional distribution of successes and failures in both groups. The alternative hypothesis is a larger success proportion in the treatment group in at least one endpoint. The tests are based on the multivariate permutation distribution of subjects between the two groups. For this permutation distribution, rejection regions are calculated that satisfy one of different possible optimization criteria. In particular, regions with maximal exhaustion of the nominal significance level, maximal power under a specified alternative or maximal number of elements can be found. Optimization is achieved by a branch-and-bound algorithm. By application of the closed testing principle, the global hypothesis tests are extended to multiple testing procedures. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-multiapply</a>	2.1.1	The base apply function and its variants, as well as the related functions in the ‘plyr’ package, typically apply user-defined functions to a single argument (or a list of vectorized arguments in the case of mapply). The ‘multiApply’ package extends this paradigm with its only function, Apply, which efficiently applies functions taking one or a list of multiple unidimensional or multidimensional arrays (or combinations thereof) as input. The input arrays can have different numbers of dimensions as well as different dimension lengths, and the applied function can return one or a list of unidimensional or multidimensional arrays as output. This saves development time by preventing the R user from writing often error-prone and memory-inefficient loops dealing with multiple complex arrays. Also, a remarkable feature of Apply is the transparent use of multi-core through its parameter ‘ncores’. In contrast to the base apply function, this package suggests the use of ‘target dimensions’ as opposite to the ‘margins’ for specifying the dimensions relevant to the function to be applied. / LGPL-3	noarch
<a href="#">r-multiassetoptions</a>	0.1.1	Efficient finite difference method for valuing European and American multi-asset options. / GPL-2   GPL-3	noarch
<a href="#">r-multiband</a>	0.1.0	Algorithms for performing joint parameter estimation in astronomical survey data acquired in multiple bands. / MIT	noarch
<a href="#">r-multica</a>	1.1	Implements a generalization of the Cochran-Armitage trend test to multinomial data. In addition to an overall test, multiple testing adjusted p-values for trend in individual outcomes and power calculation is available. / GPL-2	noarch
<a href="#">r-multicomp</a>	1.1	A toolkit containing statistical analysis models motivated by multivariate forms of the Conway-Maxwell-Poisson (COM-Poisson) distribution for flexible modeling of multivariate count data, especially in the presence of data dispersion. Currently the package only supports bivariate data, via the bivariate COM-Poisson distribution described in Sellers et al. (2016) <doi:10.1016/j.jmva.2016.04.007>. Future development will extend the package to higher-dimensional data. / GPL-3	noarch
<a href="#">r-multicnvdetect</a>	0.1.1	This package provides a tool for analysis of multiple CNV. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-multicoll</a>	1.0	The detection of worrying approximate collinearity in a multiple linear regression model is a problem addressed in all existing statistical packages. However, we have detected deficits regarding to the incorrect treatment of qualitative independent variables and the role of the intercept of the model. The objective of this package is to correct these deficits. In this package will be available detection and treatment techniques traditionally used as the recently developed. D.A. Belsley (1982) <doi:10.1016/0304-4076(82)90020-3>. D. A. Belsley (1991, ISBN: 978-0471528890). C. Garcia, R. Salmeron and C.B. Garcia (2019) <doi:10.1080/00949655.2018.1543423>. R. Salmeron, C.B. Garcia and J. Garcia (2018) <doi:10.1080/00949655.2018.1463376>. G.W. Stewart (1987) <doi:10.1214/ss/1177013444>. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-multicool</a>	0.1_10	A set of tools to permute multisets without loops or hash tables and to generate integer partitions. The permutation functions are based on C code from Aaron Williams. Cool-lex order is similar to colexicographical order. The algorithm is described in Williams, A. (2009) <DOI:10.1145/1496770.1496877> Loopless Generation of Multiset Permutations by Prefix Shifts. Symposium on Discrete Algorithms, New York, United States. The permutation code is distributed without restrictions. The code for stable and efficient computation of multinomial coefficients comes from Dave Barber. The code can be download from < <a href="http://tamivox.org/dave/multinomial/code.html">http://tamivox.org/dave/multinomial/code.html</a> > and is distributed without conditions. The package also generates the integer partitions of a positive, non-zero integer n. The C code for this is based on Python code from Jerome Kelleher which can be found here < <a href="http://jeromekelleher.net/tag/integer-partitions.html">http://jeromekelleher.net/tag/integer-partitions.html</a> >. The C code and Python code are distributed without conditions. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-multifit</a>	1.0.0	Test for independence of two random vectors, learn and report the dependency structure. For more information, see Gorsky and Ma (2018) <arXiv:1806.06777>. / CC0	linux-64, osx-64, win-64
<a href="#">r-multifwf</a>	0.2.2	Read a table of fixed width formatted data of different types into a data.frame for each type. / GPL-2	noarch
<a href="#">r-multigroup</a>	0.4.4	Several functions are presented in order to study data in a group structure, where the same set of variables are measured on different groups of individuals. / GPL-3	noarch
<a href="#">r-multijoin</a>	0.1.1	Wrapper around the Unix join facility which is more efficient than the built-in R routine merge(). The package enables the joining of multiple files on disk at once. The files can be compressed and various filters can be deployed before joining. Compiles only under Unix. / GPL-3	noarch
<a href="#">r-multilaterals</a>	1.0	Computing transitive (and non-transitive) index numbers (Coelli et al., 2005 <doi:10.1007/b136381>) for cross-sections and panel data. For the calculation of transitive indexes, the EKS (Coelli et al., 2005 <doi:10.1007/b136381>; Rao et al., 2002 <doi:10.1007/978-1-4615-0851-9_4>) and Minimum spanning tree (Hill, 2004 <doi:10.1257/0002828043052178>) methods are implemented. Traditional fixed-base and chained indexes, and their growth rates, can also be derived using the Paasche, Laspeyres, Fisher and Tornqvist formulas. / GPL-3	noarch
<a href="#">r-multilevel</a>	2.6	The functions in this package are designed to be used in the analysis of multilevel data by applied psychologists. The package includes functions for estimating common within-group agreement and reliability indices. The package also contains basic data manipulation functions that facilitate the analysis of multilevel and longitudinal data. / GPL-2	noarch
<a href="#">r-multinbmod</a>	1.0	This is a likelihood approach for the regression analysis of overdispersed correlated count data with cluster varying covariates. The approach fits a multivariate negative binomial model by maximum likelihood and provides robust estimates of the regression coefficients. / GPL-2	noarch
<a href="#">r-multinet</a>	3.0.3	Functions for the creation/generation and analysis of multilayer social networks. / GPL-3	linux-64, osx-64

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Name	Version	Summary/License	Platforms
<a href="#">r-multinomialci</a>	1.1	An implementation of a method for building simultaneous confidence intervals for the probabilities of a multinomial distribution given a set of observations, proposed by Sison and Glaz in their paper: Sison, C.P and J. Glaz. Simultaneous confidence intervals and sample size determination for multinomial proportions. Journal of the American Statistical Association, 90:366-369 (1995). The method is an R translation of the SAS code implemented by May and Johnson in their paper: May, W.L. and W.D. Johnson. Constructing two-sided simultaneous confidence intervals for multinomial proportions for small counts in a large number of cells. Journal of Statistical Software 5(6) (2000). Paper and code available at <DOI:10.18637/jss.v005.i06>. / LGPL-3	noarch
<a href="#">r-multiord</a>	2.4.1	A method for multivariate ordinal data generation given marginal distributions and correlation matrix based on the methodology proposed by Demirtas (2006). / GPL-2	noarch
<a href="#">r-multiplebubbles</a>	0.2.0	Provides the Augmented Dickey-Fuller test and its variations to check the existence of bubbles (explosive behavior) for time series, based on the article by Peter C. B. Phillips, Shuping Shi and Jun Yu (2015a) <doi:10.1111/iere.12131>. Some functions may take a while depending on the size of the data used, or the number of Monte Carlo replications applied. / GPL-2	noarch
<a href="#">r-multiplesc</a>	1.2.1	Fit Cox proportional hazard models with a weighted partial likelihood. It handles one or multiple endpoints, additional matching and makes it possible to reuse controls for other endpoints. / GPL-2	noarch
<a href="#">r-multiplex</a>	2.9	Algebraic procedures for the analysis of multiple social networks are delivered with this package. Among other things, it makes possible to create and manipulate multivariate network data with different formats, and there are effective ways available to treat multiple networks with routines that combine algebraic systems like the partially ordered semigroup or the semiring structure together with the relational bundles occurring in different types of multivariate network data sets. It also provides an algebraic approach for two-mode networks through Galois derivations between families of the pairs of subsets in the two domains. / GPL-3	noarch
<a href="#">r-multipol</a>	1.0.7	Various utilities to manipulate multivariate polynomials. / GPL-3	noarch
<a href="#">r-multirdpg</a>	1.0.1	Fits the Multiple Random Dot Product Graph Model and performs a test for whether two networks come from the same distribution. Both methods are proposed in Nielsen, A.M., Witten, D., (2018) The Multiple Random Dot Product Graph Model, arXiv preprint <arXiv:1811.12172> (Submitted to Journal of Computational and Graphical Statistics). / GPL-2	noarch
<a href="#">r-multirich</a>	2.1.1	Functions to calculate Unique Trait Combinations (UTC) and scaled Unique Trait Combinations (sUTC) as measures of multivariate richness. The package can also calculate beta-diversity for trait richness and can partition this into nestedness-related and turnover components. The code will also calculate several measures of overlap. / GPL-2	noarch
<a href="#">r-multirng</a>	1.2.2	Pseudo-random number generation for 11 multivariate distributions: Normal, t, Uniform, Bernoulli, Hypergeometric, Beta (Dirichlet), Multinomial, Dirichlet-Multinomial, Laplace, Wishart, and Inverted Wishart. The details of the method are explained in Demirtas (2004) <DOI:10.22237/jmasm/1099268340>. / GPL-2   GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-multirobust	1.0.5	Multiply robust estimation for population mean (Han and Wang 2013) <doi:10.1093/biomet/ass087>, regression analysis (Han 2014) <doi:10.1080/01621459.2014.880058> (Han 2016) <doi:10.1111/sjos.12177> and quantile regression (Han et al. 2019) <doi:10.1111/rssb.12309>. / GPL-2	noarch
r-multiroc	1.1.1	Tools to solve real-world problems with multiple classes classifications by computing the areas under ROC and PR curve via micro-averaging and macro-averaging. The vignettes of this package can be found via < <a href="https://github.com/WandeRum/multiROC">https://github.com/WandeRum/multiROC</a> >. The methodology is described in V. Van Asch (2013) < <a href="https://www.clips.uantwerpen.be/~vincent/pdf/microaverage.pdf">https://www.clips.uantwerpen.be/~vincent/pdf/microaverage.pdf</a> > and Pedregosa et al. (2011) < <a href="http://scikit-learn.org/stable/auto_examples/model_selection/plot_roc.html">http://scikit-learn.org/stable/auto_examples/model_selection/plot_roc.html</a> >. / GPL-3	noarch
r-multirr	1.1	Calculates bias, precision, and power for multi-level random regressions. Random regressions are types of hierarchical models in which data are structured in groups and (regression) coefficients can vary by groups. Tools to estimate model performance are designed mostly for scenarios where (regression) coefficients vary at just one level. ‘MultiRR’ provides simulation and analytical tools (based on ‘lme4’) to study model performance for random regressions that vary at more than one level (multi-level random regressions), allowing researchers to determine optimal sampling designs. / GPL-2	noarch
r-multisom	1.3	Implements two versions of the algorithm namely: stochastic and batch. The package determines also the best number of clusters and offers to the user the best clustering scheme from different results. / GPL-2	noarch
r-multispatialccm	1.0	The multispatial convergent cross mapping algorithm can be used as a test for causal associations between pairs of processes represented by time series. This is a combination of convergent cross mapping (CCM), described in Sugihara et al., 2012, Science, 338, 496-500, and dew-drop regression, described in Hsieh et al., 2008, American Naturalist, 171, 71â€“80. The algorithm allows CCM to be implemented on data that are not from a single long time series. Instead, data can come from many short time series, which are stitched together using bootstrapping. / GPL-2	linux-64, osx-64, win-64
r-multisv	0.0_6	MultiSV is an R package for identification of structural variations in multiple populations based on whole genome resequencing. It fits linear mixed model and identifies structural variations in multiple populations using whole genome sequencing data. It could also be manipulated to use on RNA-seq data for differential gene expression (implementation in future releases). Main steps for analysis include generating read depth in bins using ComputeBinCounts. conversion of bins to MultiSV format using Bin2MultiSV. Finally, identification of structural variations using CallMultiSV. / LGPL-3	noarch
r-multitaper	1.0_14	Implements multitaper spectral analysis using discrete prolate spheroidal sequences (Slepians) and sine tapers. It includes an adaptive weighted multitaper spectral estimate, a coherence estimate, Thomson’s Harmonic F-test, and complex demodulation. The Slepians sequences are generated efficiently using a tridiagonal matrix solution, and jackknifed confidence intervals are available for most estimates. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-multivariate</a>	2.2.0	Distance multivariate is a measure of dependence which can be used to detect and quantify dependence. The necessary functions are implemented in this packages, and examples are given. For the theoretic background we refer to the papers: B. Böttcher, Dependence and Dependence Structures: Estimation and Visualization Using Distance Multivariate. <arXiv:1712.06532>. B. Böttcher, M. Keller-Ressel, R.L. Schilling, Detecting independence of random vectors: generalized distance covariance and Gaussian covariance. VMSTA, 2018, Vol. 5, No. 3, 353-383. <arXiv:1711.07778>. B. Böttcher, M. Keller-Ressel, R.L. Schilling, Distance multivariate: New dependence measures for random vectors. <arXiv:1711.07775>. G. Berschneider, B. Böttcher, On complex Gaussian random fields, Gaussian quadratic forms and sample distance multivariate. <arXiv:1808.07280>. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-multivariaterandomforest</a>	1.1.5	Models and predicts multiple output features in single random forest considering the linear relation among the output features, see details in Rahman et al (2017)<doi:10.1093/bioinformatics/btw765>. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-multivarsel</a>	1.1.3	It performs variable selection in a multivariate linear model by estimating the covariance matrix of the residuals then use it to remove the dependence that may exist among the responses and eventually performs variable selection by using the Lasso criterion. The method is described in the paper Perrot-Dockès et al. (2017) <arXiv:1704.00076>. / GPL-2	noarch
<a href="#">r-multivator</a>	1.1_9	A multivariate generalization of the emulator package. / GPL-2	noarch
<a href="#">r-multiwave</a>	1.4	Computation of an estimation of the long-memory parameters and the long-run covariance matrix using a multivariate model (Lobato (1999) <doi:10.1016/S0304-4076(98)00038-4>; Shimotsu (2007) <doi:10.1016/j.jeconom.2006.01.003>). Two semi-parametric methods are implemented: a Fourier based approach (Shimotsu (2007) <doi:10.1016/j.jeconom.2006.01.003>) and a wavelet based approach (Achard and Gannaz (2016) <doi:10.1111/jtsa.12170>). / GPL-2	noarch
<a href="#">r-multiway</a>	1.0_6	Fits multi-way component models via alternating least squares algorithms with optional constraints. Fit models include N-way Canonical Polyadic Decomposition, Individual Differences Scaling, Multiway Covariates Regression, Parallel Factor Analysis (1 and 2), Simultaneous Component Analysis, and Tucker Factor Analysis. / GPL-2	noarch
<a href="#">r-multiwayregression</a>	1.2	Functions to predict one multi-way array (i.e., a tensor) from another multi-way array, using a low-rank CANDECOMP/PARAFAC (CP) factorization and a ridge (L_2) penalty [Lock, EF (2018) <doi:10.1080/10618600.2017.1401544>]. Also includes functions to sample from the Bayesian posterior of a tensor-on-tensor model. / GPL-3	noarch
<a href="#">r-multiwayvcov</a>	1.2.3	Exports two functions implementing multi-way clustering using the method suggested by Cameron, Gelbach, & Miller (2011) and cluster (or block) bootstrapping for estimating variance-covariance matrices. Normal one and two-way clustering matches the results of other common statistical packages. Missing values are handled transparently and rudimentary parallelization support is provided. / BSD_2_clause	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-multnonparam</a>	1.2.8	A collection of multivariate nonparametric methods, selected in part to support an MS level course in nonparametric statistical methods. Methods include adjustments for multiple comparisons, implementation of multivariate Mann-Whitney-Wilcoxon testing, inversion of these tests to produce a confidence region, some permutation tests for linear models, and some algorithms for calculating exact probabilities associated with one- and two- stage testing involving Mann-Whitney-Wilcoxon statistics. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-multxpt</a>	0.1	Implementation of commonly used p-value-based and parametric multiple testing procedures (computation of adjusted p-values and simultaneous confidence intervals) and parallel gatekeeping procedures based on the methodology presented in the book Multiple Testing Problems in Pharmaceutical Statistics (edited by Alex Dmitrienko, Ajit C. Tamhane and Frank Bretz) published by Chapman and Hall/CRC Press 2009. / GPL-2	noarch
<a href="#">r-mumin</a>	1.43.6	Tools for performing model selection and model averaging. Automated model selection through subsetting the maximum model, with optional constraints for model inclusion. Model parameter and prediction averaging based on model weights derived from information criteria (AICc and alike) or custom model weighting schemes. / GPL-2	noarch
<a href="#">r-munsell</a>	0.5.0	Provides easy access to, and manipulation of, the Munsell colours. Provides a mapping between Munsell's original notation (e.g. 5R 5/10) and hexadecimal strings suitable for use directly in R graphics. Also provides utilities to explore slices through the Munsell colour tree, to transform Munsell colours and display colour palettes. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-murl</a>	0.1_1	Provides mailmerge methods for reading spreadsheets of addresses and other relevant information to create standardized but customizable letters. Provides a method for mapping US ZIP codes, including those of letter recipients. Provides a method for parsing and processing html code from online job postings of the American Political Science Association. / GPL-2	noarch
<a href="#">r-murphydiagram</a>	0.11	Data and code for the paper by Ehm, Gneiting, Jordan and Krueger ('Of Quantiles and Expectiles: Consistent Scoring Functions, Choquet Representations, and Forecast Rankings', 2015). / GPL-3	noarch
<a href="#">r-murty</a>	0.3.0	Calculates k-best solutions and costs for an assignment problem following the method outlined in Murty (1968) <doi:10.1287/opre.16.3.682>. / MIT	noarch
<a href="#">r-mus</a>	0.1.6	Sampling and evaluation methods to apply Monetary Unit Sampling (or in older literature Dollar Unit Sampling) during an audit of financial statements. / GPL-2	noarch
<a href="#">r-music</a>	0.1.1	An aid for learning and using music theory. You can build chords, scales, and chord progressions using 12-note equal temperament tuning (12-ET) or user-defined tuning. Includes functions to visualize notes on a piano using ASCII plots in the console and to plot waveforms using base graphics. It allows simple playback of notes and chords using the 'audio' package. / GPL-3	noarch
<a href="#">r-mustat</a>	1.7.0	Performs Wilcox rank sum test, Kruskal rank sum test, Friedman rank sum test and McNemar test. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-mvar</a>	2.0.9	Package for multivariate analysis, having functions that perform simple correspondence analysis (CA) and multiple correspondence analysis (MCA), principal components analysis (PCA), canonical correlation analysis (CCA), factorial analysis (FA), multidimensional scaling (MDS), linear (LDA) and quadratic discriminant analysis (QDA), hierarchical and non-hierarchical cluster analysis, simple and multiple linear regression, multiple factor analysis (MFA) for quantitative, qualitative, frequency (MFACT) and mixed data, projection pursuit (PP), grant tour method and other useful functions for the multivariate analysis. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-mvar.pt</a>	2.0.9	Pacote para analise multivariada, tendo funcoes que executam analise de correspondencia simples (CA) e multipla (MCA), analise de componentes principais (PCA), analise de correlacao canonica (CCA), analise fatorial (FA), escalonamento multidimensional (MDS), analise discriminante linear (LDA) e quadratica (QDA), analise de cluster hierarquico e nao hierarquico, regressao linear simples e multipla, analise de multiplos fatores (MFA) para dados quantitativos, qualitativos, de frequencia (MFACT) e dados mistos, projection pursuit (PP), grant tour e outras funcoes uteis para a analise multivariada. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-mvb</a>	1.1	Fit log-linear model for multivariate Bernoulli distribution with mixed effect models and LASSO / GPL (>= 2.0)	linux-64, osx-64, win-64
<a href="#">r-mvbinary</a>	1.1	Modelling Multivariate Binary Data with Blocks of Specific One-Factor Distribution. Variables are grouped into independent blocks. Each variable is described by two continuous parameters (its marginal probability and its dependency strength with the other block variables), and one binary parameter (positive or negative dependency). Model selection consists in the estimation of the repartition of the variables into blocks. It is carried out by the maximization of the BIC criterion by a deterministic (faster) algorithm or by a stochastic (more time consuming but optimal) algorithm. Tool functions facilitate the model interpretation. / GPL-2	noarch
<a href="#">r-mvbutils</a>	2.8.23	Hierarchical workspace tree, code editing and backup, easy package prep, editing of packages while loaded, per-object lazy-loading, easy documentation, macro functions, and miscellaneous utilities. Needed by debug package. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-mvcluster</a>	1.0	Implementation of multi-view bi-clustering algorithms. When a sample is characterized by two or more sets of input features, it creates multiple data matrices for the same set of examples, each corresponding to a view. For instance, individuals who are diagnosed with a disorder can be described by their clinical symptoms (one view) and their genomic markers (another view). Rows of a data matrix correspond to examples and columns correspond to features. A multi-view bi-clustering algorithm groups examples (rows) consistently across the views and simultaneously identifies the subset of features (columns) in each view that are associated with the row groups. This mvcluster package includes three such methods. (1) MVSVDL1: multi-view bi-clustering based on singular value decomposition where the left singular vectors are used to identify row clusters and the right singular vectors are used to identify features (columns) for each row cluster. Each singular vector is regularized by the L1 vector norm. (2) MVLRRLO: multi-view bi-clustering based on sparse low rank representation (i.e., matrix approximation) where the decomposed components are regularized by the so-called L0 vector norm (which is not really a vector norm). (3) MVLRRLL1: multi-view bi-clustering based on sparse low rank representation (i.e., matrix approximation) where the decomposed components are regularized by the L1 vector norm. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-mvcwt</a>	1.3.1	Computes the continuous wavelet transform of irregularly sampled time series. / GPL-3	noarch
<a href="#">r-mvglmmrank</a>	1.2.2	Maximum likelihood estimates are obtained via an EM algorithm with either a first-order or a fully exponential Laplace approximation. / GPL-2	noarch
<a href="#">r-mvisage</a>	0.2.1	Pearson and Spearman correlation coefficients are commonly used to quantify the strength of bivariate associations of genomic variables. For example, correlations of gene-level DNA copy number and gene expression measurements may be used to assess the impact of DNA copy number changes on gene expression in tumor tissue. ‘MVisAGE’ enables users to quickly compute and visualize the correlations in order to assess the effect of regional genomic events such as changes in DNA copy number or DNA methylation level. Please see Walter V, Du Y, Danilova L, Hayward MC, Hayes DN, 2018. Cancer Research <doi:10.1158/0008-5472.CAN-17-3464>. / GPL-3	noarch
<a href="#">r-mvglm</a>	0.1.4	Allows a user to conduct multivariate multiple regression using analytic p-values rather than classic approximate F-tests. / GPL-2	noarch
<a href="#">r-mvmeta</a>	0.4.1	Collection of functions to perform fixed and random-effects multivariate and univariate meta-analysis and meta-regression. / GPL-2	noarch
<a href="#">r-mvmise</a>	1.0	Offers a general framework of multivariate mixed-effects models for the joint analysis of multiple correlated outcomes with clustered data structures and potential missingness proposed by Wang et al. (2018) <doi:10.1093/biostatistics/kxy022>. The missingness of outcome values may depend on the values themselves (missing not at random and non-ignorable), or may depend on only the covariates (missing at random and ignorable), or both. This package provides functions for two models: 1) mvMISE_b() allows correlated outcome-specific random intercepts with a factor-analytic structure, and 2) mvMISE_e() allows the correlated outcome-specific error terms with a graphical lasso penalty on the error precision matrix. Both functions are motivated by the multivariate data analysis on data with clustered structures from labelling-based quantitative proteomic studies. These models and functions can also be applied to univariate and multivariate analyses of clustered data with balanced or unbalanced design and no missingness. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-mvna</a>	2.0.1	Computes the Nelson-Aalen estimator of the cumulative transition hazard for arbitrary Markov multistate models <ISBN:978-0-387-68560-1>. / MIT	linux-64, osx-64, win-64
<a href="#">r-mvnbayesian</a>	0.0.8	Tools of Bayesian analysis framework using the method suggested by Berger (1985) <doi:10.1007/978-1-4757-4286-2> for multivariate normal (MVN) distribution and multivariate normal mixture (MixMVN) distribution: a) calculating Bayesian posteriori of (Mix)MVN distribution; b) generating random vectors of (Mix)MVN distribution; c) Markov chain Monte Carlo (MCMC) for (Mix)MVN distribution. / GPL-2	noarch
<a href="#">r-mvnfast</a>	0.2.5	Provides computationally efficient tools related to the multivariate normal and Student's t distributions. The main functionalities are: simulating multivariate random vectors, evaluating multivariate normal or Student's t densities and Mahalanobis distances. These tools are very efficient thanks to the use of C code and of the OpenMP API. / GPL (>= 2.0)	linux-64, osx-64, win-64
<a href="#">r-mvnggrad</a>	0.1.5	Package for moving grid adjustment in plant breeding field trials. / GPL-2	noarch
<a href="#">r-mvnmle</a>	0.1.1	Finds the maximum likelihood estimate of the mean vector and variance-covariance matrix for multivariate normal data with missing values. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-mvnormtest</a>	0.1.9	Generalization of shapiro-wilk test for multivariate variables. / GPL-3	noarch
<a href="#">r-mvnpermute</a>	1.0.0	Given a vector of multivariate normal data, a matrix of covariates and the data covariance matrix, generate new multivariate normal samples that have the same covariance matrix based on permutations of the transformed data residuals. / GPL (>= 3.0)	noarch
<a href="#">r-mvntest</a>	1.1.0	Routines for assessing multivariate normality. Implements three Wald's type chi-squared tests; non-parametric Anderson-Darling and Cramer-von Mises tests; Doornik-Hansen test, Royston test and Henze-Zirkler test. / GPL-2	noarch
<a href="#">r-mvprobit</a>	0.1.8	Tools for estimating multivariate probit models, calculating conditional and unconditional expectations, and calculating marginal effects on conditional and unconditional expectations. / GPL-2	noarch
<a href="#">r-mvprpb</a>	1.0.4	Computes orthant probabilities multivariate normal distribution. / BSD_3_clause	noarch
<a href="#">r-mvrtm</a>	1.0	Mean, variance, and random variates for left/right truncated normal distributions. / LGPL (>= 2.0, < 3)   Mozilla Public License	linux-64, osx-64, win-64
<a href="#">r-mvshapirotest</a>	1.0	This package implements the generalization of the Shapiro-Wilk test for multivariate normality proposed by Villasenor-Alva and Gonzalez-Estrada (2009). / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-mvt</a>	0.3	Routines to perform estimation and inference under the multivariate t-distribution. Currently, the following methodologies are implemented: multivariate mean and covariance estimation, hypothesis testing about the mean, equicorrelation and homogeneity of variances, the Wilson-Hilferty transformation, QQ-plots with envelopes and random variate generation. Some auxiliary functions are also provided. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-mvtmeta</a>	1.0	This package contains functions to run fixed effects or random effects multivariate meta-analysis. / GPL-2	noarch
<a href="#">r-mvtnorm</a>	1.0_1	Computes multivariate normal and t probabilities, quantiles, random deviates and densities. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-mvtsplot</a>	1.0_1	A function for plotting multivariate time series data / GPL-2	noarch
<a href="#">r-mwaved</a>	1.1.7	Computes the Wavelet deconvolution estimate of a common signal present in multiple channels that have possible different levels of blur and long memory additive error, see Kulik, Sapatinas and Wishart (2015), <doi:10.1016/j.acha.2014.04.004>. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-mwlasso</a>	1.3.1	The Moving-Window Lasso (MWLasso) method for genome-wide association studies. A window scans the design matrix. For predictors in the same window, their coefficients estimates are smoothed. / GPL-3	noarch
<a href="#">r-mwridge</a>	1.0.0	A two stage moving-window Ridge method for coefficients estimation and model prediction. In the first stage, moving-window penalty and L1 penalty are applied. In the second stage, ridge regression is applied. / GPL-3	noarch
<a href="#">r-mwright</a>	0.3.2	Implements random number generation, plotting, and estimation algorithms for the two-parameter one-sided and two-sided M-Wright (Mainardi-Wright) family. The M-Wright distributions naturally generalize the widely used one-sided (Airy and half-normal or half-Gaussian) and symmetric (Airy and Gaussian or normal) models. These are widely studied in time-fractional differential equations. References: Cahoy and Minkabo (2017) <doi:10.3233/MAS-170388>; Cahoy (2012) <doi:10.1007/s00180-011-0269-x>; Cahoy (2012) <doi:10.1080/03610926.2010.543299>; Cahoy (2011); Mainardi, Mura, and Pagnini (2010) <doi:10.1155/2010/104505>. / GPL-3	noarch
<a href="#">r-mwshiny</a>	2.0.0	A simple function, mwsApp(), that runs a ‘shiny’ app spanning multiple, connected windows. This uses all standard ‘shiny’ conventions, and depends only on the ‘shiny’ package. / MIT	noarch
<a href="#">r-mxkssd</a>	1.1	mxkssd is a package that generates efficient balanced mixed-level k-circulant supersaturated designs by interchanging the elements of the generator vector. The package tries to generate a supersaturated design that has EfNOD efficiency more than user specified efficiency level (mef). The package also displays the progress of generation of an efficient mixed-level k-circulant design through a progress bar. The progress of 100 per cent means that one full round of interchange is completed. More than one full round (typically 4-5 rounds) of interchange may be required for larger designs. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-mycobacrvr</a>	1.0	The mycobacrvR package contains utilities to provide detailed information for B cell and T cell epitopes for predicted adhesins from various servers such as ABCpred, Bcepred, Bimas, Propred, NetMHC and IEDB. Please refer the URL below to download data files (data_mycobacrvR.zip) used in functions of this package. / GPL-2	noarch
<a href="#">r-mycor</a>	0.1.1	Perform correlation and linear regression test among the numeric fields in a data.frame automatically and make plots using pairs or lattice::parallelplot. / CC0	noarch
<a href="#">r-myepisodes</a>	1.1.1	Useful functions for accessing MyEpisodes feeds and episode information as well as other tv episode related actions through www.myepisodes.com / GPL-2	noarch
<a href="#">r-myrrixjars</a>	1.0_2	External jars required for package ‘Myrrix’. ‘Myrrix’ is a recommendation engine. / Apache License (== 2.0)	noarch
<a href="#">r-nlqn1</a>	6.0.1	Provides ‘Scilab’ ‘nlqn1’, or Quasi-Newton BFGS qn without constraints and ‘qnbnd’ or Quasi-Newton BFGS with constraints. This takes more memory than traditional L-BFGS. The nlqn1 routine is useful since it allows prespecification of a Hessian. If the Hessian is near enough the truth in optimization it can speed up the optimization problem. Both algorithms are described in the ‘Scilab’ optimization documentation located at < <a href="http://www.scilab.org/content/download/250/1714/file/optimization_in_scilab.pdf">http://www.scilab.org/content/download/250/1714/file/optimization_in_scilab.pdf</a> >. / CeCILL-2	linux-64, osx-64, win-64
<a href="#">r-na.tools</a>	0.3.1	This comprehensive toolkit provide a consistent and extensible framework for working with missing values in vectors. The companion package ‘tidyimpute’ provides similar functionality for list-like and table-like structures). Functions exist for detection, removal, replacement, imputation, recollection, etc. of ‘NAs’. / GPL-3	noarch
<a href="#">r-nabor</a>	0.5.0	An R wrapper for ‘libnabo’, an exact or approximate k nearest neighbour library which is optimised for low dimensional spaces (e.g. 3D). ‘libnabo’ has speed and space advantages over the ‘ANN’ library wrapped by package ‘RANN’. ‘nabor’ includes a knn function that is designed as a drop-in replacement for ‘RANN’ function nn2. In addition, objects which include the k-d tree search structure can be returned to speed up repeated queries of the same set of target points. / BSD_3_clause	linux-64, osx-64, win-64
<a href="#">r-nada</a>	1.6_1	Contains methods described by Dennis Helsel in his book Nondetects And Data Analysis: Statistics for Censored Environmental Data. / GPL-2	noarch
<a href="#">r-nadiv</a>	2.16.0	Constructs (non)additive genetic relationship matrices, and their inverses, from a pedigree to be used in linear mixed effect models (A.K.A. the ‘animal model’). Also includes other functions to facilitate the use of animal models. Some functions have been created to be used in conjunction with the R package ‘asreml’ for the ‘ASReml’ software, which can be obtained upon purchase from ‘VSN’ international (< <a href="http://www.vsn.co.uk/software/asreml">http://www.vsn.co.uk/software/asreml</a> >). / GPL-2	linux-64, osx-64, win-64
<a href="#">r-naepprimer</a>	1.0.1	Contains a sample of the 2005 Grade 8 Mathematics data from the National Assessment of Educational Progress (NAEP). This data set is called the NAEP Primer. / GPL-2	noarch
<a href="#">r-naivebayes</a>	0.9.6	In this implementation of the Naive Bayes classifier following class conditional distributions are available: Bernoulli, Categorical, Gaussian, Poisson and non-parametric representation of the class conditional density estimated via Kernel Density Estimation. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-nam	1.7.2	Designed for association studies in nested association mapping (NAM) panels, experimental and random panels. The method is described by Xavier et al. (2015) <doi:10.1093/bioinformatics/btv448>. It includes tools for genome-wide associations of multiple populations, marker quality control, population genetics analysis, genome-wide prediction, solving mixed models and finding variance components through likelihood and Bayesian methods. / GPL-3	linux-64, osx-64, win-64
r-namedcapture	2019.1.30	user-friendly wrappers for named capture regular expressions. / GPL-3	noarch
r-nameneedle	1.2.4	The Needleman-Wunsch global alignment algorithm can be used to find approximate matches between sample names in different data sets. See Wang et al. (2010) <doi:10.4137/CIN.S5613>. / Apache License (== 2.0)	noarch
r-namespace	0.9.1	This package provides user-level functions to manage namespaces not (yet) available in base R: 'registerNamespace', 'unregisterNamespace', 'makeNamespace', and 'getRegisteredNamespace'. ('makeNamespaces' is extracted from the R 'base' package source code: src/library/base/R/namespace.R) / GPL-2	linux-64, osx-64, win-64
r-naptime	1.3.0	Provides a near drop-in replacement for base::Sys.sleep() that allows more types of input to produce delays in the execution of code and can silence/prevent typical sources of error. / GPL-2	noarch
r-nardl	0.1.5	Computes the nonlinear cointegrating autoregressive distributed lag model with p lags of the dependent variables and q lags of independent variables proposed by (Shin, Yu & Greenwood-Nimmo, 2014 <doi:10.1007/978-1-4899-8008-3_9>). / GPL-3	noarch
r-nasaweather	0.1	This package contains tidied data from the ASA 2006 data expo, as well as a number of useful other related data sets. / GPL-3	noarch
r-nat.utils	0.5.1	Utility functions that may be of general interest but are specifically required by the 'NeuroAnatomy Toolbox' ('nat'). Includes functions to provide a basic make style system to update files based on timestamp information, file locking and 'touch' utility. Convenience functions for working with file paths include 'abs2rel', 'split_path' and 'common_path'. Finally there are utility functions for working with 'zip' and 'gzip' files including integrity tests. / GPL-3	noarch
r-natural	0.9.0	Implementation of the two error variance estimation methods in high-dimensional linear models of Yu, Bien (2017) <arXiv:1712.02412>. / GPL-3	linux-64, osx-64, win-64
r-naturalsort	0.1.3	Provides functions related to human natural ordering. It handles adjacent digits in a character sequence as a number so that natural sort function arranges a character vector by their numbers, not digit characters. It is typically seen when operating systems lists file names. For example, a sequence a-1.png, a-2.png, a-10.png looks naturally ordered because 1 < 2 < 10 and natural sort algorithm arranges so whereas general sort algorithms arrange it into a-1.png, a-10.png, a-2.png owing to their third and fourth characters. / BSD_3_clause	noarch
r-naturesounds	1.0.1	Collection of example animal sounds for bioacoustic analysis. / GPL-2	noarch
r-nb	0.9	Estimate the effective population size of a closed population using genetic data collected from two or more data points. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<code>r-nb.mclust</code>	1.1.1	Model-based clustering of high-dimensional non-negative data that follow Generalized Negative Binomial distribution. All functions in this package applies to either continuous or integer data. Correlation between variables are allowed, while samples are assumed to be independent. / GPL-2	noarch
<code>r-nbc4va</code>	1.1	An implementation of the Naive Bayes Classifier (NBC) algorithm used for Verbal Autopsy (VA) built on code from Miasnikof et al (2015) <DOI:10.1186/s12916-015-0521-2>. / GPL-3	noarch
<code>r-nbclust</code>	3.0	It provides 30 indexes for determining the optimal number of clusters in a data set and offers the best clustering scheme from different results to the user. / GPL-2	noarch
<code>r-nbconvert</code>	1.0.2	Calls the ‘Jupyter’/‘IPython’ script ‘nbconvert’ to create vignettes from notebooks. Those notebooks (‘.ipynb’ files) are files containing rich text, code, and its output. Code cells can be edited and evaluated interactively. See < <a href="http://ipython.org/notebook.html">http://ipython.org/notebook.html</a> > for more information. / GPL-3	noarch
<code>r-nbdirichlet</code>	1.3	The Dirichlet (aka NBD-Dirichlet) model describes the purchase incidence and brand choice of consumer products. We estimate the model and summarize various theoretical quantities of interest to marketing researchers. Also provides functions for making tables that compare observed and theoretical statistics. / GPL-3	noarch
<code>r-ncbit</code>	2013.03.19	Making NCBI taxonomic data locally available and searchable as an R object / GPL-2	noarch
<code>r-ncdf4</code>	1.16	Provides a high-level R interface to data files written using Unidata’s netCDF library (version 4 or earlier), which are binary data files that are portable across platforms and include metadata information in addition to the data sets. Using this package, netCDF files (either version 4 or classic version 3) can be opened and data sets read in easily. It is also easy to create new netCDF dimensions, variables, and files, in either version 3 or 4 format, and manipulate existing netCDF files. This package replaces the former ncdf package, which only worked with netcdf version 3 files. For various reasons the names of the functions have had to be changed from the names in the ncdf package. The old ncdf package is still available at the URL given below, if you need to have backward compatibility. It should be possible to have both the ncdf and ncdf4 packages installed simultaneously without a problem. However, the ncdf package does not provide an interface for netcdf version 4 files. / GPL-3	linux-64, osx-64
<code>r-ncdunnett</code>	1.1.0	Computes the noncentral Dunnett’s test distribution (pdf, cdf and quantile) and generates random numbers. / GPL-2	noarch
<code>r-ncf</code>	1.2_8	R functions for analyzing spatial (cross-)covariance: the nonparametric (cross-)covariance function, the spline correlogram, the nonparametric phase coherence function, local indicators of spatial association (LISA), (Mantel) correlogram, (Partial) Mantel test. / GPL-3	noarch
<code>r-ncg</code>	0.1.1	Computes the noncentral gamma function: pdf, cdf, quantile function and inverse for the noncentrality parameter. / GPL-2	noarch
<code>r-ncopula</code>	0.1.1	Construct and manipulate hierarchical Archimedean copulas with multivariate compound distributions. The model used is the one of Cossette et al. (2017) <doi:10.1016/j.insmatheco.2017.06.001>. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-ncpen</a>	1.0.0	An efficient unified nonconvex penalized estimation algorithm for Gaussian (linear), binomial Logit (logistic), Poisson, multinomial Logit, and Cox proportional hazard regression models. The unified algorithm is implemented based on the convex concave procedure and the algorithm can be applied to most of the existing nonconvex penalties. The algorithm also supports convex penalty: least absolute shrinkage and selection operator (LASSO). Supported nonconvex penalties include smoothly clipped absolute deviation (SCAD), minimax concave penalty (MCP), truncated LASSO penalty (TLP), clipped LASSO (CLASSO), sparse ridge (SRIDGE), modified bridge (MBRIDGE) and modified log (MLOG). For high-dimensional data (data set with many variables), the algorithm selects relevant variables producing a parsimonious regression model. Kim, D., Lee, S. and Kwon, S. (2018) <arXiv:1811.05061>, Lee, S., Kwon, S. and Kim, Y. (2016) <doi:10.1016/j.csda.2015.08.019>, Kwon, S., Lee, S. and Kim, Y. (2015) <doi:10.1016/j.csda.2015.07.001>. (This research is funded by Julian Virtue Professorship from Center for Applied Research at Pepperdine Graziadio Business School and the National Research Foundation of Korea.) / GPL-3	linux-64, osx-64, win-64
<a href="#">r-ncvreg</a>	3.11	Fits regularization paths for linear regression, GLM, and Cox regression models using lasso or nonconvex penalties, in particular the minimax concave penalty (MCP) and smoothly clipped absolute deviation (SCAD) penalty, with options for additional L2 penalties (the elastic net idea). Utilities for carrying out cross-validation as well as post-fitting visualization, summarization, inference, and prediction are also provided. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-ndp</a>	0.1.0	An interactive presentation on the topic of normal distribution using ‘rmarkdown’ and ‘shiny’ packages. It is helpful to those who want to learn normal distribution quickly and get a hands on experience. The presentation has a template for solving problems on normal distribution. Runtime examples are provided in the package function as well as at < <a href="https://kartikeyastat.shinyapps.io/NormalDistribution/">https://kartikeyastat.shinyapps.io/NormalDistribution/</a> >. / GPL-2	noarch
<a href="#">r-nearender</a>	1.5	Performs network enrichment analysis against functional gene sets. Benchmarks networks. Renders raw gene profile matrices of dimensionality N genes x N samples into the space of gene set (typically pathway) enrichment scores of dimensionality N pathways x N samples. / GPL-3	noarch
<a href="#">r-neariso</a>	1.0.1	Implements a path algorithm for Near-Isotonic Regression. For more details see the help files. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-neat</a>	1.1.3	Includes functions and examples to compute NEAT, the Network Enrichment Analysis Test described in Signorelli et al. (2016, <DOI:10.1186/s12859-016-1203-6>). / GPL-3	noarch
<a href="#">r-neatranges</a>	0.1.0	Collapse, partition, combine, fill gaps in and expand date/time ranges. / MIT	noarch
<a href="#">r-needs</a>	0.0.3	A simple function for easier package loading and auto-installation. / MIT	noarch
<a href="#">r-needy</a>	0.2	needy is a small utility library designed to make testing function inputs less difficult. R is a dynamically typed language, but larger projects need input checking for scalability. needy offers a single function, <code>require_a()</code> , which lets you specify the traits an input object should have, such as class, size, numerical properties or number of parameters, while reducing boilerplate code and aiding debugging. / MIT	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-negbinbetabinreg</a>	1.0	The Negative Binomial regression with mean and shape modeling and mean and variance modeling and Beta Binomial regression with mean and dispersion modeling. / GPL-2	noarch
<a href="#">r-negenes</a>	1.0_1	Estimating the number of essential genes in a genome on the basis of data from a random transposon mutagenesis experiment, through the use of a Gibbs sampler. Lamichhane et al. (2003) <doi:10.1073/pnas.1231432100>. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-neighbr</a>	1.0.2	Classification, regression, and clustering with k nearest neighbors algorithm. Implements several distance and similarity measures, covering continuous and logical features. Outputs ranked neighbors. Most features of this package are directly based on the PMML specification for KNN. / GPL (>= 2.1)	noarch
<a href="#">r-nephro</a>	1.2	Set of functions to estimate renal function and other phenotypes of interest in nephrology based on different biomechimal traits. MDRD, CKD-EPI, and Virga equations are compared in Pattaro (2013) <doi:10.1159/000351043>, where the respective references are given. In addition, the software includes Stevens (2008) <doi:10.1053/j.ajkd.2007.11.018> and Cockcroft (1976) <doi:10.1159/000180580> formulas. / GPL-3	noarch
<a href="#">r-nestedcohort</a>	1.1_3	Estimate hazard ratios, survival curves and attributable risks for cohorts with missing covariates, using Cox models or Kaplan-Meier estimated for strata. This handles studies nested within cohorts, such as case-cohort studies with stratified sampling. See <a href="http://www.r-project.org/doc/Rnews/Rnews_2008-1.pdf">http://www.r-project.org/doc/Rnews/Rnews_2008-1.pdf</a> / GPL-2	noarch
<a href="#">r-nestfs</a>	0.9.2	Implementation of forward selection based on cross-validated linear and logistic regression. / GPL-2	noarch
<a href="#">r-netchain</a>	0.1.0	In networks, treatments may spill over from the treated individual to his or her social contacts and outcomes may be contagious over time. Under this setting, causal inference on the collective outcome observed over all network is often of interest. We use chain graph models approximating the projection of the full longitudinal data onto the observed data to identify the causal effect of the intervention on the whole outcome. Justification of such approximation is demonstrated in Ogburn et al. (2018) <arXiv:1812.04990>. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-netcoh</a>	0.2	Model fitting procedures for regression with network cohesion effects, when a network connecting sample individuals is available in a regression problem. In the future, other commonly used statistical models will be added, such as gaussian graphical model. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-netcomp</a>	1.6	This package contains functions to carry out high throughput data analysis and to conduct data set comparisons. Similarity matrices from high throughput phenotypic data containing uninformative (e.g. wild type) or missing data can be calculated to report similarity of response. A suite of graph comparisons using an adjacency or correlation matrix format are included to facilitate quick network analysis. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-netdata</a>	0.3	This package contains all data needed for Dan McFarland's SNA R labs. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-netindices</a>	1.4.4	Given a network (e.g. a food web), estimates several network indices. These include: Ascendency network indices, Direct and indirect dependencies, Effective measures, Environ network indices, General network indices, Pathway analysis, Network uncertainty indices and constraint efficiencies and the trophic level and omnivory indices of food webs. / GPL-2	noarch
<a href="#">r-netrankr</a>	0.2.1	Implements methods for centrality related analyses of networks. While the package includes the possibility to build more than 20 indices, its main focus lies on index-free assessment of centrality via partial rankings obtained by neighborhood-inclusion or positional dominance. These partial rankings can be analyzed with different methods, including probabilistic methods like computing expected node ranks and relative rank probabilities (how likely is it that a node is more central than another?). The methodology is described in depth in the vignettes and in Schoch (2018) <doi:10.1016/j.socnet.2017.12.003>. / MIT	linux-64, osx-64, win-64
<a href="#">r-netregr</a>	1.0.1	Regress network responses (both directed and undirected) onto covariates of interest that may be actor-, relation-, or network-valued. In addition, compute principled variance estimates of the coefficients assuming that the errors are jointly exchangeable. Missing data is accommodated. Additionally implements building and inversion of covariance matrices under joint exchangeability, and generates random covariance matrices from this class. For more detail on methods, see Marrs, Fosdick, and McCormick (2017) <arXiv:1701.05530>. / MIT	noarch
<a href="#">r-nets</a>	0.9	Sparse VAR estimation based on LASSO. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-netsimr</a>	0.1.0	Assists actuaries and other insurance modellers in pricing, reserving and capital modelling for non-life insurance and reinsurance modelling. Provides functions that help model excess levels, capping and pure Incurred but not reported claims (pure IBNR). Includes capped mean, exposure curves and increased limit factor curves (ILFs) for LogNormal, Gamma, Pareto, Sliced LogNormal-Pareto and Sliced Gamma-Pareto distributions. Includes mean, probability density function (pdf), cumulative probability function (cdf) and inverse cumulative probability function for Sliced LogNormal-Pareto and Sliced Gamma-Pareto distributions. Includes calculating pure IBNR exposure with LogNormal and Gamma distribution for reporting delay. / GPL-3	noarch
<a href="#">r-netswan</a>	0.1	A set of functions for studying network robustness, resilience and vulnerability. / GPL-2	noarch
<a href="#">r-netweaver</a>	0.0.6	Implements various simple function utilities and flexible pipelines to generate circular images for visualizing complex genomic and network data analysis features. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-networkd3</a>	0.4	Creates 'D3' 'JavaScript' network, tree, dendrogram, and Sankey graphs from 'R'. / GPL (>= 3)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-networkgen</a>	0.1.1	A network Maze generator that creates different types of network mazes. / GPL-3	noarch
<a href="#">r-neural</a>	1.4.2	RBF and MLP neural networks with graphical user interface / GPL-2	noarch
<a href="#">r-neuralnet</a>	1.44.2	Training of neural networks using backpropagation, resilient backpropagation with (Riedmiller, 1994) or without weight backtracking (Riedmiller and Braun, 1993) or the modified globally convergent version by Anastasiadis et al. (2005). The package allows flexible settings through custom-choice of error and activation function. Furthermore, the calculation of generalized weights (Intrator O & Intrator N, 1993) is implemented. / GPL-2	noarch
<a href="#">r-neuroblastoma</a>	1.0	Annotated neuroblastoma copy number profiles, a benchmark data set for change-point detection algorithms. / GPL-3	noarch
<a href="#">r-neurohcp</a>	0.8.1	Downloads and reads data from Human 'Connectome' Project < <a href="https://db.humanconnectome.org">https://db.humanconnectome.org</a> > using Amazon Web Services ('AWS') 'S3' buckets. / GPL-2	noarch
<a href="#">r-neurosims</a>	0.2.1	The package allows users to generate fMRI time series or 4D data. Some high-level functions are created for fast data generation with only a few arguments and a diversity of functions to define activation and noise. For more advanced users it is possible to use the low-level functions and manipulate the arguments. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-neverhpfiler</a>	0.2.0	In the working paper titled Why You Should Never Use the Hodrick-Prescott Filter, James D. Hamilton proposes an interesting new alternative to economic time series filtering. The neverhpfiler package provides functions for implementing his solution. Hamilton (2017) <doi:10.3386/w23429>. / GPL-3	noarch
<a href="#">r-newdistns</a>	2.1	Computes the probability density function, cumulative distribution function, quantile function, random numbers and measures of inference for the following general families of distributions (each family defined in terms of an arbitrary cdf G): Marshall Olkin G distributions, exponentiated G distributions, beta G distributions, gamma G distributions, Kumaraswamy G distributions, generalized beta G distributions, beta extended G distributions, gamma G distributions, gamma uniform G distributions, beta exponential G distributions, Weibull G distributions, log gamma G I distributions, log gamma G II distributions, exponentiated generalized G distributions, exponentiated Kumaraswamy G distributions, geometric exponential Poisson G distributions, truncated-exponential skew-symmetric G distributions, modified beta G distributions, and exponentiated exponential Poisson G distributions. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-newtestsurvrec</a>	1.0.2	Implements the routines to compare the survival curves with recurrent events, including the estimations of survival curves. The first model is a model for recurrent event, when the data are correlated or not correlated. It was proposed by Wang and Chang (1999) <doi:10.2307/2669690>. In the independent case, the survival function can be estimated by the generalization of the limit product model of Pena (2001) <doi:10.1198/016214501753381922>. / GPL-2	noarch
<a href="#">r-nfactors</a>	2.3.3	Indices, heuristics and strategies to help determine the number of factors/components to retain: 1. Acceleration factor (af with or without Parallel Analysis); 2. Optimal Coordinates (noc with or without Parallel Analysis); 3. Parallel analysis (components, factors and bootstrap); 4. lambda > mean(lambda) (Kaiser, CFA and related); 5. Cattell-Nelson-Gorsuch (CNG); 6. Zoski and Jurs multiple regression (b, t and p); 7. Zoski and Jurs standard error of the regression coefficient (sescree); 8. Nelson R2; 9. Bartlett khi-2; 10. Anderson khi-2; 11. Lawley khi-2 and 12. Bentler-Yuan khi-2. / GPL-2	noarch
<a href="#">r-nfca</a>	0.3	Numerical Formal Concept Analysis (nFCA) is a modern unsupervised learning tool for analyzing general numerical data. Given input data, this R package nFCA outputs two nFCA graphs: a H-graph and an I-graph that reveal systematic, hierarchical clustering and inherent structure of the data. / GPL-2	noarch
<a href="#">r-nfwdist</a>	0.1.0	Density, distribution function, quantile function and random generation for the 3D Navarro, Frenk & White (NFW) profile. For details see Robotham & Howlett (2018) <arXiv:1805.09550>. / GPL-3	noarch
<a href="#">r-ngram</a>	3.0.4	An n-gram is a sequence of n words taken, in order, from a body of text. This is a collection of utilities for creating, displaying, summarizing, and babbling n-grams. The ‘tokenization’ and babbling are handled by very efficient C code, which can even be built as its own standalone library. The babbler is a simple Markov chain. The package also offers a vignette with complete example ‘workflows’ and information about the utilities offered in the package. / BSD_2_clause	linux-64, osx-64, win-64
<a href="#">r-ngspatial</a>	1.2_1	Provides tools for analyzing spatial data, especially non- Gaussian areal data. The current version supports the sparse restricted spatial regression model of Hughes and Haran (2013) <DOI:10.1111/j.1467-9868.2012.01041.x>, the centered autologistic model of Caragea and Kaiser (2009) <DOI:10.1198/jabes.2009.07032>, and the Bayesian spatial filtering model of Hughes (2017) <arXiv:1706.04651>. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-nhanes</a>	2.1.0	Body Shape and related measurements from the US National Health and Nutrition Examination Survey (NHANES, 1999-2004). See <a href="http://www.cdc.gov/nchs/nhanes.htm">http://www.cdc.gov/nchs/nhanes.htm</a> for details. / GPL-2	noarch
<a href="#">r-nhds</a>	1.0.3	The National Hospital Discharge Survey (2010) summarizes the state of patients at the end of their hospital admissions. The US CDC publishes the data in the public domain, and describes it as follows: The National Hospital Discharge Survey (NHDS) is a continuing nationwide sample survey of short-stay hospitals in the United States. The scope of NHDS encompasses patients discharged from noninstitutional hospitals, exclusive of military and Department of Veterans Affairs hospitals, located in the 50 States and the District of Columbia. Only hospitals having six or more beds for in-patient use are included in the survey. See < <a href="https://www.cdc.gov/nchs/nhds">https://www.cdc.gov/nchs/nhds</a> > for more information. / GPL-3	noarch
<a href="#">r-nhldata</a>	1.0.0	Each dataset contains scores for every game during a specific season of the NHL. / CC0	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-nhsrdatasets</a>	0.1.1	Free United Kingdom National Health Service (NHS) and other healthcare, or population health-related data for education and training purposes. This package currently contains a single simulated hospital dataset for teaching regression methods, with the addition of more datasets planned for future releases. This package exists to support skills development in the NHS-R community: <a href="https://nhsrcommunity.com/">https://nhsrcommunity.com/</a> . / CC0	noarch
<a href="#">r-nice</a>	0.4_1	Get or set UNIX priority (niceness) of running R process. / MIT	linux-64, osx-64
<a href="#">r-nicherover</a>	1.0	This package uses a probabilistic method to calculate niche regions and pairwise niche overlap using multidimensional niche indicator data (e.g., stable isotopes, environmental variables, etc.). The niche region is defined as the joint probability density function of the multidimensional niche indicators at a user-defined probability alpha (e.g., 95%). Uncertainty is accounted for in a Bayesian framework, and the method can be extended to three or more indicator dimensions. It provides directional estimates of niche overlap, accounts for species-specific distributions in multivariate niche space, and produces unique and consistent bivariate projections of the multivariate niche region. A forthcoming article by Swanson et al. (Ecology, 2014) provides a detailed description of the methodology. See the package vignette for a worked example using fish stable isotope data. / GPL-2	noarch
<a href="#">r-nightday</a>	1.0.1	Computes and plots the boundary between night and day. / GPL-3	noarch
<a href="#">r-nilde</a>	1.1_3	Routines for enumerating all existing nonnegative integer solutions of a linear Diophantine equation. The package provides routines for solving 0-1, bounded and unbounded knapsack problems; 0-1, bounded and unbounded subset sum problems; additive partitioning of natural numbers; and one-dimensional bin-packing problem. / GPL-2	noarch
<a href="#">r-nimble</a>	0.8.0	A system for writing hierarchical statistical models largely compatible with ‘BUGS’ and ‘JAGS’, writing nimbleFunctions to operate models and do basic R-style math, and compiling both models and nimbleFunctions via custom-generated C. ‘NIMBLE’ includes default methods for MCMC, particle filtering, Monte Carlo Expectation Maximization, and some other tools. The nimbleFunction system makes it easy to do things like implement new MCMC samplers from R, customize the assignment of samplers to different parts of a model from R, and compile the new samplers automatically via C alongside the samplers ‘NIMBLE’ provides. ‘NIMBLE’ extends the ‘BUGS’/‘JAGS’ language by making it extensible: New distributions and functions can be added, including as calls to external compiled code. Although most people think of MCMC as the main goal of the ‘BUGS’/‘JAGS’ language for writing models, one can use ‘NIMBLE’ for writing arbitrary other kinds of model-generic algorithms as well. A full User Manual is available at <a href="https://r-nimble.org/">https://r-nimble.org/</a> . / BSD_3_clause   GPL-2	linux-64, osx-64, win-64
<a href="#">r-nipals</a>	0.5	Principal Components Analysis of a matrix using Non-linear Iterative Partial Least Squares with Gram-Schmidt orthogonalization of the scores and loadings. Optimized for speed. See Andrecut (2009) <doi:10.1089/cmb.2008.0221>. / GPL-3	noarch
<a href="#">r-nistnls</a>	0.9_1	Datasets for testing nonlinear regression routines. / GPL-2	noarch
<a href="#">r-nistunits</a>	1.0.1	Fundamental physical constants (Quantity, Value, Uncertainty, Unit) for SI (International System of Units) and non-SI units, plus unit conversions Based on the data from NIST (National Institute of Standards and Technology, USA) / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-nlar	0.4.0	Client for programmatic access to the 2007 and 2012 National Lakes Assessment database < <a href="https://www.epa.gov/national-aquatic-resource-surveys/nla">https://www.epa.gov/national-aquatic-resource-surveys/nla</a> > containing data for hundreds of lakes in the lower 48 states of the contiguous US. / GPL-3	noarch
r-nlcoptim	0.6	Optimization for nonlinear objective and constraint functions. Linear or nonlinear equality and inequality constraints are allowed. It accepts the input parameters as a constrained matrix. / GPL-3	noarch
r-nleqslv	3.3.2	Solve a system of nonlinear equations using a Broyden or a Newton method with a choice of global strategies such as line search and trust region. There are options for using a numerical or user supplied Jacobian, for specifying a banded numerical Jacobian and for allowing a singular or ill-conditioned Jacobian. / GPL-2	linux-64, osx-64, win-64
r-nlgeocoder	0.1.3	R interface to the open location server API of ‘Publieke Diensten Op de Kaart’ (< <a href="http://www.pdok.nl">http://www.pdok.nl</a> >). It offers geocoding, address suggestions and lookup of geographical objects. Included is an utility function for displaying leaflet tiles restricted to the Netherlands. / GPL-2	noarch
r-nlirms	3.4.4	Design of non-life insurance rate-making system with a frequency and a severity component based on the a posteriori criteria. The rate-making system is a general form of bonus-malus system introduced by Lemaire (1995), <doi:10.1007/978-94-011-0631-3> and Frangos and Vrontos (2001), <doi:10.2143/AST.31.1.991>. / MIT	noarch
r-nlme	3.1.1	Fit and compare Gaussian linear and nonlinear mixed-effects models. / GPL (>= 2)   file LICENCE	linux-32, linux-64, osx-64, win-32, win-64
r-nlmeode	1.1	This package combines the odesolve and nlme packages for mixed-effects modelling using differential equations. / LGPL-2.1	noarch
r-nlmeu	0.70.3	nlmeU: Datasets and utility functions enhancing functionality of nlme package. Datasets, functions and scripts are described in book titled ‘Linear Mixed-Effects Models: A Step-by-Step Approach’ by Galecki and Burzykowski (2013). Package is under development. / GPL-2	noarch
r-nlmrt	2016.32	Replacement for nls() tools for working with nonlinear least squares problems. The calling structure is similar to, but much simpler than, that of the nls() function. Moreover, where nls() specifically does NOT deal with small or zero residual problems, nlmrt is quite happy to solve them. It also attempts to be more robust in finding solutions, thereby avoiding ‘singular gradient’ messages that arise in the Gauss-Newton method within nls(). The Marquardt-Nash approach in nlmrt generally works more reliably to get a solution, though this may be one of a set of possibilities, and may also be statistically unsatisfactory. Added print and summary as of August 28, 2012. / GPL-2	noarch
r-nlms	1.1	Package to select best model among several linear and nonlinear models. The main function uses the gnls() function from the ‘nlme’ package to fit the data to nine regression models, named: linear, quadratic, cubic, logistic, exponential, power, monod, haldane, logit. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-nloptr</a>	1.2.1	nloptr is an R interface to NLOpt. NLOpt is a free/open-source library for nonlinear optimization, providing a common interface for a number of different free optimization routines available online as well as original implementations of various other algorithms. See <a href="http://ab-initio.mit.edu/wiki/index.php/NLOpt_Introduction">http://ab-initio.mit.edu/wiki/index.php/NLOpt_Introduction</a> for more information on the available algorithms. During installation on Unix the NLOpt code is downloaded and compiled from the NLOpt website. / LGPL-3	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-nlp</a>	0.2.0	Basic classes and methods for Natural Language Processing. / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-nlroot</a>	1.0	This is a package which can help you search for the root of a equation. / GPL-2	noarch
<a href="#">r-nls2</a>	0.2	Adds brute force and multiple starting values to nls. / GPL-2	noarch
<a href="#">r-nlshrink</a>	1.0.1	Non-linear shrinkage estimation of population eigenvalues and covariance matrices, based on publications by Ledoit and Wolf (2004, 2015, 2016). / GPL-3	noarch
<a href="#">r-nlsmns</a>	0.0.4	Fit univariate non-linear scale mixture of skew-normal(NL-SMSN) regression. / GPL (>= 3.0)	noarch
<a href="#">r-nlsr</a>	2019.07	Provides tools for working with nonlinear least squares problems. It is intended to eventually supersede the 'nls()' function in the R distribution. For example, 'nls()' specifically does NOT deal with small or zero residual problems as its Gauss-Newton method frequently stops with 'singular gradient' messages. 'nlsr' is based on the now-deprecated package 'nlmrt', and has refactored functions and R-language symbolic derivative features. / GPL-2	noarch
<a href="#">r-nlsrk</a>	1.1	Performs univariate or multivariate computation of a single ODE or of a set of ODE (ordinary differential equations). / GPL-2	noarch
<a href="#">r-nlstools</a>	1.0.2	Several tools for assessing the quality of fit of a gaussian nonlinear model are provided. / GPL-2	noarch
<a href="#">r-nlsylinks</a>	2.0.6	Utilities and kinship information for behavior genetics and developmental research using the National Longitudinal Survey of Youth (NLSY; < <a href="http://www.bls.gov/nls/">http://www.bls.gov/nls/</a> >). / GPL-3	noarch
<a href="#">r-nltm</a>	1.4.2	Fits a non-linear transformation model ('nltm') for analyzing survival data, see Tsodikov (2003) <doi:10.1111/1467-9868.00414>. The class of 'nltm' includes the following currently supported models: Cox proportional hazard, proportional hazard cure, proportional odds, proportional hazard - proportional hazard cure, proportional hazard - proportional odds cure, Gamma frailty, and proportional hazard - proportional odds. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-nlitt</a>	1.4.1	Provides functions to calculate the normalised Lineage-Through- Time (nLTT) statistic, given two phylogenetic trees. The nLTT statistic measures the difference between two Lineage-Through-Time curves, where each curve is normalised both in time and in number of lineages. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-nlwaldtest</a>	1.1.3	Wald Test for nonlinear restrictions on model parameters and confidence intervals for nonlinear functions of parameters using delta-method. Applicable after ANY model, provided parameters estimates and their covariance matrix are available. / GPL-2	noarch
<a href="#">r-nmainla</a>	0.1.2	Performs network meta-analysis using integrated nested Laplace approximations ('INLA'). Includes methods to assess the heterogeneity and inconsistency in the network. Contains more than ten different network meta-analysis data. 'INLA' package can be obtained from < <a href="http://www.r-inla.org">http://www.r-inla.org</a> >. We recommend the testing version. / GPL-2	noarch
<a href="#">r-nmf</a>	0.21.0	Provides a framework to perform Non-negative Matrix Factorization (NMF). The package implements a set of already published algorithms and seeding methods, and provides a framework to test, develop and plug new/custom algorithms. Most of the built-in algorithms have been optimized in C, and the main interface function provides an easy way of performing parallel computations on multicore machines. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-nmfgpu4r</a>	0.2.5.2	Wrapper package for the nmfgpu library, which implements several Non-negative Matrix Factorization (NMF) algorithms for CUDA platforms. By using the acceleration of GPGPU computing, the NMF can be used for real-world problems inside the R environment. All CUDA devices starting with Kepler architecture are supported by the library. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-nmfn</a>	2.0	Non-negative Matrix Factorization / GPL-3	noarch
<a href="#">r-nmi</a>	2.0	Calculates the normalized mutual information (NMI) of two community structures in network analysis. / GNU General Public License version 2	noarch
<a href="#">r-nmof</a>	1.6_0	Functions, examples and data from the book Numerical Methods and Optimization in Finance by M. Gilli, D. Maringer and E. Schumann (2011), ISBN 978-0123756626. The package provides implementations of several optimisation heuristics, such as Differential Evolution, Genetic Algorithms and Threshold Accepting. There are also functions for the valuation of financial instruments, such as bonds and options, and functions that help with stochastic simulations. / GPL-3	noarch
<a href="#">r-nmw</a>	0.1.4	This shows how NONMEM(R) < <a href="http://www.iconplc.com/innovation/nonmem/">http://www.iconplc.com/innovation/nonmem/</a> > software works. NONMEM's classical estimation methods like 'First Order(FO) approximation', 'First Order Conditional Estimation(FOCE)', and 'Laplacian approximation' are explained. / GPL-3	noarch
<a href="#">r-nna</a>	0.0.2	Calculates spatial pattern analysis using a T-square sample procedure. This method is based on two measures x and y. x - Distance from the random point to the nearest individual. y - Distance from individual to its nearest neighbor. This is a methodology commonly used in phytosociology or marine benthos ecology to analyze the species' distribution (random, uniform or clumped patterns). Ludwig & Reynolds (1988, ISBN:0471832359). / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<code>r-nnet</code>	7.3.1	Software for feed-forward neural networks with a single hidden layer, and for multinomial log-linear models. / GPL-2   GPL-3	linux-32, linux-64, osx-64, win-32, win-64
<code>r-nnlasso</code>	0.3	Estimates of coefficients of lasso penalized linear regression and generalized linear models subject to non-negativity constraints on the parameters using multiplicative iterative algorithm. Entire regularization path for a sequence of lambda values can be obtained. Functions are available for creating plots of regularization path, cross validation and estimating coefficients at a given lambda value. There is also provision for obtaining standard error of coefficient estimates. / GPL-2	noarch
<code>r-nnlm</code>	0.4.3	This is a package for Non-Negative Linear Models (NNLM). It implements fast sequential coordinate descent algorithms for non-negative linear regression and non-negative matrix factorization (NMF). It supports mean square error and Kullback-Leibler divergence loss. Many other features are also implemented, including missing value imputation, domain knowledge integration, designable W and H matrices and multiple forms of regularizations. / BSD_2_clause	linux-64, osx-64, win-64
<code>r-nnls</code>	1.4	An R interface to the Lawson-Hanson implementation of an algorithm for non-negative least squares (NNLS). Also allows the combination of non-negative and non-positive constraints. / GPL-2	linux-64, osx-64, win-64
<code>r-nnmmis</code>	1.0.1	Imputation for both missing covariates and censored observations (optional) for survival data with missing covariates by the nearest neighbor based multiple imputation algorithm as described in Hsu et al. (2006) <doi:10.1002/sim.2452>, and Hsu and Yu (2018) <doi:10.1177/0962280218772592>. Note that the current version can only impute for a situation with one missing covariate. / LGPL-2	noarch
<code>r-noaa oceans</code>	0.1.0	Provides a small set of tools for collecting data from National Oceanic and Atmospheric Administration (NOAA) data sources. The functions provided in the package are wrappers around NOAA's existing APIs which is found at < <a href="https://tidesandcurrents.noaa.gov/api/">https://tidesandcurrents.noaa.gov/api/</a> >. / MIT	noarch
<code>r-nodbi</code>	0.2.0	Simplified document database manipulation and analysis, including support for many 'NoSQL' databases, including document databases ('Elasticsearch', 'CouchDB', 'MongoDB'), 'key-value' databases ('Redis'), and other 'NoSQL' types ('etcd'). / MIT	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-nodeharvest</a>	0.7.3	Node harvest is a simple interpretable tree-like estimator for high-dimensional regression and classification. A few nodes are selected from an initially large ensemble of nodes, each associated with a positive weight. New observations can fall into one or several nodes and predictions are the weighted average response across all these groups. The package offers visualization of the estimator. Predictions can return the nodes a new observation fell into, along with the mean response of training observations in each node, offering a simple explanation of the prediction. / GPL-3	noarch
<a href="#">r-nofrills</a>	0.3.0	Provides a compact variation of the usual syntax of function declaration, in order to support tidyverse-style quasiquotation of a function's arguments and body. / MIT	noarch
<a href="#">r-noia</a>	0.97.1	The NOIA model, as described extensively in Alvarez-Castro & Carlborg (2007), is a framework facilitating the estimation of genetic effects and genotype-to-phenotype maps. This package provides the basic tools to perform linear and multilinear regressions from real populations (provided the phenotype and the genotype of every individuals), estimating the genetic effects from different reference points, the genotypic values, and the decomposition of genetic variances in a multi-locus, 2 alleles system. This package is presented in Le Rouzic & Alvarez-Castro (2008). / GPL-2	noarch
<a href="#">r-noisyce2</a>	1.0.0	Cross-Entropy optimisation of unconstrained deterministic and noisy functions illustrated in Rubinstein and Kroese (2004, ISBN: 978-1-4419-1940-3) through a highly flexible and customisable function which allows user to define custom variable domains, sampling distributions, updating and smoothing rules, and stopping criteria. Several built-in methods and settings make the package very easy-to-use under standard optimisation problems. / GPL-2	noarch
<a href="#">r-nomclust</a>	1.1.1	Package for hierarchical clustering of objects characterized by nominal variables. / GPL-2	noarch
<a href="#">r-nomnoml</a>	0.1.0	A tool for drawing sassy 'UML' diagrams based on a simple syntax, see < <a href="http://www.nomnoml.com">http://www.nomnoml.com</a> >. Supports styling, R Markdown and exporting diagrams in the PNG format. / MIT	noarch
<a href="#">r-noncensus</a>	0.1	A collection of various regional information determined by the U.S. Census Bureau along with demographic data. / MIT	noarch
<a href="#">r-noncompart</a>	0.4.4	Conduct a noncompartmental analysis as closely as possible to the most widely used commercial software for pharmacokinetic analysis, i.e. 'Phoenix(R) WinNonlin(R)' < <a href="https://www.certara.com/software/pkpd-modeling-and-simulation/phoenix-winnonlin/">https://www.certara.com/software/pkpd-modeling-and-simulation/phoenix-winnonlin/</a> >. Some features are 1) Use of CDISC SDTM terms 2) Automatic slope selection with the same criterion of WinNonlin(R) 3) Supporting both 'linear-up linear-down' and 'linear-up log-down' method 4) Interval(partial) AUCs with 'linear' or 'log' interpolation method * Reference: Gabrielsson J, Weiner D. Pharmacokinetic and Pharmacodynamic Data Analysis - Concepts and Applications. 5th ed. 2016. (ISBN:9198299107). / GPL-3	noarch
<a href="#">r-noncompliance</a>	0.2.2	A finite-population significance test of the 'sharp' causal null hypothesis that treatment exposure X has no effect on final outcome Y, within the principal stratum of Compliers. A generalized likelihood ratio test statistic is used, and the resulting p-value is exact. Currently, it is assumed that there are only Compliers and Never Takers in the population. / GPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<code>r-nonneg.cg</code>	0.1.6	Minimize a differentiable function subject to all the variables being non-negative (i.e. $\geq 0$ ), using a Conjugate-Gradient algorithm based on a modified Polak-Ribiere-Polyak formula as described in (Li, Can, 2013, < <a href="https://www.hindawi.com/journals/jam/2013/986317/abs/">https://www.hindawi.com/journals/jam/2013/986317/abs/</a> >). / BSD_2_clause	linux-64, osx-64, win-64
<code>r-nonnest2</code>	0.5.2	Testing non-nested models via theory supplied by Vuong (1989) <DOI:10.2307/1912557>. Includes tests of model distinguishability and of model fit that can be applied to both nested and non-nested models. Also includes functionality to obtain confidence intervals associated with AIC and BIC. This material is partially based on work supported by the National Science Foundation under Grant Number SES-1061334. / GPL-2   GPL-3	noarch
<code>r-nonnormvtdist</code>	1.0.1	Implements calculation of probability density function, cumulative distribution function, equicoordinate quantile function and survival function, and random numbers generation for the following multivariate distributions: Lomax (Pareto Type II), generalized Lomax, Mardia's Pareto of Type I, Logistic, Burr, Cook-Johnson's uniform, F and Inverted Beta. See Tapan Nayak (1987) <doi:10.2307/3214068>. / GPL-3	noarch
<code>r-nonpar</code>	1.0.1	Contains the following 5 nonparametric hypothesis tests: The Sign Test, The 2 Sample Median Test, Miller's Jackknife Procedure, Cochran's Q Test, & The Stuart-Maxwell Test. / GPL-3	noarch
<code>r-nonpareil</code>	3.3.4	Plot, process, and analyze NPO files produced by 'Nonpareil' < <a href="http://enve-omics.ce.gatech.edu/nonpareil">http://enve-omics.ce.gatech.edu/nonpareil</a> >. / Artistic-2.0	noarch
<code>r-nonpmodelcheck</code>	3.0	Provides tests of significance for covariates (or groups of covariates) in a fully nonparametric regression model and a variable (or group) selection procedure based on False Discovery Rate. In addition, it provides a function for local polynomial regression for any number of dimensions, using a bandwidth specified by the user or automatically chosen by cross validation or an adaptive procedure. / GPL-2	linux-64, osx-64, win-64
<code>r-nontargetdata</code>	1.1	Data sets for isotope pattern grouping of LC-HRMS peaks with package nontarget. Based on a vast set of unique PubChem molecular formulas, quantized (a) m/z, (b) m/z differences, (c) intensity ratios and (d) marker centroids of simulated centroid pairs are listed for different instrument resolutions. / GPL-3	noarch
<code>r-nopaco</code>	1.0.6	A non-parametric test for multi-observer concordance and differences between concordances in (un)balanced data. / GPL-3	linux-64, osx-64, win-64
<code>r-norlmix</code>	1.3.0	Onedimensional Normal (i.e. Gaussian) Mixture Models Classes, for, e.g., density estimation or clustering algorithms research and teaching; providing the widely used Marron-Wand densities. Efficient random number generation and graphics. Fitting to data by efficient ML (Maximum Likelihood) or traditional EM estimation. / GPL-2	noarch
<code>r-nordklimdata1</code>	1.2	The Nordklim dataset 1.0 is a unique and useful achievement for climate analysis. It includes observations of twelve different climate elements from more than 100 stations in the Nordic region, in time span over 100 years. The project contractors were NORDKLIM/NORDMET on behalf of the National meteorological services in Denmark (DMI), Finland (FMI), Iceland (VI), Norway (DNMI) and Sweden (SMHI). / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-norm	1.0_9	Analysis of multivariate normal datasets with missing values / file LICENSE	linux-64, osx-64, win-64
r-norm2	2.0.2	Functions for parameter estimation, Bayesian posterior simulation and multiple imputation from incomplete multivariate data under a normal model. / GPL-3	linux-64, osx-64, win-64
r-normalp	0.7.0	Collection of utilities referred to Exponential Power distribution, also known as General Error Distribution (see Mineo, A.M. and Ruggieri, M. (2005), A software Tool for the Exponential Power Distribution: The normalp package. In Journal of Statistical Software, Vol. 12, Issue 4). / GPL-3	noarch
r-normalr	1.0.0	The robustness of many of the statistical techniques, such as factor analysis, applied in the social sciences rests upon the assumption of item-level normality. However, when dealing with real data, these assumptions are often not met. The Box-Cox transformation (Box & Cox, 1964) < <a href="http://www.jstor.org/stable/2984418">http://www.jstor.org/stable/2984418</a> > provides an optimal transformation for non-normal variables. Yet, for large datasets of continuous variables, its application in current software programs is cumbersome with analysts having to take several steps to normalise each variable. We present an R package ‘normalr’ that enables researchers to make convenient optimal transformations of multiple variables in datasets. This R package enables users to quickly and accurately: (1) anchor all of their variables at 1.00, (2) select the desired precision with which the optimal lambda is estimated, (3) apply each unique exponent to its variable, (4) rescale resultant values to within their original X1 and X(n) ranges, and (5) provide original and transformed estimates of skewness, kurtosis, and other inferential assessments of normality. / GPL-3	noarch
r-normexpression	0.1.0	It provides a framework and a fast and simple way for researchers to evaluate methods (particularly some data-driven methods or their own methods) and then select a best one for data normalization in the gene expression analysis, based on the consistency of metrics and the consistency of datasets. Zhenfeng Wu, Weixiang Liu, Xiufeng Jin, Deshui Yu, Hua Wang, Gustavo Glusman, Max Robinson, Lin Liu, Jishou Ruan and Shan Gao (2018) <doi:10.1101/251140>. / Artistic-2.0	noarch
r-normt3	1.0_3	Evaluates the probability density function of the sum of the Gaussian and Student’s t density on 3 degrees of freedom. Evaluates the p.d.f. of the sphered Student’s t density function. Also evaluates the erf, and erfc functions on complex-valued arguments. Thanks to Krishna Myneni the function is calculates the Faddeeva function also! / GPL-2	linux-64, osx-64, win-64
r-normtest	1.1	Tests for the composite hypothesis of normality / GPL-3	noarch
r-normwhn.test	1.0	Includes Omnibus Univariate and Multivariate Normality Tests (See Doornik and Hansen (1994)). One variation allows for the possibility of weak dependence rather than independence in the variable(s). Also included is an univariate white noise test where the null hypothesis is white noise rather than strict white noise. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-nortara</a>	1.0.0	An implementation of a specific method for generating n-dimensional random vectors with given marginal distributions and correlation matrix. The method uses the NORTA (NORmal To Anything) approach which generates a standard normal random vector and then transforms it into a random vector with specified marginal distributions and the RA (Retrospective Approximation) algorithm which is a generic stochastic root-finding algorithm. The marginals can be continuous or discrete. See the vignette of package for more details. / MIT	noarch
<a href="#">r-nortest</a>	1.0_4	Five omnibus tests for testing the composite hypothesis of normality. / GPL-2	noarch
<a href="#">r-nortestarma</a>	1.0.2	Tests the goodness-of-fit to the Normal distribution for the errors of an ARMA model. / GPL (> 2)	linux-64, osx-64, win-64
<a href="#">r-nose</a>	1.0	The nose package consists of a collection of three functions for classifying sparseness in typical 2 x 2 data sets with at least one cell should have zero count. These functions are based on the three widely applied summary measures for 2 x 2 categorical data viz, Risk Difference (RD), Relative Risk (RR), Odds Ratio (OR). This package helps to identify suitable continuity correction for zero cells when a multi centre analysis or a meta analysis is carried out. Further, it can be considered as a tool for sensitivity analysis for adding a continuity correction and to identify the presence of Simpson's paradox. / GPL-2	noarch
<a href="#">r-not</a>	1.2	Provides efficient implementation of the Narrowest-Over-Threshold methodology for detecting an unknown number of change-points occurring at unknown locations in one-dimensional data following deterministic signal noise model, see R. Baranowski, Y. Chen and P. Fryzlewicz (2019) <doi:10.1111/rssb.12322>. Currently implemented scenarios are: piecewise-constant signal, piecewise-constant signal with a heavy-tailed noise, piecewise-linear signal, piecewise-quadratic signal, piecewise-constant signal and with piecewise-constant variance of the noise. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-notemnd</a>	0.1.0	When building a 'shiny' app to generate reports (pdf or 'word'), we can insert a comment box in front-end side for user to write down them notes and use this package to document those notes in reports. / MIT	noarch
<a href="#">r-notifyr</a>	1.02	This Package provides a connection to the pushover.net API to send push notification to your smartphone directly from R. (ACCOUNT REQUIRED!) / GPL-2	noarch
<a href="#">r-noweb</a>	1.0_4	The noweb system for source code, implemented in R. / LGPL-2	noarch
<a href="#">r-nozzle.r1</a>	1.1_1	The Nozzle package provides an API to generate HTML reports with dynamic user interface elements based on JavaScript and CSS (Cascading Style Sheets). Nozzle was designed to facilitate summarization and rapid browsing of complex results in data analysis pipelines where multiple analyses are performed frequently on big data sets. The package can be applied to any project where user-friendly reports need to be created. / LGPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-np</a>	0.60_9	Nonparametric (and semiparametric) kernel methods that seamlessly handle a mix of continuous, unordered, and ordered factor data types. We would like to gratefully acknowledge support from the Natural Sciences and Engineering Research Council of Canada (NSERC, < <a href="http://www.nserc-crsng.gc.ca">http://www.nserc-crsng.gc.ca</a> >), the Social Sciences and Humanities Research Council of Canada (SSHRC, < <a href="http://www.sshrc-crsh.gc.ca">http://www.sshrc-crsh.gc.ca</a> >), and the Shared Hierarchical Academic Research Computing Network (SHARCNET, < <a href="http://www.sharcnet.ca">http://www.sharcnet.ca</a> >). / GPL-3	linux-64, osx-64, win-64
<a href="#">r-nparcomp</a>	3.0	With this package, it is possible to compute nonparametric simultaneous confidence intervals for relative contrast effects in the unbalanced one way layout. Moreover, it computes simultaneous p-values. The simultaneous confidence intervals can be computed using multivariate normal distribution, multivariate t-distribution with a Satterthwaite Approximation of the degree of freedom or using multivariate range preserving transformations with Logit or Probit as transformation function. 2 sample comparisons can be performed with the same methods described above. There is no assumption on the underlying distribution function, only that the data have to be at least ordinal numbers. See Konietzschke et al. (2015) <doi:10.18637/jss.v064.i09> for details. / GPL-3	noarch
<a href="#">r-nparld</a>	2.1	The package nparLD is designed to perform nonparametric analysis of longitudinal data in factorial experiments. Longitudinal data are those which are collected from the same subjects over time, and they frequently arise in biological sciences. Nonparametric methods do not require distributional assumptions, and are applicable to a variety of data types (continuous, discrete, purely ordinal, and dichotomous). Such methods are also robust with respect to outliers and for small sample sizes. / GPL-2	noarch
<a href="#">r-nparsurv</a>	0.1.0	Nonparametric Tests for Main Effects, Simple Effects and Interaction Effect with Censored Data and Two Factorial Influencing Variables. / GPL-2	noarch
<a href="#">r-npbayesimputecat</a>	0.1	These routines create multiple imputations of missing at random categorical data, and create multiply imputed synthesis of categorical data, with or without structural zeros. Imputations and syntheses are based on Dirichlet process mixtures of multinomial distributions, which is a non-parametric Bayesian modeling approach that allows for flexible joint modeling. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-npcd</a>	1.0_10	An array of nonparametric and parametric estimation methods for cognitive diagnostic models, including nonparametric classification of examinee attribute profiles, joint maximum likelihood estimation (JMLE) of examinee attribute profiles and item parameters, and nonparametric refinement of the Q-matrix, as well as conditional maximum likelihood estimation (CMLE) of examinee attribute profiles given item parameters and CMLE of item parameters given examinee attribute profiles. Currently the nonparametric methods in the package support both conjunctive and disjunctive models, and the parametric methods in the package support the DINA model, the DINO model, the NIDA model, the G-NIDA model, and the R-RUM model. / LGPL-2.1	noarch
<a href="#">r-npcoptest</a>	1.03	A non parametric test for change points detection in the dependence between the components of multivariate data, with or without (multiple) changes in the marginal distributions. The full details, justification and examples are published in Rohmer (2016) <doi:10.1016/j.spl.2016.06.026>. / GPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-npcp	0.1_1	Provides nonparametric CUSUM tests for detecting changes in possibly serially dependent univariate or multivariate observations. Tests sensitive to changes in the expectation, the variance, the covariance, the autocovariance, the distribution function, Spearman's rho, Kendall's tau, Gini's mean difference, and the copula are provided, as well as a test for detecting changes in the distribution of independent block maxima (with environmental studies in mind). The latest additions are a test sensitive to changes in the autocopula and a combined test of stationarity sensitive to changes in the distribution function and the autocopula. / GPL-3	linux-64, osx-64, win-64
r-npexact	0.2	Provides several novel exact hypothesis tests with minimal assumptions on the errors. The tests are exact, meaning that their p-values are correct for the given sample sizes (the p-values are not derived from asymptotic analysis). The test for stochastic inequality is for ordinal comparisons based on two independent samples and requires no assumptions on the errors. The other tests include tests for the mean and variance of a single sample and comparing means in independent samples. All these tests only require that the data has known bounds (such as percentages that lie in [0,100]). These bounds are part of the input. / GPL-2	noarch
r-nphazardrate	0.1	Provides functions and examples for histogram, kernel (classical, variable bandwidth and transformations based), discrete and semiparametric hazard rate estimators. / GPL-2	noarch
r-nplplot	4.5	This package provides routines for plotting linkage and association results along a chromosome, with marker names displayed along the top border. There are also routines for generating BED and BedGraph custom tracks for viewing in the UCSC genome browser. The data reformatting program Mega2 uses this package to plot output from a variety of programs. / GPL-3	noarch
r-nplr	0.1_7	Performing drug response analyses and IC50 estimations using n-Parameter logistic regression. Can also be applied to proliferation analyses. / GPL-3	noarch
r-npmla	1.0.0	Support the book: Wu CO and Tian X (2018). Nonparametric Models for Longitudinal Data. Chapman & Hall/CRC (to appear); and provide fit for using global and local smoothing methods for the conditional-mean and conditional-distribution based models with longitudinal Data. / GPL-2	noarch
r-npmlecmprsk	3.0	Given a failure type, the function computes covariate-specific probability of failure over time and covariate-specific conditional hazard rate based on possibly right-censored competing risk data. Specifically, it computes the non-parametric maximum-likelihood estimates of these quantities and their asymptotic variances in a semi-parametric mixture model for competing-risks data, as described in Chang et al. (2007a). / Artistic-2.0	noarch
r-npmlence	1.0	To compute the non-parametric maximum likelihood estimates (NPMLEs) and penalized NPMLEs with SCAD, HARD and LASSO penalties for nested case-control or case-cohort sampling design with time matching under Cox's regression model. It also proposes the standard error formula for estimator using observed profile likelihood. For details about (penalized) NPMLEs see the original paper Penalized Full Likelihood Approach to Variable Selection for Cox's Regression Model under Nested Case-Control Sampling by Wang et al. (2019) <doi:10.1007/s10985-019-09475-z>. / GPL-2	noarch
r-npmr	1.2	Fit multinomial logistic regression with a penalty on the nuclear norm of the estimated regression coefficient matrix, using proximal gradient descent. Reference: Powers S, Hastie T and Tibshirani R (2018) <doi:10.1177/1471082X18777669>. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-npmv	2.4.0	Performs analysis of one-way multivariate data, for small samples using Nonparametric techniques. Using approximations for ANOVA Type, Wilks' Lambda, Lawley Hotelling, and Bartlett Nanda Pillai Test statics, the package compares the multivariate distributions for a single explanatory variable. The comparison is also performed using a permutation test for each of the four test statistics. The package also performs an all-subsets algorithm regarding variables and regarding factor levels. / GPL-2	noarch
r-npmvcp	1.1	Nonparametric Multivariate Change Point Model / GPL-2	noarch
r-npordtests	1.1	Performs nonparametric tests for equality of location against ordered alternatives. / GPL-2	noarch
r-npp	0.2.0	Posterior sampling in several commonly used distributions using normalized power prior as described in Duan, Ye and Smith (2006) <doi:10.1002/env.752> and Ibrahim et.al. (2015) <doi:10.1002/sim.6728>. Sampling of the power parameter is achieved via either independence Metropolis-Hastings or random walk Metropolis-Hastings based on transformation. / GPL-2	noarch
r-nppbib	1.1_0	Implements a nonparametric statistical test for rank or score data from partially-balanced incomplete block-design experiments. / GPL-2	noarch
r-npreg	1.0_0	Multiple and generalized nonparametric regression using smoothing spline ANOVA models and generalized additive models. Includes support for Gaussian and non-Gaussian responses, smoothers for multiple types of predictors, interactions between smoothers of mixed types, and eight different methods for smoothing parameter selection. / GPL-2	noarch
r-nprocregression	1.0_5	Implements several nonparametric regression approaches for the inclusion of covariate information on the receiver operating characteristic (ROC) framework. / GPL-3	linux-64, osx-64, win-64
r-nps	1.1	Small functions to make working with survey data in the context of a Net Promoter programme easier. Specifically, data transformation methods, some methods for examining the statistical properties of the NPS, such as its variance and standard errors, and some simple inferential testing procedures. Net Promoter and NPS are registered trademarks of Bain & Company, Satmetrix Systems and Fred Reichheld. / GPL-2	noarch
r-npsimex	0.2_1	This package contains a collection of functions to to perform nonparametric deconvolution using simulation extrapolation (SIMEX). We propose an estimator that adopts the SIMEX idea but bypasses the simulation step in the original SIMEX algorithm. There is no bandwidth parameter and the estimate is determined by appropriately selecting design points. See details in: Wang, X.F., Sun, J. and Fan, Z. (2011). Deconvolution density estimation with heteroscedastic errors using SIMEX. / GPL-3	linux-64, osx-64, win-64
r-npst	2.0	Package 'npst' generalizes Hewitt's (1971) test for seasonality and Rogerson's (1996) extension based on Monte-Carlo simulation. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-nptest</a>	1.0.0	Robust permutation tests for location, correlation, and regression problems, as described in Helwig (2019) <doi:10.1002/wics.1457>. Univariate and multivariate tests are supported. For each problem, exact tests and Monte Carlo approximations are available. Parallel computing is implemented via the ‘parallel’ package. / GPL-2	noarch
<a href="#">r-nricens</a>	1.6	Calculating the net reclassification improvement (NRI) for risk prediction models with time to event and binary data. / GPL-2	noarch
<a href="#">r-nscancor</a>	0.6.1	Two implementations of canonical correlation analysis (CCA) that are based on iterated regression. By choosing the appropriate regression algorithm for each data domain, it is possible to enforce sparsity, non-negativity or other kinds of constraints on the projection vectors. Multiple canonical variables are computed sequentially using a generalized deflation scheme, where the additional correlation not explained by previous variables is maximized. ‘nscancor’ is used to analyze paired data from two domains, and has the same interface as the ‘cancor’ function from the ‘stats’ package (plus some extra parameters). ‘mcancor’ is appropriate for analyzing data from three or more domains. See < <a href="http://sigg-iten.ch/learningbits/2014/01/20/canonical-correlation-analysis-under-constraints/">http://sigg-iten.ch/learningbits/2014/01/20/canonical-correlation-analysis-under-constraints/</a> > and Sigg et al. (2007) <doi:10.1109/MLSP.2007.4414315> for more details. / GPL-2	noarch
<a href="#">r-nscluster</a>	1.3.1	Simulation and estimation for Neyman-Scott spatial cluster point process models and their extensions, based on the methodology in Tanaka, Ogata, and Stoyan (2008) <doi:10.1002/bimj.200610339>. To estimate parameters by the simplex method, parallel computation using ‘OpenMP’ application programming interface is available. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-nseval</a>	0.4	Facilities to capture, inspect, manipulate, and create lazy values (promises), ... lists, and active calls. / GPL (>= 2.0)	linux-64, osx-64, win-64
<a href="#">r-nsgp</a>	1.0.5	A Gaussian process regression using a Gaussian kernel for both one-sample and two-sample cases. Includes non-stationary Gaussian kernel (exponential decay function) and several likelihood ratio tests for differential testing along target points. / GPL-2	noarch
<a href="#">r-nso1212</a>	1.0.0	National Statistical Office of Mongolia (NSO) is the national statistical service and an organization of Mongolian government. NSO provides open access and official data via its web site < <a href="http://www.1212.mn/">http://www.1212.mn/</a> > and API < <a href="http://opendata.1212.mn/en/doc">http://opendata.1212.mn/en/doc</a> >. The package NSO1212 has functions for accessing the API service. The functions are compatible with the API v2.0 and get data sets and its detailed informations from the API. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-nsprcomp</a>	0.5.1	Two methods for performing a constrained principal component analysis (PCA), where non-negativity and/or sparsity constraints are enforced on the principal axes (PAs). The function ‘nsprcomp’ computes one principal component (PC) after the other. Each PA is optimized such that the corresponding PC has maximum additional variance not explained by the previous components. In contrast, the function ‘nscumcomp’ jointly computes all PCs such that the cumulative variance is maximal. Both functions have the same interface as the ‘prcomp’ function from the ‘stats’ package (plus some extra parameters), and both return the result of the analysis as an object of class ‘nsprcomp’, which inherits from ‘prcomp’. See < <a href="https://sigg-iten.ch/learningbits/2013/05/27/nsprcomp-is-on-cran/">https://sigg-iten.ch/learningbits/2013/05/27/nsprcomp-is-on-cran/</a> > and Sigg et al. (2008) <doi:10.1145/1390156.1390277> for more details. / GPL-2	noarch
<a href="#">r-nsrfa</a>	0.7.1	A collection of statistical tools for objective (non-supervised) applications of the Regional Frequency Analysis methods in hydrology. The package refers to the index-value method and, more precisely, helps the hydrologist to: (1) regionalize the index-value; (2) form homogeneous regions with similar growth curves; (3) fit distribution functions to the empirical regional growth curves. Most of the methods are those described in the Flood Estimation Handbook (Centre for Ecology & Hydrology, 1999, ISBN:9781906698003). Homogeneity tests from Hosking and Wallis (1993) <doi:10.1029/92WR01980> and Viglione et al. (2007) <doi:10.1029/2006WR005095> are available. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-nsrr</a>	0.1.2	Allows users to access data from the National Sleep Research Resource (‘NSRR’) < <a href="https://sleepdata.org/">https://sleepdata.org/</a> >. / GPL-3	noarch
<a href="#">r-numbers</a>	0.7.1	Provides number-theoretic functions for factorization, prime numbers, twin primes, primitive roots, modular logarithm and inverses, extended GCD, Farey series and continuous fractions. Includes Legendre and Jacobi symbols, some divisor functions, Euler’s Phi function, etc. / GPL-3	noarch
<a href="#">r-numbersbr</a>	0.0.2	Validate, format and compare identification numbers used in Brazil. These numbers are used to identify individuals (CPF), vehicles (RENAVAN), companies (CNPJ) and etc. Functions to format, validate and compare these numbers have been implemented in a vectorized way in order to speed up validations and comparisons in big datasets. / MIT	noarch
<a href="#">r-numderiv</a>	2016.8	Methods for calculating (usually) accurate numerical first and second order derivatives. Accurate calculations are done using ‘Richardson’s’ extrapolation or, when applicable, a complex step derivative is available. A simple difference method is also provided. Simple difference is (usually) less accurate but is much quicker than ‘Richardson’s’ extrapolation and provides a useful cross-check. Methods are provided for real scalar and vector valued functions. / GPL-2	linux-32, linux-64, noarch, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
<code>r-numero</code>	1.2.0	High-dimensional datasets that do not exhibit a clear intrinsic clustered structure pose a challenge to conventional clustering algorithms. For this reason, we developed an unsupervised framework that helps scientists to better subgroup their datasets based on visual cues, please see Gao S, Mutter S, Casey A, Makinen V-P (2018) Numero: a statistical framework to define multivariable subgroups in complex population-based datasets, Int J Epidemiology, dyy113, <doi:10.1093/ije/dyy113>. The framework includes the necessary functions to construct a self-organizing map of the data, to evaluate the statistical significance of the observed data patterns, and to visualize the results. / GPL-2	linux-64, osx-64, win-64
<code>r-numform</code>	0.5.0	Format numbers and plots for publication; includes the removal of leading zeros, standardization of number of digits, addition of affixes, and a p-value formatter. These tools combine the functionality of several ‘base’ functions such as ‘paste()’, ‘format()’, and ‘sprintf()’ into specific use case functions that are named in a way that is consistent with usage, making their names easy to remember and easy to deploy. / GPL-2	noarch
<code>r-numgen</code>	0.1.1	A number series generator that creates number series items based on cognitive models. / GPL-3	noarch
<code>r-numkm</code>	0.1.0	To add the table of numbers at risk below the Kaplan-Meier plot. / GPL-3	noarch
<code>r-numosl</code>	2.6	Package for optimizing regular numeric problems in optically stimulated luminescence dating, such as: equivalent dose calculation, dose rate determination, growth curve fitting, decay curve decomposition, statistical age model optimization, and statistical plot visualization. / GPL-3	linux-64, osx-64, win-64
<code>r-nutshell.audioscrobber</code>	1.0	This package contains the Audio Scrobber data set used as an example in the book R in a Nutshell from O’Reilly Media. For more information about this book, see <a href="http://shop.oreilly.com/product/0636920022008.do">http://shop.oreilly.com/product/0636920022008.do</a> / CC BY-NC-SA 3.0	noarch
<code>r-nutshell.bbdb</code>	1.0	This package contains the baseball databank data set used as an example in the book R in a Nutshell from O’Reilly Media. For more information about this book, see <a href="http://shop.oreilly.com/product/0636920022008.do">http://shop.oreilly.com/product/0636920022008.do</a> / CC BY-NC-ND 3.0 US	noarch
<code>r-nvennr</code>	0.2.1	Provides an interface for the nVenn algorithm (Perez-Silva et al. 2018) <DOI:10.1093/bioinformatics/bty109>. This algorithm works for any number of sets, and usually yields pleasing and informative Venn diagrams with proportionality information. However, representing more than six sets takes a long time and is hard to interpret, unless many of the regions are empty. If you cannot make sense of the result, you may want to consider ‘UpSetR’ < <a href="https://cran.r-project.org/package=UpSetR/README.html">https://cran.r-project.org/package=UpSetR/README.html</a> >. / MIT	linux-64, osx-64, win-64
<code>r-nws</code>	1.7.0	Provides coordination and parallel execution facilities, as well as limited cross-language data exchange, using the netWorkSpaces server developed by REvolution Computing / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-nycflights13</a>	1.0.0	Airline on-time data for all flights departing NYC in 2013. Also includes useful ‘metadata’ on airlines, airports, weather, and planes. / CC0	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-nzelect</a>	0.4.0	Convenient access to New Zealand election results by voting place. Voting places have been matched to Regional Council, Territorial Authority, and Area Unit, to facilitate matching with additional data. Opinion polls since 2002 and some convenience analytical function are also supplied. / GPL-3	noarch
<a href="#">r-nzilbb.labbc</a>	0.2.2	‘LaBB-CAT’ is a web-based language corpus management system developed by the New Zealand Institute of Language, Brain and Behaviour (NZILBB) - see < <a href="https://labbc.canterbury.ac.nz">https://labbc.canterbury.ac.nz</a> >. This package defines functions for accessing corpus data in a ‘LaBB-CAT’ instance. You must have at least version 20190425.1121 of ‘LaBB-CAT’ to use this package. For more information about ‘LaBB-CAT’, see Robert Fromont and Jennifer Hay (2008) <doi:10.3366/E1749503208000142> or Robert Fromont (2017) <doi:10.1016/j.csl.2017.01.004>. / GPL-3	noarch
<a href="#">r-nzpullover</a>	0.3.0	Datasets of driving offences and fines in New Zealand between 2009 and 2017. Originally published by the New Zealand Police at < <a href="http://www.police.govt.nz/about-us/publication/road-policing-driver-offence-data-january-2009-december-2017">http://www.police.govt.nz/about-us/publication/road-policing-driver-offence-data-january-2009-december-2017</a> >. / CC0	noarch
<a href="#">r-oacolors</a>	0.0.4	Provides carefully chosen color palettes as used a.o. at OpenAnalytics < <a href="http://www.openanalytics.eu">http://www.openanalytics.eu</a> >. / GPL-3	noarch
<a href="#">r-oaiharvester</a>	0.3.0	Harvest metadata using the Open Archives Initiative Protocol for Metadata Harvesting (OAI-PMH) version 2.0 (for more information, see < <a href="http://www.openarchives.org/OAI/openarchivesprotocol.html">http://www.openarchives.org/OAI/openarchivesprotocol.html</a> >). / GPL-2	noarch
<a href="#">r-oak</a>	0.2.3	Functions and classes to create and manipulate trees and nodes. / MIT	noarch
<a href="#">r-oaqc</a>	1.0	Implements the efficient algorithm by Ortmann and Brandes (2017) <doi:10.1007/s41109-017-0027-2> to compute the orbit-aware frequency distribution of induced and non-induced quads, i.e. subgraphs of size four. Given an edge matrix, data frame, or a graph object (e.g., ‘igraph’), the orbit-aware counts are computed respective each of the edges and nodes. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-oarray</a>	1.4.9	Generalise the starting point of the array index. / GPL-3	noarch
<a href="#">r-objectsignals</a>	0.10.2	A mutable Signal object can report changes to its state, clients could register functions so that they are called whenever the signal is emitted. The signal could be emitted, disconnected, blocked, unblocked, and buffered. / GPL-2	noarch
<a href="#">r-obliclus</a>	0.9	This package conducts factor rotation techniques which intend to identify a simple and well-clustered structure in a factor loading matrix. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-obmbpkg</a>	1.0.0	Applies an objective Bayesian method to the Mb capture-recapture model to estimate the population size N. The Mb model is a class of capture-recapture methods used to account for variations in capture probability due to animal behavior. Under the Mb formulation, the initial capture of an animal may effect the probability of subsequent captures due to their becoming trap happy or trap shy. / GPL-3	noarch
<a href="#">r-obs.agree</a>	1.0	The package includes two functions for measuring agreement. Raw Agreement Indices (RAI) to categorical data and Information-Based Measure of Disagreement (IBMD) to continuous data. It can be used for multiple raters and multiple readings cases. / GPL-2	noarch
<a href="#">r-obsmd</a>	5.0	Implements the objective Bayesian methodology proposed in Consonni and Deldossi in order to choose the optimal experiment that better discriminate between competing models. G.Consonni, L. Deldossi (2014) Objective Bayesian Model Discrimination in Follow-up Experimental Designs, Test. <DOI:10.1007/s11749-015-0461-3>. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-obssens</a>	1.3	Observational studies are limited in that there could be an unmeasured variable related to both the response variable and the primary predictor. If this unmeasured variable were included in the analysis it would change the relationship (possibly changing the conclusions). Sensitivity analysis is a way to see how much of a relationship needs to exist with the unmeasured variable before the conclusions change. This package provides tools for doing a sensitivity analysis for regression (linear, logistic, and cox) style models. / GPL-2	noarch
<a href="#">r-oca</a>	0.1	Computes optimal capital allocations based on some standard principles such as Haircut, Overbeck type II and the Covariance Allocation Principle. It also provides some shortcuts for obtaining the Value at Risk and the Expectation Shortfall, using both the normal and the t-student distribution, see Urbina and Guill��n (2014)<doi:10.1016/j.eswa.2014.05.017> and Urbina (2013)<http://hdl.handle.net/2099.1/19443>. / GPL-2	noarch
<a href="#">r-occ</a>	1.1	Generic function for estimating positron emission tomography (PET) neuroreceptor occupancies from the total volumes of distribution of a set of regions of interest. Fittings methods include the simple ‘reference region’ and ‘ordinary least squares’ (sometimes known as occupancy plot) methods, as well as the more efficient ‘restricted maximum likelihood estimation’. / GPL-3	noarch
<a href="#">r-oce</a>	1.0.1	Supports the analysis of Oceanographic data, including ‘ADCP’ measurements, measurements made with ‘argo’ floats, ‘CTD’ measurements, sectional data, sea-level time series, coastline and topographic data, etc. Provides specialized functions for calculating seawater properties such as potential temperature in either the ‘UNESCO’ or ‘TEOS-10’ equation of state. Produces graphical displays that conform to the conventions of the Oceanographic literature. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-ocedata</a>	0.1.5	Several important and Oceanographic data sets are provided. These are particularly useful to the ‘oce’ package, but can also be helpful in a general context. / GPL-2	noarch
<a href="#">r-ocomposition</a>	1.1	Regression model where the response variable is a rank-indexed compositional vector (non-negative values that sum up to one and are ordered from the largest to the smallest). Parameters are estimated in the Bayesian framework using MCMC methods. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-ocp	0.1.1	Implements the Bayesian online changepoint detection method by Adams and MacKay (2007) <arXiv:0710.3742> for univariate or multivariate data. Gaussian and Poisson probability models are implemented. Provides post-processing functions with alternative ways to extract changepoints. / GPL-3	noarch
r-odata	0.6	Helper methods for accessing data from web service based on OData Protocol. It provides several helper methods to access the service metadata, the data from datasets and to download some file resources (it only support CSV for now). For more information about OData go to < <a href="http://www.odata.org/documentation/">http://www.odata.org/documentation/</a> >. / GPL-2	noarch
r-odb	1.1.1	This package provides functions to create, connect, update and query HSQL databases embedded in Open Document Databases (.odb) files, as OpenOffice and LibreOffice do. / GPL-3	noarch
r-odbc	1.1.5	A DBI-compatible interface to ODBC databases. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-odds.converter	1.4.8	Conversion between the most common odds types for sports betting. Hong Kong odds, US odds, Decimal odds, Indonesian odds, Malaysian odds, and raw Probability are covered in this package. / GPL-3	noarch
r-odds.n.ends	0.1.1	Computes odds ratios and 95% confidence intervals from a generalized linear model object. It also computes model significance with the chi-squared statistic and p-value and it computes model fit using a contingency table to determine the percent of observations for which the model correctly predicts the value of the outcome. Calculates model sensitivity and specificity. / CC0	noarch
r-odeintr	1.7.1	Wraps the Boost odeint library for integration of differential equations. / GPL-2	linux-64, osx-64, win-64
r-odenetwork	1.3.1	Simulates a network of ordinary differential equations of order two. The package provides an easy interface to construct networks. In addition you are able to define different external triggers to manipulate the trajectory. The method is described by Surmann, Ligges, and Weihs (2014) <doi:10.1109/ENERGYCON.2014.6850482>. / LGPL-3	noarch

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Name	Version	Summary/License	Platforms
r-odr	1.0.0	Calculate the optimal sample allocation that minimizes the variance of treatment effect in multilevel randomized trials under fixed budget and cost structure, perform power analyses with and without accommodating costs and budget. The references for proposed methods are: (1) Shen, Z. (in progress). Using optimal sample allocation to improve statistical precision and design efficiency for multilevel randomized trials. (unpublished doctoral dissertation). University of Cincinnati, Cincinnati, OH. (2) Shen, Z., & Kelcey, B. (revise & resubmit). Optimal sample allocation accounts for the full variation of sampling costs in cluster-randomized trials. Journal of Educational and Behavioral Statistics. (3) Shen, Z., & Kelcey, B. (2018, April). Optimal design of cluster randomized trials under condition- and unit-specific cost structures. Roundtable discussion presented at American Educational Research Association (AERA) annual conference. (4) Champely, S. (2018). pwr: Basic functions for power analysis (Version 1.2-2) [Software]. Available from < <a href="https://CRAN.R-project.org/package=pwr">https://CRAN.R-project.org/package=pwr</a> >. / GPL-3	noarch
r-ods	0.2.0	Outcome-dependent sampling (ODS) schemes are cost-effective ways to enhance study efficiency. In ODS designs, one observes the exposure/covariates with a probability that depends on the outcome variable. Popular ODS designs include case-control for binary outcome, case-cohort for time-to-event outcome, and continuous outcome ODS design (Zhou et al. 2002) <doi: 10.1111/j.0006-341X.2002.00413.x>. Because ODS data has biased sampling nature, standard statistical analysis such as linear regression will lead to biased estimates of the population parameters. This package implements four statistical methods related to ODS designs: (1) An empirical likelihood method analyzing the primary continuous outcome with respect to exposure variables in continuous ODS design (Zhou et al., 2002). (2) A partial linear model analyzing the primary outcome in continuous ODS design (Zhou, Qin and Longnecker, 2011) <doi: 10.1111/j.1541-0420.2010.01500.x>. (3) Analyze a secondary outcome in continuous ODS design (Pan et al. 2018) <doi: 10.1002/sim.7672>. (4) An estimated likelihood method analyzing a secondary outcome in case-cohort data (Pan et al. 2017) <doi: 10.1111/biom.12838>. / GPL-2	noarch
r-oem	2.0.9	Solves penalized least squares problems for big tall data using the orthogonalizing EM algorithm of Xiong et al. (2016) <doi:10.1080/00401706.2015.1054436>. The main fitting function is oem() and the functions cv.oem() and xval.oem() are for cross validation, the latter being an accelerated cross validation function for linear models. The big.oem() function allows for out of memory fitting. / GPL-2	linux-64, osx-64, win-64
r-officer	0.3.5	Access and manipulate ‘Microsoft Word’ and ‘Microsoft PowerPoint’ documents from R. The package focuses on tabular and graphical reporting from R; it also provides two functions that let users get document content into data objects. A set of functions lets add and remove images, tables and paragraphs of text in new or existing documents. When working with ‘PowerPoint’ presentations, slides can be added or removed; shapes inside slides can also be added or removed. When working with ‘Word’ documents, a cursor can be used to help insert or delete content at a specific location in the document. The package does not require any installation of Microsoft products to be able to write Microsoft files. / GPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-offlinechange</a>	0.0.2	Detect the number and locations of change points. The locations can be either exact or in terms of ranges, depending on the available computational resource. The method is based on Jie Ding, Yu Xiang, Lu Shen, Vahid Tarokh (2016) <arXiv:1605.00346v2>. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-ogi</a>	1.0.0	Consider a data matrix of n individuals with p variates. The objective general index (OGI) is a general index that combines the p variates into a univariate index in order to rank the n individuals. The OGI is always positively correlated with each of the variates. More details can be found in Sei (2016) <doi:10.1016/j.jmva.2016.02.005>. / GPL-3	noarch
<a href="#">r-oglmx</a>	3.0.0	Ordered models such as ordered probit and ordered logit presume that the error variance is constant across observations. In the case that this assumption does not hold estimates of marginal effects are typically biased (Weiss (1997)). This package allows for generalization of ordered probit and ordered logit models by allowing the user to specify a model for the variance. Furthermore, the package includes functions to calculate the marginal effects. Wrapper functions to estimate the standard limited dependent variable models are also included. / GPL-2	noarch
<a href="#">r-ohit</a>	1.0.0	Ing and Lai (2011) <doi:10.5705/ss.2010.081> proposed a high-dimensional model selection procedure that comprises three steps: orthogonal greedy algorithm (OGA), high-dimensional information criterion (HDIC), and Trim. The first two steps, OGA and HDIC, are used to sequentially select input variables and determine stopping rules, respectively. The third step, Trim, is used to delete irrelevant variables remaining in the second step. This package aims at fitting a high-dimensional linear regression model via OGAHDICTrim. / GPL-2	noarch
<a href="#">r-ohpl</a>	1.4	Ordered homogeneity pursuit lasso (OHPL) algorithm for group variable selection proposed in Lin et al. (2017) <DOI:10.1016/j.chemolab.2017.07.004>. The OHPL method exploits the homogeneity structure in high-dimensional data and enjoys the grouping effect to select groups of important variables automatically. This feature makes it particularly useful for high-dimensional datasets with strongly correlated variables, such as spectroscopic data. / GPL-3	noarch
<a href="#">r-ohtadstats</a>	2.1.0	Calculate's Tomoka Ohta's partitioning of linkage disequilibrium, deemed D-statistics, for pairs of loci. Beissinger et al. (2016) <doi:10.1038/hdy.2015.81>. / MIT	noarch
<a href="#">r-oidata</a>	1.0	A collection of data sets from several sources that may be useful for teaching, practice, or other purposes. Functions have also been included to assist in the retrieval of table data from websites or in visualizing sample data. / GPL-2   GPL-3	noarch
<a href="#">r-okcupiddata</a>	0.1.0	Cleaned profile data from OkCupid Profile Data for Introductory Statistics and Data Science Courses (Journal of Statistics Education 2015 < <a href="http://www.amstat.org/publications/jse/v23n2/kim.pdf">http://www.amstat.org/publications/jse/v23n2/kim.pdf</a> >). / CC0	noarch
<a href="#">r-okmesonet</a>	0.1.5	okmesonet retrieves and summarizes Oklahoma (USA) Mesonet climatological data provided by the Oklahoma Climatological Survey. Measurements are recorded every five minutes at approximately 120 stations throughout Oklahoma and are available in near real-time. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-olctools</a>	0.3.0	'Open Location Codes' < <a href="http://openlocationcode.com/">http://openlocationcode.com/</a> > are a Google-created standard for identifying geographic locations. 'olctools' provides utilities for validating, encoding and decoding entries that follow this standard. / MIT	linux-64, osx-64, win-64
<a href="#">r-oligospecificitysystem</a>	1.3	Calculate the theoretical specificity of a system of multiple primers used for PCR, qPCR primers or degenerated primer design / GPL-2	noarch
<a href="#">r-olscurve</a>	0.2.0	Provides tools for more easily organizing and plotting individual ordinary least square (OLS) growth curve trajectories. / GPL-2	noarch
<a href="#">r-omd</a>	1.0	This package including two useful function, which can be used for filter the molecular descriptors matrix for QSAR. / GPL-2	noarch
<a href="#">r-omickriging</a>	1.4.0	It provides functions to generate a correlation matrix from a genetic dataset and to use this matrix to predict the phenotype of an individual by using the phenotypes of the remaining individuals through kriging. Kriging is a geo-statistical method for optimal prediction or best unbiased linear prediction. It consists of predicting the value of a variable at an unobserved location as a weighted sum of the variable at observed locations. Intuitively, it works as a reverse linear regression: instead of computing correlation (univariate regression coefficients are simply scaled correlation) between a dependent variable Y and independent variables X, it uses known correlation between X and Y to predict Y. / GPL-3	noarch
<a href="#">r-omisc</a>	0.1.2	Primarily devoted to implementing the Univariate Bootstrap (as well as the Traditional Bootstrap). In addition there are multiple functions for DeFries-Fulker behavioral genetics models. The univariate bootstrapping functions, DeFries-Fulker functions, regression and traditional bootstrapping functions form the original core. Additional features may come online later, however this software is a work in progress. For more information about univariate bootstrapping see: Lee and Rodgers (1998) and Beasley et al (2007) < <a href="https://doi.org/10.1037/1082-989X.12.4.414">doi.org/10.1037/1082-989X.12.4.414</a> >. / GPL-3	noarch
<a href="#">r-onage</a>	1.0.1	Implementation of a likelihood ratio test of differential onset of senescence between two groups. Given two groups with measures of age and of an individual trait likely to be subjected to senescence (e.g. body mass), 'OnAge' provides an asymptotic p-value for the null hypothesis that senescence starts at the same age in both groups. The package implements the procedure used in Douhard et al. (2017) < <a href="https://doi.org/10.1111/oik.04421">doi:10.1111/oik.04421</a> >. / GPL-3	noarch
<a href="#">r-oncomodel</a>	1.0	Computing probabilistic tree models for oncogenesis based on genetic data using maximum likelihood. / GPL-2	noarch
<a href="#">r-oncotree</a>	0.3.3	Contains functions to construct and evaluate directed tree structures that model the process of occurrence of genetic alterations during carcinogenesis. / GPL-2	noarch
<a href="#">r-onearmphasetwostudy</a>	1.0.3	Purpose of this package is it to plan, monitor and evaluate oncological phase II studies. In general this kind of studies are single-arm trials with planned interim analysis and binary endpoint. To meet the resulting requirements, the package provides functions to calculate and evaluate 'Simon's two-stage designs' and 'so-called' 'subset designs'. If you are unfamiliar with this package a good starting point is to take a closer look at the functions <code>getSolutions()</code> and <code>getSolutionsSub1()</code> . The web-based tool (< <a href="https://imbi.shinyapps.io/phaseII-app/">https://imbi.shinyapps.io/phaseII-app/</a> >) extends the functionality of our R package by means of a proper dealing with over- and underrunning. The R function <code>binom.test</code> of the 'stats' R package and the package 'binom' might be helpful to assess the performance of the corresponding one-stage design as a reference. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-onehot</a>	0.1.1	Quickly create numeric matrices for machine learning algorithms that require them. It converts factor columns into onehot vectors. / MIT	linux-64, osx-64, win-64
<a href="#">r-oner</a>	2.2	Implements the One Rule (OneR) Machine Learning classification algorithm (Holte, R.C. (1993) <doi:10.1023/A:1022631118932>) with enhancements for sophisticated handling of numeric data and missing values together with extensive diagnostic functions. It is useful as a baseline for machine learning models and the rules are often helpful heuristics. / MIT	noarch
<a href="#">r-onetr</a>	1.0.3	Provides a series of functions designed to enable users to easily search and interact with occupational data from the O*NET API <www.onetonline.org>. The package produces parsed and listed XML data for custom interactions, or pre-packaged functions for easy extraction of specific data (e.g., Knowledge, Skills, Abilities, Work Styles, etc.). / GPL-3	noarch
<a href="#">r-onetwosamples</a>	1.0.3	In this package, we introduce an R function one_two_sample() which can deal with one and two (normal) samples. For one normal sample x, the function reports descriptive statistics, plot, interval estimation and test of hypothesis of x. For two normal samples x and y, the function reports descriptive statistics, plot, interval estimation and test of hypothesis of x and y, respectively. It also reports interval estimation and test of hypothesis of $\mu_1 - \mu_2$ (the difference of the means of x and y) and $\sigma_1^2 / \sigma_2^2$ (the ratio of the variances of x and y), tests whether x and y are from the same population, finds the correlation coefficient of x and y if x and y have the same length. / GPL-2	noarch
<a href="#">r-onion</a>	1.2.7	Quaternions and Octonions are four- and eight- dimensional extensions of the complex numbers. They are normed division algebras over the real numbers and find applications in spatial rotations (quaternions) and string theory and relativity (octonions). The quaternions are noncommutative and the octonions nonassociative. See RKS Hankin 2006, Rnews Volume 6/2: 49-51, and the package vignette, for more details. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-onlinevar</a>	0.1.1	Functions for recursive online fitting of time-adaptive lasso vector auto regression. A recursive coordinate descent algorithm is used to estimate sparse vector auto regressive models and exponential forgetting is applied to allow model changes. Details can be found in Jakob W. Messner and Pierre Pinson (2018). Online adaptive LASSO estimation in Vector Auto Regressive models for wind power forecasting in high dimension. International Journal of Forecasting, in press. <doi:10.1016/j.ijforecast.2018.02.001>. / GPL-2   GPL-3	linux-64, osx-64, win-64
<a href="#">r-onnx</a>	0.0.2	R Interface to ‘ONNX’ - Open Neural Network Exchange < <a href="https://onnx.ai/">https://onnx.ai/</a> >. ‘ONNX’ provides an open source format for machine learning models. It defines an extensible computation graph model, as well as definitions of built-in operators and standard data types. / MIT License file LICENSE	noarch
<a href="#">r-ontologyindex</a>	2.5	Functions for reading ontologies into R as lists and manipulating sets of ontological terms - ‘ontologyX: A suite of R packages for working with ontological data’, Greene et al 2017 <doi:10.1093/bioinformatics/btw763>. / GPL-2	noarch
<a href="#">r-oomisc</a>	1.2	Includes miscellaneous functions. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-oompabase</a>	3.2.9	Provides the class unions that must be preloaded in order for the basic tools in the OOMPA (Object-Oriented Microarray and Proteomics Analysis) project to be defined and loaded. It also includes vectorized operations for row-by-row means, variances, and t-tests. Finally, it provides new color schemes. Details on the packages in the OOMPA project can be found at <a href="http://oompa.r-forge.r-project.org/">http://oompa.r-forge.r-project.org/</a> . / Apache License (== 2.0)	noarch
<a href="#">r-oompadata</a>	3.1.1	This is a data-only package to provide example data for other packages that are part of the Object-Oriented Microarray and Proteomics Analysis suite of packages. These are described in more detail at the package URL. / Apache License (== 2.0)	noarch
<a href="#">r-oor</a>	0.1.2	Implementation of optimistic optimization methods for global optimization of deterministic or stochastic functions. The algorithms feature guarantees of the convergence to a global optimum. They require minimal assumptions on the (only local) smoothness, where the smoothness parameter does not need to be known. They are expected to be useful for the most difficult functions when we have no information on smoothness and the gradients are unknown or do not exist. Due to the weak assumptions, however, they can be mostly effective only in small dimensions, for example, for hyperparameter tuning. / LGPL-3	noarch
<a href="#">r-opalr</a>	1.2.0	Data integration Web application for biobanks by ‘OBiBa’. ‘Opal’ is the core database application for biobanks. Participant data, once collected from any data source, must be integrated and stored in a central data repository under a uniform model. ‘Opal’ is such a central repository. It can import, process, validate, query, analyze, report, and export data. ‘Opal’ is typically used in a research center to analyze the data acquired at assessment centres. Its ultimate purpose is to achieve seamless data-sharing among biobanks. This ‘Opal’ client allows to interact with ‘Opal’ web services and to perform operations on the R server side. ‘DataSHIELD’ administration tools are also provided. / GPL-3	noarch
<a href="#">r-opart</a>	2019.10	AO reference implementation of standard optimal partitioning algorithm in C using square-error loss and Poisson loss functions as described by Robert Maidstone (2016) <doi:10.1007/s11222-016-9636-3>, Toby Hocking (2016) <doi:10.1007/s11222-016-9636-3>, Guillem Rigaill (2016) <doi:10.1007/s11222-016-9636-3>, Paul Fearnhead (2016) <doi:10.1007/s11222-016-9636-3>. It scales quadratically with number of data points in terms of time-complexity. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-opencv</a>	0.1	Experimenting with computer vision and machine learning in R. This package exposes some of the available ‘OpenCV’ vision algorithms, such as edge, body or face detection. These can either be applied to analyze static images, or to filter live video footage from a camera device. / MIT	linux-64, osx-64
<a href="#">r-openintro</a>	1.7.1	Supplemental functions and data for ‘OpenIntro’ resources, which includes open-source textbooks and resources for introductory statistics at <a href="http://www.openintro.org">http://www.openintro.org</a> . The package contains data sets used in our open-source textbooks along with custom plotting functions for reproducing book figures. Note that many functions and examples include color transparency; some plotting elements may not show up properly (or at all) when run in some versions of Windows operating system. / GPL-2   GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-openmpcontroller	0.2.5	The OpenMPController package provides a function <code>omp_set_num_threads()</code> to set the number of OpenMP threads to be used. This may be useful, for example, when linking against a vendor optimised BLAS/LAPACK library (e.g. the AMD Core Math Library), since the defaults used by those libraries may not be highly performant. / GPL-2	linux-64, osx-64, win-64
r-opennlpdata	1.5.3	Apache OpenNLP jars and basic English language models. / GPL-3	noarch
r-openssl	1.3	Bindings to OpenSSL libssl and libcrypto, plus custom SSH pubkey parsers. Supports RSA, DSA and EC curves P-256, P-384 and P-521. Cryptographic signatures can either be created and verified manually or via x509 certificates. AES can be used in cbc, ctr or gcm mode for symmetric encryption; RSA for asymmetric (public key) encryption or EC for Diffie Hellman. High-level envelope functions combine RSA and AES for encrypting arbitrary sized data. Other utilities include key generators, hash functions (md5, sha1, sha256, etc), base64 encoder, a secure random number generator, and 'bignum' math methods for manually performing crypto calculations on large multibyte integers. / MIT file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
r-openxlsx	4.1.0	Simplifies the creation of Excel .xlsx files by providing a high level interface to writing, styling and editing worksheets. Through the use of 'Rcpp', read/write times are comparable to the 'xlsx' and 'XLConnect' packages with the added benefit of removing the dependency on Java. / MIT file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
r-opera	1.0	Misc methods to form online predictions, for regression-oriented time-series, by combining a finite set of forecasts provided by the user. / LGPL-3	noarch
r-operator.tools	1.6.3	Provides a collection of utilities that allow programming with R's operators. Routines allow classifying operators, translating to and from an operator and its underlying function, and inverting some operators (e.g. comparison operators), etc. All methods can be extended to custom infix operators. / GPL-2	noarch
r-operators	0.1.8	A set of binary operators for common tasks such as regex manipulation. / MIT	noarch
r-opi	2.7	Implementation of the Open Perimetry Interface (OPI) for simulating and controlling visual field machines using R. The OPI is a standard for interfacing with visual field testing machines (perimeters). It specifies basic functions that allow many visual field tests to be constructed. As of October 2017 it is fully implemented on the Octopus 900 and partially on the Heidelberg Edge Perimeter, the Kowa AP 7000, the CrewT imo and the Centervue Compass. It also has a cousin: the R package 'visualFields', which has tools for analysing and manipulating visual field data. / GPL-3	noarch
r-opportunistic	1.2	Computes the routing distribution, the expectation of the number of broadcasts, transmissions and receptions considering an Opportunistic transport model. It provides theoretical results and also estimated values based on Monte Carlo simulations. / GPL-2	noarch
r-ops	1.0	Comparison of data by Pearson product-moment correlation coefficients is prone to outliers. The problem can be alleviated by normalizing data with outliers before computing the Pearson correlation coefficient. The sample provides such normalization by optimal power space transformation. / Apache License 2.0	noarch

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Name	Version	Summary/License	Platforms
r-optauc	1.0	Searches for optimal linear combination of multiple diagnostic tests (markers) that maximizes the area under the receiver operating characteristic curve (AUC); performs an approximated cross-validation for estimating the AUC associated with the estimated coefficients. / GPL-2	noarch
r-optextras	2016_10	Tools to assist in safely applying user generated objective and derivative function to optimization programs. These are primarily function minimization methods with at most bounds and masks on the parameters. Provides a way to check the basic computation of objective functions that the user provides, along with proposed gradient and Hessian functions, as well as to wrap such functions to avoid failures when inadmissible parameters are provided. Check bounds and masks. Check scaling or optimality conditions. Perform an axial search to seek lower points on the objective function surface. Includes forward, central and backward gradient approximation codes. / GPL-2	noarch
r-optgs	1.1.1	Functions to find near-optimal multi-stage designs for continuous outcomes. / GPL-2	linux-64, osx-64, win-64
r-opthedging	1.0	Estimation of value and hedging strategy of call and put options, based on optimal hedging and Monte Carlo method, from Chapter 3 of ‘Statistical Methods for Financial Engineering’, by Bruno Remillard, CRC Press, (2013). / GPL-2	linux-64, osx-64, win-64
r-optifunset	1.0	A single function ‘options.ifunset(...)’ is contained herewith, which allows the user to set a global option ONLY if it is not already set. By this token, for package maintainers this function can be used in preference to the standard ‘options(...)’ function, making provision for THEIR end user to place ‘options(...)’ directives within their ‘.Rprofile’ file, which will not be overridden at the point when a package is loaded. / GPL-2	noarch
r-optigrab	0.9.2	Parse options from the command-line using a simple, clean syntax. It requires little or no specification and supports short and long options, GNU-, Java- or Microsoft- style syntaxes, verb commands and more. / GPL-3	noarch
r-optimalcutpoints	1.1_4	Computes optimal cutpoints for diagnostic tests or continuous markers. Various approaches for selecting optimal cutoffs have been implemented, including methods based on cost-benefit analysis and diagnostic test accuracy measures (Sensitivity/Specificity, Predictive Values and Diagnostic Likelihood Ratios). Numerical and graphical output for all methods is easily obtained. / GPL-3	noarch
<b>‘r-optimaldesign &lt; http://www.iam.fmph.uniba.sk/de Riga/</b>	0.2	Algorithms for D-, A- and IV-optimal designs of experiments. Some of the functions in this package require the ‘gurobi’ software and its accompanying package. For their installation, please follow the instructions at <www.gurobi.com> and the file gurobi_inst.txt, respectively. / GPL-3	noarch
r-optimbase	1.0_9	Provides a set of commands to manage an abstract optimization method. The goal is to provide a building block for a large class of specialized optimization methods. This package manages: the number of variables, the minimum and maximum bounds, the number of non linear inequality constraints, the cost function, the logging system, various termination criteria, etc... / CeCILL-2	noarch

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Name	Version	Summary/License	Platforms
r-optimization	1.0.7	Flexible optimizer with numerous input specifications for detailed parameterisation. Designed for complex loss functions with state and parameter space constraints. Visualization tools for validation and analysis of the convergence are included. / GPL-2	linux-64, osx-64, win-64
r-optimparallel	0.8.1	Provides a parallel version of the L-BFGS-B method of optim(). The main function of the package is optimParallel(), which has the same usage and output as optim(). Using optimParallel() can significantly reduce the optimization time. / GPL-2	noarch
r-optimstrat	2.0	Intended to assist in the choice of the sampling strategy to implement in a survey. / GPL-2	noarch
r-optimx	2018.7.10	Provides a replacement and extension of the optim() function to call to several function minimization codes in R in a single statement. These methods handle smooth, possibly box constrained functions of several or many parameters. Note that function 'optimr()' was prepared to simplify the incorporation of minimization codes going forward. Also implements some utility codes and some extra solvers, including safeguarded Newton methods. Many methods previously separate are now included here. / GPL-2	noarch
r-optinterim	3.0.1	Optimal two and three stage designs monitoring time-to-event endpoints at a specified timepoint / GPL-2	noarch
r-optional	2.0	Introduces optional types with some() and none, as well as match_with() from functional languages. / BSL	noarch
r-optionpricing	0.1	Efficient Monte Carlo Algorithms for the price and the sensitivities of Asian and European Options under Geometric Brownian Motion. / GPL-2   GPL-3	noarch
r-optionstrat	1.4.0	Utilizes the Black-Scholes-Merton option pricing model to calculate key option analytics and perform graphical analysis of various option strategies. Provides functions to calculate the option premium and option greeks of European-style options. / GPL-3	noarch
r-optiscale	1.1	Tools for performing an optimal scaling transformation on a data vector / GPL-2	noarch
r-optismixture	0.1	Code for optimal mixture weights in importance sampling. Workhorse functions penoptersp() and penoptersp.alpha.only() minimize estimated variances with and without control variates respectively. It can be used in adaptive mixture importance sampling, for example, function batch.estimation() does two stages, a pilot estimate of mixing alpha and a following importance sampling. / GPL-2	noarch
r-optparse	1.6.2	A command line parser inspired by Python's 'optparse' library to be used with Rscript to write #! shebang scripts that accept short and long flag/options. / GPL-2	noarch
r-optr	1.2.5	Solves linear systems of form Ax=b via Gauss elimination, LU decomposition, Gauss-Seidel, Conjugate Gradient Method (CGM) and Cholesky methods. / GPL-2	noarch
r-optrees	1.0	Finds optimal trees in weighted graphs. In particular, this package provides solving tools for minimum cost spanning tree problems, minimum cost arborescence problems, shortest path tree problems and minimum cut tree problem. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-opusminer</a>	0.1_0	Provides a simple R interface to the OPUS Miner algorithm (implemented in C) for finding the top-k productive, non-redundant itemsets from transaction data. The OPUS Miner algorithm uses the OPUS search algorithm to efficiently discover the key associations in transaction data, in the form of self-sufficient itemsets, using either leverage or lift. See <a href="http://i.giwebb.com/index.php/research/association-discovery/">http://i.giwebb.com/index.php/research/association-discovery/</a> for more information in relation to the OPUS Miner algorithm. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-orca</a>	1.1_1	Implements orbit counting using a fast combinatorial approach. Counts orbits of nodes and edges from edge matrix or data frame, or a graph object from the graph package. / LGPL-3	linux-64, osx-64, win-64
<a href="#">r-orclus</a>	0.2_6	Functions to perform subspace clustering and classification. / GPL-2	noarch
<a href="#">r-orcutt</a>	2.3	Solve first order autocorrelation problems using an iterative method. This procedure estimates both autocorrelation and beta coefficients recursively until we reach the convergence (8th decimal as default). The residuals are computed after estimating Beta using EGLS approach and Rho is estimated using the previous residuals. / GPL-2	noarch
<a href="#">r-orddisp</a>	1.0.1	Estimate location-shift models or rating-scale models accounting for response styles (RSRS) for the regression analysis of ordinal responses. / GPL-2	noarch
<a href="#">r-orddom</a>	3.1	Computes ordinal, statistics and effect sizes as an alternative to mean comparison: Cliff's delta or success rate difference (SRD), Vargha and Delaney's A or the Area Under a Receiver Operating Characteristic Curve (AUC), the discrete type of McGraw & Wong's Common Language Effect Size (CLES) or Grissom & Kim's Probability of Superiority (PS), and the Number needed to treat (NNT) effect size. Moreover, comparisons to Cohen's d are offered based on Huberty & Lowman's Percentage of Group (Non-)Overlap considerations. / GPL-2	noarch
<a href="#">r-order2parent</a>	1.0	This package uses B-spline based nonparametric smooth estimators to estimate parent distributions given observations on multiple order statistics. / GPL-2	noarch
<a href="#">r-ordering</a>	0.7.0	Functions to test/check/verify/investigate the ordering of vectors. The 'is_ <b>strictly</b> _*' family of functions test vectors for 'sorted', 'monotonic', 'increasing', 'decreasing' order; 'is_constant' and 'is_incremental' test for the degree of ordering. <i>ordering</i> provides a numeric indication of ordering -2 (strictly decreasing) to 2 (strictly increasing). / GPL-2	noarch
<a href="#">r-orderstats</a>	0.1.0	All the methods in this package generate a vector of uniform order statistics using a beta distribution and use an inverse cumulative distribution function for some distribution to give a vector of random order statistic variables for some distribution. This is much more efficient than using a loop since it is directly sampling from the order statistic distribution. / GPL-2	noarch
<a href="#">r-ordfacreg</a>	1.0.6	In biomedical studies, researchers are often interested in assessing the association between one or more ordinal explanatory variables and an outcome variable, at the same time adjusting for covariates of any type. The outcome variable may be continuous, binary, or represent censored survival times. In the absence of a precise knowledge of the response function, using monotonicity constraints on the ordinal variables improves efficiency in estimating parameters, especially when sample sizes are small. This package implements an active set algorithm that efficiently computes such estimators. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-ordinalclust</a>	1.3.4	Ordinal data classification, clustering and co-clustering using model-based approach with the Bos distribution for ordinal data (Christophe Biernacki and Julien Jacques (2016) <doi:10.1007/s11222-015-9585-2>). / GPL-2	linux-64, osx-64, win-64
<a href="#">r-ordinalcont</a>	2.0.1	A regression framework for response variables which are continuous self-rating scales such as the Visual Analog Scale (VAS) used in pain assessment, or the Linear Analog Self-Assessment (LASA) scales in quality of life studies. These scales measure subjects' perception of an intangible quantity, and cannot be handled as ratio variables because of their inherent non-linearity. We treat them as ordinal variables, measured on a continuous scale. A function (the g function) connects the scale with an underlying continuous latent variable. The link function is the inverse of the CDF of the assumed underlying distribution of the latent variable. A variety of link functions are currently implemented. / GPL-2	noarch
<a href="#">r-ordinalgmifs</a>	1.0.6	Provides a function for fitting cumulative link, adjacent category, forward and backward continuation ratio, and stereotype ordinal response models when the number of parameters exceeds the sample size, using the the generalized monotone incremental forward stagewise method. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-ordinalbm</a>	1.0	It implements functions for simulation and estimation of the ordinal latent block model (OLBM), as described in Corneli, Bouveyron and Latouche (2019). / GPL-2	noarch
<a href="#">r-ordinalnet</a>	2.6	Fits ordinal regression models with elastic net penalty. Supported model families include cumulative probability, stopping ratio, continuation ratio, and adjacent category. These families are a subset of vector glm's which belong to a model class we call the elementwise link multinomial-ordinal (ELMO) class. Each family in this class links a vector of covariates to a vector of class probabilities. Each of these families has a parallel form, which is appropriate for ordinal response data, as well as a nonparallel form that is appropriate for an unordered categorical response, or as a more flexible model for ordinal data. The parallel model has a single set of coefficients, whereas the nonparallel model has a set of coefficients for each response category except the baseline category. It is also possible to fit a model with both parallel and nonparallel terms, which we call the semi-parallel model. The semi-parallel model has the flexibility of the nonparallel model, but the elastic net penalty shrinks it toward the parallel model. For details, refer to Wurm, Hanlon, and Rathouz (2017) <arXiv:1706.05003>. / MIT	noarch
<a href="#">r-ordmonreg</a>	1.0.3	We consider the problem of estimating two isotonic regression curves $g_1^*$ and $g_2^*$ under the constraint that they are ordered, i.e. $g_1^* \leq g_2^*$ . Given two sets of $n$ data points $y_1, \dots, y_n$ and $z_1, \dots, z_n$ that are observed at (the same) deterministic design points $x_1, \dots, x_n$ , the estimates are obtained by minimizing the Least Squares criterion $L(a, b) = \sum_{i=1}^n (y_i - a_i)^2 w_1(x_i) + \sum_{i=1}^n (z_i - b_i)^2 w_2(x_i)$ over the class of pairs of vectors $(a, b)$ such that $a$ and $b$ are isotonic and $a_i \leq b_i$ for all $i = 1, \dots, n$ . We offer two different approaches to compute the estimates: a projected subgradient algorithm where the projection is calculated using a PAVA as well as Dykstra's cyclical projection algorithm. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-ore	1.6.2	Provides an alternative to R's built-in functionality for handling regular expressions, based on the Onigmo library. Offers first-class compiled regex objects, partial matching and function-based substitutions, amongst other features. / BSD_3_clause	linux-64, osx-64, win-64
r-ores	0.3.1	A connector to ORES (< <a href="http://ores.wmflabs.org/">http://ores.wmflabs.org/</a> >), an AI project to provide edit scoring for content on Wikipedia and other Wikimedia projects. This lets a researcher identify if edits are likely to be reverted, damaging, or made in good faith. / MIT	noarch
r-org	2019.4	system to help you organize projects. Most analyses have three (or more) main sections: code, results, and data, each with different requirements (version control/sharing/encryption). You provide folder locations and 'org' helps you take care of the details. / GPL-3	noarch
r-orgmassspectr	0.5.3	Organic/biological mass spectrometry data analysis. / BSD_2_clause	noarch
r-oriclust	1.0.1	ORIClust is a user-friendly R-based software package for gene clustering. Clusters are given by genes matched to prespecified profiles across various ordered treatment groups. It is particularly useful for analyzing data obtained from short time-course or dose-response microarray experiments. / GPL-2	noarch
r-orientlib	0.10.3	Representations, conversions and display of orientation SO(3) data. See the orientlib help topic for details. / GPL-3	noarch
r-orndr	1.3.2	Odds ratio based multifactor-dimensionality reduction method for detecting gene-gene interactions / GPL-2	linux-64, osx-64, win-64
r-orsifronts	0.1.1	A data set package with the Orsi fronts as a 'SpatialLinesDataFrame' object. The Orsi et al. (1995) fronts are published at the Southern Ocean Atlas Database Page, please see package CITATION for details. / GPL-3	noarch
r-orisk	1.0.5	Convert odds ratio to relative risk in cohort studies with partial data information (Wang (2013) <doi:10.18637/jss.v055.i05>). / GPL-2	linux-64, osx-64, win-64
r-orthogonalsplinebasis	0.1.6	Represents the basis functions for B-splines in a simple matrix formulation that facilitates, taking integrals, derivatives, and making orthogonal the basis functions. / GPL-2	noarch
r-orthopanel	1.1.3	Implements the orthogonal reparameterization approach recommended by Lancaster (2002) to estimate dynamic panel models with fixed effects (and optionally: panel specific intercepts). The approach uses a likelihood-based estimator and produces estimates that are asymptotically unbiased as N goes to infinity, with a T as low as 2. / GPL-3	noarch
r-osc	1.0.4	Allows distance based spatial clustering of georeferenced data by implementing the City Clustering Algorithm - CCA. Multiple versions allow clustering for matrix, raster and single coordinates on a plain (euclidean distance) or on a sphere (great-circle or orthodromic distance). / GPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-oscillatorgenerator</a>	0.1.0	The supplied code allows for the generation of discrete time series of oscillating species. General shapes can be selected by means of individual functions, which are widely customizable by means of function arguments. All code was developed in the Biological Information Processing Group at the BioQuant Center at Heidelberg University, Germany. / GPL-3	noarch
<a href="#">r-osdesign</a>	1.7	The osDesign serves for planning an observational study. Currently, functionality is focused on the two-phase and case-control designs. Functions in this packages provides Monte Carlo based evaluation of operating characteristics such as powers for estimators of the components of a logistic regression model. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-osdr</a>	1.1.3	Provides routines for finding an Optimal System of Distinct Representatives (OSDR), as defined by D.Gale (1968) <doi:10.1016/S0021-9800(68)80039-0>. / GPL-2	noarch
<a href="#">r-oshka</a>	0.1.2	Expands quoted language by recursively replacing any symbol that points to quoted language with the language it points to. The recursive process continues until only symbols that point to non-language objects remain. The resulting quoted language can then be evaluated normally. This differs from the traditional ‘quote’/‘eval’ pattern because it resolves intermediate language objects that would interfere with evaluation. / GPL-2	noarch
<a href="#">r-osmose</a>	0.1.1	The multispecies and individual-based model (IBM) ‘OSMOSE’ (Shin and Curry (2001) <doi:10.1016/S0990-7440(01)01106-8> and Shin and Curry (2004) <doi:10.1139/f03-154>) focuses on fish species. This model assumes opportunistic predation based on spatial co-occurrence and size adequacy between a predator and its prey (size-based opportunistic predation). It represents fish individuals grouped into schools, which are characterized by their size, weight, age, taxonomy and geographical location (2D model), and which undergo major processes of fish life cycle (growth, explicit predation, natural and starvation mortalities, reproduction and migration) and fishing exploitation. The model needs basic biological parameters that are often available for a wide range of species, and which can be found in ‘FishBase’ for instance (see < <a href="http://www.fishbase.org/search.php">http://www.fishbase.org/search.php</a> >), and fish spatial distribution data. This package provides tools to build and run simulations using the ‘OSMOSE’ model. / CeCILL	noarch
<a href="#">r-osqp</a>	0.6.0	Provides bindings to the ‘OSQP’ solver. The ‘OSQP’ solver is a numerical optimization package or solving convex quadratic programs written in ‘C’ and based on the alternating direction method of multipliers. See < <a href="https://arxiv.org/abs/1711.08013">arXiv:1711.08013</a> > for details. / Apache License 2.0   file LICENSE	linux-64, osx-64, win-64
<a href="#">r-osrmr</a>	0.1.35	Wrapper around the ‘Open Source Routing Machine (OSRM)’ API < <a href="http://project-osrm.org/">http://project-osrm.org/</a> >. ‘osrmr’ works with API versions 4 and 5 and can handle servers that run locally as well as the ‘OSRM’ webserver. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-ote	1.0	Functions for creating ensembles of optimal trees for regression, classification and class membership probability estimation are given. A few trees are selected from an initial set of trees grown by random forest for the ensemble on the basis of their individual and collective performance. Trees are assessed on out-of-bag data and on an independent training data set for individual and collective performance respectively. The prediction functions return estimates of the test responses and their class membership probabilities. Unexplained variations, error rates, confusion matrix, Brier scores, etc. are also returned for the test data. / GPL-2	noarch
r-otrselect	1.0	A penalized regression framework that can simultaneously estimate the optimal treatment strategy and identify important variables. Appropriate for either censored or uncensored continuous response. / GPL-2	noarch
r-otutable	1.1.2	Analyses of OTU tables produced by 16S rRNA gene amplicon sequencing, as well as example data. It contains the data and scripts used in the paper Linz, et al. (2017) Bacterial community composition and dynamics spanning five years in freshwater bog lakes, <doi: 10.1128/mSphere.00169-17>. / GPL-3	noarch
r-outbreaks	1.5.0	Empirical or simulated disease outbreak data, provided either as RData or as text files. / GPL-2	noarch
r-outlierdc	0.3_0	This package provides three algorithms to detect outlying observations for censored survival data. / GPL-3	noarch
r-outliers	0.14	A collection of some tests commonly used for identifying outliers. / GPL-2	noarch
r-outrankingtools	1.0	Functions to process “outranking” ELECTRE methods existing in the literature. See, e.g., < <a href="http://en.wikipedia.org/wiki/ELECTRE">http://en.wikipedia.org/wiki/ELECTRE</a> > about the outranking approach and the foundations of ELECTRE methods. / GPL-2	noarch
r-overlap	0.3.2	Provides functions to fit kernel density functions to data on temporal activity patterns of animals; estimate coefficients of overlapping of densities for two species; and calculate bootstrap estimates of confidence intervals. / GPL-3	linux-64, osx-64, win-64
r-overture	0.4_0	Simplifies MCMC setup by automatically looping through sampling functions and saving the results. Reduces the memory footprint of running MCMC and saves samples to disk as the chain runs. Allows samples from the chain to be analyzed while the MCMC is still running. Provides functions for commonly performed operations such as calculating Metropolis acceptance ratios and creating adaptive Metropolis samplers. References: Roberts and Rosenthal (2009) <doi:10.1198/jcgs.2009.06134>. / LGPL-3	noarch
r-owea	0.1.1	An implementation of optimal weight exchange algorithm Yang(2013) <doi:10.1080/01621459.2013.806268> for three models. They are Crossover model with subject dropout, crossover model with proportional first order residual effects and interference model. You can use it to find either A-opt or D-opt approximate designs. Exact designs can be automatically rounded from approximate designs and relative efficiency is provided as well. / GPL-3	noarch
r-oxcaar	1.0.0	A set of tools that enables using ‘OxCal’ from within R. ‘OxCal’ (< <a href="https://c14.arch.ox.ac.uk/oxcal.html">https://c14.arch.ox.ac.uk/oxcal.html</a> >) is a standard archaeological tool intended to provide 14C calibration and analysis of archaeological and environmental chronological information. ‘OxcAAR’ allows simple calibration with ‘Oxcal’ and plotting of the results as well as the execution of sophisticated (‘OxCal’) code and the import of the results of bulk analysis and complex Bayesian sequential calibration. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-oxybs	1.5	Provides utilities for processing of Oxy-Bisulfite microarray data (e.g. via the Illumina Infinium platform, < <a href="http://www.illumina.com">http://www.illumina.com</a> >) with tandem arrays, one using conventional bisulfite conversion, the other using oxy-bisulfite conversion. / GPL-2	noarch
r-oz	1.0_2	Functions for plotting Australia's coastline and state boundaries. / GPL-2	noarch
r-p2distance	1.0.1	The welfare's synthetic indicator provides an ideal tool for measuring multi-dimensional concepts such as welfare, development, living standards, etc. It enables information from the various indicators to be aggregated into a single synthetic measure. / GPL-3	noarch
r-p3state.msm	1.3	Analyzing survival data from illness-death model / GPL-3	noarch
r-pabonlasso	1.0	Pabon Lasso is a graphical method for monitoring the efficiency of different wards of a hospital or different hospitals. Pabon Lasso graph is divided into 4 parts which are created after drawing the average of BTR and BOR. The part in the left-down side is Zone I, left-up side is Zone II, Right-up side part is Zone III and the last part is Zone IV. / GPL-2	noarch
r-pacbo	0.1.0	A function for clustering online datasets. The number of cells is data-driven which need not to be chosen in advance by the user. The method is introduced and fully described in Le Li, Benjamin Guedj and Sebastien Loustau (2016), PAC-Bayesian Online Clustering (arXiv preprint: < <a href="https://arxiv.org/abs/1602.00522">https://arxiv.org/abs/1602.00522</a> >). / GPL-2	linux-64, osx-64, win-64
r-pacbpred	0.92	This package is intended to perform estimation and prediction in high-dimensional additive models, using a sparse PAC-Bayesian point of view and a MCMC algorithm. The method is fully described in Guedj and Alquier (2013), 'PAC-Bayesian Estimation and Prediction in Sparse Additive Models', Electronic Journal of Statistics, 7, 264–291. / GPL-2	noarch
r-pack	0.1_1	Functions to easily convert data to binary formats other programs/machines can understand. / GPL-3	noarch
r-packcircles	0.3.3	Simple algorithms for circle packing. / MIT	linux-64, osx-64, win-64
r-packclassic	0.5.2	This package comes to illustrate the book Petit Manuel de Programmation Orientee Objet sous R / GPL (>= 2.0)	noarch
r-packrat	0.5.0	Manage the R packages your project depends on in an isolated, portable, and reproducible way. / GPL-2	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-packs4	0.9.3	Illustration of the book Petit Manuel de Programmation Orientee Objet sous R. The english version A (Not so) Short Introduction to S4 is on CRAN, 'Contributed documentation'. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-pacman	0.5.1	Tools to more conveniently perform tasks associated with add-on packages. pacman conveniently wraps library and package related functions and names them in an intuitive and consistent fashion. It seeks to combine functionality from lower level functions which can speed up workflow. / GPL-2	noarch
r-pact	0.5.0	A prediction-based approach to the analysis of data from randomized clinical trials is implemented. Based on response and covariate data from a randomized clinical trial comparing a new experimental treatment E versus a control C, the objective is to develop and internally validate a model that can identify subjects likely to benefit from E rather than C. Currently, survival and binary response types are permitted. / GPL-3	noarch
r-pade	0.1.4	Given a vector of Taylor series coefficients of sufficient length as input, the function returns the numerator and denominator coefficients for the Padé approximant of appropriate order. / GPL-2   BSD_2_clause	noarch
r-paf	1.0	Calculate unadjusted/adjusted attributable fraction function of a set of covariates for a censored survival outcome from a Cox model using the method proposed by Chen, Lin and Zeng (Biometrika 97, 713-726., 2010). / GPL-2	noarch
r-pagenum	1.1	A simple way to add page numbers to base/ggplot/lattice graphics. / GPL-3	noarch
r-pageviews	0.3.0	Pageview data from the ‘Wikimedia’ sites, such as ‘Wikipedia’ < <a href="https://www.wikipedia.org/">https://www.wikipedia.org/</a> >, from entire projects to per-article levels of granularity, through the new RESTful API and data source < <a href="https://wikimedia.org/api/rest_v1/?doc">https://wikimedia.org/api/rest_v1/?doc</a> >. / MIT	noarch
r-pagi	1.0	The package can identify the dysregulated KEGG pathways based on global influence from the internal effect of pathways and crosstalk between pathways. (1) The Pagi package can prioritize the pathways associated with two biological states by statistical significance or FDR. (2) The Pagi package can evaluate the global influence factor (GIF) score in the global gene-gene network constructed based on the relationships of genes extracted from each pathway in KEGG database and the overlapped genes between pathways. / GPL-2	noarch
r-pagwas	2.0	Bayesian hierarchical methods for pathway analysis of genomewide association data: Normal/Bayes factors and Sparse Normal/Adaptive lasso. The Frequentist Fisher’s product method is included as well. / GPL-2	noarch
r-painter	0.1.0	Functions for creating color palettes, visualizing palettes, modifying colors, and assigning colors for plotting. / GPL-3	noarch
r-paintmap	1.0	Plots matrices of colours as grids of coloured squares - aka heatmaps, guaranteeing legible row and column names, without transformation of values, without re-ordering rows or columns, and without dendrograms. / GPL-2	noarch
r-pairedci	0.5.4	The package contains two functions: paired.Loc and paired.Scale. A parametric and nonparametric confidence interval can be computed for the ratio of locations (paired.Loc) and the ratio of scales (paired.Scale). The samples must be paired and expected values must be positive. / GPL-2	noarch
r-pairheatmap	1.0.1	A tool to compare two heatmaps and discover patterns within and across groups. In the context of biology, group can be defined based on gene ontology. / GPL-2	noarch
r-pairsd3	0.1.0	Creates an interactive scatterplot matrix using the D3 JavaScript library. See < <a href="http://d3js.org/">http://d3js.org/</a> > for more information on D3. / GPL-3	noarch
r-pairwise	0.4.4	Performs the explicit calculation – not estimation! – of the Rasch item parameters for dichotomous and polytomous item responses, using a pairwise comparison approach. Person parameters (WLE) are calculated according to Warm’s weighted likelihood approach. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-pairwised	0.9.62	Pairing observations according to a chosen formula and facilitates bilateral analysis of the panel data. Paring is possible for observations, as well as for vectors of observations ordered with respect to time. / GPL-2	noarch
r-pakpmics2014ch	0.1.0	Provides data set and functions for exploration of Multiple Indicator Cluster Survey (MICS) 2014 Child questionnaire data for Punjab, Pakistan (< <a href="http://www.mics.unicef.org/surveys">http://www.mics.unicef.org/surveys</a> >). / GPL-2	noarch
r-pakpmics2014hh	0.1.0	Provides data set and function for exploration of Multiple Indicator Cluster Survey (MICS) 2014 Household questionnaire data for Punjab, Pakistan (< <a href="http://www.mics.unicef.org/surveys">http://www.mics.unicef.org/surveys</a> >). / GPL-2	noarch
r-pakpmics2014hl	0.1.0	Provides data set and function for exploration of Multiple Indicator Cluster Survey (MICS) 2014 Household Listing questionnaire data for Punjab, Pakistan (< <a href="http://www.mics.unicef.org/surveys">http://www.mics.unicef.org/surveys</a> >). / GPL-2	noarch
r-pakpmics2014wm	0.1.0	Provides data set and function for exploration of Multiple Indicator Cluster Survey (MICS) 2014 Women (age 15-49 years) questionnaire data for Punjab, Pakistan (< <a href="http://www.mics.unicef.org/surveys">http://www.mics.unicef.org/surveys</a> >). / GPL-2	noarch
r-palasso	0.0.5	Implements sparse regression with paired covariates (Rauschenberger et al. 2019). For the optional shrinkage, install ashR (< <a href="https://github.com/stephens999/ashr">https://github.com/stephens999/ashr</a> >) and CorShrink (< <a href="https://github.com/kkdey/CorShrink">https://github.com/kkdey/CorShrink</a> >) from GitHub (see README). / GPL-3	noarch
r-paleobiodb	0.6.0	Includes 19 functions to wrap each endpoint of the PaleobioDB API, plus 8 functions to visualize and process the fossil data. The API documentation for the Paleobiology Database can be found in < <a href="http://paleobiodb.org/data1.1/">http://paleobiodb.org/data1.1/</a> >. / GPL-2	noarch
r-paleomorph	0.1.4	Fill missing symmetrical data with mirroring, calculate Procrustes alignments with or without scaling, and compute standard or vector correlation and covariance matrices (congruence coefficients) of 3D landmarks. Tolerates missing data for all analyses. / MIT	noarch
r-paleots	0.5.2	Facilitates analysis of paleontological sequences of trait values. Functions are provided to fit, using maximum likelihood, simple evolutionary models (including unbiased random walks, directional evolution, stasis, Ornstein-Uhlenbeck, covariate-tracking) and complex models (punctuation, mode shifts). / GPL-3	noarch
r-palettesforr	0.1.2	A set of palettes imported from ‘Gimp’ distributed under GPL3 (< <a href="https://www.gimp.org/about/COPYING">https://www.gimp.org/about/COPYING</a> >), and ‘Inkscape’ distributed under GPL2 (< <a href="https://inkscape.org/about/license/">https://inkscape.org/about/license/</a> >). / GPL-2	noarch
r-palettetown	0.1.1	Use Pokemon(R) inspired palettes with additional ‘ggplot2’ scales. Palettes are the colours in each Pokemon’s sprite, ordered by how common they are in the image. The first 386 Pokemon are currently provided. / MIT	noarch
r-palinsol	0.93	R package to compute Incoming Solar Radiation (insolation) for palaeoclimate studies. Features three solutions: Berger (1978), Berger and Loutre (1991) and Laskar et al. (2004). Computes daily-mean, season-averaged and annual means for all latitudes. / file LICENSE (FOSS)	noarch
r-palr	0.0.6	Colour palettes for data, based on some well known public data sets. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-pameasures	0.1.0	We propose a pair of summary measures for the predictive power of a prediction function based on a regression model. The regression model can be linear or nonlinear, parametric, semi-parametric, or nonparametric, and correctly specified or mis-specified. The first measure, R-squared, is an extension of the classical R-squared statistic for a linear model, quantifying the prediction function's ability to capture the variability of the response. The second measure, L-squared, quantifies the prediction function's bias for predicting the mean regression function. When used together, they give a complete summary of the predictive power of a prediction function. Please refer to Gang Li and Xiaoyan Wang (2016) <arXiv:1611.03063> for more details. / GPL-3	noarch
r-pampe	1.1.2	Implements the Panel Data Approach Method for program evaluation as developed in Hsiao, Ching and Ki Wan (2012). pampe estimates the effect of an intervention by comparing the evolution of the outcome for a unit affected by an intervention or treatment to the evolution of the unit had it not been affected by the intervention. / GPL-2	noarch
r-pamr	1.56	Some functions for sample classification in microarrays. / GPL-2	linux-64, osx-64, win-64
r-pan	1.6	It provides functions and examples for maximum likelihood estimation for generalized linear mixed models and Gibbs sampler for multivariate linear mixed models with incomplete data, as described in Schafer JL (1997) Imputation of missing covariates under a multivariate linear mixed model. Technical report 97-04, Dept. of Statistics, The Pennsylvania State University. / GPL-3	linux-64, osx-64, win-64
r-pander	0.6.3	Contains some functions catching all messages, 'stdout' and other useful information while evaluating R code and other helpers to return user specified text elements (like: header, paragraph, table, image, lists etc.) in 'pandoc' markdown or several type of R objects similarly automatically transformed to markdown format. Also capable of exporting/converting (the resulting) complex 'pandoc' documents to e.g. HTML, 'PDF', 'docx' or 'odt'. This latter reporting feature is supported in brew syntax or with a custom reference class with a smarty caching 'backend'. / AGPL-3	linux-64, osx-64, win-64
r-pandocfilters	0.1_3	The document converter 'pandoc' < <a href="http://pandoc.org/">http://pandoc.org/</a> > is widely used in the R community. One feature of 'pandoc' is that it can produce and consume JSON-formatted abstract syntax trees (AST). This allows to transform a given source document into JSON-formatted AST, alter it by so called filters and pass the altered JSON-formatted AST back to 'pandoc'. This package provides functions which allow to write such filters in native R code. Although this package is inspired by the Python package 'pandocfilters' < <a href="https://github.com/jgm/pandocfilters/">https://github.com/jgm/pandocfilters/</a> >, it provides additional convenience functions which make it simple to use the 'pandocfilters' package as a report generator. Since 'pandocfilters' inherits most of it's functionality from 'pandoc' it can create documents in many formats (for more information see < <a href="http://pandoc.org/">http://pandoc.org/</a> >) but is also bound to the same limitations as 'pandoc'. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-panelaggregation	0.1.1	Aggregate Business Tendency Survey Data (and other qualitative surveys) to time series at various aggregation levels. Run aggregation of survey data in a speedy, re-traceable and a easily deployable way. Aggregation is substantially accelerated by use of data.table. This package intends to provide an interface that is less general and abstract than data.table but rather geared towards survey researchers. / GPL-2	noarch
r-paneldata	1.0	Linear models for panel data: the fixed effect model and the random effect model / Artistic-2.0	noarch
r-panjen	1.6	A central decision in a parametric regression is how to specify the relation between an dependent variable and each explanatory variable. This package provides a semi-parametric tool for comparing different transformations of an explanatory variables in a parametric regression. The functions is relevant in a situation, where you would use a box-cox or Box-Tidwell transformations. In contrast to the classic power-transformations, the methods in this package allows for theoretical driven user input and the possibility to compare with a non-parametric transformation. / GPL-2	noarch
r-paperplanes	0.0.1	This is a data only package, that provides distances from a paper plane experiment. / GPL-3	noarch
r-parade	0.1	Tool for producing Pen's parade graphs, useful for visualizing inequalities in income, wages or other variables, as proposed by Pen (1971, ISBN: 978-0140212594). Income or another economic variable is captured by the vertical axis, while the population is arranged in ascending order of income along the horizontal axis. Pen's income parades provide an easy-to-interpret visualization of economic inequalities. / GPL-2	noarch
r-parallelize.dynamic	0.9_1	Passing a given function name or a call to the parallelize/parallelize_call functions analyses and executes the code, if possible in parallel. Parallel code execution can be performed locally or on remote batch queuing systems. / LGPL-3	noarch
r-parallelmap	1.4	Unified parallelization framework for multiple back-end, designed for internal package and interactive usage. The main operation is parallel mapping over lists. Supports 'local', 'multicore', 'mpi' and 'BatchJobs' mode. Allows tagging of the parallel operation with a level name that can be later selected by the user to switch on parallel execution for exactly this operation. / BSD_2_clause	noarch
r-parallelmcmccombine	1.0	Recent Bayesian Markov chain Monto Carlo (MCMC) methods have been developed for big data sets that are too large to be analyzed using traditional statistical methods. These methods partition the data into non-overlapping subsets, and perform parallel independent Bayesian MCMC analyses on the data subsets, creating independent subposterior samples for each data subset. These independent subposterior samples are combined through four functions in this package, including averaging across subset samples, weighted averaging across subsets samples, and kernel smoothing across subset samples. The four functions assume the user has previously run the Bayesian analysis and has produced the independent subposterior samples outside of the package; the functions use as input the array of subposterior samples. The methods have been demonstrated to be useful for Bayesian MCMC models including Bayesian logistic regression, Bayesian Gaussian mixture models and Bayesian hierarchical Poisson-Gamma models. The methods are appropriate for Bayesian hierarchical models with hyperparameters, as long as data values in a single level of the hierarchy are not split into subsets. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-parallelml</a>	1.2	By sampling your data, running the provided classifier on these samples in parallel on your own machine and letting your models vote on a prediction, we return much faster predictions than the regular machine learning algorithm and possibly even more accurate predictions. / GPL-2	noarch
<a href="#">r-parallelpc</a>	1.2	Parallelise constraint based causality discovery and causal inference methods. The parallelised algorithms in the package will generate the same results as that of the 'pcalg' package but will be much more efficient. / GPL-2	noarch
<a href="#">r-parallelsvm</a>	0.1.9	By sampling your data, running the Support-Vector-Machine algorithm on these samples in parallel on your own machine and letting your models vote on a prediction, we return much faster predictions than the regular Support-Vector-Machine and possibly even more accurate predictions. / GPL-2	noarch
<a href="#">r-params</a>	0.6.1	An interface to simplify organizing parameters used in a package, using external configuration files. This attempts to provide a cleaner alternative to options(). / GPL-2	noarch
<a href="#">r-paramtest</a>	0.1.0	Run simulations or other functions while easily varying parameters from one iteration to the next. Some common use cases would be grid search for machine learning algorithms, running sets of simulations (e.g., estimating statistical power for complex models), or bootstrapping under various conditions. See the 'paramtest' documentation for more information and examples. / GPL-3	noarch
<a href="#">r-paran</a>	1.5.2	An implementation of Horn's technique for numerically and graphically evaluating the components or factors retained in a principle components analysis (PCA) or common factor analysis (FA). Horn's method contrasts eigenvalues produced through a PCA or FA on a number of random data sets of uncorrelated variables with the same number of variables and observations as the experimental or observational data set to produce eigenvalues for components or factors that are adjusted for the sample error-induced inflation. Components with adjusted eigenvalues greater than one are retained. paran may also be used to conduct parallel analysis following Gorfeld's (1995) suggestions to reduce the likelihood of over-retention. / GPL-2	noarch
<a href="#">r-parentoffspring</a>	1.0	Conduct the Parent-Offspring Test Using Monomorphic SNP Markers. The similarity to the parents is computed for each offspring, and a plot of similarity for all offspring is produced. One can keep the offspring above some threshold for the similarity for further studies. / GPL-2	noarch
<a href="#">r-parglm</a>	0.1.3	Provides a parallel estimation method for generalized linear models without compiling with a multithreaded LAPACK or BLAS. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-parmigene</a>	1.0.2	The package provides a parallel estimation of the mutual information based on entropy estimates from k-nearest neighbors distances and algorithms for the reconstruction of gene regulatory networks. / AGPL-3	linux-64, osx-64, win-64
<a href="#">r-parse</a>	0.1.0	Model-based clustering and identifying informative features based on regularization methods. The package includes three regularization methods - PAir-wise Reciprocal fuSE (PARSE) penalty proposed by Wang, Zhou and Hoeting (2016), the adaptive L1 penalty (APL1) and the adaptive pairwise fusion penalty (APFP). Heatmaps are included to shown the identification of informative features. / CC0	noarch

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Name	Version	Summary/License	Platforms
r-parsetools	0.1.1	Tools and utilities for dealing with parse data. Parse data represents the parse tree as data with location and type information. This package provides functions for navigating the parse tree as a data frame. / GPL-2	noarch
r-partdsa	0.9.14	A novel tool for generating a piecewise constant estimation list of increasingly complex predictors based on an intensive and comprehensive search over the entire covariate space. / GPL-2	noarch
r-partiallyoverlapping	2.0	Tests for a comparison of two partially overlapping samples. A comparison of means using the partially overlapping samples t-test: See Derrick, Russ, Toher and White (2017), Test statistics for the comparison of means for two samples which include both paired observations and independent observations, Journal of Modern Applied Statistical Methods, 16(1). A comparison of proportions using the partially overlapping samples z-test: See Derrick, Dobson-Mckittrick, Toher and White (2015), Test statistics for comparing two proportions with partially overlapping samples. Journal of Applied Quantitative Methods, 10(3). / GPL-3	noarch
r-partialor	0.9	Computes Odds Ratio adjusted for a vector of possibly continuous covariates / GPL-2	noarch
r-partitionbefsp	1.0	A collection of functions that can be used to estimate selection and complementarity effects, sensu Loreau & Hector (2001) <doi:10.1038/35083573>, even in cases where data are only available for a random subset of species (i.e. incomplete sample-level data). A full derivation and explanation of the statistical corrections used here is available in Clark et al. (2019) <doi:10.1111/2041-210X.13285>. / GPL-3	noarch
r-partitionmap	0.5	Low-dimensional embedding, using Random Forests for multiclass classification / GPL-3	noarch
r-partitionmetric	1.1	partitionMetric computes a distance between two partitions of a set. / BSD_2_clause	noarch
r-partsm	1.1_2	This package performs basic functions to fit and predict periodic autoregressive time series models. These models are discussed in the book P.H. Franses (1996) Periodicity and Stochastic Trends in Economic Time Series, Oxford University Press. Data set analyzed in that book is also provided. NOTE: the package was orphaned during several years. It is now only maintained, but no major enhancement are expected, and the maintainer cannot provide any support. / GPL-2	noarch
r-party	1.3_3	A computational toolbox for recursive partitioning. The core of the package is ctree(), an implementation of conditional inference trees which embed tree-structured regression models into a well defined theory of conditional inference procedures. This non-parametric class of regression trees is applicable to all kinds of regression problems, including nominal, ordinal, numeric, censored as well as multivariate response variables and arbitrary measurement scales of the covariates. Based on conditional inference trees, cforest() provides an implementation of Breiman's random forests. The function mob() implements an algorithm for recursive partitioning based on parametric models (e.g. linear models, GLMs or survival regression) employing parameter instability tests for split selection. Extensible functionality for visualizing tree-structured regression models is available. The methods are described in Hothorn et al. (2006) <doi:10.1198/106186006X133933>, Zeileis et al. (2008) <doi:10.1198/106186008X319331> and Strobl et al. (2007) <doi:10.1186/1471-2105-8-25>. / GPL-2	linux-64, osx-64, win-64
r-pas	1.2.5	An R package for polygenic trait analysis. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-pass.lme</a>	0.9.0	Power and sample size calculation for testing fixed effect coefficients in multilevel linear mixed effect models with one or more than one independent populations. Laird, Nan M. and Ware, James H. (1982) <doi:10.2307/2529876>. / GPL-3	noarch
<a href="#">r-passport</a>	0.2.0	Smooths the process of working with country names and codes via powerful parsing, standardization, and conversion utilities arranged in a simple, consistent API. Country name formats include multiple sources including the Unicode Common Locale Data Repository (CLDR, < <a href="http://cldr.unicode.org/">http://cldr.unicode.org/</a> >) common-sense standardized names in hundreds of languages. / GPL-3	noarch
<a href="#">r-password</a>	1.0_0	Create random passwords of letters, numbers and punctuation. / GPL-3	noarch
<a href="#">r-pastecs</a>	1.3.21	Regularisation, decomposition and analysis of space-time series. The pastecs R package is a PNEC-Art4 and IFREMER (Benoit Beliaeff < <a href="mailto:Benoit.Beliaeff@ifremer.fr">Benoit.Beliaeff@ifremer.fr</a> >) initiative to bring PASSTEC 2000 functionalities to R. / GPL-2	noarch
<a href="#">r-pastis</a>	0.1_2	A pre-processor for mrBayes that assimilates sequences, taxonomic information and tree constraints as per xxx. The main functions of interest for most users will be <code>pastis_simple</code> , <code>pastis_main</code> and <code>conch</code> . The main analysis is conducted with <code>pastis_simple</code> or <code>pastis_main</code> followed by a manual execution of mrBayes (>3.2). The placement of taxa not contained in the tree constraint can be investigated using <code>conch</code> . / GPL-3	noarch
<a href="#">r-paswr</a>	1.1	Data and functions for the book PROBABILITY and STATISTICS WITH R. / GPL-2	noarch
<a href="#">r-patchdvi</a>	1.9.16	Functions to patch specials in .dvi files, or entries in .synctex files. Works with concordance=TRUE in Sweave or knitr to link sources to previews. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-patchplot</a>	0.1.5	Functions to generate scatterplots with images patches instead of usual glyphs, with associated utilities. / LGPL-3	noarch
<a href="#">r-patchsynctex</a>	0.1_4	This utility eases the debugging of literate documents ('noweb' files) by patching the synchronization information (the '.synctex.gz' file) produced by 'pdflatex' with concordance information produced by 'Sweave' or 'knitr' and 'Sweave' or 'knitr' ; this allows for bilateral communication between a text editor (visualizing the 'noweb' source) and a viewer (visualizing the resultant 'PDF'), thus bypassing the intermediate 'TeX' file. / GPL-2	noarch
<a href="#">r-patentsview</a>	0.2.2	Provides functions to simplify the 'PatentsView' API (< <a href="http://www.patentsview.org/api/doc.html">http://www.patentsview.org/api/doc.html</a> >) query language, send GET and POST requests to the API's seven endpoints, and parse the data that comes back. / MIT	noarch
<a href="#">r-pathlibr</a>	0.1.0	An OO Interface for path manipulation, emulating python's pathlib. / MIT	noarch
<a href="#">r-pathmapping</a>	1.0.2	Functions to compute and display the area-based deviation between spatial paths and to compute a mapping based on minimizing area and distance-based cost. For details, see: Mueller, S. T., Perelman, B. S., & Veinott, E. S. (2016) <DOI:10.3758/s13428-015-0562-7>. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-patternator	0.1.0	Provides a set of functions to efficiently recognize and clean the continuous dorsal pattern of a female brown anole lizard ( <i>Anolis sagrei</i> ) traced from ‘ImageJ’, an open platform for scientific image analysis (see < <a href="https://imagej.net">https://imagej.net</a> > for more information), and extract common features such as the pattern sinuosity indices, coefficient of variation, and max-min width. / GPL-2	noarch
r-pawacc	1.2.2	This is a collection of functions to process, format and store accelerometer data. / GPL-2	noarch
r-pawls	1.0.0	Efficient algorithms for fitting weighted least squares regression with eqn{L_{1}}{L1} regularization on both the coefficients and weight vectors, which is able to perform simultaneous variable selection and outliers detection efficiently. / GPL-2	linux-64, osx-64, win-64
r-paws.common	0.2.0	Functions for making low-level API requests to Amazon Web Services < <a href="https://aws.amazon.com">https://aws.amazon.com</a> >. The functions handle building, signing, and sending requests, and receiving responses. They are designed to help build higher-level interfaces to individual services, such as Simple Storage Service (S3). / Apache License (>= 2.0)	noarch
r-pbapply	1.4_2	A lightweight package that adds progress bar to vectorized R functions (*apply’). The implementation can easily be added to functions where showing the progress is useful (e.g. bootstrap). The type and style of the progress bar (with percentages or remaining time) can be set through options. Supports several parallel processing backends. / GPL-2	noarch
r-pbdncdf4	0.1_4	This package adds collective parallel read and write capability to the R package ncdf4 version 1.8. Typical use is as a parallel NetCDF4 file reader in SPMD style programming. Each R process reads and writes its own data in a synchronized collective mode, resulting in faster parallel performance. Performance improvement is conditional on a parallel file system. / GPL-3	linux-64, osx-64, win-64
r-pbdprof	0.3_1	MPI profiling tools. / Mozilla Public License 2.0	osx-64, win-64
r-pbdrpc	0.2_1	A very light implementation yet secure for remote procedure calls with unified interface via ssh (OpenSSH) or plink/plink.exe (PuTTY). / Mozilla Public License 2.0	linux-64, osx-64, win-64
r-pbdzmq	0.3_3	‘ZeroMQ’ is a well-known library for high-performance asynchronous messaging in scalable, distributed applications. This package provides high level R wrapper functions to easily utilize ‘ZeroMQ’. We mainly focus on interactive client/server programming frameworks. For convenience, a minimal ‘ZeroMQ’ library (4.2.2) is shipped with ‘pbdZMQ’, which can be used if no system installation of ‘ZeroMQ’ is available. A few wrapper functions compatible with ‘rzmq’ are also provided. / GPL-3	linux-32, linux-64, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-pbibd</a>	1.3	The PBIB designs are important type of incomplete block designs having wide area of their applications for example in agricultural experiments, in plant breeding, in sample surveys etc. This package constructs various series of PBIB designs and assists in checking all the necessary conditions of PBIB designs and the association scheme on which these designs are based on. It also assists in calculating the efficiencies of PBIB designs with any number of associate classes. The package also constructs Youden-m square designs which are Row-Column designs for the two-way elimination of heterogeneity. The incomplete columns of these Youden-m square designs constitute PBIB designs. With the present functionality, the package will be of immense importance for the researchers as it will help them to construct PBIB designs, to check if their PBIB designs and association scheme satisfy various necessary conditions for the existence, to calculate the efficiencies of PBIB designs based on any association scheme and to construct Youden-m square designs for the two-way elimination of heterogeneity. R. C. Bose and K. R. Nair (1939) < <a href="http://www.jstor.org/stable/40383923">http://www.jstor.org/stable/40383923</a> >. / GPL-2	noarch
<a href="#">r-pbimisc</a>	1.0	A set of datasets and functions used in the book ‘Modele liniowe i mieszane w R, wraz z przykladami w analizie danych’. Datasets either come from real studies or are created to be as similar as possible to real studies. / GPL-2	noarch
<a href="#">r-pbivnorm</a>	0.6.0	Provides a vectorized R function for calculating probabilities from a standard bivariate normal CDF. / GPL (>= 2)	linux-64, osx-64, win-32, win-64
<a href="#">r-pbkrtest</a>	0.4.7	Test in mixed effects models. Attention is on mixed effects models as implemented in the ‘lme4’ package. This package implements a parametric bootstrap test and a Kenward Roger modification of F-tests for linear mixed effects models and a parametric bootstrap test for generalized linear mixed models. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-pbm</a>	1.1.0	Binding models which are useful when analysing protein-ligand interactions by techniques such as Biolayer Interferometry (BLI) or Surface Plasmon Resonance (SPR). Naman B. Shah, Thomas M. Duncan (2014) < <a href="https://doi.org/10.3791/51383">doi:10.3791/51383</a> >. Hoang H. Nguyen et al. (2015) < <a href="https://doi.org/10.3390/s150510481">doi:10.3390/s150510481</a> >. After initial binding parameters are known, binding curves can be simulated and parameters can be varied. The models within this package may also be used to fit a curve to measured binding data using non-linear regression. / MIT	noarch

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Name	Version	Summary/License	Platforms
r-pbmcapply	1.5.0	A light-weight package helps you track and visualize the progress of parallel version of vectorized R functions (mc*apply). Parallelization (mc.core > 1) works only on *nix (Linux, Unix such as macOS) system due to the lack of fork() functionality, which is essential for mc*apply, on Windows. / MIT	linux-64, osx-64, win-64
r-pbo	1.3.4	Following the method of Bailey et al., computes for a collection of candidate models the probability of backtest overfitting, the performance degradation and probability of loss, and the stochastic dominance. / MIT	noarch
r-pbrackets	1.0	Adds different kinds of brackets to a plot, including braces, chevrons, parentheses or square brackets. / GPL (>= 2.0)	noarch
r-pbrf	1.0.0	Provides three ways to estimate the probability of being in response function (PBRF) The estimates are presented in Tsai, Luo and Crowley (2017) <doi: 10.1007/978-981-10-0126-0_10>. / GPL-2	linux-64, osx-64, win-64
r-pbs	1.1	Periodic B Splines Basis / GPL-2	noarch
r-pbsddesolve	1.12.4	Routines for solving systems of delay differential equations by interfacing numerical routines written by Simon N. Wood , with contributions by Benjamin J. Cairns. These numerical routines first appeared in Simon Wood's 'solv95' program. This package includes a vignette and a complete user's guide. 'PB-Sddesolve' originally appeared on CRAN under the name 'ddesolve'. That version is no longer supported. The current name emphasizes a close association with other PBS packages, particularly 'PBSmodelling'. / GPL-2	linux-64, osx-64, win-64
r-pbsmapping	2.72.1	This software has evolved from fisheries research conducted at the Pacific Biological Station (PBS) in 'Nanaimo', British Columbia, Canada. It extends the R language to include two-dimensional plotting features similar to those commonly available in a Geographic Information System (GIS). Embedded C code speeds algorithms from computational geometry, such as finding polygons that contain specified point events or converting between longitude-latitude and Universal Transverse Mercator (UTM) coordinates. Additionally, we include 'C' code developed by Angus Johnson for the 'Clipper' library, data for a global shoreline, and other data sets in the public domain. Under the user's R library directory '.libPaths()', specifically in './PBSmapping/doc', a complete user's guide is offered and should be consulted to use package functions effectively. / GPL-2	linux-64, osx-64, win-64
r-pbsmodelling	2.68.8	Provides software to facilitate the design, testing, and operation of computer models. It focuses particularly on tools that make it easy to construct and edit a customized graphical user interface ('GUI'). Although our simplified 'GUI' language depends heavily on the R interface to the 'Tcl/Tk' package, a user does not need to know 'Tcl/Tk'. Examples illustrate models built with other R packages, including 'PBSmapping', 'PBSddesolve', and 'BRugs'. A complete user's guide 'PBSmodelling-UG.pdf' shows how to use this package effectively. / GPL-2	linux-64, osx-64, win-64
r-pbv	0.2.1	Computes probabilities of the bivariate normal distribution in a vectorized R function (Drezner & Wesolowsky, 1990, <doi:10.1080/00949659008811236>). / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-pca4ts</a>	0.1	To seek for a contemporaneous linear transformation for a multivariate time series such that the transformed series is segmented into several lower-dimensional subseries, and those subseries are uncorrelated with each other both contemporaneously and serially. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-pcamixdata</a>	3.1	Implements principal component analysis, orthogonal rotation and multiple factor analysis for a mixture of quantitative and qualitative variables. / GPL (>= 2.0)	noarch
<a href="#">r-pcapp</a>	1.9_7	Provides functions for robust PCA by projection pursuit. The methods are described in Croux et al. (2006) <doi:10.2139/ssrn.968376>, Croux et al. (2013) <doi:10.1080/00401706.2012.727746>, Todorov and Filzmoser (2013) <doi:10.1007/978-3-642-33042-1_31>. / GPL (>= 3)	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-pcensmix</a>	1.2_1	Functions for generating progressively Type-II censored data in a mixture structure and fitting models using a constrained EM algorithm. It can also create a progressive Type-II censored version of a given real dataset to be considered for model fitting. / GPL-2	noarch
<a href="#">r-pcfam</a>	1.0	We provide several algorithms to compute the genotype ancestry scores (such as eigenvector projections) in the case where highly correlated individuals are involved. / GPL-2	noarch
<a href="#">r-pcg</a>	1.1	The package solves linear system of equations $Ax=b$ by using Preconditioned Conjugate Gradient Algorithm where A is real symmetric positive definite matrix. A suitable preconditioner matrix may be provided by user. This can also be used to minimize quadratic function $(x'Ax)/2-bx$ for unknown x. / GPL-2	noarch
<a href="#">r-pch</a>	1.3	Using piecewise constant hazards models is a very flexible approach for the analysis of survival data. The time line is divided into sub-intervals; for each interval, a different hazard is estimated using Poisson regression. / GPL-2	noarch
<a href="#">r-pcict</a>	0.5_4	Provides a work-alike to R's POSIXct class which implements 360- and 365-day calendars in addition to the gregorian calendar. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-peirt</a>	0.2.4	Estimates the multidimensional polytomous Rasch model (Rasch, 1961) with conditional maximum likelihood estimation. / GPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-pcit	1.5_3	Apply Partial Correlation coefficient with Information Theory (PCIT) to a correlation matrix. The PCIT algorithm identifies meaningful correlations to define edges in a weighted network. The algorithm can be applied to any correlation-based network including but not limited to gene co-expression networks. To reduce compute time by making use of multiple compute cores, simply run PCIT on a computer with has multiple cores and also has the Rmpi package installed. PCIT will then auto-detect the multicore environment and run in parallel mode without the need to rewrite your scripts. This makes scripts, using PCIT, portable across single core (or no Rmpi package installed) computers which will run in serial mode and multicore (with Rmpi package installed) computers which will run in parallel mode. / GPL-3	linux-64, osx-64, win-64
r-pco	1.0.1	Computation of the Pedroni (1999) panel cointegration test statistics. Reported are the empirical and the standardized values. / GPL-2	noarch
r-pcse	1.9.1	A function to estimate panel-corrected standard errors. Data may contain balanced or unbalanced panels. / GPL-3	noarch
r-pcsirr	0.1.0	Parallel Constraint Satisfaction (PCS) models are an increasingly common class of models in Psychology, with applications to reading and word recognition (McClelland & Rumelhart, 1981), judgment and decision making (Glöckner & Betsch, 2008; Glöckner, Hilbig, & Jekel, 2014), and several other fields (e.g. Read, Vanman, & Miller, 1997). In each of these fields, they provide a quantitative model of psychological phenomena, with precise predictions regarding choice probabilities, decision times, and often the degree of confidence. This package provides the necessary functions to create and simulate basic Parallel Constraint Satisfaction networks within R. / GPL-3	noarch
r-pdc	1.0.3	Permutation Distribution Clustering is a clustering method for time series. Dissimilarity of time series is formalized as the divergence between their permutation distributions. The permutation distribution was proposed as measure of the complexity of a time series. / GPL-3	linux-64, osx-64, win-64
r-pder	1.0_1	Data sets for the Panel Data Econometrics with R <doi:10.1002/9781119504641> book. / GPL-2	noarch
r-pdfestimator	0.1_3	Farmer, J., D. Jacobs (2108) <DOI:10.1371/journal.pone.0196937>. A non-parametric density estimator based on the maximum-entropy method. Accurately predicts a probability density function (PDF) for random data using a novel iterative scoring function to determine the best fit without overfitting to the sample. / GPL-2	linux-64, osx-64, win-64
r-pdftables	0.1	Allows the user to convert PDF tables to formats more amenable to analysis ('.csv', '.xml', or '.xlsx') by wrapping the PDFTables API. In order to use the package, the user needs to sign up for an API account on the PDFTables website (< <a href="https://pdf tables.com/pdf-to-excel-api">https://pdf tables.com/pdf-to-excel-api</a> >). The package works by taking a PDF file as input, uploading it to PDFTables, and returning a file with the extracted data. / CC0	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-pdftools</a>	2.2	Utilities based on ‘libpoppler’ for extracting text, fonts, attachments and meta-data from a PDF file. Also supports high quality rendering of PDF documents into PNG, JPEG, TIFF format, or into raw bitmap vectors for further processing in R. / MIT file LICENSE	linux-64, osx-64, win-32, win-64
<a href="#">r-pdist</a>	1.2	Computes the euclidean distance between rows of a matrix X and rows of another matrix Y. Previously, this could be done by binding the two matrices together and calling ‘dist’, but this creates unnecessary computation by computing the distances between a row of X and another row of X, and likewise for Y. pdist strictly computes distances across the two matrices, not within the same matrix, making computations significantly faster for certain use cases. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-pdm</a>	0.1	Measures real distances in pictures. With PDM() function, you can choose one ‘*.jpg’ file, select the measure in mm of scale, starting and finishing point in the graphical scale, the name of the measure, and starting and finishing point of the measures. After, ask the user for a new measure. / GPL-3	noarch
<a href="#">r-pdsce</a>	1.2	A package to compute and tune some positive definite and sparse covariance estimators / GPL-2	linux-64, osx-64, win-64
<a href="#">r-pdshiny</a>	0.1.0	Interactive shiny application for working with Probability Distributions. Calculations and Graphs are provided. / GPL-2	noarch
<a href="#">r-peacock.test</a>	1.0	The original definition of the two and three dimensional Kolmogorov-Smirnov two-sample test statistics given by Peacock (1983) is implemented. Two R-functions: peacock2 and peacock3, are provided to compute the test statistics in two and three dimensional spaces, respectively. Note the Peacock test is different from the Fasano and Franceschini test (1987). The latter is a variant of the Peacock test. / GPL-2	noarch
<a href="#">r-peacots</a>	1.3	Calculates the periodogram of a time series, maximum-likelihood fits an Ornstein-Uhlenbeck state space (OUSS) null model and evaluates the statistical significance of periodogram peaks against the OUSS null hypothesis. The OUSS is a parsimonious model for stochastically fluctuating variables with linear stabilizing forces, subject to uncorrelated measurement errors. Contrary to the classical white noise null model for detecting cyclicity, the OUSS model can account for temporal correlations typically occurring in ecological and geological time series. / GPL-3	noarch
<a href="#">r-peakerror</a>	2017.06.19	Chromatin immunoprecipitation DNA sequencing results in genomic tracks that show enriched regions or peaks where proteins are bound. This package implements fast C code that computes the true and false positives with respect to a database of annotated regions. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-peakpick</a>	0.11	Biologically inspired methods for detecting peaks in one-dimensional data, such as time series or genomics data. The algorithms were originally designed by Weber, Ramachandran, and Henikoff, see documentation. / MIT	noarch

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Name	Version	Summary/License	Platforms
r-peakram	1.0.2	When working with big data sets, RAM conservation is critically important. However, it is not always enough to just monitor the size of the objects created. So-called copy-on-modify behavior, characteristic of R, means that some expressions or functions may require an unexpectedly large amount of RAM overhead. For example, replacing a single value in a matrix duplicates that matrix in the back-end, making this task require twice as much RAM as that used by the matrix itself. This package makes it easy to monitor the total and peak RAM used so that developers can quickly identify and eliminate RAM hungry code. / GPL-2	noarch
r-peaksegdisk	2019.08.16	Disk-based implementation of Functional Pruning Optimal Partitioning with up-down constraints <arXiv:1810.00117> for single-sample peak calling (independently for each sample and genomic problem), can handle huge data sets ( $10^7$ or more). / GPL-3	linux-64, osx-64, win-64
r-peaksegdp	2017.08.16	Quadratic time dynamic programming algorithm can be used to compute an approximate solution to the problem of finding the most likely changepoints with respect to the Poisson likelihood, subject to a constraint on the number of segments, and the changes which must alternate: up, down, up, down, etc. For more info read < <a href="http://proceedings.mlr.press/v37/hocking15.html">http://proceedings.mlr.press/v37/hocking15.html</a> > PeakSeg: constrained optimal segmentation and supervised penalty learning for peak detection in count data by TD Hocking et al, proceedings of ICML2015. / GPL-3	linux-64, osx-64, win-64
r-pear	1.2	Package for estimating periodic autoregressive models. Datasets: monthly ozone and Fraser riverflow. Plots: periodic versions of boxplot, auto/partial correlations, moving-average expansion. / GPL-2	noarch
r-pearson7	1.0_2	Supports maximum likelihood inference for the Pearson VII distribution with shape parameter 3/2 and free location and scale parameters. This distribution is relevant when estimating the velocity of processive motor proteins with random detachment. / GPL-2	noarch
r-pearsonds	1.1	Implementation of the Pearson distribution system, including full support for the (d,p,q,r)-family of functions for probability distributions and fitting via method of moments and maximum likelihood method. / GPL-2	linux-64, osx-64, win-64
r-pearsonica	1.2_4	The Pearson-ICA algorithm is a mutual information-based method for blind separation of statistically independent source signals. It has been shown that the minimization of mutual information leads to iterative use of score functions, i.e. derivatives of log densities. The Pearson system allows adaptive modeling of score functions. The flexibility of the Pearson system makes it possible to model a wide range of source distributions including asymmetric distributions. The algorithm is designed especially for problems with asymmetric sources but it works for symmetric sources as well. / GPL-2	noarch
r-pedigreemm	0.3_3	Fit pedigree-based mixed-effects models. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-pedigreetools	0.1	Tools to sort, edit and prune pedigrees and to extract the inbreeding coefficients and the relationship matrix (includes code for pedigrees from self-pollinated species). The use of pedigree data is central to genetics research within the animal and plant breeding communities to predict breeding values. The relationship matrix between the individuals can be derived from pedigree structure following the algorithms described for example in Vazquez et al., 2010 <doi:10.2527/jas.2009-1952>. / GPL-3	linux-64, osx-64, win-64
r-pedometrics	0.6.6	Functions to employ many of the tools and techniques used in the field of pedometrics. / GPL-2	linux-64, osx-64, win-64
r-peerperformance	2.2.1	Provides functions to perform the peer performance analysis of funds' returns as described in Ardia and Boudt (2018) <doi:10.1016/j.jbankfin.2017.10.014>. / GPL-2	noarch
r-pegrouptest	1.0	The population proportion using group testing can be estimated by different methods. Four functions including p.mle(), p.gart(), p.burrow() and p.order() are provided to implement four estimating methods including the maximum likelihood estimate, Gart's estimate, Burrow's estimate, and order statistic estimate. / GPL-2	noarch
r-pemm	1.0	This package provides functions to perform multivariate Gaussian parameter estimation based on data with abundance-dependent missingness. It implements a penalized Expectation-Maximization (EM) algorithm. The package is tailored for but not limited to proteomics data applications, in which a large proportion of the data are often missing-not-at-random with lower values (or absolute values) more likely to be missing. / GPL-3	noarch
r-penalized	0.9.5	Fitting possibly high dimensional penalized regression models. The penalty structure can be any combination of an L1 penalty (lasso and fused lasso), an L2 penalty (ridge) and a positivity constraint on the regression coefficients. The supported regression models are linear, logistic and Poisson regression and the Cox Proportional Hazards model. Cross-validation routines allow optimization of the tuning parameters. / GPL-2	linux-64, osx-64, win-64
r-pencoxfrail	1.0.1	A regularization approach for Cox Frailty Models by penalization methods is provided. / GPL-2	linux-64, osx-64, win-64
r-penmsm	0.99	Structured fusion Lasso penalized estimation of multi-state models with the penalty applied to absolute effects and absolute effect differences (i.e., effects on transition-type specific hazard rates). / GPL-2	linux-64, osx-64, win-64
r-pense	1.2.5	Robust penalized elastic net S and MM estimator for linear regression. The method is described in detail in Cohen Freue, G. V., Kepplinger, D., Salibian-Barrera, M., and Smucler, E. (2017) < <a href="https://gcohenfr.github.io/pdfs/PENSE_manuscript.pdf">https://gcohenfr.github.io/pdfs/PENSE_manuscript.pdf</a> >. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-pepsavims</a>	0.9.1	An implementation of the data processing and data analysis portion of a pipeline named the PepSAVI-MS which is currently under development by the Hicks laboratory at the University of North Carolina. The statistical analysis package presented herein provides a collection of software tools used to facilitate the prioritization of putative bioactive peptides from a complex biological matrix. Tools are provided to deconvolute mass spectrometry features into a single representation for each peptide charge state, filter compounds to include only those possibly contributing to the observed bioactivity, and prioritize these remaining compounds for those most likely contributing to each bioactivity data set. / CC BY-NC-SA 4.0	noarch
<a href="#">r-peptides</a>	2.4.1	Includes functions to calculate several physicochemical properties and indices for amino-acid sequences as well as to read and plot 'XVG' output files from the 'GROMACS' molecular dynamics package. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-perc</a>	0.1.3	To find the certainty of dominance interactions with indirect interactions being considered. / GPL-2	noarch
<a href="#">r-perccal</a>	1.0	Contains functions which allow the user to compute confidence intervals quickly using the double bootstrap-based percentile calibrated ('perc-cal') method for linear regression coefficients. 'perccal_interval()' is the primary user-facing function within this package. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-performanceanalytics</a>	1.5.3	Collection of econometric functions for performance and risk analysis. In addition to standard risk and performance metrics, this package aims to aid practitioners and researchers in utilizing the latest research in analysis of non-normal return streams. In general, it is most tested on return (rather than price) data on a regular scale, but most functions will work with irregular return data as well, and increasing numbers of functions will work with P&L or price data where possible. / GPL-2   GPL-3	linux-64, osx-64, win-64
<a href="#">r-periodictable</a>	0.1.2	Provides a dataset containing properties for chemical elements. Helper functions are also provided to access some atomic properties. / GPL-3	noarch
<a href="#">r-perm</a>	1.0_0	Perform Exact or Asymptotic permutation tests / GPL	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-permalgo</a>	1.1	This version of the permutational algorithm generates a dataset in which event and censoring times are conditional on an user-specified list of covariates, some or all of which are time-dependent. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-permallows</a>	1.13	Includes functions to work with the Mallows and Generalized Mallows Models. The considered distances are Kendall's-tau, Cayley, Hamming and Ulam and it includes functions for making inference, sampling and learning such distributions, some of which are novel in the literature. As a by-product, PerMallows also includes operations for permutations, paying special attention to those related with the Kendall's-tau, Cayley, Ulam and Hamming distances. It is also possible to generate random permutations at a given distance, or with a given number of inversions, or cycles, or fixed points or even with a given length on LIS (longest increasing subsequence). / GPL-2	linux-64, osx-64, win-64
<a href="#">r-permdep</a>	1.0.2	Implementations of permutation approach to hypothesis testing for quasi-independence of truncation time and failure time. The implemented approaches are powerful against non-monotone alternatives and thereby offer protection against erroneous assumptions of quasi-independence. The proposed tests use either a conditional or an unconditional method to evaluate the permutation p-value. The conditional method was first developed in Tsai (1980) <doi:10.2307/2336059> and Efron and Petrosian (1992) <doi:10.1086/171931>. The unconditional method provides a valid approximation to the conditional method, yet computationally simpler and does not hold fixed the size of each risk sets. Users also have an option to carry out the proposed permutation tests in a parallel computing fashion. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-permgs</a>	0.2.5	Permutational group-sequential tests for time-to-event data based on the log-rank test statistic. Supports exact permutation test when the censoring distributions are equal in the treatment and the control group and approximate imputation-permutation methods when the censoring distributions are different. / GPL-3	noarch
<a href="#">r-permute</a>	0.9.5	A set of restricted permutation designs for freely exchangeable, line transects (time series), and spatial grid designs plus permutation of blocks (groups of samples) is provided. 'permute' also allows split-plot designs, in which the whole-plots or split-plots or both can be freely-exchangeable or one of the restricted designs. The 'permute' package is modelled after the permutation schemes of 'Canoco 3.1' (and later) by Cajo ter Braak. / GPL-2	noarch
<a href="#">r-persiandictionary</a>	1.0	Translate words from English to Persian (Over 67,000 words) / GPL-2	noarch
<a href="#">r-persianstemmer</a>	1.0	Allows users to stem Persian texts for text analysis. / GPL-2	noarch
<a href="#">r-perturb</a>	2.10	Use the perturb() function to evaluates collinearity by adding random noise to selected variables (Hendrickx & Pelzer 2004). The colldiag function() calculates condition numbers and variance decomposition proportions to test for collinearity and uncover its sources (Belsley 1980). / GPL-2	noarch
<a href="#">r-pesel</a>	0.7.2	Automatic estimation of number of principal components in PCA with PEnalized SEmi-integrated Likelihood (PESEL). See Piotr Sobczyk, Malgorzata Bogdan, Julie Josse 'Bayesian dimensionality reduction with PCA using penalized semi-integrated likelihood' (2017) <doi:10.1080/10618600.2017.1340302>. / GPL-3	noarch
<a href="#">r-pet</a>	0.5.1	Implementation of different analytic/direct and iterative reconstruction methods of radon transformed data such as PET data. It also offer the possibility to simulate PET data. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-petfinder	2.0.0	Wrapper of the ‘Petfinder API’ < <a href="https://www.petfinder.com/developers/v2/docs/">https://www.petfinder.com/developers/v2/docs/</a> > that implements methods for interacting with and extracting data from the ‘Petfinder’ database. The ‘Petfinder REST API’ allows access to the ‘Petfinder’ database, one of the largest online databases of adoptable animals and animal welfare organizations across North America. / MIT	noarch
r-petitr	1.0	Calculates the relative growth rate (RGR) of a series of individuals by building a life table and solving the Lotka-Birch equation. (See Birch, L. C. 1948. The intrinsic rate of natural increase of an insect population. - Journal of Animal Ecology 17: 15-26) <doi:10.2307/1605>. / GPL-2	noarch
r-pgam	0.4.15	This work is an extension of the state space model for Poisson count data, Poisson-Gamma model, towards a semiparametric specification. Just like the generalized additive models (GAM), cubic splines are used for covariate smoothing. The semiparametric models are fitted by an iterative process that combines maximization of likelihood and backfitting algorithm. / GPL-2	linux-64, osx-64, win-64
r-pgbart	0.6.16	The Particle Gibbs sampler and Gibbs/Metropolis-Hastings sampler were implemented to fit Bayesian additive regression tree model. Construction of the model (training) and prediction for a new data set (testing) can be separated. Our reference papers are: Lakshminarayanan B, Roy D, Teh Y W. Particle Gibbs for Bayesian additive regression trees[C], Artificial Intelligence and Statistics. 2015: 553-561, < <a href="http://proceedings.mlr.press/v38/lakshminarayanan15.pdf">http://proceedings.mlr.press/v38/lakshminarayanan15.pdf</a> > and Chipman, H., George, E., and McCulloch R. (2010) Bayesian Additive Regression Trees. The Annals of Applied Statistics, 4,1, 266-298, <doi:10.1214/09-aoas285>. / GPL-2	linux-64, osx-64, win-64
r-pgdraw	1.1	Generates random samples from the Polya-Gamma distribution using an implementation of the algorithm described in J. Windle’s PhD thesis (2013) < <a href="https://repositories.lib.utexas.edu/bitstream/handle/2152/21842/WINDLE-DISSERTATION-2013.pdf">https://repositories.lib.utexas.edu/bitstream/handle/2152/21842/WINDLE-DISSERTATION-2013.pdf</a> >. The underlying implementation is in C. / GPL-3	linux-64, osx-64, win-64
r-pgee	1.5	Fits penalized generalized estimating equations to longitudinal data with high-dimensional covariates. / GPL-2	noarch
r-pgee.mixed	0.1.0	Perform simultaneous estimation and variable selection for correlated bivariate mixed outcomes (one continuous outcome and one binary outcome per cluster) using penalized generalized estimating equations. In addition, clustered Gaussian and binary outcomes can also be modeled. The SCAD, MCP, and LASSO penalties are supported. Cross-validation can be performed to find the optimal regularization parameter(s). / GPL-2	linux-64, osx-64, win-64
r-pgls	0.0_1	Based on the Generalized Least Square model for comparative Phylogenetics (ref). / GPL-2	noarch
<b>r-pgm2</b> < <a href="https://sites.google.com/site/robmccallinfield/">https://sites.google.com/site/robmccallinfield/</a> > >‘_	1.0_1	Construction method of nested resolvable designs from a projective geometry defined on Galois field of order 2. The obtained Resolvable designs are used to build uniform design. The presented results are based on < <a href="https://eudml.org/doc/219563">https://eudml.org/doc/219563</a> > and A. Boudraa et al. (See references). / GPL-3	noarch
r-pgmm	1.2.3	Carries out model-based clustering or classification using parsimonious Gaussian mixture models. McNicholas and Murphy (2008) <doi:10.1007/s11222-008-9056-0>, McNicholas (2010) <doi:10.1016/j.jsps.2009.11.006>, McNicholas and Murphy (2010) <doi:10.1093/bioinformatics/btq498>, McNicholas et al. (2010) <doi:10.1016/j.csda.2009.02.011>. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-pgnorm</a>	2.0	Evaluation of the pdf and the cdf of the univariate, noncentral, p-generalized normal distribution. Sampling from the univariate, noncentral, p-generalized normal distribution using either the p-generalized polar method, the p-generalized rejecting polar method, the Monty Python method, the Ziggurat method or the method of Nardon and Pianca. The package also includes routines for the simulation of the bivariate, p-generalized uniform distribution and the simulation of the corresponding angular distribution. / GPL-2	noarch
<a href="#">r-pgsc</a>	1.0.0	Computes the generalized synthetic control estimator described in Powell (2017) <doi:10.7249/WR1142>. Provides both point estimates, and hypothesis testing. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-ph2bayes</a>	0.0.2	An implementation of Bayesian single-arm phase II design methods for binary outcome based on posterior probability (Thall and Simon (1994) <doi:10.2307/2533377>) and predictive probability (Lee and Liu (2008) <doi:10.1177/1740774508089279>). / GPL-3	linux-64, osx-64, win-64
<a href="#">r-ph2hetero</a>	1.0.2	Implementation of Jones (2007) <doi:10.1016/j.cct.2007.02.008> , Tournoux-Facon (2011) <doi:10.1002/sim.4148> and Parashar (2016) <doi:10.1002/pst.1742> designs. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-ph2mult</a>	0.1.1	Provide multinomial design methods under intersection-union test (IUT) and union-intersection test (UIT) scheme for Phase II trial. The design types include : Minimax (minimize the maximum sample size), Optimal (minimize the expected sample size), Admissible (minimize the Bayesian risk) and Max-power (maximize the exact power level). / GPL-2	noarch
<a href="#">r-phase123</a>	2.1	Contains three simulation functions for implementing the entire Phase 123 trial and the separate Eff-Tox and Phase 3 portions of the trial, which may be beneficial for use on clusters. The functions AssignEffTox() and RandomizeEffTox() assign doses to patient cohorts during phase 12 and Reoptimize() determines the optimal dose to continue with during Phase 3. The functions ReturnMeansAgent() and ReturnMeanControl() gives the true mean survival for the agent doses and control and ReturnOCS() gives the operating characteristics of the design. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-phd</a>	0.1	Provides permutation methods for testing in high-dimensional linear models. The tests are often robust against heteroscedasticity and non-normality and usually perform well under anti-sparsity. See Hemerik and Goeman (2018) <doi:10.1007/s11749-017-0571-1>. / GPL-3	noarch
<a href="#">r-pheatmap</a>	1.0.12	Implementation of heatmaps that offers more control over dimensions and appearance. / GPL-2	noarch
<a href="#">r-phenability</a>	2.0	An alternative to carrying out phenotypic adaptability and stability analyses, taking into account nonparametric statistics. Can be used as a robust approach, less sensitive to departures from common genotypic, environmental, and GxE effects data assumptions (e.g., normal distribution of errors). / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-phenex	1.4.5	Provides some easy-to-use functions for spatial analyses of (plant-) phenological data sets and satellite observations of vegetation. / GPL-2	linux-64, osx-64, win-64
r-pheno	1.6	Provides some easy-to-use functions for time series analyses of (plant-) phenological data sets. These functions mainly deal with the estimation of combined phenological time series and are usually wrappers for functions that are already implemented in other R packages adapted to the special structure of phenological data and the needs of phenologists. Some date conversion functions to handle Julian dates are also provided. / GPL-2	linux-64, osx-64, win-64
r-phenocamapi	0.1.5	A bundle to facilitate working with PhenoCam timeseries and data. The user would be able to obtain phenological time-series and site metadata from the PhenoCam network < <a href="https://phenocam.sr.unh.edu/webcam/">https://phenocam.sr.unh.edu/webcam/</a> >. / AGPL-3	noarch
r-pheval	0.5.4	Provides tools for the evaluation of the goodness of fit and the predictive capacity of the proportional hazards model. / GPL (>= 2.0)	noarch
r-phidelta	1.0.1	Analysis of features by phi delta diagrams. In particular, functions for reading data and calculating phi and delta as well as the functionality to plot it. Moreover it is possible to do further analysis on the data by generating rankings. For more information on phi delta diagrams, see also Giuliano Armano (2015) <doi:10.1016/j.ins.2015.07.028>. / GPL-2	noarch
r-phmm	0.7.1	Fits proportional hazards model incorporating random effects using an EM algorithm using Markov Chain Monte Carlo at E-step. Vaida and Xu (2000) <DOI:10.1002/1097-0258(20001230)19:24%3C3309::AID-SIM825%3E3.0.CO;2-9>. / GPL-3	linux-64, osx-64, win-64
r-phonenum	0.2.2	Convert English letters to numbers or numbers to English letters as on a telephone keypad. When converting letters to numbers, a character vector is returned with A, B, or C becoming 2, D, E, or F becoming 3, etc. When converting numbers to letters, a character vector is returned with multiple elements (i.e., 2 becomes a vector of A, B, and C). / MIT	noarch
r-phonics	1.3.2	Provides a collection of phonetic algorithms including Soundex, Metaphone, NYSIIS, Caverphone, and others. / BSD_2_clause	linux-64, osx-64, win-64
r-phontools	0.2.2	Contains tools for the organization, display, and analysis of the sorts of data frequently encountered in phonetics research and experimentation, including the easy creation of IPA vowel plots, and the creation and manipulation of WAVE audio files. / BSD_2_clause	noarch
r-phreeqc	3.4.10	A geochemical modeling program developed by the US Geological Survey that is designed to perform a wide variety of aqueous geochemical calculations, including speciation, batch-reaction, one-dimensional reactive-transport, and inverse geochemical calculations. / GPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-phtt	3.1.2	The package provides estimation procedures for panel data with large dimensions $n$ , $T$ , and general forms of unobservable heterogeneous effects. Particularly, the estimation procedures are those of Bai (2009) and Kneip, Sickles, and Song (2012), which complement one another very well: both models assume the unobservable heterogeneous effects to have a factor structure. The method of Bai (2009) assumes that the factors are stationary, whereas the method of Kneip et al. (2012) allows the factors to be non-stationary. Additionally, the ‘phtt’ package provides a wide range of dimensionality criteria in order to estimate the number of the unobserved factors simultaneously with the remaining model parameters. / GPL-2	noarch
r-phuassess	1.1	Assessment of habitat selection by means of the permutation-based combination of sign tests (Fattorini et al., 2014 <DOI:10.1007/s10651-013-0250-7>). To exemplify the application of this procedure, habitat selection is assessed for a population of European Brown Hares settled in central Italy. / GPL-2	noarch
r-phuse	0.1.8	Make it easy to review, download and execute scripts stored in Github ‘phuse-scripts’ repository < <a href="https://github.com/phuse-org/phuse-scripts">https://github.com/phuse-org/phuse-scripts</a> >. Some examples included show the web application framework using the script meta-data. The ‘PhUSE’ is Pharmaceutical Users Software Exchange < <a href="http://www.phuse.eu">http://www.phuse.eu</a> >. / MIT	noarch
r-phyclust	0.1_2	Phylogenetic clustering (phyloclustering) is an evolutionary Continuous Time Markov Chain model-based approach to identify population structure from molecular data without assuming linkage equilibrium. The package phyclust (Chen 2011) provides a convenient implementation of phyloclustering for DNA and SNP data, capable of clustering individuals into subpopulations and identifying molecular sequences representative of those subpopulations. It is designed in C for performance, interfaced with R for visualization, and incorporates other popular open source programs including ms (Hudson 2002) <doi:10.1093/bioinformatics/18.2.337>, seq-gen (Rambaut and Grassly 1997) <doi:10.1093/bioinformatics/13.3.235>, Hap-Clustering (Tzeng 2005) <doi:10.1002/gepi.20063> and PAML baseml (Yang 1997, 2007) <doi:10.1093/bioinformatics/13.5.555>, <doi:10.1093/molbev/msm088>, for simulating data, additional analyses, and searching the best tree. See the phyclust website for more information, documentations and examples. / GPL-2	linux-64, osx-64, win-64
r-phylin	2.0	The spatial interpolation of genetic distances between samples is based on a modified kriging method that accepts a genetic distance matrix and generates a map of probability of lineage presence. This package also offers tools to generate a map of potential contact zones between groups with user-defined thresholds in the tree to account for old and recent divergence. Additionally, it has functions for IDW interpolation using genetic data and midpoints. / GPL-2	noarch
r-phyloclim	0.9.5	Implements some methods in phyloclimatic modeling: estimation of ancestral climatic niches, age-range-correlation, niche equivalency test and background-similarity test. / GPL-2	noarch
r-phylogr	1.0.10	Manipulation and analysis of phylogenetically simulated data sets and phylogenetically based analyses using GLS. / GPL-2	noarch
r-phylogram	2.1.0	Contains functions for developing phylogenetic trees as deeply-nested lists (dendrogram objects). Enables bi-directional conversion between dendrogram and phylo objects (see Paradis et al (2004) <doi:10.1093/bioinformatics/btg412>), and features several tools for command-line tree manipulation and import/export via Newick parenthetical text. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-phyloland	1.3	Phyloland package models a space colonization process mapped onto a phylogeny, it aims at estimating limited dispersal and ecological competitive exclusion in a Bayesian MCMC statistical phylogeographic framework (please refer to phyloland-package help for details.) / GPL-2	linux-64, osx-64, win-64
r-phylomeasures	2.1	Given a phylogenetic tree T and an assemblage S of species represented as a subset of tips in T, we want to compute a measure of the diversity of the species in S with respect to T. The current package offers efficient algorithms that can process large phylogenetic data for several such measures. Most importantly, the package includes algorithms for computing efficiently the standardized versions of phylogenetic measures and their p-values, which are essential for null model comparisons. Among other functions, the package provides efficient computation of richness-standardized versions for indices such as the net relatedness index (NRI), nearest taxon index (NTI), phylogenetic diversity index (PDI), and the corresponding indices of two-sample measures. The package also introduces a new single-sample measure, the Core Ancestor Cost (CAC); the package provides functions for computing the value and the standardised index of the CAC and, more than that, there is an extra function available that can compute exactly any statistical moment of the measure. The package supports computations under different null models, including abundance-weighted models. / GPL-3	linux-64, osx-64, win-64
r-phylometrics	0.0.1	Provides functions to estimate statistical errors of phylogenetic metrics particularly to detect binary trait influence on diversification, as well as a function to simulate trees with fixed number of sampled taxa and trait prevalence. / GPL-2	noarch
r-phylotate	1.3	Functions to read and write APE-compatible phylogenetic trees in NEXUS and Newick formats, while preserving annotations. / MIT	noarch
r-phylotools	0.2.2	A collection of tools for building RAxML supermatrix using PHYLIP or aligned FASTA files. These functions will be useful for building large phylogenies using multiple markers. / GPL-2	noarch
r-phyreg	1.0.2	Provides general linear model facilities (single y-variable, multiple x-variables with arbitrary mixture of continuous and categorical and arbitrary interactions) for cross-species data. The method is, however, based on the nowadays rather uncommon situation in which uncertainty about a phylogeny is well represented by adopting a single polytomous tree. The theory is in A. Grafen (1989, Proc. R. Soc. B 326, 119-157) and aims to cope with both recognised phylogeny (closely related species tend to be similar) and unrecognised phylogeny (a polytomy usually indicates ignorance about the true sequence of binary splits). / GPL-2   GPL-3	noarch
r-physactbedrest	1.0	Contains a function to categorize accelerometer readings collected in free-living (e.g., for 24 hours/day for 7 days), preprocessed and compressed as counts (unit-less value) in a specified time period termed epoch (e.g., 1 minute) as either bedrest (sleep) or active. The input is a matrix with a timestamp column and a column with number of counts per epoch. The output is the same dataframe with an additional column termed bedrest. In the bedrest column each line (epoch) contains a function-generated classification 'br' or 'a' denoting bedrest/sleep and activity, respectively. The package is designed to be used after wear/nonwear marking function in the 'PhysicalActivity' package. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-physicalactivity</a>	0.2.2	It provides a function wearingMarking for classification of monitor wear and nonwear time intervals in accelerometer data collected to assess physical activity. The package also contains functions for making plot for accelerometer data and obtaining the summary of various information including daily monitor wear time and the mean monitor wear time during valid days. The revised package version 0.2-1 improved the functions in the previous version regarding speed and robustness. In addition, several functions were added: markDelivery can classify days for ActiGraph delivery by mail; markPAI can categorize physical activity intensity level based on user-defined cut-points of accelerometer counts. It also supports importing ActiGraph AGD files with readActigraph and queryActigraph functions. The package also better supports time zones and daylight saving. / GPL-3	noarch
<a href="#">r-physiology</a>	1.2.1	A variety of formulae are provided for estimation of physiologic characteristics of infants, children, and adults. Calculations include: body surface area, ideal weight, airway dead-space, the alveolar gas equation, and GFR. Each formula is referenced to the original publication. Future functions will cover more material with a focus on anaesthesia, critical care and peri-operative medicine. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-picasso</a>	1.3.1	Computationally efficient tools for fitting generalized linear model with convex or non-convex penalty. Users can enjoy the superior statistical property of non-convex penalty such as SCAD and MCP which has significantly less estimation error and overfitting compared to convex penalty such as lasso and ridge. Computation is handled by multi-stage convex relaxation and the Pathwise CALibrated Sparse Shooting algorithm (PICASSO) which exploits warm start initialization, active set updating, and strong rule for coordinate preselection to boost computation, and attains a linear convergence to a unique sparse local optimum with optimal statistical properties. The computation is memory-optimized using the sparse matrix output. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-pieceexpintensity</a>	1.0.4	This function fits a reversible jump Bayesian piecewise exponential model that also includes the intensity of each event considered along with the rate of events. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-piggyback</a>	0.0.10	Because larger (> 50 MB) data files cannot easily be committed to git, a different approach is required to manage data associated with an analysis in a GitHub repository. This package provides a simple work-around by allowing larger (up to 2 GB) data files to piggyback on a repository as assets attached to individual GitHub releases. These files are not handled by git in any way, but instead are uploaded, downloaded, or edited directly by calls through the GitHub API. These data files can be versioned manually by creating different releases. This approach works equally well with public or private repositories. Data can be uploaded and downloaded programmatically from scripts. No authentication is required to download data from public repositories. / GPL-3	noarch
<a href="#">r-pigshift</a>	1.0.1	Fits models of gene expression evolution to expression data from coregulated groups of genes, assuming inverse gamma distributed rate variation. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-pijavski</a>	1.0	Global univariate minimization of Lipschitz functions is performed by using Pijavski method, which was published in Pijavski (1972) <DOI:10.1016/0041-5553(72)90115-2>. / LGPL-3	linux-64, osx-64, win-64
<a href="#">r-pillar</a>	1.3.1	Provides a ‘pillar’ generic designed for formatting columns of data using the full range of colours provided by modern terminals. / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-pinfsc50</a>	1.1.0	Genomic data for the plant pathogen <i>Phytophthora infestans</i> . It includes a variant file (‘VCF’), a sequence file (‘FASTA’) and an annotation file (‘GFF’). This package is intended to be used as example data for packages that work with genomic data. / GPL-3	noarch
<a href="#">r-pingr</a>	1.1.2	Check if a remote computer is up. It can either just call the system ping command, or check a specified TCP port. / MIT	linux-64, osx-64, win-64
<a href="#">r-pinnacle.api</a>	2.3.3	An interface to the API by Pinnacle that allows Pinnacle customers to interact with the sports market data in R. See < <a href="https://www.pinnacle.com/en/api">https://www.pinnacle.com/en/api</a> > for more information. The Pinnacle API can be used to place wagers, retrieve line information, retrieve account information. Please be aware that the TOC of Pinnacle apply < <a href="https://www.pinnacle.com/en/termsandconditions">https://www.pinnacle.com/en/termsandconditions</a> >. An account with Pinnacle is necessary to use the Pinnacle API. / GPL-3	noarch
<a href="#">r-pinochet</a>	0.1.0	Packages data about the victims of the Pinochet regime as compiled by the Chilean National Commission for Truth and Reconciliation Report (1991, ISBN:9780268016463). / MIT	noarch
<a href="#">r-pinp</a>	0.0.8	A ‘PNAS’-alike style for ‘rmarkdown’, derived from the ‘Proceedings of the National Academy of Sciences of the United States of America’ (‘PNAS’, see < <a href="https://www.pnas.org">https://www.pnas.org</a> >) ‘LaTeX’ style, and adapted for use with ‘markdown’ and ‘pandoc’. / GPL-3	noarch
<a href="#">r-pins</a>	0.1.2	Pin remote resources into a local cache to work offline, improve speed and avoid recomputing; discover and share resources in local folders, ‘GitHub’, ‘Kaggle’ or ‘RStudio Connect’. Resources can be anything from ‘CSV’, ‘JSON’, or image files to arbitrary R objects. / Apache License 2.0	noarch
<a href="#">r-pipefitter</a>	0.1.2	To take nested function calls and convert them to a more readable form using pipes from package ‘magrittr’. / MIT	noarch

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Name	Version	Summary/License	Platforms
r-pipegs	0.4	Code for various permutation p-values estimation methods for gene set test. The description of corresponding methods can be found in the dissertation of Yu He(2016) Efficient permutation P-value estimation for gene set tests < <a href="https://searchworks.stanford.edu/view/11849351">https://searchworks.stanford.edu/view/11849351</a> >. One of the methods also corresponds to the paper Permutation p-value approximation via generalized Stolarsky invariance <arXiv:1603.02757>. / GPL-2	noarch
r-pipeliner	0.1.1	A framework for defining ‘pipelines’ of functions for applying data transformations, model estimation and inverse-transformations, resulting in predicted value generation (or model-scoring) functions that automatically apply the entire pipeline of functions required to go from input to predicted output. / Apache License 2.0	noarch
r-piper	0.6.1	Provides various styles of function chaining methods: Pipe operator, Pipe object, and pipeline function, each representing a distinct pipeline model yet sharing almost a common set of features: A value can be piped to the first unnamed argument of a function and to dot symbol in an enclosed expression. The syntax is designed to make the pipeline more readable and friendly to a wide range of operations. / MIT	noarch
r-pips	1.0.1	Generate Predicted Interval Plots. Simulate and plot confidence intervals of an effect estimate given observed data and a hypothesis about the distribution of future data. / GPL-2	noarch
r-piton	0.1.1	A wrapper around the ‘Parsing Expression Grammar Template Library’, a C11 library for generating Parsing Expression Grammars, that makes it accessible within Repp. With this, developers can implement their own grammars and easily expose them in R packages. / MIT	linux-64, osx-64, win-64
r-pivotalr	0.1.18	Provides an R interface for the Pivotal Data stack running on ‘PostgreSQL’, ‘Greenplum’ or ‘Apache HAWQ (incubating)’ databases with parallel and distributed computation ability for big data processing. ‘PivotalR’ provides an R interface to various database operations on tables or views. These operations are almost the same as the corresponding native R operations. Thus users of R do not need to learn ‘SQL’ when they operate on objects in the database. It also provides a wrapper for ‘Apache MADlib (incubating)’, which is an open-source library for parallel and scalable in-database analytics. / GPL-2	linux-64, osx-64, win-64
r-pivotaltrackr	0.1.0	‘Pivotal Tracker’ < <a href="https://www.pivotaltracker.com">https://www.pivotaltracker.com</a> > is a project management software-as-a-service that provides a REST API. This package provides an R interface to that API, allowing you to query it and work with its responses. / MIT	noarch
r-pixels	0.1.0	Provides tools to show and draw image pixels using ‘HTML’ widgets and ‘Shiny’ applications. It can be used to visualize the ‘MNIST’ dataset for hand-written digit recognition or to create new image recognition datasets. / MIT	noarch
r-pixmap	0.4.1	Functions for import, export, plotting and other manipulations of bitmapped images. / GPL-2	noarch
r-pk	1.3.4	Estimation of pharmacokinetic parameters using non-compartmental theory. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-pkconverter</a>	1.3	Pharmacokinetics is the study of drug absorption, distribution, metabolism, and excretion. The pharmacokinetics model explains that how the drug concentration change as the drug moves through the different compartments of the body. For pharmacokinetic modeling and analysis, it is essential to understand the basic pharmacokinetic parameters. All parameters are considered, but only some of parameters are used in the model. Therefore, we need to convert the estimated parameters to the other parameters after fitting the specific pharmacokinetic model. This package is developed to help this converting work. For more detailed explanation of pharmacokinetic parameters, see Gabrielsson and Weiner (2007), ISBN-10: 9197651001; Benet and Zia-Amirhosseini (1995) <DOI: 10.1177/019262339502300203>; Mould and Upton (2012) <doi:10.1038/psp.2012.4>; Mould and Upton (2013) <doi:10.1038/psp.2013.14>. / GPL-2	noarch
<a href="#">r-pkgbuild</a>	1.0.3	Provides functions used to build R packages. Locates compilers needed to build R packages on various platforms and ensures the PATH is configured appropriately so R can use them. / GPL-3	linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-pkgcond</a>	0.1.0	This provides utilities for creating classed error and warning conditions based on where the error originated. / GPL-2	noarch
<a href="#">r-pkgconfig</a>	2.0.2	Set configuration options on a per-package basis. Options set by a given package only apply to that package, other packages are unaffected. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-pkgdown</a>	1.4.1	Generate an attractive and useful website from a source package. ‘pkgdown’ converts your documentation, vignettes, ‘README’, and more to ‘HTML’ making it easy to share information about your package online. / MIT	noarch
<a href="#">r-pkgkitten</a>	0.1.4	Provides a function kitten() which creates cute little packages which pass R package checks. This sets it apart from package.skeleton() which it calls, and which leaves imperfect files behind. As this is not exactly helpful for beginners, kitten() offers an alternative. / GPL-2	noarch
<a href="#">r-pkgload</a>	1.0.2	Simulates the process of installing a package and then attaching it. This is a key part of the ‘devtools’ package as it allows you to rapidly iterate while developing a package. / GPL-3	linux-64, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
r-pkgmaker	0.27	Provides some low-level utilities to use for package development. It currently provides managers for multiple package specific options and registries, vignette, unit test and bibtex related utilities. It serves as a base package for packages like NMF, RcppOctave, doRNG, and as an incubator package for other general purposes utilities, that will eventually be packaged separately. It is still under heavy development and changes in the interface(s) are more than likely to happen. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-pki	0.1_5	PKI functions such as verifying certificates, RSA encryption and signing which can be used to build PKI infrastructure and perform cryptographic tasks. / GPL-2   GPL-3   file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
r-pkmon	1.0	We implement two least-squares estimators under k-monotony constraint using a method based on the Support Reduction Algorithm from Groeneboom et al (2008) <DOI:10.1111/j.1467-9469.2007.00588.x>. The first one is a projection estimator on the set of k-monotone discrete functions. The second one is a projection on the set of k-monotone discrete probabilities. This package provides functions to generate samples from the spline basis from Lefevre and Loisel (2013) <DOI:10.1239/jap/1378401239>, and from mixtures of splines. / CC BY 4.0	noarch
r-pkpdmodels	0.3.2	Provides functions to evaluate common pharmacokinetic/pharmacodynamic models and their gradients. / GPL-2	noarch
r-pksea	0.0.1	A tool for inferring kinase activity changes from phosphoproteomics data. 'pKSEA' uses kinase-substrate prediction scores to weight observed changes in phosphopeptide abundance to calculate a phosphopeptide-level contribution score, then sums up these contribution scores by kinase to obtain a phosphoproteome-level kinase activity change score (KAC score). 'pKSEA' then assesses the significance of changes in predicted substrate abundances for each kinase using permutation testing. This results in a permutation score (pKSEA significance score) reflecting the likelihood of a similarly high or low KAC from random chance, which can then be interpreted in an analogous manner to an empirically calculated p-value. 'pKSEA' contains default databases of kinase-substrate predictions from 'NetworKIN' (NetworKINPred_db) < <a href="http://networkin.info">http://networkin.info</a> > Horn, et. al (2014) <doi:10.1038/nmeth.2968> and of known kinase-substrate links from 'PhosphoSitePlus' (KSEAdb) < <a href="https://www.phosphosite.org/">https://www.phosphosite.org/</a> > Hornbeck PV, et. al (2015) <doi:10.1093/nar/gku1267>. / MIT	noarch

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Name	Version	Summary/License	Platforms
r-pla	0.2	Parallel Line Assays: Completely randomized design, Randomized Block design, and Latin squares design. Balanced data are fitted as described in the Ph.Eur. In the presence of missing values complete data analysis can be performed (with computation of Fieller's confidence intervals for the estimated potency), or imputation of values can be applied. The package contains a script such that a pdf-document with a report of an analysis of an assay can be produced from an input file with data of the assay. Here no knowledge of R is needed by the user. / GPL-2	noarch
r-plac	0.1.1	A semi-parametric estimation method for the Cox model with left-truncated data using augmented information from the marginal of truncation times. / GPL-3	linux-64, osx-64, win-64
r-plan	0.4.3	Supports the creation of 'burndown' charts and 'gantt' diagrams. / GPL-2	noarch
r-planesmuestra	0.1	Calculates an acceptance sampling plan, (sample size and acceptance number) based in MIL STD 105E, Dodge Romig and MIL STD 414 tables and procedures. The arguments for each function are related to lot size, inspection level and quality level. The specific plan operating curve (OC), is calculated by the binomial distribution. / GPL-2	noarch
r-planets	0.1.0	The goal of 'planets' is to provide of very simple and accessible data containing basic information from all known planets. / MIT	noarch
r-planor	1.5.1	Automatic generation of regular factorial designs, including fractional designs, orthogonal block designs, row-column designs and split-plots. / GPL-2	linux-64, osx-64, win-64
r-plantecophys	1.4.4	Coupled leaf gas exchange model, A-Ci curve simulation and fitting, Ball-Berry stomatal conductance models, leaf energy balance using Penman-Monteith, Cowan-Farquhar optimization, humidity unit conversions. See Duruma (2015) <doi:10.1371/journal.pone.0143346>. / GPL-3	noarch
r-plaqr	2.0	Estimation, prediction, thresholding, transformation, and plotting for partially linear additive quantile regression. Intuitive functions for fitting and plotting partially linear additive quantile regression models. Uses and works with functions from the 'quantreg' package. / GPL-2	noarch
r-playerratings	1.0.3	Implements schemes for estimating player or team skill based on dynamic updating. Implemented methods include Elo, Glicko, Glicko-2 and Stephenson. Contains pdf documentation of a reproducible analysis using approximately two million chess matches. / GPL-3	linux-64, osx-64, win-64
r-plde	0.1.2	We present a penalized log-density estimation method using Legendre polynomials with lasso penalty to adjust estimate's smoothness. Re-expressing the logarithm of the density estimator via a linear combination of Legendre polynomials, we can estimate parameters by maximizing the penalized log-likelihood function. Besides, we proposed an implementation strategy that builds on the coordinate decent algorithm, together with the Bayesian information criterion (BIC). / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-plfm	2.2.2	Functions for estimating probabilistic latent feature models with a disjunctive, conjunctive or additive mapping rule on (aggregated) binary three-way data. / GPL-2	linux-64, osx-64, win-64
r-pliable	1.1	Fits a pliable lasso model. For details see Tibshirani and Friedman (2018) <arXiv:1712.00484>. / GPL-3	linux-64, osx-64, win-64
r-plis	1.1	PLIS is a multiple testing procedure for testing several groups of hypotheses. Linear dependency is expected from the hypotheses within the same group and is modeled by hidden Markov Models. It is noted that, for PLIS, a smaller p value does not necessarily imply more significance because of dependency among the hypotheses. A typical application of PLIS is to analyze genome wide association studies datasets, where SNPs from the same chromosome are treated as a group and exhibit strong linear genomic dependency. / GPL-3	noarch
r-plm	1.7_0	A set of estimators and tests for panel data econometrics. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-pln	0.2_1	Performs bivariate composite likelihood and full information maximum likelihood estimation for polytomous logit-normit (graded logistic) item response theory (IRT) models. / GPL-3	linux-64, osx-64, win-64
r-plogr	0.2.0	A simple header-only logging library for C. Add 'LinkingTo: plogr' to 'DESCRIPTION', and '#include <plogr.h>' in your C modules to use it. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
r-plordprob	1.1	Multivariate ordered probit model, i.e. the extension of the scalar ordered probit model where the observed variables have dimension greater than one. Estimation of the parameters is done via maximization of the pairwise likelihood, a special case of the composite likelihood obtained as product of bivariate marginal distributions. The package uses the Fortran 77 subroutine SADMVN by Alan Genz, with minor adaptations made by Adelchi Azzalini in his mvnrmf package for evaluating the two-dimensional Gaussian integrals involved in the pairwise log-likelihood. Optimization of the latter objective function is performed via quasi-Newton box-constrained optimization algorithm, as implemented in nlminb. / GPL-2	linux-64, osx-64, win-64
r-plot.matrix	1.2	Visualizes a matrix object plainly as heatmap. It provides S3 functions to plot simple matrices and loading matrices. / GPL-3	noarch
r-plotcontour	0.1.0	This function plots a contour line with a user-defined probability and tightness of fit. / GPL-2	noarch
r-plotfunctions	1.3	When analyzing data, plots are a helpful tool for visualizing data and interpreting statistical models. This package provides a set of simple tools for building plots incrementally, starting with an empty plot region, and adding bars, data points, regression lines, error bars, gradient legends, density distributions in the margins, and even pictures. The package builds further on R graphics by simply combining functions and settings in order to reduce the amount of code to produce for the user. As a result, the package does not use formula input or special syntax, but can be used in combination with default R plot functions. Note: Most of the functions were part of the package 'itsadug', which is now split in two packages: 1. the package 'itsadug', which contains the core functions for visualizing and evaluating nonlinear regression models, and 2. the package 'plotfunctions', which contains more general plot functions. / GPL-2	noarch
r-plotly	4.9.0	Create interactive web graphics from 'ggplot2' graphs and/or a custom interface to the (MIT-licensed) JavaScript library 'plotly.js' inspired by the grammar of graphics. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-plotlygeoassets	0.0.2	Includes 'JavaScript' files that allow 'plotly' maps to render without an internet connection. / MIT	noarch
r-plotmcmc	2.0_0	Markov chain Monte Carlo diagnostic plots. The purpose of the package is to combine existing tools from the 'coda' and 'lattice' packages, and make it easy to adjust graphical details. / GPL-2	noarch
r-plotpc	1.0.4	Plot principal component histograms around a bivariate scatter plot. / GPL-3	noarch
r-plotregionhighlighter	1.0	Creates an envelope around a set of plotted points. The envelope is compact with a boundary that is continuous, smooth and convex. Each point is represented as a circle and the circles and connecting lines are the solution to the multiple pulley problem. This method can be used to highlight regions in a two-dimensional space. / GPL-2	noarch
r-plotrix	3.7_6	Lots of plots, various labeling, axis and color scaling functions. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-plotscale	0.1.6	Figures rendered on graphics devices are usually rescaled to fit pre-determined device dimensions. ‘plotscale’ implements the reverse: desired plot dimensions are specified and device dimensions are calculated to accommodate marginal material, giving consistent proportions for plot elements. Default methods support grid graphics such as lattice and ggplot. See example(‘devsize’) and vignette(‘plotscale’). / GPL-3	noarch
r-plotwidgets	0.4	Small self-contained plots for use in larger plots or to delegate plotting in other functions. Also contains a number of alternative color palettes and HSL color space based tools to modify colors or palettes. / GPL (>= 2.0)	noarch
r-plrasch	1.0	Fit Log Linear by Linear Association models and Rasch family models by pseudolikelihood estimation / GPL-2	noarch
r-plrmodels	1.1	This package provides statistical inference tools applied to Partial Linear Regression (PLR) models. Specifically, point estimation, confidence intervals estimation, bandwidth selection, goodness-of-fit tests and analysis of covariance are considered. Kernel-based methods, combined with ordinary least squares estimation, are used and time series errors are allowed. In addition, these techniques are also implemented for both parametric (linear) and nonparametric regression models. / GPL-3	noarch
r-pls	2.7_1	Multivariate regression methods Partial Least Squares Regression (PLSR), Principal Component Regression (PCR) and Canonical Powered Partial Least Squares (CPPLS). / GPL-2	linux-64, noarch, osx-64, win-32, win-64
r-plsbiplot1	0.1	Principal Component Analysis (PCA) biplots, Covariance monoplots and biplots, Partial Least Squares (PLS) biplots, Partial Least Squares for Generalized Linear Model (PLS-GLM) biplots, Sparse Partial Least Squares (SPLS) biplots and Sparse Partial Least Squares for Generalized Linear Model (SPLS-GLM) biplots. / GPL-2	noarch
r-plsdepot	0.1.17	plsdepot contains different methods for PLS analysis of one or two data tables such as Tucker’s Inter-Battery, NIPALS, SIMPLS, SIMPLS-CA, PLS Regression, and PLS Canonical Analysis. The main reference for this software is the awesome book (in French) ‘La Regression PLS: Theorie et Pratique’ by Michel Tenenhaus. / GPL-3	noarch
r-plsdof	0.2_9	The plsdof package provides Degrees of Freedom estimates for Partial Least Squares (PLS) Regression. Model selection for PLS is based on various information criteria (aic, bic, gmdl) or on cross-validation. Estimates for the mean and covariance of the PLS regression coefficients are available. They allow the construction of approximate confidence intervals and the application of test procedures. Further, cross-validation procedures for Ridge Regression and Principal Components Regression are available. / GPL-2	noarch
r-plugdensity	0.8_3	Kernel density estimation with global bandwidth selection via plug-in. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-plumber	0.4.6	Gives the ability to automatically generate and serve an HTTP API from R functions using the annotations in the R documentation around your functions. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-plus	1.0	Efficient procedures for fitting an entire regression sequences with different model types. / GPL-2	noarch
r-pluscode	0.1.0	Retrieves a 'pluscode' by inputting latitude and longitude. Includes additional functions to retrieve neighbouring 'pluscodes'. / GPL-2	noarch
r-plusser	0.4.0	plusser provides an API interface to Google so that posts, profiles and pages can be automatically retrieved. / GPL-3	noarch
r-plyr	1.8.4	A set of tools that solves a common set of problems: you need to break a big problem down into manageable pieces, operate on each piece and then put all the pieces back together. For example, you might want to fit a model to each spatial location or time point in your study, summarise data by panels or collapse high-dimensional arrays to simpler summary statistics. The development of 'plyr' has been generously supported by 'Becton Dickinson'. / MIT file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
r-pmcmmr	4.3	Note, that the 'PMCMR' package is superseded by the novel 'PMCMRplus' package. The 'PMCMRplus' package contains all functions from 'PMCMR' and many more parametric and non-parametric multiple comparison procedures, one-factorial trend tests, as well as improved method functions, such as print, summary and plot. The 'PMCMR' package is no longer maintained, but kept for compatibility of reverse depending packages for some time. / GPL-3	noarch
r-pmml	2.0.0	The Predictive Model Markup Language (PMML) is an XML-based language which provides a way for applications to define machine learning, statistical and data mining models and to share models between PMML compliant applications. More information about the PMML industry standard and the Data Mining Group can be found at < <a href="http://www.dmg.org">http://www.dmg.org</a> >. The generated PMML can be imported into any PMML consuming application, such as Zementis Predictive Analytics products, which integrate with web services, relational database systems and deploy natively on Hadoop in conjunction with Hive, Spark or Storm, as well as allow predictive analytics to be executed for IBM z Systems mainframe applications and real-time, streaming analytics platforms. The package isoform (used for anomaly detection) can be installed with devtools::install_github(Zelazny7/isoform). / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-pmmltransformations	1.3.3	Allows for data to be transformed before using it to construct models. Builds structures to allow functions in the PMML package to output transformation details in addition to the model in the resulting PMML file. The Predictive Model Markup Language (PMML) is an XML-based language which provides a way for applications to define machine learning, statistical and data mining models and to share models between PMML compliant applications. More information about the PMML industry standard and the Data Mining Group can be found at <a href="http://www.dmg.org">http://www.dmg.org</a> . The generated PMML can be imported into any PMML consuming application, such as Zementis Predictive Analytics products, which integrate with web services, relational database systems and deploy natively on Hadoop in conjunction with Hive, Spark or Storm, as well as allow predictive analytics to be executed for IBM z Systems mainframe applications and real-time, streaming analytics platforms. / GPL (>= 2.1)	noarch
r-pmr	1.2.5	Descriptive statistics (mean rank, pairwise frequencies, and marginal matrix), Analytic Hierarchy Process models (with Saaty's and Koczkodaj's inconsistencies), probability models (Luce models, distance-based models, and rank-ordered logit models) and visualization with multidimensional preference analysis for ranking data are provided. Current, only complete rankings are supported by this package. / GPL-2	noarch
r-pmsampsize	1.0.1	Computes the minimum sample size required for the development of a new multivariable prediction model using the criteria proposed by Riley et al. (2018) <doi: 10.1002/sim.7992>. pmsampsize can be used to calculate the minimum sample size for the development of models with continuous, binary or survival (time-to-event) outcomes. Riley et al. (2018) <doi: 10.1002/sim.7992> lay out a series of criteria the sample size should meet. These aim to minimise the overfitting and to ensure precise estimation of key parameters in the prediction model. / GPL-3	noarch
r-pmultinom	1.0.0	Implements multinomial CDF ( $P(N_1 \leq n_1, \dots, N_k \leq n_k)$ ) and tail probabilities ( $P(N_1 > n_1, \dots, N_k > n_k)$ ), as well as probabilities with both constraints ( $P(l_1 < N_1 \leq u_1, \dots, l_k < N_k \leq u_k)$ ). Uses a method suggested by Bruce Levin (1981) <doi:10.1214/aos/1176345593>. / AGPL-3	noarch
r-png	0.1_7	This package provides an easy and simple way to read, write and display bitmap images stored in the PNG format. It can read and write both files and in-memory raw vectors. / GPL-2   GPL-3	linux-32, linux-64, osx-64, win-32, win-64
r-pnmtrem	1.3	An R package for Probit-Normal Marginalized Transition Random Effects Models / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-pnn	1.0.1	The program pnn implements the algorithm proposed by Specht (1990). It is written in the R statistical language. It solves a common problem in automatic learning. Knowing a set of observations described by a vector of quantitative variables, we classify them in a given number of groups. Then, the algorithm is trained with this datasets and should guess afterwards the group of any new observation. This neural network has the main advantage to begin generalization instantaneously even with a small set of known observations. It is delivered with four functions (learn, smooth, perf and guess) and a dataset. The functions are documented with examples and provided with unit tests. / AGPL-3	noarch
r-pocrm	0.12	Provides functions to implement and simulate the partial order continual reassessment method (PO-CRM) of Wages, Conaway and O’Quigley (2011) <doi:10.1177/1740774511408748> for use in Phase I trials of combinations of agents. Provides a function for generating a set of initial guesses (skeleton) for the toxicity probabilities at each combination that correspond to the set of possible orderings of the toxicity probabilities specified by the user. / GPL-2	noarch
r-pod	1.1.4	This tool computes the probability of detection (POD) curve and the limit of detection (LOD), i.e. the number of copies of the target DNA sequence required to ensure a 95 % probability of detection (LOD95). Other quantiles of the LOD can be specified. This is a reimplement of the mathematical-statistical modelling of the validation of qualitative polymerase chain reaction (PCR) methods within a single laboratory as provided by the commercial tool ‘PROLab’ < <a href="http://quodata.de/">http://quodata.de/</a> >. The modelling itself has been described by Uhlig et al. (2015) <doi:10.1007/s00769-015-1112-9>. / GPL-3	noarch
r-poet	2.0	Estimate large covariance matrices in approximate factor models by thresholding principal orthogonal complements. / GPL-2	noarch
r-poibin	1.3	Implementation of both the exact and approximation methods for computing the cdf of the Poisson binomial distribution. It also provides the pmf, quantile function, and random number generation for the Poisson binomial distribution. / GPL-2	linux-64, osx-64, win-64
r-poiclaclu	1.0.2	Implements the methods described in the paper, Witten (2011) Classification and Clustering of Sequencing Data using a Poisson Model, Annals of Applied Statistics 5(4) 2493-2518. / GPL-2	noarch
r-poiilog	0.4	Functions for obtaining the density, random deviates and maximum likelihood estimates of the Poisson lognormal distribution and the bivariate Poisson lognormal distribution. / GPL-3	linux-64, osx-64, win-64
r-pointdensity	0.3.4	The function pointdensity returns a density count and the temporal average for every point in the original list. The dataframe returned includes four columns: lat, lon, count, and date_avg. The lat column is the original latitude data; the lon column is the original longitude data; the count is the density count of the number of points within a radius of radius*grid_size (the neighborhood); and the date_avg column includes the average date of each point in the neighborhood. / MIT	noarch

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Name	Version	Summary/License	Platforms
r-poisbinnonnor	1.3.1	Generation of multiple count, binary and continuous variables simultaneously given the marginal characteristics and association structure. Throughout the package, the word ‘Poisson’ is used to imply count data under the assumption of Poisson distribution. / GPL-2   GPL-3	noarch
r-poisbinom	1.0.1	Provides the probability, distribution, and quantile functions and random number generator for the Poisson-Binomial distribution. This package relies on FFTW to implement the discrete Fourier transform, so that it is much faster than the existing implementation of the same algorithm in R. / GPL-2	linux-64, osx-64, win-64
r-poisdoublesamp	1.1	Functions to create confidence intervals for ratios of Poisson rates under misclassification using double sampling. / GPL-2	linux-64, osx-64, win-64
r-poisnonnor	1.6.1	Generation of count (assuming Poisson distribution) and continuous data (using Fleishman polynomials) simultaneously. / GPL-2   GPL-3	noarch
r-poisnor	1.3.1	Generates multivariate data with count and continuous variables with a pre-specified correlation matrix. The count and continuous variables are assumed to have Poisson and normal marginals, respectively. The data generation mechanism is a combination of the normal to anything principle and a connection between Poisson and normal correlations in the mixture. / GPL-2	noarch
r-poisson	1.0	Contains functions and classes for simulating, plotting and analysing homogeneous and non-homogenous Poisson processes. / GPL-2	noarch
r-poisson.glm.mix	1.2	High dimensional mixtures of Poisson Generalized Linear models with three different parameterizations of Poisson means are considered. Moreover, partitioning the response variables into a set of blocks is possible. The package estimates parameters via EM algorithm. For an efficient initialization, a random splitting small-EM is introduced. / GPL-2	noarch
r-poissonpca	1.0.2	For a multivariate dataset with independent Poisson measurement error, calculates principal components of transformed latent Poisson means. T. Kenney, T. Huang, H. Gu (2019) <arXiv:1904.11745>. / GPL-3	linux-64, osx-64, win-64
r-poissonseq	1.1.2	This package implements a method for normalization, testing, and false discovery rate estimation for RNA-sequencing data. The description of the method is in Li J, Witten DM, Johnstone I, Tibshirani R (2012). Normalization, testing, and false discovery rate estimation for RNA-sequencing data. Biostatistics 13(3): 523-38. We estimate the sequencing depths of experiments using a new method based on Poisson goodness-of-fit statistic, calculate a score statistic on the basis of a Poisson log-linear model, and then estimate the false discovery rate using a modified version of permutation plug-in method. A more detailed instruction as well as sample data is available at <a href="http://www.stanford.edu/~junli07/research.html">http://www.stanford.edu/~junli07/research.html</a> . In this version, we changed the way of calculating log foldchange for two-class data. The FDR estimation part remains unchanged. / GPL-2	noarch
r-poistweedie	1.0	Simulation of models Poisson-Tweedie. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-poker	0.8.8	Type testRoundOfPoker() to demonstrate the game of Texas Hold ~Em poker. Rotate the dealer button, deal cards, rank each hand, compare ranks, break ties (if necessary), determine the winner, output a textual summary, and output a graphical user interface. / GPL-2	noarch
r-polidata	0.1.0	This package provides easy access to various political data APIs directly from R. For example, you can access Google Civic Information API < <a href="https://developers.google.com/civic-information/">https://developers.google.com/civic-information/</a> > or Sunlight Congress API < <a href="https://sunlightlabs.github.io/congress/">https://sunlightlabs.github.io/congress/</a> > for US Congress data, and POPONG API < <a href="http://data.popong.com/">http://data.popong.com/</a> > for South Korea National Assembly data. / MIT	noarch
r-politicaldata	0.1.3	Provides useful functions for obtaining commonly-used data in political analysis and political science, including from sources such as the Comparative Agendas Project < <a href="https://www.comparativeagendas.net/">https://www.comparativeagendas.net/</a> >, which provides data on politics and policy from 20 countries, the MIT Election and Data Science Lab < <a href="https://www.electionlab.mit.edu/">https://www.electionlab.mit.edu/</a> >, and FiveThirtyEight < <a href="https://www.FiveThirtyEight.com/">https://www.FiveThirtyEight.com/</a> >. / MIT	noarch
r-pollstr	2.0.1	Client for the HuffPost Pollster API, which provides access to U.S. polls on elections and political opinion. / GPL-2	noarch
r-polspline	1.1.14	Routines for the polynomial spline fitting routines hazard regression, hazard estimation with flexible tails, logspline, lspec, polyclass, and polymars, by C. Kooperberg and co-authors. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
r-polyaaeppli	2.0	Functions for evaluating the mass density, cumulative distribution function, quantile function and random variate generation for the Polya-Aeppli distribution, also known as the geometric compound Poisson distribution. / GPL-2	noarch
r-polyclip	1.10	R port of Angus Johnson's open source library Clipper. Performs polygon clipping operations (intersection, union, set minus, set difference) for polygonal regions of arbitrary complexity, including holes. Computes offset polygons (spatial buffer zones, morphological dilations, Minkowski dilations) for polygonal regions and polygonal lines. Computes Minkowski Sum of general polygons. There is a function for removing self-intersections from polygon data. / BSL	linux-64, osx-64, win-64
r-polycor	0.7.1	Computes polychoric and polyserial correlations by quick two-step methods or ML, optionally with standard errors; tetrachoric and biserial correlations are special cases. / GPL-2	noarch
r-polycub	0.7.1	Numerical integration of continuously differentiable functions f(x,y) over simple closed polygonal domains. The following cubature methods are implemented: product Gauss cubature (Sommariva and Vianello, 2007, < <a href="https://doi.org/10.1007/s10543-007-0131-2">doi:10.1007/s10543-007-0131-2</a> >), the simple two-dimensional midpoint rule (wrapping 'spatstat' functions), adaptive cubature for radially symmetric functions via line integrate() along the polygon boundary (Meyer and Held, 2014, < <a href="https://doi.org/10.1214/14-AOAS743">doi:10.1214/14-AOAS743</a> >, Supplement B), and integration of the bivariate Gaussian density based on polygon triangulation. For simple integration along the axes, the 'cubature' package is more appropriate. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-polyfreqs	1.0.2	Implements a Gibbs sampling algorithm to perform Bayesian inference on biallelic SNP frequencies, genotypes and heterozygosity (observed and expected) in a population of autopolyploids. See the published paper in Molecular Ecology Resources: Blischak et al. (2016) <doi:10.1111/1755-0998.12493>. / GPL-2	linux-64, osx-64, win-64
r-polylabelr	0.1.0	A wrapper around the C library 'polylabel' from 'Mapbox', providing an efficient routine for finding the approximate pole of inaccessibility of a polygon, which usually serves as an excellent candidate for labeling of a polygon. / MIT	linux-64, osx-64, win-64
r-polynom	1.4_0	A collection of functions to implement a class for univariate polynomial manipulations. / GPL-2	noarch
r-polynomf	2.0_2	Implements univariate polynomial operations in R, including polynomial arithmetic, finding zeros, plotting, and some operations on lists of polynomials. / GPL-2	linux-64, osx-64, win-64
r-polypatex	0.9.2	Functions to perform paternity exclusion via allele matching, in autopolyploid species having ploidy 4, 6, or 8. The marker data used can be genotype data (copy numbers known) or 'allelic phenotype data' (copy numbers not known). / GPL-3	noarch
r-polysat	1.7_4	A collection of tools to handle microsatellite data of any ploidy (and samples of mixed ploidy) where allele copy number is not known in partially heterozygous genotypes. It can import and export data in ABI 'GeneMapper', 'Structure', 'ATetra', 'Tetrasat'/'Tetra', 'GenoDive', 'SPAGeDi', 'POPDIST', 'STRand', and binary presence/absence formats. It can calculate pairwise distances between individuals using a stepwise mutation model or infinite alleles model, with or without taking ploidies and allele frequencies into account. These distances can be used for the calculation of clonal diversity statistics or used for further analysis in R. Allelic diversity statistics and Polymorphic Information Content are also available. polysat can assist the user in estimating the ploidy of samples, and it can estimate allele frequencies in populations, calculate pairwise or global differentiation statistics based on those frequencies, and export allele frequencies to 'SPAGeDi' and 'ade-genet'. Functions are also included for assigning alleles to isoloci in cases where one pair of microsatellite primers amplifies alleles from two or more independently segregating isoloci. polysat is described by Clark and Jasieniuk (2011) <doi:10.1111/j.1755-0998.2011.02985.x> and Clark and Schreier (2017) <doi:10.1111/1755-0998.12639>. / GPL-2	linux-64, osx-64, win-64
r-polysegratio	0.2_5	Perform classic chi-squared tests and Ripol et al(1999) binomial confidence interval approach for autopolyploid dominant markers. Also, dominant markers may be generated for families of offspring where either one or both of the parents possess the marker. Missing values and misclassified markers may be generated at random. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-polytrend	1.2	This algorithm classifies the trends into linear, quadratic, cubic, concealed and no-trend types. The concealed trends are those trends that possess quadratic or cubic forms, but the net change from the start of the time period to the end of the time period hasn't been significant. The no-trend category includes simple linear trends with statistically in-significant slope coefficient. / GPL-2	noarch
r-pomaspu	1.0.0	POM-aSPU test evaluates an association between an ordinal response and multiple phenotypes, for details see Kim and Pan (2017) <DOI:10.1002/gepi.22033>. / GPL-3	linux-64, osx-64, win-64
r-pomdp	0.9.1	Provides an interface to pomdp-solve, a solver for Partially Observable Markov Decision Processes (POMDP). The package enables the user to simply define all components of a POMDP model and solve the problem using several methods. The package also contains functions to analyze and visualize the POMDP solutions (e.g., the optimal policy). / GPL-3	linux-64, osx-64
r-pomic	1.0.4	Calculations of an information criterion are proposed to check the quality of simulations results of Agent-based models (ABM/IBM) or other non-linear rule-based models. The POMDEV measure (Pattern Oriented Modelling Deviance) is based on the Kullback-Leibler divergence and likelihood theory. It basically indicates the deviance of simulation results from field observations. Once POMDEV scores and metropolis-hasting sampling on different model versions are effectuated, POMIC scores (Pattern Oriented Modelling Information Criterion) can be calculated. This method could be further developed to incorporate multiple patterns assessment. Piou C, U Berger and V Grimm (2009) <doi:10.1016/j.ecolmodel.2009.05.003>. / GPL-2	noarch
r-pomp	2.3	Tools for data analysis with partially observed Markov process (POMP) models (also known as stochastic dynamical systems, hidden Markov models, and nonlinear, non-Gaussian, state-space models). The package provides facilities for implementing POMP models, simulating them, and fitting them to time series data by a variety of frequentist and Bayesian methods. It is also a versatile platform for implementation of inference methods for general POMP models. / GPL-3	linux-64, osx-64, win-64
r-pooh	0.3.2	Finds equivalence classes corresponding to a symmetric relation or undirected graph. Finds total order consistent with partial order or directed graph (so-called topological sort). / MIT	linux-64, osx-64, win-64
r-pool	0.1.4	Enables the creation of object pools, which make it less computationally expensive to fetch a new object. Currently the only supported pooled objects are 'DBI' connections. / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
r-pooledmeangroup	1.0	Calculates the pooled mean group (PMG) estimator for dynamic panel data models, as described by Pesaran, Shin and Smith (1999) <doi:10.1080/01621459.1999.10474156>. / GPL-2	noarch
r-poolfstat	1.1.0	Functions for the computation of F-statistics from Pool-Seq data in population genomics studies. The package also includes several utilities to manipulate Pool-Seq data stored in standard format ('vcf' or 'rsync' files generated by the the 'PoPoolation' software) and perform conversion to alternative format (as used in the 'BayPass' and 'SelEstim' software). / GPL-2	noarch
r-pop	0.1	Population dynamic models underpin a range of analyses and applications in ecology and epidemiology. The various approaches for analysing population dynamics models (MPMs, IPMs, ODEs, POMP, PVA) each require the model to be defined in a different way. This makes it difficult to combine different modelling approaches and data types to solve a given problem. 'pop' aims to provide a flexible and easy to use common interface for constructing population dynamic models and enabling them to be fitted and analysed in lots of different ways. / MIT	noarch
r-pop.wolf	0.1	Simulate the dynamic of wolf populations using a specific Individual-Based Model (IBM) compiled in C. / GPL-3	linux-64, osx-64, win-64
r-popbio	2.4.4	Construct and analyze projection matrix models from a demography study of marked individuals classified by age or stage. The package covers methods described in Matrix Population Models by Caswell (2001) and Quantitative Conservation Biology by Morris and Doak (2002). / GPL-3	noarch
r-popdemog	1.0.3	Plot demographic graphs for single/multiple populations from coalescent simulation program input. Currently, this package can support the 'ms', 'msHot', 'MaCS', 'msprime', 'SCRM', and 'Cosi2' simulation programs. It does not check the simulation program input for correctness, but assumes the simulation program input has been validated by the simulation program. More features will be added to this package in the future, please check the 'GitHub' page for the latest updates: < <a href="https://github.com/YingZhou001/POPdemog">https://github.com/YingZhou001/POPdemog</a> >. / GPL-2	noarch
r-popgenkit	1.0	There are two main purposes to this package. The first is to allow batch conversion of Genepop (Rousset 2008) input files for use with Arlequin (Excoffier and Lischer 2010), which has a simple GUI to analyze batch files. Two commonly used simulation software, BottleSim (Kuo & Janzen 2003) and EasyPop (Balloux 2001) produce Genepop output files that can be analyzed this way. There are also functions to convert to and from BottleSim format, to quickly produce allele frequency tables or to convert a file directly for use in ordination analyses (e.g. principal component analysis). This package also includes functions to calculate allele rarefaction curves, confidence intervals on heterozygosity and allelic richness with resampling strategies (bootstrap and jackknife). / GPL-2	noarch
r-popkin	1.2.2	Provides functions to estimate the kinship matrix of individuals from a large set of biallelic SNPs, and extract inbreeding coefficients and the generalized FST (Wright's fixation index). Method described in Ochoa and Storey (2016) <doi:10.1101/083923>. / GPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-popkorn	0.3_0	Provides a suite of tools for various methods of estimating confidence intervals for the mean of selected populations. / MIT	noarch
r-poprange	1.1.3	Runs a forward genetic simulator / MIT	noarch
r-popreconstruct	1.0_5	Implements the Bayesian hierarchical model described by Wheldon, Raftery, Clark and Gerland (see: <doi:10.1080/01621459.2012.737729>) for simultaneously estimating age-specific population counts, fertility rates, mortality rates and net international migration flows, at the national level. / GPL-3	noarch
r-poptrend	0.1.0	Functions to estimate and plot smooth or linear population trends, or population indices, from animal or plant count survey data. / GPL-3	noarch
r-population	0.2	Run population simulations using an Individual-Based Model (IBM) compiled in C. / GPL-3	linux-64, osx-64, win-64
r-portfolio	0.4_7	Classes for analysing and implementing equity portfolios. / GPL-2	noarch
r-portsort	0.1.0	Designed to aid both academic researchers and asset managers in conducting factor based portfolio sorts. Provides functionality to sort assets into portfolios for up to three factors via a conditional or unconditional sorting procedure. / GPL-2	noarch
r-posi	1.0	In linear LS regression, calculate for a given design matrix the multiplier K of coefficient standard errors such that the confidence intervals [b - K*SE(b), b + K*SE(b)] have a guaranteed coverage probability for all coefficient estimates b in any submodels after performing arbitrary model selection. / GPL-3	noarch
r-postcodesior	0.1.1	Free UK geocoding using data from Office for National Statistics. It is using several functions to get information about post codes, outward codes, reverse geocoding, nearest post codes/outward codes, validation, or randomly generate a post code. API wrapper around < <a href="https://postcodes.io">https://postcodes.io</a> >. / GPL-3	noarch
r-postinfectious	0.1.0	Functions to estimate the incubation period distribution of post-infectious syndrome which is defined as the time between the symptom onset of the antecedent infection and that of the post-infectious syndrome. / GPL-2	noarch
r-postlogic	0.1.0	Provides adds postfix and infix logic operators for if, then, unless, and otherwise. / GPL-2	noarch
r-pot	1.1_7	Some functions useful to perform a Peak Over Threshold analysis in univariate and bivariate cases, see Beirlant et al. (2004) <doi:10.1002/0470012382>. A user's guide is available. / GPL-2	linux-64, osx-64, win-64
r-potts	0.5_8	Do Markov chain Monte Carlo (MCMC) simulation of Potts models (Potts, 1952, <doi:10.1017/S0305004100027419>), which are the multi-color generalization of Ising models (so, as a special case, also simulates Ising models). Use the Swendsen-Wang algorithm (Swendsen and Wang, 1987, <doi:10.1103/PhysRevLett.58.86>) so MCMC is fast. Do maximum composite likelihood estimation of parameters (Besag, 1975, <doi:10.2307/2987782>, Lindsay, 1988, <doi:10.1090/conm/080>). / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-power	1.0.7	Functions for the computation of power and level tables for hypothesis tests, in Latex format, functions to build explanatory graphs for studying power of test statistics. / GPL-2	linux-64, osx-64, win-64
r-poweranalysis	0.2.1	Basic functions for power analysis and effect size calculation. / GPL-2	noarch
r-powercomprisk	1.0.1	A power analysis tool for jointly testing the cause-1 cause-specific hazard and the any-cause hazard with competing risks data. / GPL-2	noarch
r-powerfulmaxeigenpair	0.1.0	An implementation for using powerful algorithm to compute the maximal eigenpair of Hermitizable tridiagonal matrices in R. It provides two algorithms to find the maximal and the next to maximal eigenpairs under the tridiagonal matrix. Besides, it also provides two auxiliary algorithms to generate tridiagonal matrix and solve the linear equation by Thomas algorithm. Several examples are included in the vignettes to illustrate the usage of the functions. / MIT	noarch
r-powerlaw	0.70.2	An implementation of maximum likelihood estimators for a variety of heavy tailed distributions, including both the discrete and continuous power law distributions. Additionally, a goodness-of-fit based approach is used to estimate the lower cut-off for the scaling region. / GPL-2   GPL-3	noarch
r-powerlmm	0.4.0	Calculate power for the ‘time x treatment’ effect in two- and three-level multilevel longitudinal studies with missing data. Both the third-level factor (e.g. therapists, schools, or physicians), and the second-level factor (e.g. subjects), can be assigned random slopes. Studies with partially nested designs, unequal cluster sizes, unequal allocation to treatment arms, and different dropout patterns per treatment are supported. For all designs power can be calculated both analytically and via simulations. The analytical calculations extends the method described in Galbraith et al. (2002) <doi:10.1016/S0197-2456(02)00205-2>, to three-level models. Additionally, the simulation tools provides flexible ways to investigate bias, Type I errors and the consequences of model misspecification. / GPL-3	noarch
r-powermediation	0.2.9	Functions to calculate power and sample size for testing (1) mediation effects; (2) the slope in a simple linear regression; (3) odds ratio in a simple logistic regression; (4) mean change for longitudinal study with 2 time points; (5) interaction effect in 2-way ANOVA; and (6) the slope in a simple Poisson regression. / GPL-2	noarch
r-powernormal	1.2.0	Miscellaneous functions for a descriptive analysis and initial Bayesian and classical inference for the power parameter of the the Power Normal (PN) distribution. This miscellaneous will be extend for more distributions into the power family and the three-parameter model. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-powerpkg	1.5	(1) To estimate the power of testing for linkage using an affected sib pair design, as a function of the recurrence risk ratios. We will use analytical power formulae as implemented in R. These are based on a Mathematica notebook created by Martin Farrall. (2) To examine how the power of the transmission disequilibrium test (TDT) depends on the disease allele frequency, the marker allele frequency, the strength of the linkage disequilibrium, and the magnitude of the genetic effect. We will use an R program that implements the power formulae of Abel and Muller-Myhsok (1998). These formulae allow one to quickly compute power of the TDT approach under a variety of different conditions. This R program was modeled on Martin Farrall's Mathematica notebook. / GPL-2	noarch
r-powersurvepi	0.1.0	Functions to calculate power and sample size for testing main effect or interaction effect in the survival analysis of epidemiological studies (non-randomized studies), taking into account the correlation between the covariate of the interest and other covariates. Some calculations also take into account the competing risks and stratified analysis. This package also includes a set of functions to calculate power and sample size for testing main effect in the survival analysis of randomized clinical trials. / GPL-2	noarch
r-powerupr	1.0.4	Includes tools to calculate statistical power, minimum detectable effect size (MDES), MDES difference (MDESd), and minimum required sample size for various multilevel randomized experiments with continuous outcomes. Some of the functions can assist with planning two- and three-level cluster-randomized trials (CRTs) sensitive to multilevel moderation and mediation (2-1-1, 2-2-1, and 3-2-1). See 'PowerUp!' Excel series at < <a href="https://www.causalevaluation.org/">https://www.causalevaluation.org/</a> >. / GPL-3	noarch
r-pp	0.6.2	The PP package includes estimation of (MLE, WLE, MAP, EAP, ROBUST) person parameters for the 1,2,3,4-PL model and the GPCM (generalized partial credit model). The parameters are estimated under the assumption that the item parameters are known and fixed. The package is useful e.g. in the case that items from an item pool / item bank with known item parameters are administered to a new population of test-takers and an ability estimation for every test-taker is needed. / GPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-pp3</a>	1.2	Exploratory projection pursuit is a method to discovers structure in multivariate data. At heart this package uses a projection index to evaluate how interesting a specific three-dimensional projection of multivariate data (with more than three dimensions) is. Typically, the main structure finding algorithm starts at a random projection and then iteratively changes the projection direction to move to a more interesting one. In other words, the projection index is maximised over the projection direction to find the most interesting projection. This maximum is, though, a local maximum. So, this code has the ability to restart the algorithm from many different starting positions automatically. Routines exist to plot a density estimate of projection indices over the runs, this enables the user to obtain an idea of the distribution of the projection indices, and, hence, which ones might be interesting. Individual projection solutions, including those identified as interesting, can be extracted and plotted individually. The package can make use of the <code>mclapply()</code> function to execute multiple runs in parallel to speed up index discovery. Projection pursuit is similar to independent component analysis. This package uses a projection index that maximises an entropy measure to look for projections that exhibit non-normality, and operates on sphered data. Hence, information from this package is different from that obtained from principal components analysis, but the rationale behind both methods is similar. Nason, G. P. (1995) <doi:10.2307/2986135>. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-ppcc</a>	1.1	Calculates the Probability Plot Correlation Coefficient (PPCC) between a continuous variable X and a specified distribution. The corresponding composite hypothesis test that was first introduced by Filliben (1975) <doi: 10.1080/00401706.1975.10489279> can be performed to test whether the sample X is element of either the Normal, log-Normal, Exponential, Uniform, Cauchy, Logistic, Generalized Logistic, Gumbel (GEVI), Weibull, Generalized Extreme Value, Pearson III (Gamma 2), Mielke's Kappa, Rayleigh or Generalized Logistic Distribution. The PPCC test is performed with a fast Monte-Carlo simulation. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-ppcor</a>	1.1	Calculates partial and semi-partial (part) correlations along with p-value. / GPL-2	noarch
<a href="#">r-ppls</a>	1.6_1	Contains linear and nonlinear regression methods based on Partial Least Squares and Penalization Techniques. Model parameters are selected via cross-validation, and confidence intervals and tests for the regression coefficients can be conducted via jackknifing. / GPL-2	noarch
<a href="#">r-ppmr</a>	1.0	Efficient statistical inference of two-sample MR (Mendelian Randomization) analysis. It can account for the correlated instruments and the horizontal pleiotropy, and can provide the accurate estimates of both causal effect and horizontal pleiotropy effect as well as the two corresponding p-values. There are two main functions in the 'PPMR' package. One is <code>PMR_individual()</code> for individual level data, the other is <code>PMR_summary()</code> for summary data. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-pps</a>	0.94	The pps package contains functions to select samples using PPS (probability proportional to size) sampling. It also includes a function for stratified simple random sampling, a function to compute joint inclusion probabilities for Sampford's method of PPS sampling, and a few utility functions. The user's guide <code>pps-ug.pdf</code> is included. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-pqantimalarials</a>	0.2	This package allows users to calculate the number of under-five child deaths caused by consumption of poor quality antimalarials across 39 sub-Saharan nations. The package supports one function, that starts an interactive web tool created using the shiny R package. The web tool runs locally on the user's machine. The web tool allows users to set input parameters (prevalence of poor quality antimalarials, case fatality rate of children who take poor quality antimalarials, and sample size) which are then used to perform an uncertainty analysis following the Latin hypercube sampling scheme. Users can download the output figures as PDFs, and the output data as CSVs. Users can also download their input parameters for reference. This package was designed to accompany the analysis presented in: J. Patrick Renschler, Kelsey Walters, Paul Newton, Ramanan Laxminarayan Estimated under-five deaths associated with poor-quality antimalarials in sub-Saharan Africa, 2014. Paper submitted. / GPL-3	noarch
<a href="#">r-pqlseq</a>	1.1	An efficient tool designed for differential analysis of large-scale RNA sequencing (RNAseq) data and Bisulfite sequencing (BSseq) data in the presence of individual relatedness and population structure. 'PQLseq' first fits a Generalized Linear Mixed Model (GLMM) with adjusted covariates, predictor of interest and random effects to account for population structure and individual relatedness, and then performs Wald tests for each gene in RNAseq or site in BSseq. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-pracma</a>	2.2.5	Provides a large number of functions from numerical analysis and linear algebra, numerical optimization, differential equations, time series, plus some well-known special mathematical functions. Uses 'MATLAB' function names where appropriate to simplify porting. / GPL-3	noarch
<a href="#">r-practools</a>	1.2	Functions and datasets to support Valliant, Dever, and Kreuter, "Practical Tools for Designing and Weighting Survey Samples" (2nd edition, 2018). Contains functions for sample size calculation for survey samples using stratified or clustered one-, two-, and three-stage sample designs. Other functions compute variance components for multistage designs and sample sizes in two-phase designs. A number of example data sets are included. / GPL-2	noarch
<a href="#">r-pragma</a>	0.1.3	pragma allows for the use of pragma (also sometimes called directives or keywords. These allow assigning arbitrary functionality to a word without requiring the standard function call syntax i.e. with parens. / GPL-2	noarch
<a href="#">r-prais</a>	1.1.1	The Prais-Winsten estimator (Prais & Winsten, 1954) takes into account AR(1) serial correlation of the errors in a linear regression model. The procedure recursively estimates the coefficients and the error autocorrelation of the specified model until sufficient convergence of the AR(1) coefficient is attained. / GPL-2	noarch
<a href="#">r-praise</a>	1.0.0	Build friendly R packages that praise their users if they have done something good, or they just need it to feel better. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
r-praktikum	0.1	Kasulikud funktsioonid kvantitatiivsete mudelite kursuse (SHPH.00.004) jaoks / GPL-2	noarch
r-praznik	6.0.0	A collection of feature selection filters performing greedy optimisation of mutual information-based usefulness criteria, inspired by the overview by Brown, Pocock, Zhao and Lujan (2012) < <a href="http://www.jmlr.org/papers/v13/brown12a.html">http://www.jmlr.org/papers/v13/brown12a.html</a> >. Implements, among other, minimum redundancy maximal relevancy ('mRMR') method by Peng, Long and Ding (2005) <doi:10.1109/TPAMI.2005.159>; joint mutual information ('JMI') method by Yang and Moody (1999) < <a href="http://papers.nips.cc/paper/1779-data-visualization-and-feature-selection-new-algorithms-for-nongaussian-data">http://papers.nips.cc/paper/1779-data-visualization-and-feature-selection-new-algorithms-for-nongaussian-data</a> >; double input symmetrical relevance ('DISR') method by Meyer and Bontempi (2006) <doi:10.1007/11732242_9> as well as joint mutual information maximisation ('JMIM') method by Bennasar, Hicks and Setchi (2015) <doi:10.1016/j.eswa.2015.07.007>. / GPL-3	linux-64, osx-64, win-64
r-prclust	1.3	Clustering is unsupervised and exploratory in nature. Yet, it can be performed through penalized regression with grouping pursuit. In this package, we provide two algorithms for fitting the penalized regression-based clustering (PRclust) with non-convex grouping penalties, such as group truncated lasso, MCP and SCAD. One algorithm is based on quadratic penalty and difference convex method. Another algorithm is based on difference convex and ADMM, called DC-ADD, which is more efficient. Generalized cross validation and stability based method were provided to select the tuning parameters. Rand index, adjusted Rand index and Jaccard index were provided to estimate the agreement between estimated cluster memberships and the truth. / GPL-2   GPL-3	linux-64, osx-64, win-64
r-precisesums	0.3	Most of the time floating point arithmetic does approximately the right thing. When adding sums or having products of numbers that greatly differ in magnitude, the floating point arithmetic may be incorrect. This package implements the Kahan (1965) sum <doi:10.1145/363707.363723>, Neumaier (1974) sum <doi:10.1002/zamm.19740540106>, pairwise-sum (adapted from 'NumPy', See Castaldo (2008) <doi:10.1137/070679946> for a discussion of accuracy), and arbitrary precision sum (adapted from the fsum in 'Python'; Shewchuk (1997) < <a href="http://www.cs.berkeley.edu/~jrs/papers/robustr.pdf">http://www.cs.berkeley.edu/~jrs/papers/robustr.pdf</a> >). In addition, products are changed to long double precision for accuracy, or changed into a log-sum for accuracy. / GPL-2	linux-64, osx-64, win-64
r-prediction	0.3.14	A one-function package containing 'prediction()', a type-safe alternative to 'predict()' that always returns a data frame. The 'summary()' method provides a data frame with average predictions, possibly over counterfactual versions of the data (a la the 'margins' command in 'Stata'). Marginal effect estimation is provided by the related package, 'margins' < <a href="https://cran.r-project.org/package=margins">https://cran.r-project.org/package=margins</a> >. The package currently supports common model types (e.g., lm, glm) from the 'stats' package, as well as numerous other model classes from other add-on packages. See the README or main package documentation page for a complete listing. / MIT	noarch
r-predictiveregression	0.1_4	Three prediction algorithms described in the paper On-line predictive linear regression Annals of Statistics 37, 1566 - 1590 (2009) / file LICENSE (Restricts use)	noarch

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Name	Version	Summary/License	Platforms
r-predkmeans	0.1.0	Implements the predictive k-means method for clustering observations, using a mixture of experts model to allow covariates to influence cluster centers. Motivated by air pollution epidemiology settings, where cluster membership needs to be predicted across space. Includes functions for predicting cluster membership using spatial splines and principal component analysis (PCA) scores using either multinomial logistic regression or support vector machines (SVMs). For method details see Keller et al. (2017) <doi:10.1214/16-AOAS992>. / GPL-3	linux-64, osx-64, win-64
r-predmixcor	1.1.1	train_predict_mix predicts the binary response with binary features / GPL-2	noarch
r-preknitposthtmlrender	0.1.0	Dynamize headers or R code within 'Rmd' files to prevent proliferation of 'Rmd' files for similar reports. Add in external HTML document within 'rmarkdown' rendered HTML doc. / GPL-2	noarch
r-preputils	1.0.2	Miscellaneous small utilities are provided to mitigate issues with messy, inconsistent or high dimensional data and help for preprocessing and preparing analyses. / GPL-3	noarch
r-prereg	0.4.0	Provides a collection of templates to author preregistration documents for scientific studies in PDF format. / GPL-3	noarch
r-presenceabsence	1.1.9	This package provides a set of functions useful when evaluating the results of presence-absence models. Package includes functions for calculating threshold dependent measures such as confusion matrices, pcc, sensitivity, specificity, and Kappa, and produces plots of each measure as the threshold is varied. It will calculate optimal threshold choice according to a choice of optimization criteria. It also includes functions to plot the threshold independent ROC curves along with the associated AUC (area under the curve). / Unlimited	noarch
r-prettyb	0.2.1	Drop-in replacements for standard base graphics functions. The replacements are prettier versions of the originals. / GPL-2   GPL-3	noarch
r-prettycode	1.0.2	Replace the standard print method for functions with one that performs syntax highlighting, using ANSI colors, if the terminal supports them. / MIT	noarch
r-prettydoc	0.3.0	Creating tiny yet beautiful documents and vignettes from R Markdown. The package provides the 'html_pretty' output format as an alternative to the 'html_document' and 'html_vignette' engines that convert R Markdown into HTML pages. Various themes and syntax highlight styles are supported. / Apache License (>= 2.0)	noarch
r-prettygraphs	2.1.6	Simple and crisp publication-quality graphics for the ExPosition family of packages. See An ExPosition of the Singular Value Decomposition in R (Beaton et al 2014) <doi:10.1016/j.csda.2013.11.006>. / GPL-2	noarch
r-prettymapr	0.2.2	Automates the process of creating a scale bar and north arrow in any package that uses base graphics to plot in R. Bounding box tools help find and manipulate extents. Finally, there is a function to automate the process of setting margins, plotting the map, scale bar, and north arrow, and resetting graphic parameters upon completion. / GPL-2	noarch
r-prettyr	2.2.3	Functions for conventionally formatting descriptive stats, reshaping data frames and formatting R output as HTML. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-prettyunits	1.0.2	Pretty, human readable formatting of quantities. Time intervals: 1337000 -> 15d 11h 23m 20s. Vague time intervals: 2674000 -> about a month ago. Bytes: 1337 -> 1.34 kB. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-prevederer	0.0.1	Easy and efficient access to the API provided by ‘Prevedere’, an industry insights and predictive analytics company. Query and download indicators, models and workbenches built with ‘Prevedere’ for further analysis and reporting < <a href="https://www.prevedere.com/">https://www.prevedere.com/</a> >. / MIT	noarch
r-primefactr	0.1.1	Use Prime Factorization for simplifying computations, for instance for ratios of large factorials. / GPL-3	noarch
r-primes	0.1.0	Functions to test whether a number is prime and generate the prime numbers within a specified range. Based around an implementation of Wilson’s theorem for testing for an integer’s primality. / MIT	linux-64, osx-64, win-64
r-primme	3.0_0	R interface to PRIMME, a C library for computing a few eigenvalues and their corresponding eigenvectors of a real symmetric or complex Hermitian matrix. It can also compute singular values and vectors of a square or rectangular matrix. It can find largest, smallest, or interior singular/eigenvalues and can use preconditioning to accelerate convergence. / GPL-3	linux-64, osx-64
r-princurve	2.1.4	Fitting a principal curve to a data matrix in arbitrary dimensions. Hastie and Stuetzle (1989) <doi:10.2307/2289936>. / GPL-2	linux-64, osx-64, win-64
r-prinsimp	0.8_8	Provides capabilities beyond principal components analysis to focus on finding structure in low variability subspaces. Constructs and plots simple basis vectors for pre-defined and user-defined measures of simplicity. / AGPL-3	noarch
r-printr	0.1	Extends the S3 generic function knit_print() in ‘knitr’ to automatically print some objects using an appropriate format such as Markdown or LaTeX. For example, data frames are automatically printed as tables, and the help() pages can also be rendered in ‘knitr’ documents. / GPL-3	noarch
r-priogene	0.99.0	In gene sequencing methods, the topological features of protein-protein interaction (PPI) networks are often used, such as ToppNet < <a href="https://toppgene.cchmc.org">https://toppgene.cchmc.org</a> >. In this study, a candidate gene prioritization method was proposed for non-communicable diseases considering disease risks transferred between genes in weighted disease PPI networks with weights for nodes and edges based on functional information. / Artistic-2.0	noarch
r-prioritizrdata	0.2.2	Conservation planning data sets for learning how to use the ‘prioritizr’ package < <a href="https://CRAN.R-project.org/package=prioritizr">https://CRAN.R-project.org/package=prioritizr</a> >. / GPL-3	noarch
r-prioritylasso	0.2.2	Fits successive Lasso models for several blocks of (omics) data with different priorities and takes the predicted values as an offset for the next block. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-prism.forecast</a>	0.1.6	Implements Penalized Regression with Inferred Seasonality Module (PRISM) to generate forecast estimation of weekly unemployment initial claims using ‘Google Trends’ data. It includes required data and tools for backtesting the performance in 2007-2016. / GPL-2	noarch
<a href="#">r-prithulib</a>	1.0.2	Enables user to perform the following: 1. Roll ‘n’ number of die/dice (roll()). 2. Toss ‘n’ number of coin(s) (toss()). 3. Play the game of Rock, Paper, Scissors. 4. Choose ‘n’ number of card(s) from a pack of 52 playing cards (Joker optional). / GPL-3	noarch
<a href="#">r-privatelr</a>	1.2.2	Implements two differentially private algorithms for estimating L2-regularized logistic regression coefficients. A randomized algorithm F is epsilon-differentially private (C. Dwork, Differential Privacy, ICALP 2006 <DOI:10.1007/11681878_14>), if $ \log(P(F(D) \text{ in } S)) - \log(P(F(D') \text{ in } S))  \leq \epsilon$ for any pair D, D’ of datasets that differ in exactly one record, any measurable set S, and the randomness is taken over the choices F makes. / GPL-2	noarch
<a href="#">r-prnsamplr</a>	0.1.0	Survey sampling using permanent random numbers (PRN’s). A solution to the problem of unknown overlap between survey samples, which leads to a low precision in estimates when the survey is repeated or combined with other surveys. The PRN solution is to supply the U(0, 1) random numbers to the sampling procedure, instead of having the sampling procedure generate them. In Lindblom (2014) <doi:10.2478/jos-2014-0047>, and therein cited articles, it is shown how this is carried out and how it improves the estimates. This package supports two common fixed-size sampling procedures (simple random sampling and probability-proportional-to-size sampling) and includes a function for transforming the PRN’s in order to control the sample overlap. / MIT	noarch
<a href="#">r-pro</a>	0.1.1	Optogenetics is a new tool to study neuronal circuits that have been genetically modified to allow stimulation by flashes of light. This package implements the methodological framework, Point-process Response model for Optogenetics (PRO), for analyzing data from these experiments. This method provides explicit nonlinear transformations to link the flash point-process with the spiking point-process. Such response functions can be used to provide important and interpretable scientific insights into the properties of the biophysical process that governs neural spiking in response to optogenetic stimulation. / GPL-2	noarch
<a href="#">r-probmod</a>	0.2.1	Contains functions that are useful for probing moderation effects (or interactions) including techniques such as pick-a-point (also known as spotlight analysis) and Johnson-Neyman (also known as floodlight analysis). Plot function is also provided to facilitate visualization of results from each of these techniques. / GPL-3	noarch
<a href="#">r-probfda</a>	1.0.1	Probabilistic Fisher discriminant analysis (pFDA) is a probabilistic version of the popular and powerful Fisher linear discriminant analysis for dimensionality reduction and classification. / GPL-2	noarch
<a href="#">r-probhat</a>	0.1.1	Computes nonparametric probability distributions (probability density functions, cumulative distribution functions and quantile functions) using kernel smoothing. Supports univariate, multivariate and conditional distributions, and weighted data (possibly useful mixed with fuzzy clustering or frequency data). Also, supports empirical continuous cumulative distribution functions and their inverses, and random number generation. / GPL-2	noarch
<a href="#">r-probsvm</a>	1.00	This package provides multiclass conditional probability estimation for the SVM, which is distributional assumption free. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-proc	1.14.0	Tools for visualizing, smoothing and comparing receiver operating characteristic (ROC curves). (Partial) area under the curve (AUC) can be compared with statistical tests based on U-statistics or bootstrap. Confidence intervals can be computed for (p)AUC or ROC curves. / GPL (>= 3)	linux-32, linux-64, osx-64, win-32, win-64
r-proccalibrad	0.14	Package for processing downloaded MODIS Calibrated radiances Product HDF files. Specifically, MOD02 calibrated radiance product files, and the associated MOD03 geolocation files (for MODIS-TERRA). The package will be most effective if the user installs MRTSwath (MODIS Reprojection Tool for swath products; < <a href="https://lpdaac.usgs.gov/tools/modis_reprojection_tool_swath">https://lpdaac.usgs.gov/tools/modis_reprojection_tool_swath</a> >, and adds the directory with the MRTSwath executable to the default R PATH by editing ~/.Rprofile. / GPL-2	noarch
r-processcontrol	0.1.0	Generate time series chart for individual values with mean and +/- 3 standard deviation lines and the corresponding mR chart with the upper control limit. Also execute the 8 Shewhart stability run tests and display the violations. / MIT	noarch
r-processx	3.3.0	Portable tools to run system processes in the background. It can check if a background process is running; wait on a background process to finish; get the exit status of finished processes; kill background processes and their children; restart processes. It can read the standard output and error of the processes, using non-blocking connections. 'processx' can poll a process for standard output or error, with a timeout. It can also poll several processes at once. / MIT file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
r-prodigendr	0.5.0	Create a project directory structure, along with typical files for that project. This allows projects to be quickly and easily created, as well as for them to be standardized. Designed specifically with scientists in mind (mainly biomedical researchers, but likely applies to other fields). / MIT	noarch
r-prodlim	2018.04.18	Fast and user friendly implementation of nonparametric estimators for censored event history (survival) analysis. Kaplan-Meier and Aalen-Johansen method. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
r-profdpm	3.3	This package facilitates profile inference (inference at the posterior mode) for a class of product partition models (PPM). The Dirichlet process mixture is currently the only available member of this class. These methods search for the maximum posterior (MAP) estimate for the data partition in a PPM. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-profilelikelihood</a>	1.1	This package provides profile likelihoods for a parameter of interest in commonly used statistical models. The models include linear models, generalized linear models, proportional odds models, linear mixed-effects models, and linear models for longitudinal responses fitted by generalized least squares. The package also provides plots for normalized profile likelihoods as well as the maximum profile likelihood estimates and the kth likelihood support intervals. / GPL-3	noarch
<a href="#">r-profilemodel</a>	0.6.0	Provides tools that can be used to calculate, evaluate, plot and use for inference the profiles of <i>arbitrary</i> inference functions for <i>arbitrary</i> ‘glm’-like fitted models with linear predictors. More information on the methods that are implemented can be found in Kosmidis (2008) < <a href="https://www.r-project.org/doc/Rnews/Rnews_2008-2.pdf">https://www.r-project.org/doc/Rnews/Rnews_2008-2.pdf</a> >. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-profmem</a>	0.5.0	A simple and light-weight API for memory profiling of R expressions. The profiling is built on top of R’s built-in memory profiler (‘utils::Rprofmem()’), which records every memory allocation done by R (also native code). / LGPL-2.1	noarch
<a href="#">r-profr</a>	0.3.3	An alternative data structure and visual rendering for the profiling information generated by Rprof. / MIT	noarch
<a href="#">r-proftools</a>	0.99	Tools for examining Rprof profile output. / GPL-3	noarch
<a href="#">r-profvis</a>	0.3.5	Interactive visualizations for profiling R code. / GPL-3   file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-prognosticroc</a>	0.7	Prognostic ROC curve is an alternative graphical approach to represent the discriminative capacity of the marker: a receiver operating characteristic (ROC) curve by plotting 1 minus the survival in the high-risk group against 1 minus the survival in the low-risk group. This package contains functions to assess prognostic ROC curve. The user can enter the survival according to a model previously estimated or the user can also enter individual survival data for estimating the prognostic ROC curve by using Kaplan-Meier estimator. The area under the curve (AUC) corresponds to the probability that a patient in the low-risk group has a longer lifetime than a patient in the high-risk group. The prognostic ROC curve provides complementary information compared to survival curves. The AUC is assessed by using the trapezoidal rules. When survival curves do not reach 0, the prognostic ROC curve is incomplete and the extrapolations of the AUC are performed by assuming pessimist, optimist and non-informative situations. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-progress	1.2.0	Configurable Progress bars, they may include percentage, elapsed time, and/or the estimated completion time. They work in terminals, in ‘Emacs’ ‘ESS’, ‘RStudio’, ‘Windows’ ‘Rgui’ and the ‘macOS’ ‘R.app’. The package also provides a ‘C’ ‘API’, that works with or without ‘Rcpp’. / MIT file LICENSE	noarch
r-proj4	1.0_8	A simple interface to lat/long projection and datum transformation of the PROJ.4 cartographic projections library. It allows transformation of geographic coordinates from one projection and/or datum to another. / GPL-2	linux-64, osx-64
r-projecttemplate	0.9.0	Provides functions to automatically build a directory structure for a new R project. Using this structure, ‘ProjectTemplate’ automates data loading, pre-processing, library importing and unit testing. / GPL-3	noarch
r-projmgr	0.1.0	Provides programmatic access to ‘GitHub’ API with a focus on project management. Key functionality includes setting up issues and milestones from R objects or ‘YAML’ configurations, querying outstanding or completed tasks, and generating progress updates in tables, charts, and RMarkdown reports. Useful for those using ‘GitHub’ in personal, professional, or academic settings with an emphasis on streamlining the workflow of data analysis projects. / MIT	noarch
r-proliferativeindex	1.0.1	Provides functions for calculating and analyzing the proliferative index (PI) from an RNA-seq dataset. As described in Ramaker & Lasseigne, et al. bioRxiv, 2016 <doi:10.1101/063057>. / MIT	noarch
r-promethee	1.1	Functions which can be used to support the Multicriteria Decision Analysis (MCDA) process involving multiple criteria, by PROMETHEE (Preference Ranking Organization METHod for Enrichment of Evaluations). / GPL-3	noarch
r-promises	1.0.1	Provides fundamental abstractions for doing asynchronous programming in R using promises. Asynchronous programming is useful for allowing a single R process to orchestrate multiple tasks in the background while also attending to something else. Semantics are similar to ‘JavaScript’ promises, but with a syntax that is idiomatic R. / MIT file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
r-promote	1.1.1	Deploy, maintain, and invoke predictive models using the ‘Alteryx Promote’ REST API. ‘Alteryx Promote’ is available at the URL: < <a href="https://www.alteryx.com/products/alteryx-promote">https://www.alteryx.com/products/alteryx-promote</a> >. / FreeBSD	noarch
r-propcis	0.3_0	Computes two-sample confidence intervals for single, paired and independent proportions. / GPL-3	noarch
r-properties	0.0_9	Allows to parse ‘Java’ properties files in the context of ‘R Service Bus’ applications. / GPL-2	noarch
r-propscrand	1.1	This package contains functions to run propensity-biased allocation to balance covariate distributions in sequential trials and propensity-constrained randomization to balance covariate distributions in trials with known baseline covariates at time of randomization. Currently this package only supports trials comparing two groups. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-proscorer</a> <a href="#">tools</a>	0.0.1	Provides a reliable and flexible toolbox to score patient-reported outcome (PRO), Quality of Life (QOL), and other psychometric measures. The guiding philosophy is that scoring errors can be eliminated by using a limited number of well-tested, well-behaved functions to score PRO-like measures. The workhorse of the package is the ‘scoreScale’ function, which can be used to score most single-scale measures. It can reverse code items that need to be reversed before scoring and pro-rate scores for missing item data. Currently, three different types of scores can be output: summed item scores, mean item scores, and scores scaled to range from 0 to 100. The ‘PROscorerTools’ functions can be used to write new functions that score more complex measures. In fact, ‘PROscorerTools’ functions are the building blocks of the scoring functions in the ‘PROscorer’ package (which is a repository of functions that score specific commonly-used instruments). Users are encouraged to use ‘PROscorerTools’ to write scoring functions for their favorite PRO-like instruments, and to submit these functions for inclusion in ‘PROscorer’ (a tutorial vignette will be added soon). The long-term vision for the ‘PROscorerTools’ and ‘PROscorer’ packages is to provide an easy-to-use system to facilitate the incorporation of PRO measures into research studies in a scientifically rigorous and reproducible manner. These packages and their vignettes are intended to help establish and promote best practices for scoring and describing PRO-like measures in research. / MIT	noarch
<a href="#">r-prospectr</a>	0.1.3	The package provides functions for pretreatment and sample selection of visible and near infrared diffuse reflectance spectra / GPL-3	linux-64, osx-64, win-64
<a href="#">r-prosper</a>	0.3.0	An environment to simulate the development of annual plant populations with regard to population dynamics and genetics, especially herbicide resistance. It combines genetics on the individual level (Renton et al. 2011) with a stochastic development on the population level (Daedlow, 2015). Renton, M, Diggle, A, Manalil, S and Powles, S (2011) <doi:10.1016/j.jtbi.2011.05.010> Daedlow, Daniel (2015, doctoral dissertation: University of Rostock, Faculty of Agriculture and Environmental Sciences.) / GPL-3	noarch
<a href="#">r-proteindescriptors</a>	0.1.0	An implementation of protein descriptors in R. These descriptors combine the advantages of being fixed length and including partial sequential effect: Various length of protein sequences are described with fixed length vectors that are suitable for machine learning algorithms, and still includes partial sequential effect. / BSD_3_clause	noarch
<a href="#">r-proteomicdesign</a>	2.0	This package provides functions to identify the optimal solution that maximizes numbers of detectable differentiated proteins from a multi-stage clinical proteomic study. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-proto	1.0.0	An object oriented system using object-based, also called prototype-based, rather than class-based object oriented ideas. / GPL-2	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-protoclass	1.0	Greedy algorithm described in Bien and Tibshirani (2011) Prototype Selection for Interpretable Classification. Annals of Applied Statistics. 5(4). 2403-2424 / GPL-3	noarch
r-protoclust	1.6.3	Performs minimax linkage hierarchical clustering. Every cluster has an associated prototype element that represents that cluster as described in Bien, J., and Tibshirani, R. (2011), Hierarchical Clustering with Prototypes via Minimax Linkage, The Journal of the American Statistical Association, 106(495), 1075-1084. / GPL-2	linux-64, osx-64, win-64
r-protolidar	0.1	PROTOLIDAR package contains functions for analyze the LIDAR scan of plants (grapevine) and make 3D maps in GRASS GIS. / GPL-3	noarch
r-protolite	1.9	Optimized C implementations for reading and writing protocol-buffers. Currently supports 'rexp.proto' for serializing R objects and 'geobuf.proto' for geojson data. This lightweight package is complementary to the much larger 'RProtoBuf' package which provides a full featured toolkit for working with protocol-buffers in R. / MIT	linux-64, osx-64, win-64
r-proton	1.0	'The Proton Game' is a console-based data-crunching game for younger and older data scientists. Act as a data-hacker and find Slawomir Pietraszko's credentials to the Proton server. You have to solve four data-based puzzles to find the login and password. There are many ways to solve these puzzles. You may use loops, data filtering, ordering, aggregation or other tools. Only basics knowledge of R is required to play the game, yet the more functions you know, the more approaches you can try. The knowledge of dplyr is not required but may be very helpful. This game is linked with the „Pietraszko's Cave" story available at <a href="http://biecek.pl/BetaBit/Warsaw">http://biecek.pl/BetaBit/Warsaw</a> . It's a part of Beta and Bit series. You will find more about the Beta and Bit series at <a href="http://biecek.pl/BetaBit">http://biecek.pl/BetaBit</a> . / GPL-2	noarch
r-protr	1.6_2	Comprehensive toolkit for generating various numerical features of protein sequences described in Xiao et al. (2015) <DOI:10.1093/bioinformatics/btv042>. For full functionality, the software 'ncbi-blast' is needed, see < <a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi?PAGE_TYPE=BlastDocs&amp;DOC_TYPE=Download">https://blast.ncbi.nlm.nih.gov/Blast.cgi?PAGE_TYPE=BlastDocs&amp;DOC_TYPE=Download</a> > for more information. / BSD_3_clause	noarch
r-protviz	0.4.0	Helps with quality checks, visualizations and analysis of mass spectrometry data, coming from proteomics experiments. The package is developed, tested and used at the Functional Genomics Center Zurich. We use this package mainly for prototyping, teaching, and having fun with proteomics data. But it can also be used to do data analysis for small scale data sets. / GPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-provparser	0.2	R functions to access provenance information collected by ‘rdt’ or ‘rdtLite’. The information is stored inside a ‘ProvInfo’ object and can be accessed through a collection of functions that will return the requested data. The exact format of the JSON created by ‘rdt’ and ‘rdtLite’ is described in < <a href="https://github.com/End-to-end-provenance/ExtendedProvJson">https://github.com/End-to-end-provenance/ExtendedProvJson</a> >. / GPL-3	noarch
r-provviz	1.0.6	Displays provenance graphically for provenance collected by the ‘rdt’ or ‘rdtLite’ packages, or other tools providing compatible PROV JSON output. The exact format of the JSON created by ‘rdt’ and ‘rdtLite’ is described in < <a href="https://github.com/End-to-end-provenance/ExtendedProvJson">https://github.com/End-to-end-provenance/ExtendedProvJson</a> >. More information about rdtLite and associated tools is available at < <a href="https://github.com/End-to-end-provenance/">https://github.com/End-to-end-provenance/</a> > and Barbara Lerner, Emery Boose, and Luis Perez (2018), Using Introspection to Collect Provenance in R, Informatics, <doi:10.3390/informatics5010012>. / GPL-3	noarch
r-proxy	0.4_2	Provides an extensible framework for the efficient calculation of auto- and cross-proximities, along with implementations of the most popular ones. / GPL-2	linux-64, osx-64, win-64
r-prroc	1.3.1	Computes the areas under the precision-recall (PR) and ROC curve for weighted (e.g., soft-labeled) and unweighted data. In contrast to other implementations, the interpolation between points of the PR curve is done by a non-linear piecewise function. In addition to the areas under the curves, the curves themselves can also be computed and plotted by a specific S3-method. References: Davis and Goadrich (2006) <doi:10.1145/1143844.1143874>; Keilwagen et al. (2014) <doi:10.1371/journal.pone.0092209>; Grau et al. (2015) <doi:10.1093/bioinformatics/btv153>. / GPL-3	noarch
r-prsr	3.1.1_2	Tests periodicity in short time series using response surface regression. / GPL-2	linux-64, osx-64, win-64
r-pryr	0.1.4	Useful tools to pry back the covers of R and understand the language at a deeper level. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
r-ps	1.3.0	List, query and manipulate all system processes, on ‘Windows’, ‘Linux’ and ‘macOS’. / BSD_3_clause file LICENSE	linux-64, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
r-psagraphics	2.1.1	A collection of functions that primarily produce graphics to aid in a Propensity Score Analysis (PSA). Functions include: cat.psa and box.psa to test balance within strata of categorical and quantitative covariates, circ.psa for a representation of the estimated effect size by stratum, loess.psa that provides a graphic and loess based effect size estimate, and various balance functions that provide measures of the balance achieved via a PSA in a categorical covariate. / GPL-2	noarch
r-pscl	1.5.2	Bayesian analysis of item-response theory (IRT) models, roll call analysis; computing highest density regions; maximum likelihood estimation of zero-inflated and hurdle models for count data; goodness-of-fit measures for GLMs; data sets used in writing and teaching at the Political Science Computational Laboratory; seats-votes curves. / GPL-2	linux-64, osx-64, win-64
r-pseval	1.3.1	Contains the core methods for the evaluation of principal surrogates in a single clinical trial. Provides a flexible interface for defining models for the risk given treatment and the surrogate, the models for integration over the missing counterfactual surrogate responses, and the estimation methods. Estimated maximum likelihood and pseudo-score can be used for estimation, and the bootstrap for inference. A variety of post-estimation summary methods are provided, including print, summary, plot, and testing. / MIT	noarch
r-psi	1.1	This package contains functions to calculate the Specificity Index statistic, which can be used for comparative quantitative analysis to identify genes enriched in specific cell populations across a large number of profiles, as well as perform numerous post-processing operations. NOTE:Supplementary data (human & mouse expression sets, calculated pSI datasets, etc.) can be found in pSI.data package located at the following URL: <a href="http://genetics.wustl.edu/jdlab/psi_package/">http://genetics.wustl.edu/jdlab/psi_package/</a> / GPL-2	noarch
r-psy	1.0.3	The package provides an implementation of PSO consistent with the standard PSO 2007/2011 by Maurice Clerc et al. Additionally a number of ancillary routines are provided for easy testing and graphics. / LGPL-3	noarch
r-psoptim	1.0	Particle swarm optimization - a basic variant. / GPL (>= 2.0)	noarch
r-pspearman	0.3_0	Spearman's rank correlation test with precomputed exact null distribution for n <= 22. / GPL-3	linux-64, osx-64, win-64
r-pspline	1.0_1	Smoothing splines with penalties on order m derivatives. / Unlimited	linux-32, linux-64, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
r-pstat	1.2	Calculating Pst values to assess differentiation among populations from a set of quantitative traits is the primary purpose of such a package. The bootstrap method provides confidence intervals and distribution histograms of Pst. Variations of Pst in function of the parameter $c/h^2$ are studied as well. Finally, the package proposes different transformations especially to eliminate any variation resulting from allometric growth (calculation of residuals from linear regressions, Reist standardizations or Aitchison transformation). / GPL-2	noarch
r-psumtsim	0.4	Functions to simulate Poisson or Normally distributed responses relative to a baseline and compute achieved significance level and powers for tests on the simulated responses. / GPL-3	noarch
r-psy	1.1	Kappa, ICC, Cronbach alpha, screeplot, mtmm / GPL-2	noarch
r-psych	1.8.1	A general purpose toolbox for personality, psychometric theory and experimental psychology. Functions are primarily for multivariate analysis and scale construction using factor analysis, principal component analysis, cluster analysis and reliability analysis, although others provide basic descriptive statistics. Item Response Theory is done using factor analysis of tetrachoric and polychoric correlations. Functions for analyzing data at multiple levels include within and between group statistics, including correlations and factor analysis. Functions for simulating and testing particular item and test structures are included. Several functions serve as a useful front end for structural equation modeling. Graphical displays of path diagrams, factor analysis and structural equation models are created using basic graphics. Some of the functions are written to support a book on psychometric theory as well as publications in personality research. For more information, see the < <a href="https://personality-project.org/r/">https://personality-project.org/r/</a> > web page. / GPL ( $\geq 2$ )	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-psychotools	0.5.0	Infrastructure for psychometric modeling such as data classes (for item response data and paired comparisons), basic model fitting functions (for Bradley-Terry, Rasch, parametric logistic IRT, generalized partial credit, rating scale, multinomial processing tree models), extractor functions for different types of parameters (item, person, threshold, discrimination, guessing, upper asymptotes), unified inference and visualizations, and various datasets for illustration. Intended as a common lightweight and efficient toolbox for psychometric modeling and a common building block for fitting psychometric mixture models in package psychomix and trees based on psychometric models in package psychotree. / GPL-2   GPL-3	linux-64, osx-64, win-64
r-psychtools	1.9.5	Support functions, data sets, and vignettes for the ‘psych’ package. Contains several of the biggest data sets for the ‘psych’ package as well as one vignette. A few helper functions for file manipulation are included as well. For more information, see the < <a href="https://personality-project.org/r/">https://personality-project.org/r/</a> > web page. / GPL-2	noarch
r-psymonitor	0.0.2	Apply the popular real-time monitoring strategy proposed by Phillips, Shi and Yu (2015a,b;PSY) <doi:10.1111/iere.12132>, <doi:10.1111/iere.12131>, along with a new bootstrap procedure designed to mitigate the potential impact of heteroskedasticity and to effect family-wise size control in recursive testing algorithms (Phillips and Shi, forthcoming). / GPL-3	noarch
r-psyphy	0.1.9	An assortment of functions that could be useful in analyzing data from psychophysical experiments. It includes functions for calculating $d'$ from several different experimental designs, links for m-alternative forced-choice (mafc) data to be used with the binomial family in glm (and possibly other contexts) and self-Start functions for estimating gamma values for CRT screen calibrations. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-pte	1.7	We provide inference for personalized medicine models. Namely, we answer the questions: (1) how much better does a purported personalized recommendation engine for treatments do over a business-as-usual approach and (2) is that difference statistically significant? / GPL-3	noarch
r-ptest	1.0.8	Implements p-value computations using an approximation to the cumulative distribution function for a variety of tests for periodicity. These tests include harmonic regression tests with normal and double exponential errors as well as modifications of Fisher's g test. An accompanying vignette illustrates the application of these tests. / GPL-2	linux-64, osx-64, win-64
r-ptprocess	3.3.1	Fits and analyses time dependent marked point process models with an emphasis on earthquake modelling. For a more detailed introduction to the package, see the topic PtProcess. A list of recent changes can be found in the topic Change Log. / GPL-2	noarch
r-pts2polys	0.1.1	Various applications in invasive species biology, conservation biology, epidemiology and elsewhere involve sampling of sets of 2D points from a posterior distribution. The number of such point sets may be large, say 1000 or 10000. This package facilitates visualisation of such output by constructing seven nested polygons representing the location and variability of the point sets. This can be used, for example, to visualise the range boundary of a species, and uncertainty in the location of that boundary. / GPL-2	linux-64, osx-64, win-64
r-ptsuite	1.0.0	Various estimation methods for the shape parameter of Pareto distributed data. This package contains functions for various estimation methods such as maximum likelihood (Newman, 2005)<doi:10.1016/j.cities.2012.03.001>, Hill's estimator (Hill, 1975)<doi:10.1214/aos/1176343247>, least squares (Zaher et al., 2014)<doi:10.9734/BJMCS/2014/10890>, method of moments (Rytgaard, 1990)<doi:10.2143/AST.20.2.2005443>, percentiles (Bhatti et al., 2018)<doi:10.1371/journal.pone.0196456>, and weighted least squares (Nair et al., 2019) to estimate the shape parameter of Pareto distributed data. It also provides both a heuristic method (Hubert et al., 2013)<doi:10.1016/j.csda.2012.07.011> and a goodness of fit test (Gulati and Shapiro, 2008)<doi:10.1007/978-0-8176-4619-6> for testing for Pareto data as well as a method for generating Pareto distributed data. / GPL-3	linux-64, osx-64, win-64
r-ptw	1.9.1	Parametric Time Warping aligns patterns, i.e. it aims to put corresponding features at the same locations. The algorithm searches for an optimal polynomial describing the warping. It is possible to align one sample to a reference, several samples to the same reference, or several samples to several references. One can choose between calculating individual warpings, or one global warping for a set of samples and one reference. Two optimization criteria are implemented: RMS (Root Mean Square error) and WCC (Weighted Cross Correlation). Both warping of peak profiles and of peak lists are supported. / GPL-2	linux-64, osx-64, win-64
r-ptwikiwords	0.0.3	Contains a dataset of words used in 15,000 randomly extracted pages from the Portuguese Wikipedia (< <a href="https://pt.wikipedia.org/">https://pt.wikipedia.org/</a> >). / MIT	noarch
r-ptycho	1.1.4	Bayesian variable selection for linear regression models using hierarchical priors. There is a prior that combines information across responses and one that combines information across covariates, as well as a standard spike and slab prior for comparison. An MCMC samples from the marginal posterior distribution for the 0-1 variables indicating if each covariate belongs to the model for each response. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-publish	2018.04.17	Convenience functions that transform the results of some basic statistical analyses into table format nearly ready for publication. This includes descriptive tables, tables of logistic regression and Cox regression results as well as forest plots. / GPL-2	noarch
r-pullword	0.2	R Interface to Pullword Service for natural language processing in Chinese. It enables users to extract valuable words from text by deep learning models. For more details please visit the official site (in Chinese) <a href="http://pullword.com/">http://pullword.com/</a> . / LGPL-3	linux-64, osx-64, win-64
r-pulsar	0.3.6	Model selection for penalized graphical models using the Stability Approach to Regularization Selection ('StARS'), with options for speed-ups including Bounded StARS (B-StARS), batch computing, and other stability metrics (e.g., graphlet stability G-StARS). Christian L. Müller, Richard Bonneau, Zachary Kurtz (2016) <arXiv:1605.07072>. / GPL-2	noarch
r-pumilior	1.3.1	R package to query and get data out of a Pumilio sound archive system ( <a href="http://ljvillanueva.github.io/pumilio/">http://ljvillanueva.github.io/pumilio/</a> ). / GPL-3	noarch
r-purge	0.2.1	Enables the removal of training data from fitted R models while retaining predict functionality. The purged models are more portable as their memory footprints do not scale with the training sample size. / MIT	noarch
r-purging	1.0.0	Simple method of purging independent variables of mediating effects. First, regress the direct variable on the indirect variable. Then, used the stored residuals as the new purged (direct) variable in the updated specification. This purging process allows for use of a new direct variable uncorrelated with the indirect variable. Please cite the method and/or package using Waggoner, Philip D. (2018) <doi:10.1177/1532673X18759644>. / MIT	noarch
r-purrr	0.3.2	A complete and consistent functional programming toolkit for R. / GPL-3   file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
r-pushbar	0.1.0	Create sliders from left, right, top and bottom which may include any html or 'Shiny' input or output. / MIT	noarch
r-pushoverr	1.0.0	Send push notifications to mobile devices or the desktop using Pushover. These notifications can display job status, results, scraped web data, or any other text or numeric data. / BSD_2_clause	noarch
r-pvclass	1.4	Computes nonparametric p-values for the potential class memberships of new observations as well as cross-validated p-values for the training data. The p-values are based on permutation tests applied to an estimated Bayesian likelihood ratio, using a plug-in statistic for the Gaussian model, 'k nearest neighbors', 'weighted nearest neighbors' or 'penalized logistic regression'. Additionally, it provides graphical displays and quantitative analyses of the p-values. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-pvclust	2.0_0	An implementation of multiscale bootstrap resampling for assessing the uncertainty in hierarchical cluster analysis. It provides AU (approximately unbiased) p-value as well as BP (bootstrap probability) value for each cluster in a dendrogram. / GPL-2	noarch
r-pvsr	0.3	The pvsR package facilitates data retrieval from Project Vote Smart's rich on-line data base on US politics via the Project Vote Smart application programming interface (PVS API). The functions in this package cover most PVS API classes and methods and return the requested data in a data frame. / GPL-2	noarch
r-pwr	1.2_2	Power analysis functions along the lines of Cohen (1988). / GPL-3	noarch
r-pwr2	1.0	User friendly functions for power and sample size analysis at one-way and two-way ANOVA settings take either effect size or delta and sigma as arguments. They are designed for both one-way and two-way ANOVA settings. In addition, a function for plotting power curves is available for power comparison, which can be easily visualized by statisticians and clinical researchers. / GPL-2	noarch
r-pwrab	0.1.0	Power analysis for AB testing. The calculations are based on the Welch's unequal variances t-test, which is generally preferred over the Student's t-test when sample sizes and variances of the two groups are unequal, which is frequently the case in AB testing. In such situations, the Student's t-test will give biased results due to using the pooled standard deviation, unlike the Welch's t-test. / GPL-3	noarch
r-pwrrasch	0.1_2	Statistical power simulation for testing the Rasch Model based on a three-way analysis of variance design with mixed classification. / GPL-3	noarch
r-pwt	7.1_1	The Penn World Table provides purchasing power parity and national income accounts converted to international prices for 189 countries for some or all of the years 1950-2010. / GPL-2	noarch
r-pwt8	8.1_1	The Penn World Table 8.x provides information on relative levels of income, output, inputs, and productivity for 167 countries between 1950 and 2011. / GPL-2   GPL-3	noarch
r-pwt9	9.1_0	The Penn World Table 9.x (< <a href="http://www.ggd.net/pwt/">http://www.ggd.net/pwt/</a> >) provides information on relative levels of income, output, inputs, and productivity for 182 countries between 1950 and 2017. / GPL-2   GPL-3	noarch
r-pxr	0.42	Provides a set of functions for reading and writing PC-Axis files, used by different statistical organizations around the globe for data dissemination. / GPL-3	noarch
r-pxweb	0.9.1	Generic interface for the PX-Web/PC-Axis API. The PX-Web/PC-Axis API is used by organizations such as Statistics Sweden and Statistics Finland to disseminate data. The R package can interact with all PX-Web/PC-Axis APIs to fetch information about the data hierarchy, extract metadata and extract and parse statistics to R data.frame format. PX-Web is a solution to disseminate PC-Axis data files in dynamic tables on the web. Since 2013 PX-Web contains an API to disseminate PC-Axis files. / BSD_2_clause	noarch
r-pymturkr	1.1	Provides access to the latest 'Amazon Mechanical Turk' ('MTurk') < <a href="https://www.mturk.com">https://www.mturk.com</a> > Requester API (version '2017-01-17'), replacing the now deprecated 'MTurkR' package. / GPL-2	noarch
r-pyramid	1.5	Drawing population pyramid using (1) data.frame or (2) vectors. The former is named as pyramid() and the latter pyramids(), as wrapper function of pyramid(). pyramidf() is the function to draw population pyramid within the specified frame. / GPL-2	noarch
r-pzfx	0.2.0	Read and write 'GraphPad Prism' '.pzfx' files in R. / MIT	noarch

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Name	Version	Summary/License	Platforms
r-qaig	0.1.5	A tool for automatic generation of sibling items from a parent item model defined by the user. It is an implementation of the process automatic item generation (AIG) focused on generating quantitative multiple-choice type of items (see Embretson, Kingston (2018) <doi:10.1111/jedm.12166>). / GPL-3	noarch
r-qboxplot	0.2	Produce quantile-based box-and-whisker plot(s). / GPL-2	noarch
r-qcafalsepositive	1.1.1	Implements tests for Type I error in Qualitative Comparative Analysis (QCA) that take into account the multiple hypothesis tests inherent in the procedure. Tests can be carried out on three variants of QCA: crisp-set QCA (csQCA), multi-value QCA (mvQCA) and fuzzy-set QCA (fsQCA). For fsQCA, the fsQCApermTest() command implements a permutation test that provides 95% confidence intervals for the number of counterexamples and degree of consistency, respectively. The distributions of permuted values can be plotted against the observed values. For csQCA and mvQCA, simple binomial tests are implemented in csQCABinTest() and mvQCABinTest(), respectively. / GPL-3	noarch
r-qcba	0.3.1	CBA postprocessing algorithm that creates smaller models for datasets containing quantitative (numerical) attributes. Article describing QCBA is published in Tomas Kliegr (2017) <arXiv:1711.10166>. / AGPL-3	noarch
r-qcc	2.7	Shewhart quality control charts for continuous, attribute and count data. Cusum and EWMA charts. Operating characteristic curves. Process capability analysis. Pareto chart and cause-and-effect chart. Multivariate control charts. / GPL-2	noarch
r-qcewas	1.2_2	Tools for (automated and manual) quality control of the results of Epigenome-Wide Association Studies. / GPL-3	noarch
r-qcgwas	1.0_8	Tools for (automated and manual) quality control of the results of Genome Wide Association Studies / GPL-3	noarch
r-qcsis	0.1	Quantile correlation-sure independence screening (QC-SIS) and composite quantile correlation-sure independence screening (CQC-SIS) for ultrahigh-dimensional data. / GPL-2	noarch
r-qcv	1.0	Primarily, the ‘qcv’ package computes key indices related to the Quantifying Construct Validity procedure (QCV; Westen & Rosenthal, 2003 <doi:10.1037/0022-3514.84.3.608>; see also Furr & Heuckeroth, in press). The qcv() function is the heart of the ‘qcv’ package, but additional functions in the package provide useful ancillary information related to the QCV procedure. / GPL-2	noarch
r-qdapdictionaries	1.0.7	A collection of text analysis dictionaries and word lists for use with the ‘qdap’ package. / GPL-2	noarch
r-qdapregex	0.7.2	A collection of regular expression tools associated with the ‘qdap’ package that may be useful outside of the context of discourse analysis. Tools include removal/extraction/replacement of abbreviations, dates, dollar amounts, email addresses, hash tags, numbers, percentages, citations, person tags, phone numbers, times, and zip codes. / GPL-2	noarch
r-qdaptools	1.3.3	A collection of tools associated with the ‘qdap’ package that may be useful outside of the context of text analysis. / GPL-2	noarch
r-qdcomparison	3.0	Allows practitioners to determine (i) if two univariate distributions (which can be continuous, discrete, or even mixed) are equal, (ii) how two distributions differ (shape differences, e.g., location, scale, etc.), and (iii) where two distributions differ (at which quantiles), all using nonparametric LP statistics. The primary reference is Jungreis, D. (2019, Technical Report). / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-qdm	0.1.0	This package provides different specifications of a Quadrilateral Dissimilarity Model which can be used to fit same-different judgments in order to get a predicted matrix that satisfies regular minimality [Colonius & Dzhafarov, 2006, Measurement and representations of sensations, Erlbaum]. From such a matrix, Fechnerian distances can be computed. / GPL-2	noarch
r-qfrm	1.0.1	Option pricing (financial derivatives) techniques mainly following textbook ‘Options, Futures and Other Derivatives’, 9ed by John C.Hull, 2014. Prentice Hall. Implementations are via binomial tree option model (BOPM), Black-Scholes model, Monte Carlo simulations, etc. This package is a result of Quantitative Financial Risk Management course (STAT 449 and STAT 649) at Rice University, Houston, TX, USA, taught by Oleg Melnikov, statistics PhD student, as of Spring 2015. / GPL-2	noarch
r-qgglmm	0.7.2	Compute various quantitative genetics parameters from a Generalised Linear Mixed Model (GLMM) estimates. Especially, it yields the observed phenotypic mean, phenotypic variance and additive genetic variance. / GPL-2	noarch
r-qgtools	1.0	Two linear mixed model approaches: REML(restricted maximum likelihood) and MINQUE (minimum norm quadratic unbiased estimation) approaches and several resampling techniques are integrated for various quantitative genetics analyses. With these two types of approaches, various unbalanced data structures, missing data, and any irregular genetic mating designs can be analyzed and statistically tested. This package also offers fast computations for many large data sets. Other functions will be added to this R tool in the future. / GPL-2	noarch
r-qhot	0.1.0	This function produces both the numerical and graphical summaries of the QTL hotspot detection in the genomes that are available on the worldwide web including the flanking markers of QTLs. / GPL-3	noarch
r-qiitr	0.1.0	Qiita is a technical knowledge sharing and collaboration platform for programmers. See < <a href="https://qiita.com/api/v2/docs">https://qiita.com/api/v2/docs</a> > for more information. / MIT	noarch
r-qkerntool	1.19	Nonlinear machine learning tool for classification, clustering and dimensionality reduction. It integrates 12 q-kernel functions and 15 conditional negative definite kernel functions and includes the q-kernel and conditional negative definite kernel version of density-based spatial clustering of applications with noise, spectral clustering, generalized discriminant analysis, principal component analysis, multidimensional scaling, locally linear embedding, sammon’s mapping and t-Distributed stochastic neighbor embedding. / GPL-2	noarch
r-qlearn	1.0	Functions to implement Q-learning for estimating optimal dynamic treatment regimes from two stage sequentially randomized trials, and to perform inference via m-out-of-n bootstrap for parameters indexing the optimal regime. / GPL-2	noarch
r-qlearning	0.1.1	Implements Q-Learning, a model-free form of reinforcement learning, described in work by Strehl, Li, Wiewiora, Langford & Littman (2006) <doi:10.1145/1143844.1143955>. / GPL-3	noarch
r-qmrparser	0.1.5	Basic functions for building parsers, with an application to PC-AXIS format files. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-qpdf	1.1	Content-preserving transformations of PDF files such as split, combine, and compress. This package interfaces directly to the ‘qpdf’ C API and does not require any command line utilities. Note that ‘qpdf’ does not read actual content from PDF files: to extract text and data you need the ‘pdftools’ package. / Apache License 2.0	linux-64, osx-64, win-32, win-64
r-qqman	0.1.4	Create Q-Q and manhattan plots for GWAS data from PLINK results. / GPL-3	noarch
r-qqperm	1.0.1	Provides users the necessary utility functions to generate permutation-based QQ plots and also estimate inflation factor based on the empirical NULL distribution. While it has general utility, it is particularly helpful when the skewness of the Fisher’s Exact test in sparse data situations with imbalanced case-control sample sizes renders the reliance on the uniform chi-square expected distribution inappropriate. / GPL-2	noarch
r-qqvases	1.0.0	Presents an explanatory animation of normal quantile-quantile plots based on a water-filling analogy. The animation presents a normal QQ plot as the parametric plot of the water levels in vases defined by two distributions. The distributions decorate the axes in the normal QQ plot and are optionally shown as vases adjacent to the plot. The package draws QQ plots for several distributions, either as samples or continuous functions. / GPL-2	noarch
r-qrage	1.0	Tools that create D3 JavaScript force directed graph from R. D3 JavaScript was created by Michael Bostock. See <a href="http://d3js.org/">http://d3js.org/</a> and, more specifically for Force Directed Graph <a href="https://github.com/mbostock/d3/wiki/Force-Layout">https://github.com/mbostock/d3/wiki/Force-Layout</a> . / MIT	noarch
r-qrank	1.0	A Quantile Rank-score based test for the identification of expression quantitative trait loci. / GPL-2	noarch
r-qrcode	0.1.1	Create QRcode in R. / GPL-3	noarch
r-qrm	0.4.1	Accompanying package to the book Quantitative Risk Management: Concepts, Techniques and Tools by Alexander J. McNeil, Rüdiger Frey, and Paul Embrechts. / GPL (>= 2)	linux-64, osx-64, win-32, win-64
r-qrmdata	2016.01.03	Various data sets (stocks, stock indices, constituent data, FX, zero-coupon bond yield curves, volatility, commodities) for Quantitative Risk Management practice. / GPL-2   GPL-3	noarch
r-qrmix	0.9.0	Implements the robust algorithm for fitting finite mixture models based on quantile regression proposed by Emir et al., 2017 (unpublished). / LGPL-3	noarch
r-qrnn	2.0.4	Fit quantile regression neural network models with optional left censoring, partial monotonicity constraints, generalized additive model constraints, and the ability to fit multiple non-crossing quantile functions following Cannon (2011) <doi:10.1016/j.cageo.2010.07.005> and Cannon (2018) <doi:10.1007/s00477-018-1573-6>. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-qrsvm	0.2.1	Quantile Regression (QR) using Support Vector Machines under the Pinball-Loss. Estimation is based on Nonparametric Quantile Regression by I. Takeuchi, Q.V.Le , T. Sears, A.J.Smola (2004). Implementation relies on ‘quadprog’ package, package ‘kernlab’ Kernelfunctions and package ‘Matrix’ nearPD to find next Positive definite Kernelmatrix. Package estimates quantiles individually but an Implementation of non crossing constraints coming soon. Function multqrsvm() now supports parallel backend for faster fitting. / GPL-2	noarch
r-qsardata	1.3	Molecular descriptors and outcomes for several public domain data sets / GPL-3	noarch
r-qtlbook	0.18	Datasets for the book, A Guide to QTL Mapping with R/qtl. Broman and Sen (2009) <doi:10.1007/978-0-387-92125-9>. / GPL-3	noarch
r-qtlDesign	0.94	Tools for the design of QTL experiments / GPL-3	noarch
r-quadprog	1.5_5	This package contains routines and documentation for solving quadratic programming problems. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
r-quadprogxt	0.0.4	Extends the quadprog package to solve quadratic programs with absolute value constraints and absolute values in the objective function. / GPL-2	noarch
r-qualci	0.1	Exact one-sided p-values and confidence intervals for an outcome variable defined on an interval measurement scale with only qualitative and ordinal information available. / GPL-2	noarch
r-qualvar	0.2.0	Implements indices of qualitative variation proposed by Wilcox (1973). / GPL-3	noarch
r-quandl	2.10.0	Functions for interacting directly with the Quandl API to offer data in a number of formats usable in R, downloading a zip with all data from a Quandl database, and the ability to search. This R package uses the Quandl API. For more information go to < <a href="https://www.quandl.com/docs/api">https://www.quandl.com/docs/api</a> >. For more help on the package itself go to < <a href="https://www.quandl.com/help/r">https://www.quandl.com/help/r</a> >. / MIT	noarch
r-quantileda	1.1	Code for centroid, median and quantile classifiers. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-quantilegrader</a>	0.1.1	Implementation of the food safety restaurant grading system adopted by Public Health - Seattle & King County (see Ashwood, Z.C., Elias, B., and Ho. D.E. Improving the Reliability of Food Safety Disclosure: A Quantile Adjusted Restaurant Grading System for Seattle-King County (working paper)). As reported in the accompanying paper, this package allows jurisdictions to easily implement refinements that address common challenges with unadjusted grading systems. First, in contrast to unadjusted grading, where the most recent single routine inspection is the primary determinant of a grade, grading inputs are allowed to be flexible. For instance, it is straightforward to base the grade on average inspection scores across multiple inspection cycles. Second, the package can identify quantile cutoffs by inputting substantively meaningful regulatory thresholds (e.g., the proportion of establishments receiving sufficient violation points to warrant a return visit). Third, the quantile adjustment equalizes the proportion of establishments in a flexible number of grading categories (e.g., A/B/C) across areas (e.g., ZIP codes, inspector areas) to account for inspector differences. Fourth, the package implements a refined quantile adjustment that addresses two limitations with the <code>stats::quantile()</code> function when applied to inspection score datasets with large numbers of score ties. The quantile adjustment algorithm iterates over quantiles until, over all restaurants in all areas, grading proportions are within a tolerance of desired global proportions. In addition the package allows a modified definition of quantile from Nearest Rank. Instead of requiring that at least $p[1]\%$ of restaurants receive the top grade and at least $(p[1]p[2])\%$ of restaurants receive the top or second best grade for quantiles $p$ , the algorithm searches for cutoffs so that as close as possible $p[1]\%$ of restaurants receive the top grade, and as close as possible to $p[2]\%$ of restaurants receive the second top grade. / GPL-2	noarch
<a href="#">r-quantilenpci</a>	0.9.0	Based on Alan D. Hutson (1999) <doi:10.1080/02664769922458>, Calculating nonparametric confidence intervals for quantiles using fractional order statistics, Journal of Applied Statistics, 26:3, 343-353. / GPL-3	noarch
<a href="#">r-quantmod</a>	0.4.1	Specify, build, trade, and analyse quantitative financial trading strategies. / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-quantnorm</a>	1.0.5	Modifies the distance matrix obtained from data with batch effects, so as to improve the performance of sample pattern detection, such as clustering, dimension reduction, and construction of networks between subjects. The method has been published in Bioinformatics (Fei et al, 2018, <doi:10.1093/bioinformatics/bty117>). Also available on 'GitHub' <https://github.com/tengfei-emory/QuantNorm>. / GPL-2	noarch
<a href="#">r-quantpsyc</a>	1.5	Contains functions useful for data screening, testing moderation, mediation and estimating power. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-quantreg</a>	5.38	Estimation and inference methods for models of conditional quantiles: Linear and nonlinear parametric and non-parametric (total variation penalized) models for conditional quantiles of a univariate response and several methods for handling censored survival data. Portfolio selection methods based on expected shortfall risk are also included. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-quantreggrowth</a>	0.4_3	Fits non-crossing regression quantiles as a function of linear covariates and multiple smooth terms via B-splines with L1-norm difference penalties. Monotonicity constraints on the fitted curves are allowed. See Muggeo, Sciandra, Tomasello and Calvo (2013) <doi:10.1007/s10651-012-0232-1> and <doi:10.13140/RG.2.2.12924.85122> for some code example. / GPL-3	noarch
<a href="#">r-quantumops</a>	2.5.3	Contains basic structures and operations used frequently in quantum computing. Intended to be a convenient tool to help learn quantum mechanics and algorithms. Can create arbitrarily sized kets and bras and implements quantum gates, inner products, and tensor products. Creates arbitrarily controlled versions of all gates and can simulate complete or partial measurements of kets. Has functionality to convert functions into equivalent quantum gates. Includes larger applications, such as Steane error correction <DOI:10.1103/physrevlett.77.793>, Quantum Fourier Transform and Shor's algorithm (Shor 1999), Grover's algorithm (1996), Quantum Approximation Optimization Algorithm (QAOA) (Farhi, Goldstone, and Gutmann 2014) <arXiv:1411.4028>, and a variational quantum classifier (Schuld 2018) <arXiv:1804.00633>. / GPL-3	noarch
<a href="#">r-quclu</a>	0.1.0	Various quantile-based clustering algorithms: algorithm CU (Common theta and Unscaled variables), algorithm CS (Common theta and Scaled variables through lambda_j), algorithm VU (Variable-wise theta_j and Unscaled variables) and algorithm VW (Variable-wise theta_j and Scaled variables through lambda_j). Hennig, Viroli, Anderlucci (2018) <arXiv:1806.10403v1>. / GPL-2   GPL-3	noarch
<a href="#">r-queryparser</a>	0.1.1	Translate 'SQL' 'SELECT' statements into lists of 'R' expressions. / Apache License 2.0	noarch
<a href="#">r-queueing</a>	0.2.1	It provides versatile tools for analysis of birth and death based Markovian Queueing Models and Single and Multiclass Product-Form Queueing Networks. It implements M/M/1, M/M/c, M/M/Infinite, M/M/1/K, M/M/c/K, M/M/c/c, M/M/1/K/K, M/M/c/K/K, M/M/c/K/m, M/M/Infinite/K/K, Multiple Channel Open Jackson Networks, Multiple Channel Closed Jackson Networks, Single Channel Multiple Class Open Networks, Single Channel Multiple Class Closed Networks and Single Channel Multiple Class Mixed Networks. Also it provides a B-Erlang, C-Erlang and Engset calculators. This work is dedicated to the memory of D. Sixto Rios Insua. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-quiddich	1.0.0	Provides tools for an automated identification of diagnostic molecular characters, i.e. such columns in a given nucleotide or amino acid alignment that allow to distinguish taxa from each other. These characters can then be used to complement the formal descriptions of the taxa, which are often based on morphological and anatomical features. Especially for morphologically cryptic species, this will be helpful. QUIDDICH distinguishes between four different types of diagnostic characters. For more information, see Kuehn, A.L., Haase, M. 2019. QUIDDICH: QUick IDentification of DIagnostic CHaracters. / GPL-3	noarch
r-quietr	0.1.0	Simplifies output suppression logic in R packages, as it's common to develop some form of it in R. 'quietR' intends to simplify that problem and allow a set of simple toggle functions to be used to suppress console output. / MIT	noarch
r-quran	0.1.0	Full text, in data frames containing one row per verse, of the Qur'an in Arabic (with and without vowels) and in English (the Yusuf Ali and Saheeh International translations), formatted to be convenient for text analysis. / MIT	noarch
r-qvcalc	0.9.1	Functions to compute quasi variances and associated measures of approximation error. / GPL-2   GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-r.blip	1.1	Allows the user to learn Bayesian networks from datasets containing thousands of variables. It focuses on score-based learning, mainly the 'BIC' and the 'BDeu' score functions. It provides state-of-the-art algorithms for the following tasks: (1) parent set identification - Mauro Scanagatta (2015) < <a href="http://papers.nips.cc/paper/5803-learning-bayesian-networks-with-thousands-of-variables">http://papers.nips.cc/paper/5803-learning-bayesian-networks-with-thousands-of-variables</a> >; (2) general structure optimization - Mauro Scanagatta (2018) <doi:10.1007/s10994-018-5701-9>, Mauro Scanagatta (2018) < <a href="http://proceedings.mlr.press/v73/scanagatta17a.html">http://proceedings.mlr.press/v73/scanagatta17a.html</a> >; (3) bounded treewidth structure optimization - Mauro Scanagatta (2016) < <a href="http://papers.nips.cc/paper/6232-learning-treewidth-bounded-bayesian-networks-with-thousands-of-variables">http://papers.nips.cc/paper/6232-learning-treewidth-bounded-bayesian-networks-with-thousands-of-variables</a> >; (4) structure learning on incomplete data sets - Mauro Scanagatta (2018) <doi:10.1016/j.ijar.2018.02.004>. Distributed under the LGPL-3 by IDSIA. / LGPL-3	noarch
r-r.cache	0.13.0	Memoization can be used to speed up repetitive and computational expensive function calls. The first time a function that implements memoization is called the results are stored in a cache memory. The next time the function is called with the same set of parameters, the results are momentarily retrieved from the cache avoiding repeating the calculations. With this package, any R object can be cached in a key-value storage where the key can be an arbitrary set of R objects. The cache memory is persistent (on the file system). / LGPL-2.1	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-r.devices</a>	2.16.0	Functions for creating plots and image files in a unified way regardless of output format (EPS, PDF, PNG, SVG, TIFF, WMF, etc.). Default device options as well as scales and aspect ratios are controlled in a uniform way across all device types. Switching output format requires minimal changes in code. This package is ideal for large-scale batch processing, because it will never leave open graphics devices or incomplete image files behind, even on errors or user interrupts. / LGPL-2.1	noarch
<a href="#">r-r.huge</a>	0.9.0	DEPRECATED. Do not start building new projects based on this package. Cross-platform alternatives are the following packages: bigmemory (CRAN), ff (CRAN), BufferedMatrix (Bioconductor). The main usage of it was inside the aroma.affymetrix package. (The package currently provides a class representing a matrix where the actual data is stored in a binary format on the local file system. This way the size limit of the data is set by the file system and not the memory.) / LGPL-2.1	noarch
<a href="#">r-r.matlab</a>	3.6.2	Methods readMat() and writeMat() for reading and writing MAT files. For user with MATLAB v6 or newer installed (either locally or on a remote host), the package also provides methods for controlling MATLAB (trademark) via R and sending and retrieving data between R and MATLAB. / LGPL-2.1	noarch
<a href="#">r-r.methodss3</a>	1.7.1	Methods that simplify the setup of S3 generic functions and S3 methods. Major effort has been made in making definition of methods as simple as possible with a minimum of maintenance for package developers. For example, generic functions are created automatically, if missing, and naming conflict are automatically solved, if possible. The method setMethodS3() is a good start for those who in the future may want to migrate to S4. This is a cross-platform package implemented in pure R that generates standard S3 methods. / LGPL (>= 2.1)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-r.oo</a>	1.22.0	Methods and classes for object-oriented programming in R with or without references. Large effort has been made on making definition of methods as simple as possible with a minimum of maintenance for package developers. The package has been developed since 2001 and is now considered very stable. This is a cross-platform package implemented in pure R that defines standard S3 classes without any tricks. / LGPL (>= 2.1)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-r.utils</a>	2.8.0	Utility functions useful when programming and developing R packages. / LGPL (>= 2.1)	linux-32, linux-64, noarch, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
r-r0	1.2.6	Estimation of reproduction numbers for disease outbreak, based on incidence data. The R0 package implements several documented methods. It is therefore possible to compare estimations according to the methods used. Depending on the methods requested by user, basic reproduction number (commonly denoted as R0) or real-time reproduction number (referred to as R(t)) is computed, along with a 95% Confidence Interval. Plotting outputs will give different graphs depending on the methods requested : basic reproductive number estimations will only show the epidemic curve (collected data) and an adjusted model, whereas real-time methods will also show the R(t) variations throughout the outbreak time period. Sensitivity analysis tools are also provided, and allow for investigating effects of varying Generation Time distribution or time window on estimates. / GPL-2	noarch
r-r1magic	0.3.2	Utilities for sparse signal recovery suitable for compressed sensing. L1, L2 and TV penalties, DFT basis matrix, simple sparse signal generator, mutual cumulative coherence between two matrices and examples, Lp complex norm, scaling back regression coefficients. / GPL-3	noarch
r-r2admb	0.7.1	A series of functions to call 'AD Model Builder' (i.e., compile and run models) from within R, read the results back into R as 'admb' objects, and provide standard accessors (i.e. coef(), vcov(), etc.) / GPL-3	noarch
r-r2beat	1.0.0	Multivariate optimal allocation for different domains in one and two stages stratified sample design. R2BEAT extends the Neyman (1934) <doi:10.2307/2342192> – Tschuprow (1923) allocation method to the case of several variables, adopting a generalization of the Bethel's proposal (1989). R2BEAT develops this methodology but, moreover, it allows to determine the sample allocation in the multivariate and multi-domains case of estimates for two-stage stratified samples. / EUPL	noarch
r-r2d2	1.0.0	This package provides generic functions to analyze the distribution of two continuous variables: 'conf2d' to calculate a smooth empirical confidence region, and 'freq2d' to calculate a frequency distribution. / GPL-2	noarch
r-r2d3	0.2.3	Suite of tools for using 'D3', a library for producing dynamic, interactive data visualizations. Supports translating objects into 'D3' friendly data structures, rendering 'D3' scripts, publishing 'D3' visualizations, incorporating 'D3' in R Markdown, creating interactive 'D3' applications with Shiny, and distributing 'D3' based 'htmlwidgets' in R packages. / BSD_3_clause file LICENSE	noarch
r-r2dgc	1.0.3	Provides functions for aligning 2D gas chromatography mass spectrometry derived metabolite peaks obtained from primary processing and generates an alignment table that allows for a comparison of common peaks across samples and metabolite identification. Publication describing the package in detail is available at the following citation: Ryne C. Ramaker, Emily Gordon, Sara J. Cooper (2017) <doi:10.1101/179168>. / MIT	noarch
r-r2dt	0.1	Some heavily used base R functions are reconstructed to also be compliant to data.table objects. Also, some general helper functions that could be of interest for working with data.table objects are included. / GPL-3	noarch
r-r2html	2.3.2	Includes HTML function and methods to write in an HTML file. Thus, making HTML reports is easy. Includes a function that allows redirection on the fly, which appears to be very useful for teaching purpose, as the student can keep a copy of the produced output to keep all that he did during the course. Package comes with a vignette describing how to write HTML reports for statistical analysis. Finally, a driver for 'Sweave' allows to parse HTML flat files containing R code and to automatically write the corresponding outputs (tables and graphs). / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-r2openbugs</a>	3.2.3	Using this package, it is possible to call a BUGS model, summarize inferences and convergence in a table and graph, and save the simulations in arrays for easy access in R. / GPL-2	noarch
<a href="#">r-r2pmml</a>	0.23.0	R wrapper for the JPMML-R library < <a href="https://github.com/jpmml/jpmml-r">https://github.com/jpmml/jpmml-r</a> >, which converts R models to Predictive Model Markup Language (PMML). / AGPL-3	noarch
<a href="#">r-r2stl</a>	1.0.0	r2stl, R package for visualizing data using a 3D printer Package r2stl converts R data to STL (stereolithography) files that can be used to feed a 3-dimensional printer. The 3-dimensional output from an R function can be materialized into a solid surface in a plastic material, therefore allowing more detailed examination. There are many possible uses for this new R tool, such as to examine mathematical expressions with very irregular shapes, to aid teaching people with impaired vision, to create raised relief maps from digital elevation maps (DEMs), to bridge the gap between mathematical tools and rapid prototyping, and many more. Ian Walker created the function r2stl and Jose' Gama assembled the package. / CC BY-NC-SA 3.0	noarch
<a href="#">r-r2winbugs</a>	2.1.2	Invoke a 'BUGS' model in 'OpenBUGS' or 'WinBUGS', a class bugs for 'BUGS' results and functions to work with that class. Function write.model() allows a 'BUGS' model file to be written. The class and auxiliary functions could be used with other MCMC programs, including 'JAGS'. / GPL-2	noarch
<a href="#">r-r3port</a>	0.1.1	Create and combine HTML and PDF reports from within R. Possibility to design tables and listings for reporting and also include R plots. / GPL-2	noarch
<a href="#">r-r4couchdb</a>	0.7.5	Provides a collection of functions for basic database and document management operations such as add, get, list access or delete. Every cdbFunction() gets and returns a list() containing the connection setup. Such a list can be generated by cdbIni(). / MIT	noarch
<a href="#">r-r6</a>	2.4.0	Creates classes with reference semantics, similar to R's built-in reference classes. Compared to reference classes, R6 classes are simpler and lighter-weight, and they are not built on S4 classes so they do not require the methods package. These classes allow public and private members, and they support inheritance, even when the classes are defined in different packages. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-r62s3</a>	1.3.1	After defining an R6 class, R62S3 is used to automatically generate optional S3/S4 generics and methods for dispatch. Also allows piping for R6 objects. / MIT	noarch
<a href="#">r-r6ds</a>	1.2.0	Provides reference classes implementing some useful data structures. The package implements these data structures by using the reference class R6. Therefore, the classes of the data structures are also reference classes which means that their instances are passed by reference. The implemented data structures include stack, queue, double-ended queue, doubly linked list, set, dictionary and binary search tree. See for example < <a href="https://en.wikipedia.org/wiki/Data_structure">https://en.wikipedia.org/wiki/Data_structure</a> > for more information about the data structures. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-radanalysis</a>	0.5.5	It has tools for normalization of rank abundance distributions (RAD) to a desired number of ranks using MaxRank Normalization method. RADs are commonly used in biology/ecology and mathematically equivalent to complementary cumulative distributions (CCDFs) which are used in physics, linguistics and sociology and more generally in data science. / GPL-3	noarch
<a href="#">r-radar</a>	1.0.0	Fundamental formulas for Radar, for attenuation, range, velocity, effectiveness, power, scatter, doppler, geometry, radar equations, etc. Based on Nick Guy's Python package PyRadarMet / GPL-3	noarch
<a href="#">r-radarboxplot</a>	1.0.0	Creates the radar-boxplot, a plot that was created by the author during his doctoring in forest resources. The radar-boxplot is a visualization feature suited for multivariate classification/clustering. It provides an intuitive deep understanding of the data. / MIT	noarch
<a href="#">r-radarchart</a>	0.3.1	Create interactive radar charts using the 'Chart.js' 'JavaScript' library and the 'htmlwidgets' package. 'Chart.js' < <a href="http://www.chartjs.org/">http://www.chartjs.org/</a> > is a lightweight library that supports several types of simple chart using the 'HTML5' canvas element. This package provides an R interface specifically to the radar chart, sometimes called a spider chart, for visualising multivariate data. / MIT	noarch
<a href="#">r-raddata</a>	1.0.0	Nuclear Decay Data for Dosimetric Calculations from the International Commission on Radiological Protection from ICRP Publication 107. Ann. ICRP 38 (3). Eckerman, Keith and Endo, Akira 2008 < <a href="https://doi.org/10.1016/j.icrp.2008.10.004">doi:10.1016/j.icrp.2008.10.004</a> > < <a href="http://www.icrp.org/publication.asp?id=ICRP%20Publication%20107">http://www.icrp.org/publication.asp?id=ICRP%20Publication%20107</a> >. This is a database of the physical data needed in calculations of radionuclide-specific protection and operational quantities. The data is prescribed by the ICRP, the international authority on radiation dose standards, for estimating dose from the intake of or exposure to radionuclides in the workplace and the environment. The database contains information on the half-lives, decay chains, and yields and energies of radiations emitted in nuclear transformations of 1252 radionuclides of 97 elements. / GPL-2	noarch
<a href="#">r-radiosonde</a>	1.4	RadioSonde is a collection of programs for reading and plotting SKEW-T, log p diagrams and wind profiles for data collected by radiosondes (the typical weather balloon-borne instrument), which we will call flights, sondes, or profiles throughout the associated documentation. The raw data files are in a common format that has a header followed by specific variables. Use help(ExampleSonde) for the full explanation of the data files. / GPL-2	noarch
<a href="#">r-radjust</a>	0.1.0	Calculates adjusted p-values for the null hypothesis of no replicability across studies for two study designs: (i) a primary and follow-up study, where the features in the follow-up study are selected from the primary study, as described in Bogomolov and Heller (2013) < <a href="https://doi.org/10.1080/01621459.2013.829002">doi:10.1080/01621459.2013.829002</a> > and Heller, Bogomolov and Benjamini (2014) < <a href="https://doi.org/10.1073/pnas.1314814111">doi:10.1073/pnas.1314814111</a> >; (ii) two independent studies, where the features for replicability are first selected in each study separately, as described in Bogomolov and Heller (2018) < <a href="https://doi.org/10.1093/biomet/asv029">doi:10.1093/biomet/asv029</a> >. The latter design is the one encountered in a typical meta-analysis of two studies, but the inference is for replicability rather than for identifying the features that are non-null in at least one study. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-radviz</a>	0.7.0	An implementation of the radviz projection in R. It enables the visualization of multidimensional data while maintaining the relation to the original dimensions. This package provides functions to create and plot radviz projections, and a number of summary plots that enable comparison and analysis. For reference see Ankerst et al. (1996) < <a href="http://citeseer.ist.psu.edu/viewdoc/summary?doi=10.1.1.68.1811">http://citeseer.ist.psu.edu/viewdoc/summary?doi=10.1.1.68.1811</a> > for original implementation, see Di Caro et al. (2010) <DOI:10.1007/978-3-642-13672-6_13> for the original method for dimensional anchor arrangements. / CC BY-NC-SA 4.0	noarch
<a href="#">r-radwords</a>	0.1.18	Aims at loading Google Adwords data into R. Adwords is an online advertising service that enables advertisers to display advertising copy to web users (see < <a href="https://developers.google.com/adwords/">https://developers.google.com/adwords/</a> > for more information). Therefore the package implements three main features. First, the package provides an authentication process for R with the Google Adwords API (see < <a href="https://developers.google.com/adwords/api/">https://developers.google.com/adwords/api/</a> > for more information) via OAuth2. Second, the package offers an interface to apply the Adwords query language in R and query the Adwords API with ad-hoc reports. Third, the received data are transformed into suitable data formats for further data processing and data analysis. / MIT	noarch
<a href="#">r-rafalib</a>	1.0.0	A series of shortcuts for routine tasks originally developed by Rafael A. Irizarry to facilitate data exploration. / Artistic-2.0	noarch
<a href="#">r-rahrefs</a>	0.1.4	Enables downloading detailed reports from < <a href="https://ahrefs.com">https://ahrefs.com</a> > about backlinks from pointing to website, provides authentication with an API key as well as ordering, grouping and filtering functionalities. / MIT	noarch
<a href="#">r-rainfallerosivityfactor</a>	0.1.0	Determination of rainfall-runoff erosivity factor. / GPL-2	noarch
<a href="#">r-rainfarmr</a>	0.1	An implementation of the RainFARM (Rainfall Filtered Autoregressive Model) stochastic precipitation downscaling method (Rebora et al. (2006) <doi:10.1175/JHM517.1>). Adapted for climate downscaling according to D'Onofrio et al. (2018) <doi:10.1175/JHM-D-13-096.1> and for complex topography as in Terzago et al. (2018) <doi:10.5194/nhess-18-2825-2018>. The RainFARM method is based on the extrapolation to small scales of the Fourier spectrum of a large-scale precipitation field, using a fixed logarithmic slope and random phases at small scales, followed by a nonlinear transformation of the resulting linearly correlated stochastic field. RainFARM allows to generate ensembles of spatially downscaled precipitation fields which conserve precipitation at large scales and whose statistical properties are consistent with the small-scale statistics of observed precipitation, based only on knowledge of the large-scale precipitation field. / Apache License 2.0	noarch
<a href="#">r-raltmetric</a>	0.7.0	Provides a programmatic interface to the citation information and alternate metrics provided by 'Altmetric'. Data from Altmetric allows researchers to immediately track the impact of their published work, without having to wait for citations. This allows for faster engagement with the audience interested in your work. For more information, visit < <a href="https://www.altmetric.com/">https://www.altmetric.com/</a> >. / MIT	noarch
<a href="#">r-ramble</a>	0.1.1	Parser generator for R using combinatory parsers. It is inspired by combinatory parsers developed in Haskell. / MIT	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-ramchoice</a>	1.1	It is widely documented in psychology, economics and other disciplines that socio-economic agent may not pay full attention to all available alternatives, rendering standard revealed preference theory invalid. This package implements the estimation and inference procedures of Cattaneo, Ma, Masatlioglu and Suleymanov (2019) <arXiv:1712.03448>, which utilizes standard choice data to partially identify and estimate a decision maker's preference. For inference, several simulation-based critical values are provided. / GPL-2	noarch
<a href="#">r-ramify</a>	0.3.3	Additional matrix functionality for R including: (1) wrappers for the base matrix function that allow matrices to be created from character strings and lists (the former is especially useful for creating block matrices), (2) better printing of large matrices via the generic pretty print function, and (3) a number of convenience functions for users more familiar with other scientific languages like 'Julia', 'Matlab'/'Octave', or 'Python'/'NumPy'. / GPL-2	noarch
<a href="#">r-rampath</a>	0.4	We rewrite of RAMPpath software developed by John McArdle and Steven Boker as an R package. In addition to performing regular SEM analysis through the R package lavaan, RAMPpath has unique features. First, it can generate path diagrams according to a given model. Second, it can display path tracing rules through path diagrams and decompose total effects into their respective direct and indirect effects as well as decompose variance and covariance into individual bridges. Furthermore, RAMPpath can fit dynamic system models automatically based on latent change scores and generate vector field plots based upon results obtained from a bivariate dynamic system. Starting version 0.4, RAMPpath can conduct power analysis for both univariate and bivariate latent change score models. / GPL-2	noarch
<a href="#">r-randcorr</a>	1.0	Implements the algorithm by Pourahmadi and Wang (2015) <doi:10.1016/j.spl.2015.06.015> for generating a random $p \times p$ correlation matrix. Briefly, the idea is to represent the correlation matrix using Cholesky factorization and $p(p-1)/2$ hyperspherical coordinates (i.e., angles), sample the angles from a particular distribution and then convert to the standard correlation matrix form. The angles are sampled from a distribution with pdf proportional to $\sin^k(\theta)$ ( $0 < \theta < \pi$ , $k \geq 1$ ) using the efficient sampling algorithm described in Enes Makalic and Daniel F. Schmidt (2018) <arXiv:1809.05212>. / GPL-3	noarch
<a href="#">r-randgeo</a>	0.3.0	Generate random positions (latitude/longitude), Well-known text ('WKT') points or polygons, or 'GeoJSON' points or polygons. / MIT	noarch
<a href="#">r-randmeta</a>	0.1.0	A novel numerical algorithm that provides functionality for estimating the exact 95% confidence interval of the location parameter in the random effects model, and is much faster than the naive method. Works best when the number of studies is between 6-20. / GPL-2	noarch
<a href="#">r-random</a>	0.2.6	The true random number service provided by the RANDOM.ORG website created by Mads Haahr samples atmospheric noise via radio tuned to an unused broadcasting frequency together with a skew correction algorithm due to John von Neumann. More background is available in the included vignette based on an essay by Mads Haahr. In its current form, the package offers functions to retrieve random integers, randomized sequences and random strings. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-randomforest	4.6_14	Classification and regression based on a forest of trees using random inputs, based on Breiman (2001) <DOI:10.1023/A:1010933404324>. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
r-randomglm	1.02_1	The package implements a bagging predictor based on general linear models / GPL-2	noarch
r-randomizebe	0.3_5	Contains a function to randomize subjects, patients in groups of sequences (treatment sequences). If a blocksize is given, the randomization will be done within blocks. The randomization may be controlled by a Wald-Wolfowitz runs test. Functions to obtain the p-value of that test are included. The package is mainly intended for randomization of bioequivalence studies but may be used also for other clinical crossover studies. Contains two helper functions sequences() and williams() to get the sequences of commonly used designs in BE studies. / GPL (>= 2.0)	noarch
r-randtests	1.0	Several non parametric randomness tests for numeric sequences / GPL-2	noarch
r-rangemodelr	1.0.4	Generates expected values of species richness, with continuous or scattered ranges, for data across one or two dimensions. / GPL-2	noarch
r-ranger	0.11.2	A fast implementation of Random Forests, particularly suited for high dimensional data. Ensembles of classification, regression, survival and probability prediction trees are supported. Data from genome-wide association studies can be analyzed efficiently. In addition to data frames, datasets of class 'gwaa.data' (R package 'GenABEL') and 'dgCMatrx' (R package 'Matrix') can be directly analyzed. / GPL-3	linux-32, linux-64, osx-64, win-32, win-64
r-rankfd	0.0.3	The rankFD() function calculates the Wald-type statistic (WTS) and the ANOVA-type statistic (ATS) for nonparametric factorial designs, e.g., for count, ordinal or score data in a crossed design with an arbitrary number of factors. / GPL-2   GPL-3	noarch
r-rankhazard	1.1.0	Rank-hazard plots Karvanen and Harrell (2009) <DOI:10.1002/sim.3591> visualize the relative importance of covariates in a proportional hazards model. The key idea is to rank the covariate values and plot the relative hazard as a function of ranks scaled to interval [0,1]. The relative hazard is plotted in respect to the reference hazard, which can be e.g. the hazard related to the median of the covariate. / GPL-2	noarch
r-rankingproject	0.1.1	Functions to generate plots and tables for comparing independently- sampled populations. Companion package to A Primer on Visualizations for Comparing Populations, Including the Issue of Overlapping Confidence Intervals by Wright, Klein, and Wieczorek (2017, in press). / GPL-2	noarch
r-rankresponse	3.1.1	Methods for ranking responses of a single response question or a multiple response question / GPL-2	noarch
r-rap	1.1	To find the reversal association between variables. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-rapiclient	0.1.2	Access services specified in OpenAPI (formerly Swagger) format. It is not a code generator. Client is generated dynamically as a list of R functions. / MIT	noarch
r-rapidjsonr	1.1	Provides JSON parsing capability through the ‘Rapidjson’ ‘C’ header-only library. / MIT	noarch
r-rapidxmlr	0.1.0	Provides XML parsing capability through the ‘Rapidxml’ ‘C’ header-only library. / MIT	noarch
r-rappdirs	0.3.1	An easy way to determine which directories on the users computer you should use to save data, caches and logs. A port of Python’s ‘Appdirs’ ( <a href="https://github.com/ActiveState/appdirs">url{https://github.com/ActiveState/appdirs}</a> ) to R. / MIT file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
r-raptor	1.0.0	Performs wood cell anatomical data analyses on spatially explicit xylem (tracheids) datasets derived from thin sections of woody tissue. The package includes functions for visualisation, detection and alignment of continuous tracheid radial file (defined as rows) and individual tracheid position within an annual ring of coniferous species. This package is designed to be used with elaborate cell output, e.g. as provided with ROXAS (von Arx & Carrer, 2014 <doi:10.1016/j.dendro.2013.12.001>). The package has been validated for Picea abies, Larix Siberica, Pinus cembra and Pinus sylvestris. / GPL-2	noarch
r-rarity	1.3_6	Allows calculation of rarity weights for species and indices of rarity for assemblages of species according to different methods (Leroy et al. 2012, Insect. Conserv. Divers. 5:159-168 <doi:10.1111/j.1752-4598.2011.00148.x>; Leroy et al. 2013, Divers. Distrib. 19:794-803 <doi:10.1111/ddi.12040>). / GPL (>= 2.0)	noarch
r-rasciidoc	2.0.0	Inspired by Karl Broman’s reader on using ‘knitr’ with ‘asciidoc’ (< <a href="http://kbroman.org/knitr_knutshell/pages/asciidoc.html">http://kbroman.org/knitr_knutshell/pages/asciidoc.html</a> >), this is merely a wrapper to ‘knitr’ and ‘asciidoc’. / BSD_2_clause	noarch
r-raster	2.8_1	Reading, writing, manipulating, analyzing and modeling of gridded spatial data. The package implements basic and high-level functions. Processing of very large files is supported. / GPL (>= 3)	linux-32, linux-64, osx-64, win-32, win-64
r-rasterize	0.1	Provides R functions to selectively rasterize components of ‘grid’ output. / GPL-3	noarch
r-rasterlist	0.5.8	A S4 class has been created such that complex operations can be executed on each cells of a raster map. The raster of objects contains the traditional raster map with the addition of a list of generic objects: one object for each raster cells. It allows to write few lines of R code for complex map algebra. Two environmental applications about frequency analysis of raster map of precipitation and creation of a raster map of soil water retention curves have been presented. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<code>r-rastervis</code>	0.46	Methods for enhanced visualization and interaction with raster data. It implements visualization methods for quantitative data and categorical data, both for univariate and multivariate rasters. It also provides methods to display spatiotemporal rasters, and vector fields. See the website for examples. / GPL-3	noarch
<code>r-ratedistortion</code>	1.01	An implementation of routines for solving rate-distortion problems. Rate-distortion theory is a field within information theory that examines optimal lossy compression. That is, given that some information must be lost, how can a communication channel be designed that minimizes the cost of communication error? Rate-distortion theory is concerned with the optimal (minimal cost) solution to such tradeoffs. An important tool for solving rate-distortion problems is the Blahut algorithm, developed by Richard Blahut and described in: . Blahut, R. E. (1972). Computation of channel capacity and rate-distortion functions. IEEE Transactions on Information Theory, IT-18(4), 460-473. . This package implements the basic Blahut algorithm, and additionally contains a number of ‘helper’ functions, including a routine for searching for an information channel that minimizes cost subject to a constraint on information rate. / GPL-2	noarch
<code>r-ratelimitr</code>	0.4.1	Allows to limit the rate at which one or more functions can be called. / MIT	noarch
<code>r-rateratio.test</code>	1.0.2	A function which performs exact rate ratio tests and returns an object of class <code>htest</code> . / GPL-3	noarch
<code>r-raters</code>	2.0.1	The kappa statistic implemented by Fleiss is a very popular index for assessing the reliability of agreement among multiple observers. It is used both in the psychological and in the psychiatric field. Other fields of application are typically medicine, biology and engineering. Unfortunately, the kappa statistic may behave inconsistently in case of strong agreement between raters, since this index assumes lower values than it would have been expected. We propose a modification kappa implemented by Fleiss in case of nominal and ordinal variables. Monte Carlo simulations are used both to testing statistical hypotheses and to calculating percentile bootstrap confidence intervals based on proposed statistic in case of nominal and ordinal data. / GPL-2	noarch
<code>r-ratesci</code>	0.3.0	Computes confidence intervals for the rate (or risk) difference (‘RD’) or rate ratio (or relative risk, ‘RR’) for binomial proportions or Poisson rates, or for odds ratio (‘OR’, binomial only). Also confidence intervals for a single binomial or Poisson rate, and intervals for matched pairs. Includes skewness-corrected asymptotic score (‘SCAS’) methods, which have been developed in Laud (2017) <doi:10.1002/pst.1813> from Miettinen & Nurminen (1985) <doi:10.1002/sim.4780040211> and Gart & Nam (1988) <doi:10.2307/2531848>. Also includes MOVER methods (Method Of Variance Estimates Recovery) for all contrasts, derived from the Newcombe method but using equal-tailed Jeffreys intervals, and generalised for Bayesian applications incorporating prior information. So-called ‘exact’ methods for strictly conservative coverage are approximated using continuity corrections. Also includes methods for stratified calculations (e.g. meta-analysis), either assuming fixed effects or incorporating stratum heterogeneity. / GPL-3	noarch
<code>r-ratios</code>	1.2.0	Calculation of ratios between two data sets containing environmental data like element concentrations by different methods. Additionally plant element concentrations can be corrected for adhering particles (soil, airborne dust). / GPL-3	noarch
<code>r-rattle.data</code>	1.0.2	Contains the datasets used as default examples by the rattle package. The datasets themselves can be used independently of the rattle package to illustrate analytics, data mining, and data science tasks. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-raw	0.1.6	In order to facilitate R instruction for actuaries, we have organized several sets of publicly available data of interest to non-life actuaries. In addition, we suggest a set of packages, which most practicing actuaries will use routinely. Finally, there is an R markdown skeleton for basic reserve analysis. / CC0	noarch
r-rbenchmark	1.0.0	rbenchmark is inspired by the Perl module Benchmark, and is intended to facilitate benchmarking of arbitrary R code. The library consists of just one function, benchmark, which is a simple wrapper around system.time. Given a specification of the benchmarking process (counts of replications, evaluation environment) and an arbitrary number of expressions, benchmark evaluates each of the expressions in the specified environment, replicating the evaluation as many times as specified, and returning the results conveniently wrapped into a data frame. / GPL-2	noarch
r-rbiouml	1.8	Functions for connecting to BioUML server, querying BioUML repository and launching BioUML analyses. / GPL-2	noarch
r-rbit	1.0.0	A simple implementation of Binary Indexed Tree by R. The BinaryIndexedTree class supports construction of Binary Indexed Tree from a vector, update of a value in the vector and query for the sum of a interval of the vector. / MIT	noarch
r-rbitcoin	0.9.2	Utilities related to Bitcoin. Unified markets API interface (bitstamp, kraken, btce, bitmarket). Both public and private API calls. Integration of data structures for all markets. Support SSL. Read Rbitcoin documentation (command: ?btc) for more information. / MIT	noarch
r-rbitcoinchartsapi	1.0.4	An R package for the BitCoinCharts.com API. / LGPL-3	noarch
r-rbldatalicense	0.2.1	R interface to access prices and market data with the 'Bloomberg Data License' service from < <a href="https://www.bloomberg.com/professional/product/data-license/">https://www.bloomberg.com/professional/product/data-license/</a> >. As a prerequisite, a valid Data License from 'Bloomberg' is needed together with the corresponding SFTP credentials and whitelisting of the IP from which accessing the service. This software and its author are in no way affiliated, endorsed, or approved by 'Bloomberg' or any of its affiliates. 'Bloomberg' is a registered trademark. / GPL-3	noarch
r-rbmnn	0.9_2	Creation, manipulation, simulation of linear Gaussian Bayesian networks from text files and more. . . / GPL-2	noarch
r-rbokeh	0.6.3	A native R plotting library that provides a flexible declarative interface for creating interactive web-based graphics, backed by the Bokeh visualization library < <a href="http://bokeh.pydata.org/">http://bokeh.pydata.org/</a> >. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-rbtc	0.1_6	Implementation of the RPC-JSON API for Bitcoin and utility functions for address creation and content analysis of the blockchain. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-rbtt</a>	0.1.0	Tu & Zhou (1999) <doi:10.1002/(SICI)1097-0258(19991030)18:20%3C2749::AID-SIM195%3E3.0.CO;2-C> showed that comparing the means of populations whose data-generating distributions are non-negative with excess zero observations is a problem of great importance in the analysis of medical cost data. In the same study, Tu & Zhou discuss that it can be difficult to control type-I error rates of general-purpose statistical tests for comparing the means of these particular data sets. This package allows users to perform a modified bootstrap-based t-test that aims to better control type-I error rates in these situations. / GPL-3	noarch
<a href="#">r-rca</a>	2.0	Relational Class Analysis (RCA) is a method for detecting heterogeneity in attitudinal data (as described in Goldberg A., 2011, Am. J. Soc, 116(5)). / GPL-2	noarch
<a href="#">r-rcane</a>	1.0	There are different numeric optimizations which are used in order to estimate coefficients in models such as linear regression and neural networks. This package covers parameter estimation in linear regression using different methods such as batch gradient descent, stochastic gradient descent, minibatch gradient descent and coordinate descent. Kiwiel, Krzysztof C (2001) <doi:10.1007/PL00011414> Yu Nesterov (2004) <ISBN:1-4020-7553-7> Ferguson, Thomas S (1982) <doi:10.1080/01621459.1982.10477894> Zeiler, Matthew D (2012) <arXiv:1212.5701> Wright, Stephen J (2015) <arXiv:1502.04759>. / MIT	noarch
<a href="#">r-rcapture</a>	1.4.2	Estimation of abundance and other of demographic parameters for closed populations, open populations and the robust design in capture-recapture experiments using loglinear models. / GPL-2	noarch
<a href="#">r-rcarbon</a>	1.2.0	Enables the calibration and analysis of radiocarbon dates, often but not exclusively for the purposes of archaeological research. It includes functions not only for basic calibration, uncalibration, and plotting of one or more dates, but also a statistical framework for building demographic and related longitudinal inferences from aggregate radiocarbon date lists, including: Monte-Carlo simulation test (Timpson et al 2014 <doi:10.1016/j.jas.2014.08.011>), random mark permutation test (Crema et al 2016 <doi:10.1371/journal.pone.0154809>) and spatial permutation tests (Crema, Bevan, and Shennan 2017 <doi:10.1016/j.jas.2017.09.007>). / GPL-2	noarch
<a href="#">r-rcarto</a>	0.8	This package makes some maps using shapefiles and dataframes. Five kinds of maps are available : proportionnal circles, proportionnal circles colored by a discretized quantitative variable, proportionnal circles colored by the modalities of a qualitative variable, choropleth and typology. / GPL (>= 2.0)	noarch
<a href="#">r-rcbalance</a>	1.8.5	Tools for large, sparse optimal matching of treated units and control units in observational studies. Provisions are made for refined covariate balance constraints, which include fine and near-fine balance as special cases. Matches are optimal in the sense that they are computed as solutions to network optimization problems rather than greedy algorithms. / MIT	noarch
<a href="#">r-rcsubset</a>	1.1.4	Tools for optimal subset matching of treated units and control units in observational studies, with support for refined covariate balance constraints, (including fine and near-fine balance as special cases). A close relative is the 'rcbalance' package. / MIT	noarch
<a href="#">r-rcc</a>	1.0.0	Functions to implement the parametric and non-parametric bootstrap confidence interval methods described in Morrison and Simon (2017) <arXiv:1702.06986>. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-rcklibs</a>	2.0	An R interface to the Chemistry Development Kit, a Java library for chemoinformatics. Given the size of the library itself, this package is not expected to change very frequently. To make use of the CDK within R, it is suggested that you use the ‘rck’ package. Note that it is possible to directly interact with the CDK using ‘rJava’. However ‘rck’ exposes functionality in a more idiomatic way. The CDK library itself is released as LGPL and the sources can be obtained from <a href="https://github.com/cdk/cdk">https://github.com/cdk/cdk</a> . / LGPL-3	noarch
<a href="#">r-rceim</a>	0.3	An implementation of a stochastic heuristic method for performing multidimensional function optimization. The method is inspired in the Cross-Entropy Method. It does not relies on derivatives, neither imposes particularly strong requirements into the function to be optimized. Additionally, it takes profit from multi-core processing to enable optimization of time-consuming functions. / GPL-2	noarch
<a href="#">r-rclldata</a>	1.3.2	Example dataset for ‘Rcell’ package. Contains images and cell data object. / GPL-2	noarch
<a href="#">r-rcereal</a>	1.2.1	To facilitate using ‘cereal’ with Rcpp. ‘cereal’ is a header-only C11 serialization library. ‘cereal’ takes arbitrary data types and reversibly turns them into different representations, such as compact binary encodings, XML, or JSON. ‘cereal’ was designed to be fast, light-weight, and easy to extend - it has no external dependencies and can be easily bundled with other code or used standalone. Please see <a href="http://uscilab.github.io/cereal">http://uscilab.github.io/cereal</a> for more information. / BSD_2_clause	noarch
<a href="#">r-rcgmin</a>	2013.0	Conjugate gradient minimization of nonlinear functions with box constraints incorporating the Dai/Yuan update. This implementation should be used in place of the CG algorithm of the optim() function. / GPL-2	noarch
<a href="#">r-rchallenge</a>	1.3.0	A simple data science challenge system using R Markdown and Dropbox <a href="https://www.dropbox.com/">https://www.dropbox.com/</a> . It requires no network configuration, does not depend on external platforms like e.g. Kaggle <a href="https://www.kaggle.com/">https://www.kaggle.com/</a> and can be easily installed on a personal computer. / GPL-2	noarch
<a href="#">r-rcheology</a>	3.6.1	Provides a dataset of functions in all base packages of R versions 1.0.1 onwards. / CC0	noarch
<a href="#">r-rchoicedialogs</a>	1.0.6	Collection of portable choice dialog widgets / LGPL-2.1	noarch
<a href="#">r-rcircos</a>	1.2.1	A simple and flexible way to generate Circos 2D track plot images for genomic data visualization is implemented in this package. The types of plots include: heatmap, histogram, lines, scatterplot, tiles and plot items for further decorations include connector, link (lines and ribbons), and text (gene) label. All functions require only R graphics package that comes with R base installation. / GPL-2	noarch
<a href="#">r-rcites</a>	1.0.1	A programmatic interface to the Species <a href="https://speciesplus.net/">https://speciesplus.net/</a> database via the Species/CITES Checklist API <a href="https://api.speciesplus.net/">https://api.speciesplus.net/</a> . / MIT	noarch
<a href="#">r-rclean</a>	1.0.0	To create clearer, more concise code provides this toolbox helps coders to isolate the essential parts of a script that produces a chosen result, such as an object, tables and figures written to disk and even warnings and errors. This work was funded by US National Science Foundation grant SSI-1450277 for applications of End-to-End Data Provenance. / GPL-3	noarch
<a href="#">r-rclinicalcodes</a>	1.0.1	R tools for integrating with the <a href="http://www.clinicalcodes.org">www.clinicalcodes.org</a> web repository / GPL-2	noarch
<a href="#">r-rclipboard</a>	0.1.2	Leverages the functionality of ‘clipboard.js’, a JavaScript library for HTML5-based copy to clipboard from web pages (see <a href="https://clipboardjs.com">https://clipboardjs.com</a> for more information), and provides a reactive copy-to-clipboard UI button component, called ‘rclipButton’, for ‘shiny’ R applications. / MIT	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-rcclone</a>	1.0.2	R version of ‘GenClone’ (a computer program to analyse genotypic data, test for clonality and describe spatial clonal organization, Arnaud-Haond & Belkhir 2007, < <a href="http://wwz.ifremer.fr/clonix/content/download/68205/903914/file/GenClone2.0.setup.zip">http://wwz.ifremer.fr/clonix/content/download/68205/903914/file/GenClone2.0.setup.zip</a> >), this package allows clone handling as ‘GenClone’ does, plus the possibility to work with several populations, Multi-Locus Lineages (MLL) custom definition and use, and p-value calculation for psex statistic (probability of originating from distinct sexual events) and psex_Fis statistic (taking account of Hardy-Weinberg equilibrium departure) as ‘MLGsim’/‘MLGsim2’ (a program for detecting clones using a simulation approach, Stenberg et al. 2003). / GPL (>= 2.0)	noarch
<a href="#">r-rcma</a>	1.1	Tool for providing access to the Java version ‘CMAEvolutionStrategy’ of Nikolaus Hansen. ‘CMA-ES’ is the Covariance Matrix Adaptation Evolution Strategy, see <a href="https://www.lri.fr/~hansen/cmaes_inmatlab.html#java">https://www.lri.fr/~hansen/cmaes_inmatlab.html#java</a> . / GPL-3	noarch
<a href="#">r-rcmdcheck</a>	1.3.2	Run ‘R CMD check’ from ‘R’ programmatically, and capture the results of the individual checks. / MIT file LICENSE	noarch
<a href="#">r-rcolombos</a>	2.0.2	Provides programmatic access to Colombos, a web based interface for exploring and analyzing comprehensive organism-specific cross-platform expression compendia of bacterial organisms. / GPL-3	noarch
<a href="#">r-rcolorbrewer</a>	1.1_2	Provides color schemes for maps (and other graphics) designed by Cynthia Brewer as described at <a href="http://colorbrewer2.org">http://colorbrewer2.org</a> / Apache License 2.0	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-rconics</a>	1.0	Solve some conic related problems (intersection of conics with lines and conics, arc length of an ellipse, polar lines, etc.). / GPL-2	noarch
<a href="#">r-rcorpora</a>	2.0.0	A collection of small text corpora of interesting data. It contains all data sets from ‘dariusk/corpora’. Some examples: names of animals: birds, dinosaurs, dogs; foods: beer categories, pizza toppings; geography: English towns, rivers, oceans; humans: authors, US presidents, occupations; science: elements, planets; words: adjectives, verbs, proverbs, US president quotes. / CC0	noarch
<a href="#">r-rcpp</a>	1.0.1	The ‘Rcpp’ package provides R functions as well as C classes which offer a seamless integration of R and C. Many R data types and objects can be mapped back and forth to C equivalents which facilitates both writing of new code as well as easier integration of third-party libraries. Documentation about ‘Rcpp’ is provided by several vignettes included in this package, via the ‘Rcpp Gallery’ site at < <a href="http://gallery.rcpp.org">http://gallery.rcpp.org</a> >, the paper by Eddelbuettel and Francois (2011, < <a href="https://doi.org/10.18637/jss.v040.i08">doi:10.18637/jss.v040.i08</a> >), the book by Eddelbuettel (2013, < <a href="https://doi.org/10.1007/978-1-4614-6868-4">doi:10.1007/978-1-4614-6868-4</a> >) and the paper by Eddelbuettel and Balamuta (2017, < <a href="https://doi.org/10.7287/peerj.preprints.3188v1">doi:10.7287/peerj.preprints.3188v1</a> >); see ‘citation(Rcpp)’ for details. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-rcpp11</a>	3.1.2.0	Rcpp11 includes a header only C11 library that facilitates integration between R and modern C. / MIT	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-rcpparmadillo</a>	0.9.3002	'Armadillo' is a templated C linear algebra library (by Conrad Sanderson) that aims towards a good balance between speed and ease of use. Integer, floating point and complex numbers are supported, as well as a subset of trigonometric and statistics functions. Various matrix decompositions are provided through optional integration with LAPACK and ATLAS libraries. The 'RcppArmadillo' package includes the header files from the templated 'Armadillo' library. Thus users do not need to install 'Armadillo' itself in order to use 'RcppArmadillo'. From release 7.800.0 on, 'Armadillo' is licensed under Apache License 2; previous releases were under licensed as MPL 2.0 from version 3.800.0 onwards and LGPL-3 prior to that; 'RcppArmadillo' (the 'Rcpp' bindings/bridge to Armadillo) is licensed under the GNU GPL version 2 or later, as is the rest of 'Rcpp'. Note that Armadillo requires a fairly recent compiler; for the g family at least version 4.6.* is required. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-rcppeigen</a>	0.3.3.50	and 'Eigen' integration using 'Rcpp'. 'Eigen' is a C template library for linear algebra: matrices, vectors, numerical solvers and related algorithms. It supports dense and sparse matrices on integer, floating point and complex numbers, decompositions of such matrices, and solutions of linear systems. Its performance on many algorithms is comparable with some of the best implementations based on 'Lapack' and level-3 'BLAS'. The 'RcppEigen' package includes the header files from the 'Eigen' C template library (currently version 3.3.4). Thus users do not need to install 'Eigen' itself in order to use 'RcppEigen'. Since version 3.1.1, 'Eigen' is licensed under the Mozilla Public License (version 2); earlier version were licensed under the GNU LGPL version 3 or later. 'RcppEigen' (the 'Rcpp' bindings/bridge to 'Eigen') is licensed under the GNU GPL version 2 or later, as is the rest of 'Rcpp'. / GPL (>= 2)   file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-rcppprogress</a>	0.4.1	Allows to display a progress bar in the R console for long running computations taking place in c code, and support for interrupting those computations even in multithreaded code, typically using OpenMP. / GPL (>= 3)	noarch
<a href="#">r-rcpproll</a>	0.3.0	Provides fast and efficient routines for common rolling / windowed operations. Routines for the efficient computation of windowed mean, median, sum, product, minimum, maximum, standard deviation and variance are provided. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-rcppthread</a>	0.5.3	Provides a C11-style thread class and thread pool that can safely be interrupted from R; see, Nagler (2018) <arXiv:1811.00450>. / MIT	noarch
<a href="#">r-rcppxptrutils</a>	0.1.1	Provides the means to compile user-supplied C functions with 'Rcpp' and retrieve an 'XPtr' that can be passed to other C components. / MIT	noarch
<a href="#">r-rcreds</a>	0.6.6	Tools to write a list of credentials to an encrypted file and later read from that file into R. The goal is to have a useful alternative to including username/passwords as part of a script or even stored in the clear in a separate text file. Additional tools provided which are specific for connecting to a database. / MIT	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-rcriteo</a>	1.0.2	Aims at loading Criteo online advertising campaign data into R. Criteo < <a href="http://www.criteo.com/">http://www.criteo.com/</a> > is an online advertising service that enables advertisers to display commercial ads to web users. The package provides an authentication process for R with the Criteo API < <a href="http://kb.criteo.com/advertising/content/5/27/en/api.html">http://kb.criteo.com/advertising/content/5/27/en/api.html</a> >. Moreover, the package features an interface to query campaign data from the Criteo API. The data can be downloaded and will be transformed into a R data frame. / GPL-2   MIT	noarch
<a href="#">r-rcriticor</a>	2.0	Goldwin-Pierre correlogram. Research of critical periods in the past. Integrates a time series in a given window. / GPL-2	noarch
<a href="#">r-rcrypt</a>	0.1.1	Provides easy symmetric file encryption using GPG with cryptographically strong defaults. Only symmetric encryption is supported. GPG is pre-installed with most Linux distributions. Windows users will need to install ‘Gpg4win’ ( <a href="http://www.gpg4win.org/">http://www.gpg4win.org/</a> ). OS X users will need to install ‘GPGTools’ ( <a href="https://gpgtools.org/">https://gpgtools.org/</a> ). / MIT	noarch
<a href="#">r-rcssplot</a>	0.3.0	Provides a means to style plots through cascading style sheets. This separates the aesthetics from the data crunching in plots and charts. / GPL-2	noarch
<a href="#">r-rcube</a>	0.5	Provides simplified methods for managing classic Rubik’s cubes and many other modifications of it (such as NxNxN size cubes, void cubes and 8-coloured cubes - so called octa cubes). Includes functions of handling special syntax for managing such cubes; and different approach to plotting 3D cubes without using external libraries (for example ‘OpenGL’). / GPL-3	noarch
<a href="#">r-rcur</a>	1.3	Functions and objects for CUR matrix decomposition. / GPL-2	noarch
<a href="#">r-rcurl</a>	1.95	<del>Wrapper for ‘libcurl’</del> < <a href="http://curl.haxx.se/libcurl/">http://curl.haxx.se/libcurl/</a> > Provides functions to allow one to compose general HTTP requests and provides convenient functions to fetch URIs, get & post forms, etc. and process the results returned by the Web server. This provides a great deal of control over the HTTP/FTP/... connection and the form of the request while providing a higher-level interface than is available just using R socket connections. Additionally, the underlying implementation is robust and extensive, supporting FTP/FTPS/TFTP (uploads and downloads), SSL/HTTPS, telnet, dict, ldap, and also supports cookies, redirects, authentication, etc. / BSD	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-rd2md</a>	0.0.2	The native R functionalities only allow PDF exports of reference manuals. This shall be extended by converting the package documentation files into markdown files and combining them into a markdown version of the package reference manual. / GPL-3	noarch
<a href="#">r-rd2roxygen</a>	1.8	Functions to convert Rd to ‘roxygen’ documentation. It can parse an Rd file to a list, create the ‘roxygen’ documentation and update the original R script (e.g. the one containing the definition of the function) accordingly. This package also provides utilities that can help developers build packages using ‘roxygen’ more easily. The ‘formatR’ package can be used to reformat the R code in the examples sections so that the code will be more readable. / GPL-3	noarch
<a href="#">r-rda</a>	1.0.2	Shrunken Centroids Regularized Discriminant Analysis for the classification purpose in high dimensional data. / GPL-2	noarch
<a href="#">r-rdatacanvas</a>	0.1	Provides basic functionalities for writing a module for <a href="http://datacanvas.io">http://datacanvas.io</a> . The <a href="http://datacanvas.io">http://datacanvas.io</a> is a big data analytics platform that helps data scientists to build, manage and share data pipelines. / BSD_3_clause	noarch
<a href="#">r-rdataretriever</a>	2.0.0	Provides an R interface to the Data Retriever < <a href="http://data-retriever.org/">http://data-retriever.org/</a> > via the Data Retriever’s command line interface. The Data Retriever automates the tasks of finding, downloading, and cleaning public datasets, and then stores them in a local database. / MIT	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-rdbnomics</a>	0.4.7	R access to hundreds of millions data series from DBnomics API (< <a href="https://db.nomics.world/">https://db.nomics.world/</a> >). / AGPL-3	noarch
<a href="#">r-rde</a>	0.1.0	Allows caching of raw data directly in R code. This allows R scripts and R Notebooks to be shared and re-run on a machine without access to the original data. Cached data is encoded into an ASCII string that can be pasted into R code. When the code is run, the data is automatically loaded from the cached version if the original data file is unavailable. Works best for small datasets (a few hundred observations). / GPL-3	noarch
<a href="#">r-rdetools</a>	1.0	The package provides functions for estimating the relevant dimension of a data set in feature spaces, applications to model selection, graphical illustrations and prediction. / GPL-2	noarch
<a href="#">r-rdian</a>	0.1.1	A client library for ‘The Guardian’ ( <a href="https://www.guardian.com/">https://www.guardian.com/</a> ) and their API, this package allows users to search for Guardian articles and retrieve both the content and metadata. / MIT	noarch
<a href="#">r-rdice</a>	1.0.0	A collection of functions to simulate dice rolls and the like. In particular, experiments and exercises can be performed looking at combinations and permutations of values in dice rolls and coin flips, together with the corresponding frequencies of occurrences. When applying each function, the user has to input the number of times (rolls, flips) to toss the dice. Needless to say, the more the tosses, the more the frequencies approximate the actual probabilities. Moreover, the package provides functions to generate non-transitive sets of dice (like Efron’s) and to check whether a given set of dice is non-transitive with given probability. / GPL-2	noarch
<a href="#">r-rdidq</a>	1.0	The package has many function that helps to perform various quality check on the data. It basically provides many function that helps in performing Extrapolative data analysis. / GPL-2	noarch
<a href="#">r-rdistance</a>	2.1.3	Distance-sampling is a popular method for estimating density and abundance of organisms in ecology. Rdistance contains routines that assist with analysis of distance-sampling data collected on point or line transects. Distance models are specified using regression-like formula (similar to lm, glm, etc.). Abundance routines perform automated bootstrapping and automated detection-function selection. Overall (study area) and site-level (transect or point) abundance estimates are available. A large suite of classical, parametric detection functions are included along with some uncommon parametric functions (e.g., Gamma, negative exponential) and non-parametric smoothed distance functions. Custom (user-defined) detection functions are easily implemented (see vignette). The help files and vignettes have been vetted by multiple authors and tested in workshop settings. / GPL-3	noarch
<a href="#">r-rdnase</a>	1.1_1	Comprehensive toolkit for generating various numerical representation schemes of DNA sequence. The descriptors and similarity scores included are extensively used in bioinformatics and chemogenomics. / GPL-2	noarch
<a href="#">r-rdnb</a>	0.1_3	A wrapper for the ‘Deutsche Nationalbibliothek (German National Library) API’, available at < <a href="http://www.dnb.de">http://www.dnb.de</a> >. The German National Library is the German central archival library, collecting, archiving, bibliographically classifying all German and German-language publications, foreign publications about Germany, translations of German works, and the works of German-speaking emigrants published abroad between 1933 and 1945. A personal access token is required for usage. / MIT	noarch

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Name	Version	Summary/License	Platforms
r-rdocumentation	0.8.2	Wraps around the default help functionality in R. Instead of plain documentation files, documentation will show up as it does on < <a href="https://www.rdocumentation.org">https://www.rdocumentation.org</a> >, a platform that shows R documentation from ‘CRAN’, ‘GitHub’ and ‘Bioconductor’, together with informative stats to assess the package quality. / GPL-2	noarch
r-rdota2	0.1.6	An R API Client for Valve’s Dota2. RDota2 can be easily used to connect to the Steam API and retrieve data for Valve’s popular video game Dota2. You can find out more about Dota2 at < <a href="http://store.steampowered.com/app/570/">http://store.steampowered.com/app/570/</a> >. / MIT	noarch
r-rdrobust	0.99.4	Regression-discontinuity (RD) designs are quasi-experimental research designs popular in social, behavioral and natural sciences. The RD design is usually employed to study the (local) causal effect of a treatment, intervention or policy. This package provides tools for data-driven graphical and analytical statistical inference in RD designs: rdrobust() to construct local-polynomial point estimators and robust confidence intervals for average treatment effects at the cutoff in Sharp, Fuzzy and Kink RD settings, rdbwselect() to perform bandwidth selection for the different procedures implemented, and rdplot() to conduct exploratory data analysis (RD plots). / GPL-2	noarch
r-rdroolsjars	1.0.1	External jars required for package ‘Rdrools’. / Apache License 2.0	noarch
r-rdsm	2.1.1	Provides a threads-type programming environment for R. The package gives the R programmer the clearer, more concise shared memory world view, and in some cases gives superior performance as well. In addition, it enables parallel processing on very large, out-of-core matrices. / GPL-2	linux-64
r-rdstk	1.1	This package provides an R interface to Pete Warden’s Data Science Toolkit. See <a href="http://www.datasciencetoolkit.org">www.datasciencetoolkit.org</a> for more information. The source code for this package can be found at <a href="https://github.com/rtelmore/RDSTK">github.com/rtelmore/RDSTK</a> Happy hacking! / BSD_2_clause	noarch
r-rdstreeboot	1.0	A tree bootstrap method for estimating uncertainty in respondent-driven samples (RDS). Quantiles are estimated by multilevel resampling in such a way that preserves the dependencies of and accounts for the high variability of the RDS process. / GPL-2   GPL-3	noarch
r-reactlog	1.0.0	Building interactive web applications with R is incredibly easy with ‘shiny’. Behind the scenes, ‘shiny’ builds a reactive graph that can quickly become intertwined and difficult to debug. ‘reactlog’ (Schloerke 2019) < <a href="https://doi.org/10.5281/zenodo.2591517">doi:10.5281/zenodo.2591517</a> > provides a visual insight into that black box of ‘shiny’ reactivity by constructing a directed dependency graph of the application’s reactive state at any time point in a reactive recording. / GPL-3	noarch
r-reactr	0.4.1	Make it easy to use ‘React’ in R with ‘htmlwidget’ scaffolds, helper dependency functions, an embedded ‘Babel’ ‘transpiler’, and examples. / MIT	noarch
r-read.gb	1.6	Opens complete record(s) with .gb extension from the NCBI/GenBank Nucleotide database and returns a list containing shaped record(s). These kind of files contains detailed records of DNA samples (locus, organism, type of sequence, source of the sequence. ...). An example of record can be found at < <a href="https://www.ncbi.nlm.nih.gov/nuccore/HE799070">https://www.ncbi.nlm.nih.gov/nuccore/HE799070</a> >. / GPL (>= 2.0)	noarch
r-readabf	1.0.1	Loads Axon Binary Files (both ‘ABF’ and ‘ABF2’) created by Axon Instruments/Molecular Devices software such as ‘pClamp’. / GPL-3	noarch
r-readbrukerflexdata	1.8.5	Reads data files acquired by Bruker Daltonics’ matrix-assisted laser desorption/ionization-time-of-flight mass spectrometer of the *flex series. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-readbulk</a>	1.1.2	Combine multiple data files from a common directory. The data files will be read into R and bound together, creating a single large data.frame. A general function is provided along with a specific function for data that was collected using the open-source experiment builder ‘OpenSesame’ < <a href="http://osdoc.cogsci.nl/">http://osdoc.cogsci.nl/</a> >. / GPL-3	noarch
<a href="#">r-readhac</a>	1.0	Read Acoustic HAC format. / GPL-2	noarch
<a href="#">r-readjdx</a>	0.3.25	Import data written in the JCAMP-DX format. This is an instrument-independent format used in the field of spectroscopy. Examples include IR, NMR, and Raman spectroscopy. See the vignette for background and supported formats. The official JCAMP-DX site is < <a href="http://www.jcamp-dx.org/">http://www.jcamp-dx.org/</a> >. / GPL-3	noarch
<a href="#">r-readmldata</a>	0.9_7	Functions for reading data sets in different formats for testing machine learning tools are provided. This allows to run a loop over several data sets in their original form, for example if they are downloaded from UCI Machine Learning Repository. The data are not part of the package and have to be downloaded separately. / GPL-3	noarch
<a href="#">r-readmnist</a>	1.0.6	You can use the function Read.mnist() to read data and arrange them properly from MNIST dataset (the open handwriting digit database < <a href="http://yann.lecun.com/exdb/mnist/">http://yann.lecun.com/exdb/mnist/</a> >). With this package, you can conveniently get all of necessary informations and then immediately start to check whether your machine learning algorithm works well. It can automatically recognize the type of dataset and returns the informations in corresponding structure. / GPL-3	noarch
<a href="#">r-readmzxmldata</a>	2.8.1	Functions for reading mass spectrometry data in mzXML format. / GPL-3	noarch
<a href="#">r-readoffice</a>	0.2.2	Reads in text from ‘unstructured’ modern Microsoft Office files (XML based files) such as Word and PowerPoint. This does not read in structured data (from Excel or Access) as there are many other great packages to that do so already. / Unlimited	noarch
<a href="#">r-readr</a>	1.3.1	The goal of ‘readr’ is to provide a fast and friendly way to read rectangular data (like ‘csv’, ‘tsv’, and ‘fwf’). It is designed to flexibly parse many types of data found in the wild, while still cleanly failing when data unexpectedly changes. / GPL (>= 2)   file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-readxl</a>	1.3.1	Import excel files into R. Supports ‘.xls’ via the embedded ‘libxls’ C library < <a href="https://github.com/evanmiller/libxls">https://github.com/evanmiller/libxls</a> > and ‘.xlsx’ via the embedded ‘RapidXML’ C library < <a href="https://rapidxml.sourceforge.net">https://rapidxml.sourceforge.net</a> >. Works on Windows, Mac and Linux without external dependencies. / GPL-3	linux-32, linux-64, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
r-realvams	0.4.3	Fits a multivariate value-added model (VAM), see Broatch, Green, and Karl (2018) <doi:10.32614/RJ-2018-033> and Broatch and Lohr (2012) <doi:10.3102/1076998610396900>, with normally distributed test scores and a binary outcome indicator. A pseudo-likelihood approach, Wolfinger (1993) <doi:10.1080/00949659308811554>, is used for the estimation of this joint generalized linear mixed model. The inner loop of the pseudo-likelihood routine (estimation of a linear mixed model) occurs in the framework of the EM algorithm presented by Karl, Yang, and Lohr (2013) <DOI:10.1016/j.csda.2012.10.004>. This material is based upon work supported by the National Science Foundation under grants DRL-1336027 and DRL-1336265. / GPL-2	linux-64, osx-64, win-64
r-reams	0.1	Resampling methods for adaptive linear model selection. These can be thought of as extensions of the Akaike information criterion that account for searching among candidate models. / GPL-2	noarch
r-rearrangement	2.1	The rearrangement operator (Hardy, Littlewood, and Polya 1952) for univariate, bivariate, and trivariate point estimates of monotonic functions. The package additionally provides a function that creates simultaneous confidence intervals for univariate functions and applies the rearrangement operator to these confidence intervals. / GPL-2	noarch
r-reat	3.0.1	Collection of models and analysis methods used in regional and urban economics and (quantitative) economic geography, e.g. measures of inequality, regional disparities and convergence, regional specialization as well as accessibility and spatial interaction models. / GPL-2	noarch
r-rebmix	2.10.3	R functions for random univariate and multivariate finite mixture model generation, estimation, clustering, latent class analysis and classification. Variables can be continuous, discrete, independent or dependent and may follow normal, lognormal, Weibull, gamma, binomial, Poisson, Dirac or circular von Mises parametric families. / GPL-2	linux-64, osx-64, win-64
r-rebus.base	0.0.3	Build regular expressions piece by piece using human readable code. This package contains core functionality, and is primarily intended to be used by package developers. / Unlimited	noarch
r-reca	1.7	Relevant Component Analysis (RCA) tries to find a linear transformation of the feature space such that the effect of irrelevant variability is reduced in the transformed space. / GPL-3	noarch
r-rechonest	1.2	The ‘Echo nest’ < <a href="http://the.echonest.com">http://the.echonest.com</a> > is the industry’s leading music intelligence company, providing developer with deepest understanding of music content and music fans. This package can be used to access artist’s data including songs, blogs, news, reviews etc. Song’s data including audio summary, style, danceability, tempo etc can also be accessed. / MIT	noarch
r-recipe	3.0	Pathways in a database could have many redundancies among them. This package allows the user to set a maximum value for the proportion of these redundancies. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-recipes</a>	0.1.5	An extensible framework to create and preprocess design matrices. Recipes consist of one or more data manipulation and analysis steps. Statistical parameters for the steps can be estimated from an initial data set and then applied to other data sets. The resulting design matrices can then be used as inputs into statistical or machine learning models. / GPL-2	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-recoder</a>	0.1	Simple, easy to use, and flexible functionality for recoding variables. It allows for simple piecewise definition of transformations. / GPL-2	noarch
<a href="#">r-recombinator</a>	1.0.1	Turns nested lists into data.frames in an orderly manner. / MIT	noarch
<a href="#">r-recommended</a>	3.6.0	R is a free software environment for statistical computing and graphics. / GPL-3.0	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-reconstructr</a>	2.0.2	Functions to reconstruct sessions from web log or other user trace data and calculate various metrics around them, producing tabular, output that is compatible with 'dplyr' or 'data.table' centered processes. / MIT	linux-64, osx-64, win-64
<a href="#">r-recorder</a>	0.8.2	A lightweight toolkit to validate new observations when computing their predictions with a predictive model. The validation process consists of two steps: (1) record relevant statistics and meta data of the variables in the original training data for the predictive model and (2) use these data to run a set of basic validation tests on the new set of observations. / MIT	noarch
<a href="#">r-records</a>	1.0	Functions for generating k-record values and k-record times / GPL-2	noarch
<a href="#">r-recosystem</a>	0.4.2	R wrapper of the 'libmf' library < <a href="http://www.csie.ntu.edu.tw/~cjlin/libmf/">http://www.csie.ntu.edu.tw/~cjlin/libmf/</a> > for recommender system using matrix factorization. It is typically used to approximate an incomplete matrix using the product of two matrices in a latent space. Other common names for this task include collaborative filtering, matrix completion, matrix recovery, etc. High performance multi-core parallel computing is supported in this package. / BSD_3_clause	linux-64, osx-64, win-64
<a href="#">r-recurse</a>	1.1.0	Computes revisitation metrics for trajectory data, such as the number of revisitations for each location as well as the time spent for that visit and the time since the previous visit. Also includes functions to plot data. / MIT	linux-64, osx-64, win-64
<a href="#">r-redas</a>	0.9.3	Provides functions used in the 'R: Einführung durch angewandte Statistik' (second edition). / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-redm</a>	0.7.2	A new implementation of EDM algorithms based on research software previously developed for internal use in the Sugihara Lab (UCSD/SIO). Contains C compiled objects that use time delay embedding to perform state-space reconstruction and nonlinear forecasting and an R interface to those objects using 'Rcpp'. It supports both the simplex projection method from Sugihara & May (1990) <DOI:10.1038/344734a0> and the S-map algorithm in Sugihara (1994) <DOI:10.1098/rsta.1994.0106>. In addition, this package implements convergent cross mapping as described in Sugihara et al. (2012) <DOI:10.1126/science.1227079> and multiview embedding as described in Ye & Sugihara (2016) <DOI:10.1126/science.aag0863>. / file LICENSE	linux-64, osx-64, win-64
<a href="#">r-redmonder</a>	0.2.0	Provide color schemes for maps (and other graphics) based on the color palettes of several Microsoft(r) products. Forked from 'RColorBrewer' v1.1-2. / Apache License 2.0	noarch
<a href="#">r-reemtree</a>	0.90.3	This package estimates regression trees with random effects as a way to use data mining techniques to describe longitudinal or panel data. / GPL-3	noarch
<a href="#">r-reffreeewas</a>	2.2	Reference-free method for conducting EWAS while deconvoluting DNA methylation arising as mixtures of cell types. The older method (Houseman et al., 2014, <doi:10.1093/bioinformatics/btu029>) is similar to surrogate variable analysis (SVA and ISVA), except that it makes additional use of a biological mixture assumption. The newer method (Houseman et al., 2016, <doi:10.1186/s12859-016-1140-4>) is similar to non-negative matrix factorization, with additional constraints and additional utilities. / GPL-2	noarch
<a href="#">r-refinr</a>	0.3.1	These functions take a character vector as input, identify and cluster similar values, and then merge clusters together so their values become identical. The functions are an implementation of the key collision and ngram fingerprint algorithms from the open source tool Open Refine < <a href="http://openrefine.org/">http://openrefine.org/</a> >. More info on key collision and ngram fingerprint can be found here < <a href="https://github.com/OpenRefine/OpenRefine/wiki/Clustering-In-Depth">https://github.com/OpenRefine/OpenRefine/wiki/Clustering-In-Depth</a> >. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-refmanager</a>	1.2.12	Provides tools for importing and working with bibliographic references. It greatly enhances the 'bibentry' class by providing a class 'BibEntry' which stores 'BibTeX' and 'BibLaTeX' references, supports 'UTF-8' encoding, and can be easily searched by any field, by date ranges, and by various formats for name lists (author by last names, translator by full names, etc.). Entries can be updated, combined, sorted, printed in a number of styles, and exported. 'BibTeX' and 'BibLaTeX' '.bib' files can be read into 'R' and converted to 'BibEntry' objects. Interfaces to 'NCBI Entrez', 'CrossRef', and 'Zotero' are provided for importing references and references can be created from locally stored 'PDF' files using 'Poppler'. Includes functions for citing and generating a bibliography with hyperlinks for documents prepared with 'RMarkdown' or 'RHTML'. / GPL-2   GPL-3   BSD_3_clause	noarch
<a href="#">r-refnr</a>	0.1.0	A tool for refining data frame with formulas. / Apache License 2.0   file LICENSE	noarch
<a href="#">r-refset</a>	0.1.1	Provides subsets with reference semantics, i.e. subsets which automatically reflect changes in the original object, and which optionally update the original object when they are changed. / GPL-2	noarch
<a href="#">r-regclust</a>	1.0	This package clusters regression coefficients using the methods of clustering through linear regression models (CLM) (Qin and Self 2006). Maximum likelihood approach is used to infer the parameters for each cluster. Bayesian information criterion (BIC) combined with Bootstrapped maximum volume (BMV) criterion are used to determine the number of clusters. / Artistic-2.0	noarch

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Name	Version	Summary/License	Platforms
r-regent	1.0.6	Produces population distribution of disease risk and statistical risk categories, and predicts risks for individuals with genotype information. / GPL-3	noarch
r-regexpipes	0.0.1	Provides wrappers around base::grep() where the first argument is standardized to take the data object. This makes it less of a pain to use regular expressions with 'magrittr' or other pipe operators. / GPL-2	noarch
r-regexselect	1.0.0	'shiny' extension that adds regular expression filtering capabilities to the choice vector of the select list. / GPL-2   GPL-3	noarch
r-registry	0.5.1	Provides a generic infrastructure for creating and using registries. / GPL-2	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-reglogit	1.2.6	Regularized (polychotomous) logistic regression by Gibbs sampling. The package implements subtly different MCMC schemes with varying efficiency depending on the data type (binary v. binomial, say) and the desired estimator (regularized maximum likelihood, or Bayesian maximum a posteriori/posterior mean, etc.) through a unified interface. / LGPL-3	linux-64, osx-64, win-64
r-regnet	0.4.0	Network-based regularization has achieved success in variable selection for high-dimensional biological data due to its ability to incorporate correlations among genomic features. This package provides procedures of network-based variable selection for generalized linear models (Ren et al. (2017) <doi:10.1186/s12863-017-0495-5> and Ren et al. (2019) <doi:10.1002/gepi.22194>). Two recent additions are the robust network regularization for the survival response and the network regularization for continuous response. Functions for other regularization methods will be included in the forthcoming upgraded versions. / GPL-2	linux-64, osx-64, win-64
r-regpro	0.1.1	Tools are provided for (1) nonparametric regression (kernel, local linear), (2) semiparametric regression (single index, additive models), and (3) quantile regression (linear, kernel). / GPL-2	noarch
r-regress	1.3.1	Functions to fit Gaussian linear model by maximising the residual log likelihood where the covariance structure can be written as a linear combination of known matrices. Can be used for multivariate models and random effects models. Easy straight forward manner to specify random effects models, including random interactions. Code now optimised to use Sherman Morrison Woodbury identities for matrix inversion in random effects models. We've added the ability to fit models using any kernel as well as a function to return the mean and covariance of random effects conditional on the data (BLUPs). / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-regressionfactory</a>	0.7.2	The expander functions rely on the mathematics developed for the Hessian-definiteness invariance theorem for linear projection transformations of variables, described in authors' paper, to generate the full, high-dimensional gradient and Hessian from the lower-dimensional derivative objects. This greatly relieves the computational burden of generating the regression-function derivatives, which in turn can be fed into any optimization routine that utilizes such derivatives. The theorem guarantees that Hessian definiteness is preserved, meaning that reasoning about this property can be performed in the low-dimensional space of the base distribution. This is often a much easier task than its equivalent in the full, high-dimensional space. Definiteness of Hessian can be useful in selecting optimization/sampling algorithms such as Newton-Raphson optimization or its sampling equivalent, the Stochastic Newton Sampler. Finally, in addition to being a computational tool, the regression expansion framework is of conceptual value by offering new opportunities to generate novel regression problems. / GPL-2	noarch
<a href="#">r-regsel</a>	0.2	Functions for fitting linear and generalized linear models with variable selection. The functions can automatically do Stepwise Regression, Lasso or Elastic Net as variable selection methods. Lasso and Elastic net are improved and handle factors better (they can either include or exclude all factor levels). / GPL-2	noarch
<a href="#">r-regspec</a>	2.4	Computes linear Bayesian spectral estimates from multirate data for second-order stationary time series. Provides credible intervals and methods for plotting various spectral estimates. / GPL-2	noarch
<a href="#">r-regsubseq</a>	0.12	For a sequence of event occurrence times, we are interested in finding subsequences in it that are too regular. We define regular as being significantly different from a homogeneous Poisson process. The departure from the Poisson process is measured using a L1 distance. See Di and Perlman 2007 for more details. / GPL-2	noarch
<a href="#">r-regtest</a>	0.05	Functions for unary and binary regression tests / file LICENSE (Restricts use)	noarch
<a href="#">r-rehh.data</a>	1.0.0	Contains example data for the 'rehh' package. / GPL-2	noarch
<a href="#">r-reinforcelearn</a>	0.2.1	Implements reinforcement learning environments and algorithms as described in Sutton & Barto (1998, ISBN:0262193981). The Q-Learning algorithm can be used with function approximation, eligibility traces (Singh & Sutton (1996) <doi:10.1007/BF00114726>) and experience replay (Mnih et al. (2013) <arXiv:1312.5602>). / MIT	noarch
<a href="#">r-reins</a>	1.0.8	Functions from the book Reinsurance: Actuarial and Statistical Aspects (2017) by Hansjoerg Albrecher, Jan Beirlant and Jef Teugels < <a href="http://www.wiley.com/WileyCDA/WileyTitle/productCd-0470772689.html">http://www.wiley.com/WileyCDA/WileyTitle/productCd-0470772689.html</a> >. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-reinstallr</a>	0.1.4	Search R files for not installed packages and run install.packages. / GPL-3	noarch
<a href="#">r-rel</a>	1.3.1	Derives point estimates with confidence intervals for Bennett et al's S, Cohen's kappa, Conger's kappa, Fleiss' kappa, Gwet's AC, intraclass correlation coefficients, Krippendorff's alpha, Scott's pi, the standard error of measurement, and weighted kappa. / GPL-3	noarch
<a href="#">r-rela</a>	4.1	Item analysis with alpha standard error and principal axis factoring for continuous variable scales (with plots). / Artistic-2.0	noarch

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Name	Version	Summary/License	Platforms
r-relabelloadings	1.0	In confirmatory factor analysis (CFA), structural constraints typically ensure that the model is identified up to all possible reflections, i.e., column sign changes of the matrix of loadings. Such reflection invariance is problematic for Bayesian CFA when the reflection modes are not well separated in the posterior distribution. Imposing rotational constraints – fixing some loadings to be zero or positive in order to pick a factor solution that corresponds to one reflection mode – may not provide a satisfactory solution for Bayesian CFA. The function ‘relabel’ uses the relabeling algorithm of Erosheva and Curtis to correct for sign invariance in MCMC draws from CFA models. The MCMC draws should come from Bayesian CFA models that are fit without rotational constraints. / GPL-2	noarch
r-relatable	1.0.0	Functions to safely map from a vector of keys to a vector of values, determine properties of a given relation, or ensure a relation conforms to a given type, such as many-to-many, one-to-many, injective, surjective, or bijective. Permits default return values for use similar to a vectorised switch statement, as well as safely handling large vectors, NAs, and duplicate mappings. / MIT	noarch
r-relatedness	2.0	Inference of relatedness coefficients from a bi-allelic genotype matrix using a Maximum Likelihood estimation, Laporte, F., Charcosset, A. and Mary-Huard, T. (2017) <doi:10.1111/biom.12634>. / AGPL-3	linux-64, osx-64, win-64
r-relaxnet	0.3_2	Extends the glmnet package with relaxation, done by running glmnet once on the entire predictor matrix, then again on each different subset of variables from along the regularization path. Relaxation may lead to improved prediction accuracy for truly sparse data generating models, as well as fewer false positives (i.e. fewer noncontributing predictors in the final model). Penalty may be lasso (alpha = 1) or elastic net (0 < alpha < 1). For this version, family may be gaussian or binomial only. Takes advantage of fast FORTRAN code from the glmnet package. / GPL-2	noarch
r-relaxo	0.1_2	Relaxed Lasso is a generalisation of the Lasso shrinkage technique for linear regression. Both variable selection and parameter estimation is achieved by regular Lasso, yet both steps do not necessarily use the same penalty parameter. The results include all standard Lasso solutions but allow often for sparser models while having similar or even slightly better predictive performance if many predictor variables are present. The package depends on the LARS package. / GPL-3	noarch
r-relen	1.0.1	This function computes the relative entropy (H) as an index for qualitative variation of a factor. / GPL-2	noarch
r-reliability	0.0_2	Functions for estimating parameters in software reliability models. Only infinite failure models are implemented so far. / Unlimited	noarch
r-reliar	0.01	A collection of utilities for some reliability models/probability distributions. / GPL-2	noarch
r-relimp	1.0_5	Functions to facilitate inference on the relative importance of predictors in a linear or generalized linear model, and a couple of useful Tcl/Tk widgets. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-relsurv</a>	2.2_3	Contains functions for analysing relative survival data, including nonparametric estimators of net (marginal relative) survival, relative survival ratio, crude mortality, methods for fitting and checking additive and multiplicative regression models, transformation approach, methods for dealing with population mortality tables. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-relvalanalysis</a>	1.0	Classes and functions for analyzing the performance of portfolios relative to a benchmark. / GPL-2   GPL-3	noarch
<a href="#">r-rem</a>	1.3.1	Calculate endogenous network effects in event sequences and fit relational event models (REM): Using network event sequences (where each tie between a sender and a target in a network is time-stamped), REMs can measure how networks form and evolve over time. Endogenous patterns such as popularity effects, inertia, similarities, cycles or triads can be calculated and analyzed over time. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-rematch</a>	1.0.1	A small wrapper on ‘regexr’ to extract the matches and captured groups from the match of a regular expression to a character vector. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-rematch2</a>	2.1.0	Wrappers on ‘regexr’ and ‘gregexpr’ to return the match results in tidy data frames. / MIT	noarch
<a href="#">r-remindr</a>	0.0.1	Insert/extract text reminders into/from function source code comments or as the comment attribute of any object. The former can be handy in development as reminders of e.g. argument requirements, expected objects in the calling environment, required options settings, etc. The latter can be used to provide information of the object and as simple manual tooltips for users, among other things. / GPL-2   GPL-3	noarch
<a href="#">r-remmap</a>	0.2_0	remMap is developed for fitting multivariate response regression models under the high-dimension-low-sample-size setting / GPL-2	linux-64, osx-64, win-64
<a href="#">r-remotes</a>	2.0.4	Download and install R packages stored in ‘GitHub’, ‘BitBucket’, or plain ‘subversion’ or ‘git’ repositories. This package provides the ‘install_’ functions in ‘devtools’. Indeed most of the code was copied over from ‘devtools’. / GPL (>= 2)	noarch
<a href="#">r-renpow</a>	0.1_1	Supports calculations and visualization for renewable power systems and the environment. Analysis and graphical tools for DC and AC circuits and their use in electric power systems. Analysis and graphical tools for thermodynamic cycles and heat engines, supporting efficiency calculations in coal-fired power plants, gas-fired power plants. Calculations of carbon emissions and atmospheric CO2 dynamics. Analysis of power flow and demand for the grid, as well as power models for microgrids and off-grid systems. Provides resource and power generation for hydro power, wind power, and solar power. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-rentrez	1.2.2	Provides an R interface to the NCBI's 'EUtils' API, allowing users to search databases like 'GenBank' < <a href="https://www.ncbi.nlm.nih.gov/genbank/">https://www.ncbi.nlm.nih.gov/genbank/</a> > and 'PubMed' < <a href="https://www.ncbi.nlm.nih.gov/pubmed/">https://www.ncbi.nlm.nih.gov/pubmed/</a> >, process the results of those searches and pull data into their R sessions. / MIT	noarch
r-reordercluster	1.0	Tools for performing the leaf reordering for the dendrogram that preserves the hierarchical clustering result and at the same time tries to group instances from the same class together. / GPL-3	linux-64, osx-64, win-64
r-repeatedhighdim	2.0.0	Global tests for expression data of high-dimensional sets of molecular features. / GPL-2	noarch
r-repec	0.1.0	Utilities for accessing RePEc (Research Papers in Economics) through a RESTful API. You can request a code and get detailed information at the following page: < <a href="https://ideas.repec.org/api.html">https://ideas.repec.org/api.html</a> >. / MIT	noarch
r-repfd	1.2.3	Estimation of Bayes and local Bayes false discovery rates for replicability analysis (Heller & Yekutieli, 2014 <doi:10.1214/13-AOAS697> ; Heller et al., 2015 <doi: 10.1093/bioinformatics/btu434>). / GPL-2	linux-64, osx-64, win-64
r-repo	2.1.3	A data manager meant to avoid manual storage/retrieval of data to/from the file system. It builds one (or more) centralized repository where R objects are stored with rich annotations, including corresponding code chunks, and easily searched and retrieved. / GPL-3	noarch
r-repogenerator	0.0.1	Generates a project and repo for easy initialization of a GitHub repo for R workshops. The repo includes a README with instructions to ensure that all users have the needed packages, an 'RStudio' project with the right directories and the proper data. The repo can then be used for hosting code taught during the workshop. / MIT	noarch
r-repolr	3.4	Fits linear models to repeated ordinal scores using GEE methodology. / GPL-3	linux-64, osx-64, win-64
r-reportreg	0.3.0	Provides an easy way to report the results of regression analysis, including: 1. Proportional hazards regression from function 'coxph' of package 'survival'; 2. Conditional logistic regression from function 'clogit' of package 'survival'; 3. Ordered logistic regression from function 'polr' of package 'MASS'; 4. Binary logistic regression from function 'glm' of package 'stats'; 5. Linear regression from function 'lm' of package 'stats'; 6. Risk regression model for survival analysis with competing risks from function 'FGR' of package 'riskRegression'; 7. Multilevel model from function 'lme' of package 'nlme'. / GPL-3	noarch
r-reportroc	3.4	Provides an easy way to report the results of ROC analysis, including: 1. an ROC curve. 2. the value of Cutoff, AUC (Area Under Curve), ACC (accuracy), SEN (sensitivity), SPE (specificity), PLR (positive likelihood ratio), NLR (negative likelihood ratio), PPV (positive predictive value), NPV (negative predictive value). / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-reports</a>	0.1.4	Assists in writing reports and presentations by providing a frame work that brings together existing R, LaTeX/docx and Pandoc tools. The package is designed to be used with RStudio, MiKTeX/Tex Live/LibreOffice, knitr, knitrations, Pandoc and pander. The user will want to download these free programs/packages to maximize the effectiveness of the reports package. Functions with two letter names are general text formatting functions for copying text from articles for inclusion as a citation. / GPL-2	noarch
<a href="#">r-reporttools</a>	1.1.2	These functions are especially helpful when writing reports of data analysis using Sweave. / GPL-2	noarch
<a href="#">r-repr</a>	0.19.2	String and binary representations of objects for several formats / mime types. / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-represent</a>	1.0	Contains workhorse function jrparams(), as well as two helper functions Mboxtest() and JRsMahaldist(), and four example data sets. / GPL-3	noarch
<a href="#">r-represtools</a>	0.1.2	Reproducible research tools automates the creation of an analysis directory structure and work flow. There are R markdown skeletons which encapsulate typical analytic work flow steps. Functions will create appropriate modules which may pass data from one step to another. / GPL-3	noarch
<a href="#">r-reprex</a>	0.2.1	Convenience wrapper that uses the ‘rmarkdown’ package to render small snippets of code to target formats that include both code and output. The goal is to encourage the sharing of small, reproducible, and runnable examples on code-oriented websites, such as < <a href="https://stackoverflow.com">https://stackoverflow.com</a> > and < <a href="https://github.com">https://github.com</a> >, or in email. The user’s clipboard is the default source of input code and the default target for rendered output. ‘reprex’ also extracts clean, runnable R code from various common formats, such as copy/paste from an R session. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-reqs</a>	0.8.1	This package contains the function run.eqs() which calls an EQS script file, executes the EQS estimation, and, finally, imports the results as R objects. These two steps can be performed separately: call.eqs() calls and executes EQS, whereas read.eqs() imports existing EQS outputs as objects into R. It requires EQS 6.2 (build 98 or higher). / GPL-3	noarch
<a href="#">r-request</a>	0.1.0	High level and easy ‘HTTP’ client for ‘R’. Provides functions for building ‘HTTP’ queries, including query parameters, body requests, headers, authentication, and more. / MIT	noarch
<a href="#">r-requirer</a>	1.0.0	Modularizes source code. Keeps the global environment clean, explicifies interdependencies. Inspired by ‘RequireJS’ < <a href="http://requirejs.org/">http://requirejs.org/</a> >. / MIT	noarch
<a href="#">r-rerefact</a>	1.0	Executes a post-rotation algorithm that REorders and/or REFlects FACTors (REREFAC) for each replication of a simulation study with exploratory factor analysis. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<code>r-resample</code>	0.4	Bootstrap, permutation tests, and other resampling functions, featuring easy-to-use syntax. / BSD_3_clause	noarch
<code>r-resampled</code>	0.3.1	Package of data sets from Mathematical Statistics with Resampling in R (1st Ed. 2011, 2nd Ed. 2018) by Laura Chihara and Tim Hesterberg. / CC0	noarch
<code>r-resemble</code>	1.2.2	Implementation of functions for spectral similarity/dissimilarity analysis and memory-based learning (MBL) for non-linear modeling in complex spectral datasets. In chemometrics MBL is also known as local modeling. / GPL-3	linux-64, osx-64, win-64
<code>r-reservoir</code>	1.1.5	Measure single-storage water supply system performance using resilience, reliability, and vulnerability metrics; assess storage-yield-reliability relationships; determine no-fail storage with sequent peak analysis; optimize release decisions for water supply, hydropower, and multi-objective reservoirs using deterministic and stochastic dynamic programming; generate inflow replicates using parametric and non-parametric models; evaluate inflow persistence using the Hurst coefficient. / GPL-2	noarch
<code>r-reshape</code>	0.8.8	Flexibly restructure and aggregate data using just two functions: melt and cast. / MIT file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<code>r-reshape2</code>	1.4.3	Flexibly restructure and aggregate data using just two functions: melt and 'dcast' (or 'acast'). / MIT file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<code>r-resistorarray</code>	1.0_3	Electrical properties of resistor networks using matrix methods. / GPL-2	noarch
<code>r-ress</code>	1.3	Contains three functions that query AuriQ Systems' Essentia Database and return the results in R. 'essQuery' takes a single Essentia command and captures the output in R, where you can save the output to a dataframe or stream it directly into additional analysis. 'read.essentia' takes an Essentia script and captures the output csv data into R, where you can save the output to a dataframe or stream it directly into additional analysis. 'capture.essentia' takes a file containing any number of Essentia commands and captures the output of the specified statements into R dataframes. Essentia can be downloaded for free at <a href="http://www.auriq.com/documentation/source/install/index.html">http://www.auriq.com/documentation/source/install/index.html</a> . / LGPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-restimizeapi</a>	1.0.0	Provides the user with functions to develop their trading strategy, uncover actionable trading ideas, and monitor consensus shifts with crowdsourced earnings and economic estimate data directly from <www.estimize.com>. Further information regarding the web services this package invokes can be found at <www.estimize.com/api>. / LGPL-3	noarch
<a href="#">r-restorepoint</a>	0.2	Debugging with restore points instead of break points. A restore point stores all local variables when called inside a function. The stored values can later be retrieved and evaluated in a modified R console that replicates the function's environment. To debug step by step, one can simply copy & paste the function body from the R script. Particularly convenient in combination with RStudio. See the Github page <a href="#">inst/vignettes</a> for a tutorial. / GPL-2	noarch
<a href="#">r-restrictedmvn</a>	1.0	A fast Gibbs sampler for multivariate normal with affine constraints. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-rethinker</a>	1.1.0	Simple, native 'RethinkDB' client. / GPL-3	noarch
<a href="#">r-reticulate</a>	1.12	Interface to 'Python' modules, classes, and functions. When calling into 'Python', R data types are automatically converted to their equivalent 'Python' types. When values are returned from 'Python' to R they are converted back to R types. Compatible with all versions of 'Python' >= 2.7. / Apache License 2.0	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-retimes</a>	0.1_2	Reaction time analysis by maximum likelihood / GPL-3	linux-64, osx-64, win-64
<a href="#">r-retrodesign</a>	0.1.0	Provides tools for working with Type S (Sign) and Type M (Magnitude) errors, as proposed in Gelman and Tuerlinckx (2000) < <a href="https://doi.org/10.1007/s001800000040">doi.org/10.1007/s001800000040</a> > and Gelman & Carlin (2014) < <a href="https://doi.org/10.1177/1745691614551642">doi.org/10.1177/1745691614551642</a> >. In addition to simply calculating the probability of Type S/M error, the package includes functions for calculating these errors across a variety of effect sizes for comparison, and recommended sample size given tolerances for Type S/M errors. To improve the speed of these calculations, closed forms solutions for the probability of a Type S/M error from Lu, Qiu, and Deng (2018) < <a href="https://doi.org/10.1111/bmsp.12132">doi.org/10.1111/bmsp.12132</a> > are implemented. As of 1.0.0, this includes support only for simple research designs. See the package vignette for a fuller exposition on how Type S/M errors arise in research, and how to analyze them using the type of design analysis proposed in the above papers. / MIT	noarch
<a href="#">r-reval</a>	2.0.0	Simplified scenario testing and sensitivity analysis with R via a generalized function for one-factor-at-a-time (OFAT) sensitivity analysis, evaluation of parameter sets and (sampled) parameter permutations. Options for formatting output and parallel processing are also provided. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-revealjs</a>	0.9	R Markdown format for ‘reveal.js’ presentations, a framework for easily creating beautiful presentations using HTML. / MIT	noarch
<a href="#">r-revecor</a>	0.99.3	An implementation of the reverse ecology framework. Reverse ecology refers to the use of genomics to study ecology with no a priori assumptions about the organism(s) under consideration, linking organisms to their environment. It allows researchers to reconstruct the metabolic networks and study the ecology of poorly characterized microbial species from their genomic information, and has substantial potentials for microbial community ecological analysis. / GPL-2	noarch
<a href="#">r-revgeo</a>	0.15	Function revgeo() allows you to use the Photon geocoder for OpenStreetMap < <a href="http://photon.komoot.de">http://photon.komoot.de</a> >, Google Maps < <a href="http://maps.google.com">http://maps.google.com</a> >, and Bing < <a href="https://www.bingmapsportal.com">https://www.bingmapsportal.com</a> > to reverse geocode coordinate pairs with minimal hassle. / GPL (>= 3.0)	noarch
<a href="#">r-revoioq</a>	10.0.0	Test suite for Microsoft R Services. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-revomods</a>	11.0.0	Microsoft modifications and extensions to standard R functions / GPL-2	linux-64, osx-64, win-64
<a href="#">r-revoutils</a>	11.0.0	Utility functions for Microsoft R / GPL-2	linux-64, osx-64, win-64
<a href="#">r-revoutilsmath</a>	11.0.0	Utility functions for managing math threading. / file LICENSE	linux-64, win-64
<a href="#">r-reweight</a>	1.2.1	Adjusts the weights of survey respondents so that the marginal distributions of certain variables fit more closely to those from a more precise source (e.g. Census Bureau’s data). / GPL-2	noarch
<a href="#">r-rex</a>	1.1.2	A friendly interface for the construction of regular expressions. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-rexperigen</a>	0.2.1	Provides convenience functions to communicate with an Experigen server: Experigen ( <a href="http://github.com/aquincum/experigen">http://github.com/aquincum/experigen</a> ) is an online framework for creating linguistic experiments, and it stores the results on a dedicated server. This package can be used to retrieve the results from the server, and it is especially helpful with registered experiments, as authentication with the server has to happen. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-rexpokit</a>	0.26.6	Wraps some of the matrix exponentiation utilities from EXPOKIT ( <a href="http://www.maths.uq.edu.au/expokit/">http://www.maths.uq.edu.au/expokit/</a> ), a FORTRAN library that is widely recommended for matrix exponentiation (Sidje RB, 1998. Expokit: A Software Package for Computing Matrix Exponentials. ACM Trans. Math. Softw. 24(1): 130-156). EXPOKIT includes functions for exponentiating both small, dense matrices, and large, sparse matrices (in sparse matrices, most of the cells have value 0). Rapid matrix exponentiation is useful in phylogenetics when we have a large number of states (as we do when we are inferring the history of transitions between the possible geographic ranges of a species), but is probably useful in other ways as well. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-rfacebook</a>	0.6.15	Provides an interface to the Facebook API. / GPL-2	noarch
<a href="#">r-rfdsn</a>	0.0.0	This package facilitates searching for and downloading seismic time series in miniSEED format (a minimalist version of the Standard for the Exchange of Earthquake Data) from International Federation of Digital Seismograph Networks repositories. This package can also be used to gather information about seismic networks (stations, channels, locations, etc) and find historical earthquake data (origins, magnitudes, etc). / GPL-3	noarch
<a href="#">r-rferns</a>	3.0.0	Provides the random ferns classifier by Ozuysal, Calonder, Lepetit and Fua (2009) <doi:10.1109/TPAMI.2009.23>, modified for generic and multi-label classification and featuring OOB error approximation and importance measure as introduced in Kursu (2014) <doi:10.18637/jss.v061.i10>. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-rfgls</a>	1.1	RFGLS uses a generalized least-squares method to perform single-marker association analysis, in datasets of nuclear families containing parents, twins, and/or adoptees / GPL-2	noarch
<a href="#">r-rfinanceyj</a>	0.3.1	Japanese stock market from Yahoo!-finance-Japan / BSD_3_clause	noarch
<a href="#">r-rfinterval</a>	1.0.0	An integrated package for constructing random forest prediction intervals using a fast implementation package ‘ranger’. This package can apply the following three methods described in Haozhe Zhang, Joshua Zimmerman, Dan Nettleton, and Daniel J. Nordman (2019) <doi:10.1080/00031305.2019.1585288>: the out-of-bag prediction interval, the split conformal method, and the quantile regression forest. / GPL-3	noarch
<a href="#">r-rfit</a>	0.23.0	OR estimation and inference for linear models. Estimation is for general scores and a library of commonly used score functions is included. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-rflights</a>	0.1.10	Query plane tickets, from several airlines, using the ‘Kiwi’ API (similar to ‘Google Flights’). The API is documented at <a href="https://docs.kiwi.com/">https://docs.kiwi.com/</a> . / GPL-3	noarch
<a href="#">r-rflptools</a>	1.6	RFLPtools provides functions to analyse DNA fragment samples (i.e. derived from RFLP-analysis) and standalone BLAST report files (i.e. DNA sequence analysis). / LGPL-3	noarch

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Name	Version	Summary/License	Platforms
r-rfml	0.1.0	Functionality required to efficiently use R with MarkLogic NoSQL Database Server, < <a href="http://www.marklogic.com/what-is-marklogic/">http://www.marklogic.com/what-is-marklogic/</a> >. Many basic and complex R operations are pushed down into the database, which removes the main memory boundary of R and allows to make full use of MarkLogic server. In order to use the package you need a MarkLogic Server version 8 or higher. / GPL-3	noarch
r-rfoaas	2.0.0	R access to the 'FOAAS' (F... Off As A Service) web service is provided. / GPL-2	noarch
r-rfolding	1.0	The basic algorithm to perform the folding test of unimodality. Given a dataset X (d dimensional, n samples), the test checks whether the distribution of the data are rather unimodal or rather multimodal. This package stems from the following research publication: Siffer Alban, Pierre-Alain Fouque, Alexandre Termier, and Christine Largouët. Are your data gathered? In Proceedings of the 24th ACM SIGKDD International Conference on Knowledge Discovery Data Mining, pp. 2210-2218. ACM, 2018. <doi:10.1145/3219819.3219994>. / GPL-3	noarch
r-rforcecom	1.1	Insert, update, retrieve, delete and bulk operate datasets with a SaaS based CRM Salesforce.com and a PaaS based application platform Force.com from R. / Apache License 2.0	noarch
r-rfordummies	0.1.4	Contains all the code examples in the book R for Dummies (2nd edition) by Andrie de Vries and Joris Meys. You can view the table of contents as well as the sample code for each chapter. / GPL-2   GPL-3	noarch
r-rforensicbatwing	1.3.1	A modified version (with great help from Ian J. Wilson) of Ian J. Wilson's program BATWING for calculating forensic trace-suspect match probabilities. / GPL-3	linux-64, osx-64, win-64
r-rformatter	0.1.1	The R Formatter formats R source code. It is very much based on formatR, but tries to improve it by heuristics. For example, spaces can be forced around the division operator /. / GPL-3	noarch
r-rfreak	0.3.0	An R interface to a modified version of the Free Evolutionary Algorithm Kit FrEAK. FrEAK is a toolkit written in Java to design and analyze evolutionary algorithms. Both the R interface and an extended version of FrEAK are contained in the RFreak package. For more information on FrEAK see <a href="http://sourceforge.net/projects/freak427/">http://sourceforge.net/projects/freak427/</a> . / GPL-2	noarch
r-rfutilities	2.1.4	Utilities for Random Forest model selection, class balance correction, significance test, cross validation and partial dependency plots. / GPL-3	noarch
r-rga	0.4.2	Provides functions for accessing and retrieving data from the Google Analytics APIs ( <a href="https://developers.google.com/analytics/">https://developers.google.com/analytics/</a> ). Supports OAuth 2.0 authorization. Package provides access to the Management, Core Reporting, Multi-Channel Funnels Reporting, Real Time Reporting and Metadata APIs. Access to all the Google Analytics accounts which the user has access to. Auto-pagination to return more than 10,000 rows of the results by combining multiple data requests. Also package provides shiny app to explore the core reporting API dimensions and metrics. / GPL-2	noarch
r-rga4gh	0.1.1	An Interface to the GA4GH API that allows users to easily GET responses and POST requests to GA4GH Servers. See < <a href="http://ga4gh.org">http://ga4gh.org</a> > for more information about the GA4GH project. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-rgabriel</a>	0.7	This package was created to analyze multi-level one-way experimental designs. It is designed to handle vectorized observation and factor data where there are unequal sample sizes and population variance homogeneity can not be assumed. To conduct the Gabriel test, create two vectors: one for your observations and one for the factor level of each observation. The function, <code>rgabriel</code> , conduct the test and save the output as a vector to input into the <code>gabriel.plot</code> function, which produces a confidence interval plot for Multiple Comparison. / GPL-2	noarch
<a href="#">r-rgammagamma</a>	1.0.12	This package implements a Gamma convolution model for background correction. / GPL (>= 2.0)	noarch
<a href="#">r-rgb</a>	1.6.1	Classes and methods to efficiently handle (slice, annotate, draw ...) genomic features (such as genes or transcripts), and an interactive interface to browse them. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-rgbm</a>	1.0.8	Provides an implementation of Regularized LS-TreeBoost & LAD-TreeBoost algorithm for Regulatory Network inference from any type of expression data (Microarray/RNA-seq etc). See Mall et al (2017) <doi:10.1101/132670>. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-rgcca</a>	2.1.2	Multiblock data analysis concerns the analysis of several sets of variables (blocks) observed on the same group of individuals. The main aims of the RGCCA package are: (i) to study the relationships between blocks and (ii) to identify subsets of variables of each block which are active in their relationships with the other blocks. / GPL-2	noarch
<a href="#">r-rgdal</a>	1.4.4	Provides bindings to the 'Geospatial' Data Abstraction Library ('GDAL') (>= 1.11.4) and access to projection/transformation operations from the 'PROJ.4' library. The 'GDAL' and 'PROJ.4' libraries are external to the package, and, when installing the package from source, must be correctly installed first. From 'rgdal' 1.4.1, provision is made for 'PROJ6' accommodation, with 'PROJ6' functionality to follow; from 1.4.1 'rgdal' will build and function when 'PROJ' >= 6. Both 'GDAL' raster and 'OGR' vector map data can be imported into R, and 'GDAL' raster data and 'OGR' vector data exported. Use is made of classes defined in the 'sp' package. Windows and Mac Intel OS X binaries (including 'GDAL', 'PROJ.4' and 'Expat') are provided on 'CRAN'. / GPL-2	osx-64, win-64
<a href="#">r-rgdax</a>	1.0.0	Allow access to both public and private end points to Coinbase Pro (erstwhile GDAX) cryptocurrency exchange. For authenticated flow, users must have valid api, secret and passphrase to be able to connect. / MIT	noarch
<a href="#">r-rgeckoboard</a>	0.1.5	Provides an interface to Geckoboard. / MIT	noarch
<a href="#">r-rgen</a>	0.0.1	Provides popular sampling distributions C routines based in armadillo through a header file approach. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-rgendata	1.0	The GenDataSample() and GenDataPopulation() functions create, respectively, a sample or population of multivariate nonnormal data using methods described in Ruscio and Kaczetow (2008). Both of these functions call a FactorAnalysis() function to reproduce a correlation matrix. The EFACompData() function allows users to determine how many factors to retain in an exploratory factor analysis of an empirical data set using a method described in Ruscio and Roche (2012). The latter function uses populations of comparison data created by calling the GenDataPopulation() function. <DOI: 10.1080/00273170802285693>. <DOI: 10.1037/a0025697>. / MIT	noarch
r-rgenetics	0.1	R packages for genetics research / GPL-2	noarch
r-rgenoud	5.8_3	A genetic algorithm plus derivative optimizer. / GPL-3	linux-64, osx-64, win-64
r-rgeode	0.1.0	Provides the hybrid Bayesian method Geometric Density Estimation. On the one hand, it scales the dimension of our data, on the other it performs inference. The method is fully described in the paper Scalable Geometric Density Estimation by Y. Wang, A. Canale, D. Dunson (2016) < <a href="http://proceedings.mlr.press/v51/wang16e.pdf">http://proceedings.mlr.press/v51/wang16e.pdf</a> >. / GPL-2	linux-64, osx-64, win-64
r-rgeos	0.5_1	Interface to Geometry Engine - Open Source ('GEOS') using the C 'API' for topology operations on geometries. The 'GEOS' library is external to the package, and, when installing the package from source, must be correctly installed first. Windows and Mac Intel OS X binaries are provided on 'CRAN'. ('rgeos' >= 0.5-1): Up to and including 'GEOS' 3.7.1, topological operations succeeded with some invalid geometries for which the same operations fail from and including 'GEOS' 3.7.2. The 'checkValidity=' argument defaults and structure have been changed, from default FALSE to integer default '0L' for 'GEOS' < 3.7.2 (no check), '1L' 'GEOS' >= 3.7.2 (check and warn). A value of '2L' is also provided that may be used, assigned globally using 'set_RGEOS_CheckValidity(2L)', or locally using the 'checkValidity=2L' argument, to attempt zero-width buffer repair if invalid geometries are found. The previous default (FALSE, now '0L') is fastest and used for 'GEOS' < 3.7.2, but will not warn users of possible problems before the failure of topological operations that previously succeeded. / GPL-2	linux-64, osx-64, win-64
r-rgexf	0.15.3	Create, read and write GEXF (Graph Exchange XML Format) graph files (used in Gephi and others). Using the XML package, it allows the user to easily build/read graph files including attributes, GEXF viz attributes (such as color, size, and position), network dynamics (for both edges and nodes) and edge weighting. Users can build/handle graphs element-by-element or massively through data-frames, visualize the graph on a web browser through sigma.js (a javascript library) and interact with the igraph package. / GPL (>= 3)	linux-32, linux-64, osx-64, win-32, win-64
r-rgf	1.0.6	Regularized Greedy Forest wrapper of the 'Regularized Greedy Forest' < <a href="https://github.com/RGF-team/rgf/tree/master/python-package">https://github.com/RGF-team/rgf/tree/master/python-package</a> > 'python' package, which also includes a Multi-core implementation (FastRGF) < <a href="https://github.com/RGF-team/rgf/tree/master/FastRGF">https://github.com/RGF-team/rgf/tree/master/FastRGF</a> >. / MIT	noarch

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Name	Version	Summary/License	Platforms
r-rgift	0.1.5	This package provides some functions to create quizzes in the GIFT format. This format is used by several Virtual Learning Environments such as Moodle. / GPL-2	noarch
r-rgl	0.100.19	Provides medium to high level functions for 3D interactive graphics, including functions modelled on base graphics (plot3d(), etc.) as well as functions for constructing representations of geometric objects (cube3d(), etc.). Output may be on screen using OpenGL, or to various standard 3D file formats including WebGL, PLY, OBJ, STL as well as 2D image formats, including PNG, Postscript, SVG, PGF. / GPL	linux-32, linux-64, osx-64, win-32, win-64
r-rglobi	0.2.19	A programmatic interface to the web service methods provided by Global Biotic Interactions (GloBI). GloBI provides access to spatial-temporal species interaction records from sources all over the world. rglobi provides methods to search species interactions by location, interaction type, and taxonomic name. In addition, it supports Cypher, a graph query language, to allow for executing custom queries on the GloBI aggregate species interaction data set. / MIT	noarch
r-rglwidget	0.2.1	The contents of this package have been merged into rgl, so it is no longer needed. / GPL-2	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-rgooddata	0.1.1	Export raw reports from 'GoodData' business intelligence platform (see < <a href="http://www.gooddata.com">http://www.gooddata.com</a> > for more information). / GPL-3	noarch
r-rgoogleanalytics	0.1.6	Provides functions for accessing and retrieving data from the Google Analytics API. / Apache License 2.0	noarch
r-rgoogleanalyticspremium	0.1.1	It fires a query to the API to get the unsampled data in R for Google Analytics Premium Accounts. It retrieves data from the Google drive document and stores it into the local drive. The path to the excel file is returned by this package. The user can read data from the excel file into R using read.csv() function. / Apache License 2.0	noarch
r-rgooglefit	0.3.1	Provides interface to Google Fit REST API v1 (see < <a href="https://developers.google.com/fit/rest/v1/reference/">https://developers.google.com/fit/rest/v1/reference/</a> >). / MIT	noarch
r-rgooglemaps	1.4.4	Serves two purposes: (i) Provide a comfortable R interface to query the Google server for static maps, and (ii) Use the map as a background image to overlay plots within R. This requires proper coordinate scaling. / GPL-3	noarch
r-rgoogleslides	0.3.1	Previously, when one is working with in the Google Ecosystem (Using Google Drive etc), there is hardly any good workflow of getting the values calculated from R and getting that into Google Slides. The normal and easy way out would be to just copy your work over but when you have a number of analysis to present with a lot of changes between each environment, it just becomes quite cumbersome. / MIT	noarch

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Name	Version	Summary/License	Platforms
r-gr	1.1.15	Geological Survey of Canada (GSC) functions for exploratory data analysis with applied geochemical data, with special application to the estimation of background ranges and identification of outliers, ‘anomalies’, to support mineral exploration and environmental studies. Additional functions are provided to support analytical data QA/QC, ANOVA for investigations of field sampling and analytical variability, and utility tasks. NOTE: function caplot() for concentration-area plots employs package ‘akima’, however, ‘akima’ is only licensed for not-for-profit use. Therefore, not-for-profit users of ‘rgr’ will have to independently make package ‘akima’ available through library(...); and use of function caplot() by for-profit users will fail. / GPL-2	noarch
r-grass7	0.2.1	Interpreted interface between ‘GRASS’ 7 geographical information system and R, based on starting R from within the ‘GRASS’ ‘GIS’ environment, or running free-standing R in a temporary ‘GRASS’ location; the package provides facilities for using all ‘GRASS’ commands from the R command line. This package may not be used for ‘GRASS’ 6, for which ‘spgrass6’ should be used. / GPL-2	noarch
r-groovy	1.3	Integrates the Groovy scripting language with the R Project for Statistical Computing. / LGPL-3	noarch
r-gw	0.1.0	Implementation of the affine-invariant method of Goodman & Weare (2010) <DOI:10.2140/camcos.2010.5.65>, a method of producing Monte-Carlo samples from a target distribution. / MIT	noarch
r-h2	0.2.4	DBI/RJDBC interface to h2 database. h2 version 1.3.175 is included. / Mozilla Public License 1.1	noarch
r-handsontable	0.3.7	An R interface to the ‘Handsontable’ JavaScript library, which is a minimalist Excel-like data grid editor. See < <a href="https://handsontable.com/">https://handsontable.com/</a> > for details. / MIT	noarch
r-healthdatagov	1.0.1	An R interface for the HealthData.gov data API. For each data resource, you can filter results (server-side) to select subsets of data. / GPL-2	noarch
r-hive	2.0.0	RHive is an R extension facilitating distributed computing via HIVE query. It provides an easy to use HQL like SQL and R objects and functions in HQL. / Apache License (== 2.0)	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-hli	0.0.2	Complete access from ‘R’ to the FIS ‘MarketMap C-Toolkit’ (‘FAME C-HLI’). ‘FAME’ is a fully integrated software and database management system from FIS that provides the following capabilities: Time series and cross-sectional data management; Financial calculation, data analysis, econometrics, and forecasting; Table generation and detailed multicolor, presentation-quality report writing; Multicolor, presentation-quality graphics; What-if analysis; Application development and structured programming; Data transfer to and from other applications; Tools for building customized graphical user interfaces. / AGPL-3	linux-64, osx-64, win-64
r-hmc	1.0.0	Implements simple Hamiltonian Monte Carlo routines in R for sampling from any desired target distribution which is continuous and smooth. See Neal (2017) <arXiv:1701.02434> for further details on Hamiltonian Monte Carlo. Automatic parameter selection is not supported. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-rhnerm</a>	1.1	Performs the random heteroscedastic nested error regression model described in Kubokawa, Sugawara, Ghosh and Chaudhuri (2016) <doi:10.5705/ss.202014.0070>. / GPL-2	noarch
<a href="#">r-rhor</a>	1.2.1	Rho is used to test the generalization of inter rater reliability (IRR) statistics. Calculating rho starts by generating a large number of simulated, fully-coded data sets: a sizable collection of hypothetical populations, all of which have a kappa value below a given threshold – which indicates unacceptable agreement. Then kappa is calculated on a sample from each of those sets in the collection to see if it is equal to or higher than the kappa in then real sample. If less than five percent of the distribution of samples from the simulated data sets is greater than actual observed kappa, the null hypothesis is rejected and one can conclude that if the two raters had coded the rest of the data, we would have acceptable agreement (kappa above the threshold). / GPL-3	noarch
<a href="#">r-rhosp</a>	1.10	Evaluating risk (that a patient arises a side effect) during hospitalization is the main purpose of this package. Several methods (Parametric, non parametric and De Vielder estimation) to estimate the risk constant (R) are implemented in this package. There are also functions to simulate the different models of this issue in order to quantify the previous estimators. It is necessary to read at least the first six pages of the report to understand the topic. / GPL-2	noarch
<a href="#">r-rhpcbenchmark</a>	0.1.0	Microbenchmarks for determining the run time performance of aspects of the R programming environment and packages relevant to high-performance computation. The benchmarks are divided into three categories: dense matrix linear algebra kernels, sparse matrix linear algebra kernels, and machine learning functionality. / Apache License 2.0   file LICENSE	noarch
<a href="#">r-rhpcblasctl</a>	0.18.1	Control the number of threads on ‘BLAS’ (Aka ‘GotoBLAS’, ‘OpenBLAS’, ‘ACML’, ‘BLIS’ and ‘MKL’). And possible to control the number of threads in ‘OpenMP’. Get a number of logical cores and physical cores if feasible. / AGPL-3	linux-64, osx-64, win-64
<a href="#">r-rhpcc</a>	1.0	rHpcc is an R package providing an Interface between R and HPCC.Familiarity with ECL (Enterprise Control Language) is a must to use this package.HPCC is a massive parallel-processing computing platform that solves Big Data problems.ECL is the Enterprise Control Language designed specifically for huge data projects using the HPCC platform.Its extreme scalability comes from a design that allows you to leverage every query you create for re-use in subsequent queries as needed. To do this, ECL takes a dictionary approach to building queries wherein each ECL definition defines an Attribute. Each previously defined Attribute can then be used in succeeding ECL Attribute definitions as the language extends itself as you use it. / GPL-2	noarch
<a href="#">r-rht</a>	1.0	This package offers functions to perform regularized Hotelling’s T-square test for pathway or gene set analysis. The package is tailored for but not limited to proteomics data, in which sample sizes are often small, a large proportion of the data are missing and/or correlations may be present. / GPL-3	noarch
<a href="#">r-rhymer</a>	1.0.0	Wrapper for ‘Datamuse’ API to find rhyming and other associated words. This includes words of similar meaning, spelling, or other related words. Learn more about the ‘Datamuse’ API here < <a href="http://www.datamuse.com/api/">http://www.datamuse.com/api/</a> >. / MIT	noarch

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Name	Version	Summary/License	Platforms
r-ri	0.9	This package provides a set of tools for conducting exact or approximate randomization-based inference for experiments of arbitrary design. The primary functionality of the package is in the generation, manipulation and use of permutation matrices implied by given experimental designs. Among other features, the package facilitates estimation of average treatment effects, constant effects variance estimation, randomization inference for significance testing against sharp null hypotheses and visualization of data and results. / GPL-2	noarch
r-ri2by2	1.3	Computes attributable effects based confidence interval, permutation test confidence interval, or asymptotic confidence interval for the the average treatment effect on a binary outcome. / GPL-3	linux-64, osx-64, win-64
r-ridge	2.4	Linear and logistic ridge regression functions. Additionally includes special functions for genome-wide single-nucleotide polymorphism (SNP) data. / GPL-2	linux-64, osx-64, win-64
r-ridgefusion	1.0_3	This package implements ridge fusion methodology for inverse covariance matrix estimation for use in quadratic discriminant analysis. The package also contains function for model based clustering using ridge fusion for inverse matrix estimation, as well as tuning parameter selection functions. We have also implemented QDA using joint inverse covariance estimation. / MIT	noarch
r-ridigbio	0.3.5	An interface to iDigBio's search API that allows downloading specimen records. Searches are returned as a data.frame. Other functions such as the metadata end points return lists of information. iDigBio is a US project focused on digitizing and serving museum specimen collections on the web. See < <a href="https://www.idigbio.org">https://www.idigbio.org</a> > for information on iDigBio. / MIT	noarch
r-ridit	1.1	An extension of the Kruskal-Wallis Test that allow selection of arbitrary reference group. Also provide Mean Ridit for each group. Mean Ridit of a group is an estimate of probability a random observation from that group will be greater than or equal to a random observation from reference group. / GPL-2   GPL-3	noarch
r-ridittools	0.1	Functions to compute ridit scores of vectors, compute mean ridits and their standard errors for vectors compared to a reference vector, as described in Fleiss (1981, ISBN:0-471-06428-9), and compute means/SEs for multiple groups in matrices. Data can be either counts or proportions. Emphasis is on ridit analysis of ordered categorical data such as Likert items and pain-rating scales. / GPL-2   GPL-3   MIT	noarch
r-rifle	1.0	Implements the algorithms for solving sparse generalized eigenvalue problem by Tan, et. al. (2018). Sparse Generalized Eigenvalue Problem: Optimal Statistical Rates via Truncated Rayleigh Flow. To appear in Journal of the Royal Statistical Society: Series B. <arXiv:1604.08697>. / GPL-2	noarch
r-rifs	0.1_5	RIFS package provides functionality for generating & plotting prefractals in R^n with various protofractal sets and partition coefficient for iterative segments / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-rimpack</a>	1.0	The metrics() function calculates measures of scholarly impact. These include conventional measures, such as the number of publications and the total citations to all publications, as well as modern and robust metrics based on the vector of citations associated with each publication, such as the h index and many of its variants or rivals. These methods are described in Ruscio et al. (2012) <DOI: 10.1080/15366367.2012.711147>. / MIT	noarch
<a href="#">r-ring</a>	1.0.0	Circular / ring buffers in R and C. There are a couple of different buffers here with different implementations that represent different trade-offs. / MIT	linux-64, osx-64, win-64
<a href="#">r-rinside</a>	0.2.15	C classes to embed R in C applications A C class providing the R interpreter is offered by this package making it easier to have R inside your C application. As R itself is embedded into your application, a shared library build of R is required. This works on Linux, OS X and even on Windows provided you use the same tools used to build R itself. d Numerous examples are provided in the eight subdirectories of the examples/ directory of the installed package: standard, 'mpi' (for parallel computing), 'qt' (showing how to embed 'RInside' inside a Qt GUI application), 'wt' (showing how to build a web-application using the Wt toolkit), 'armadillo' (for 'RInside' use with 'RcppArmadillo') and 'eigen' (for 'RInside' use with 'RcppEigen'). The examples use 'GNUmakefile(s)' with GNU extensions, so a GNU make is required (and will use the 'GNUmakefile' automatically). 'Doxygen'-generated documentation of the C classes is available at the 'RInside' website as well. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-rinsp</a>	1.2.3	Functions to calculate several ecological indices of individual and population niche width (Araujo's E, clustering and pairwise similarity among individuals, IS, Petraitis' W, and Roughgarden's WIC/TNW) to assess individual specialization based on data of resource use. Resource use can be quantified by counts of categories, measures of mass/length or proportions. Monte Carlo resampling procedures are available for hypothesis testing against multinomial null models. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-rintervaltree</a>	0.1.0	This tool can be used to build binary interval trees using real number inputs. The tree supports queries of intervals overlapping a single number or an interval (start, end). Intervals with same bounds but different names are treated as distinct intervals. Insertion of intervals is also allowed. Deletion of intervals is not implemented at this point. See Mark de Berg, Otfried Cheong, Marc van Kreveld, Mark Overmars (2008). Computational Geometry: Algorithms and Applications, for a reference. / GPL-2	noarch
<a href="#">r-rintrojs</a>	0.2.2	A wrapper for the 'Intro.js' library (For more info: < <a href="http://www.introjs.com">http://www.introjs.com</a> >). This package makes it easy to include step-by-step introductions, and clickable hints in a 'Shiny' application. It supports both static introductions in the UI, and programmatic introductions from the server-side. / AGPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-rio</a>	0.5.16	Streamlined data import and export by making assumptions that the user is probably willing to make: ‘import()’ and ‘export()’ determine the data structure from the file extension, reasonable defaults are used for data import and export (e.g., ‘stringsAsFactors=FALSE’), web-based import is natively supported (including from SSL/HTTPS), compressed files can be read directly without explicit decompression, and fast import packages are used where appropriate. An additional convenience function, ‘convert()’, provides a simple method for converting between file types. / GPL-2	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-rip46</a>	1.0.2	Utility functions and S3 classes for IPv4 and IPv6 addresses, including conversion to and from binary representation. / GPL-3	linux-64, osx-64
<a href="#">r-rising</a>	0.1.0	Fits an Ising model to a binary dataset using L1 regularized logistic regression and extended BIC. Also includes a fast lasso logistic regression function for high-dimensional problems. Uses the ‘libLBFGS’ optimization library by Naoaki Okazaki. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-risk</a>	1.0	Computes 26 financial risk measures for any continuous distribution. The 26 financial risk measures include value at risk, expected shortfall due to Artzner et al. (1999) <DOI:10.1007/s10957-011-9968-2>, tail conditional median due to Kou et al. (2013) <DOI:10.1287/moor.1120.0577>, expectiles due to Newey and Powell (1987) <DOI:10.2307/1911031>, beyond value at risk due to Longin (2001) <DOI:10.3905/jod.2001.319161>, expected proportional shortfall due to Belzunce et al. (2012) <DOI:10.1016/j.insmatheco.2012.05.003>, elementary risk measure due to Ahmadi-Javid (2012) <DOI:10.1007/s10957-011-9968-2>, omega due to Shadwick and Keating (2002), sortino ratio due to Rollinger and Hoffman (2013), kappa due to Kaplan and Knowles (2004), Wang (1998)’s <DOI:10.1080/10920277.1998.10595708> risk measures, Stone (1973)’s <DOI:10.2307/2978638> risk measures, Luce (1980)’s <DOI:10.1007/BF00135033> risk measures, Sarin (1987)’s <DOI:10.1007/BF00126387> risk measures, Bronshtein and Kurelenkova (2009)’s risk measures. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-riskparityportfolio</a>	0.2.0	Fast design of risk parity portfolios for financial investment. The goal of the risk parity portfolio formulation is to equalize or distribute the risk contributions of the different assets, which is missing if we simply consider the overall volatility of the portfolio as in the mean-variance Markowitz portfolio. In addition to the vanilla formulation, where the risk contributions are perfectly equalized subject to no shortselling and budget constraints, many other formulations are considered that allow for box constraints and shortselling, as well as the inclusion of additional objectives like the expected return and overall variance. See vignette for a detailed documentation and comparison, with several illustrative examples. The package is based on the papers: Y. Feng, and D. P. Palomar (2015). SCRIP: Successive Convex Optimization Methods for Risk Parity Portfolio Design. IEEE Trans. on Signal Processing, vol. 63, no. 19, pp. 5285-5300. <doi:10.1109/TSP.2015.2452219>. F. Spinu (2013), An Algorithm for Computing Risk Parity Weights. <doi:10.2139/ssrn.2297383>. T. Griveau-Billion, J. Richard, and T. Roncalli (2013). A fast algorithm for computing High-dimensional risk parity portfolios. <arXiv:1311.4057>. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-riskportfolios</a>	2.1.2	Collection of functions designed to compute risk-based portfolios as described in Ardia et al. (2017) <doi:10.1007/s10479-017-2474-7> and Ardia et al. (2017) <doi:10.21105/joss.00171>. / GPL-2	noarch
<a href="#">r-riskr</a>	1.1	Computes risk measures from data, as well as performs risk management procedures. / GPL-2	noarch
<a href="#">r-risksetroc</a>	1.0.4	Compute time-dependent Incident/dynamic accuracy measures (ROC curve, AUC, integrated AUC )from censored survival data under proportional or non-proportional hazard assumption of Heagerty & Zheng (Biometrics, Vol 61 No 1, 2005, PP 92-105). / GPL-2	noarch
<a href="#">r-riskyr</a>	0.2.0	Risk-related information (like the prevalence of conditions and the sensitivity and specificity of diagnostic tests or treatment decisions) can be expressed in terms of probabilities or frequencies. By providing a toolbox of methods and metrics, 'riskyr' computes, translates, and visualizes risk-related information in a variety of ways. Offering multiple complementary perspectives on the interplay between key parameters renders teaching and training of risk literacy more transparent. / GPL-2   GPL-3	noarch
<a href="#">r-rismed</a>	2.1.7	A set of tools to extract bibliographic content from the National Center for Biotechnology Information (NCBI) databases, including PubMed. The name RISmed is a portmanteau of RIS (for Research Information Systems, a common tag format for bibliographic data) and PubMed. / GPL-2	noarch
<a href="#">r-riverbuilder</a>	0.1.1	Generates graphs, CSV files, and coordinates related to river valleys when calling the riverbuilder() function. / GPL-3	noarch
<a href="#">r-riverload</a>	1.0.1	Implements several of the most popular load estimation procedures, including averaging methods, ratio estimators and regression methods. The package provides an easy-to-use tool to rapidly calculate the load for various compounds and to compare different methods. The package also supplies additional functions to easily organize and analyze the data. / GPL-2	noarch
<a href="#">r-rivernet</a>	1.2	Functions for reading, analysing and plotting river networks. For this package, river networks consist of sections and nodes with associated attributes, e.g. to characterise their morphological, chemical and biological state. The package provides functions to read this data from text files, to analyse the network structure and network paths and regions consisting of sections and nodes that fulfill prescribed criteria, and to plot the river network and associated properties. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<code>r-riverplot</code>	0.6	Sankey plots are a type of diagram that is convenient to illustrate how flow of information, resources etc. separates and joins, much like observing how rivers split and merge. For example, they can be used to compare different clusterings. / GPL ( $\geq 2.0$ )	noarch
<code>r-rivervis</code>	0.46.0	This R package is a flexible and efficient tool to visualise both quantitative and qualitative data from river surveys. It can be used to produce diagrams with the topological structure of the river network. / GPL-2	noarch
<code>r-rivr</code>	1.2.1	A tool for undergraduate and graduate courses in open-channel hydraulics. Provides functions for computing normal and critical depths, steady-state water surface profiles (e.g. backwater curves) and unsteady flow computations (e.g. flood wave routing). / GPL-3	linux-64, osx-64, win-64
<code>r-rjacgh</code>	2.0.4	Bayesian analysis of CGH microarrays fitting Hidden Markov Chain models. The selection of the number of states is made via their posterior probability computed by Reversible Jump Markov Chain Monte Carlo Methods. Also returns probabilistic common regions for gains/losses. / GPL-3	linux-64, osx-64, win-64
<code>r-rjava</code>	0.9.1	Low-level interface to Java VM very much like .C/.Call and friends. Allows creation of objects, calling methods and accessing fields. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
<code>r-rjazz</code>	0.1.7	This is the official ‘Jazz’ client. ‘Jazz’ is a lightweight modular data processing framework, including a web server. It provides data persistence and computation capabilities accessible from ‘R’ and ‘Python’ and also through a REST API. < <a href="https://github.com/bbvadata/Jazz">https://github.com/bbvadata/Jazz</a> > See ?rjazz::rjazz to get a ‘Jazz’ server. / Apache License ( $= 2.0$ )	noarch
<code>r-rjdbc</code>	0.2.7	The RJDBC package is an implementation of R’s DBI interface using JDBC as a back-end. This allows R to connect to any DBMS that has a JDBC driver. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<code>r-rjdemetra</code>	0.1.3	Interface around ‘JDemetra’ (< <a href="https://github.com/jdemetra/jdemetra-app">https://github.com/jdemetra/jdemetra-app</a> >), the seasonal adjustment software officially recommended to the members of the European Statistical System (ESS) and the European System of Central Banks. It offers full access to all options and outputs of ‘JDemetra’, including the two leading seasonal adjustment methods TRAMO/SEATS and X-12ARIMA/X-13ARIMA-SEATS. / EUPL	noarch

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Name	Version	Summary/License	Platforms
r-rje	1.10.1	A series of functions in some way considered useful to the author. These include functions for subsetting tables and generating indices for arrays, conditioning and intervening in probability distributions, generating combinations and more... / GPL-2	linux-64, osx-64, win-64
r-rjsdmx	2.1_0	Provides functions to retrieve data and metadata from providers that disseminate data by means of SDMX web services. SDMX (Statistical Data and Metadata eXchange) is a standard that has been developed with the aim of simplifying the exchange of statistical information. More about the SDMX standard and the SDMX Web Services can be found at: < <a href="http://sdmx.org">http://sdmx.org</a> >. / EUPL	noarch
r-rjson	0.2.20	Converts R object into JSON objects and vice-versa / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
r-rjsonio	1.3_1	This is a package that allows conversion to and from data in Javascript object notation (JSON) format. This allows R objects to be inserted into Javascript/ECMAScript/ActionScript code and allows R programmers to read and convert JSON content to R objects. This is an alternative to rjson package. Originally, that was too slow for converting large R objects to JSON and was not extensible. rjson's performance is now similar to this package, and perhaps slightly faster in some cases. This package uses methods and is readily extensible by defining methods for different classes, vectorized operations, and C code and callbacks to R functions for deserializing JSON objects to R. The two packages intentionally share the same basic interface. This package (RJSONIO) has many additional options to allow customizing the generation and processing of JSON content. This package uses libjson rather than implementing yet another JSON parser. The aim is to support other general projects by building on their work, providing feedback and benefit from their ongoing development. / BSD_3_clause file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
r-rjsplot	2.5	Creates interactive graphs with 'R'. It joins the data analysis power of R and the visualization libraries of JavaScript in one package. / CC BY-NC-SA 4.0	noarch
r-rjstat	0.3.0	Read and write the 'JSON-stat' format ( <a href="http://json-stat.org">http://json-stat.org</a> ) to and from (lists of) R data frames. Not all features are supported, especially the extensive metadata features of 'JSON-stat'. / MIT	noarch
r-rjwsacruncher	0.1.0	'JDemetra' (< <a href="https://github.com/jdemetra/jdemetra-app">https://github.com/jdemetra/jdemetra-app</a> >) is the seasonal adjustment software officially recommended to the members of the European Statistical System and the European System of Central Banks. Seasonal adjustment models performed with 'JDemetra' can be stored into workspaces. 'JWSACruncher' (< <a href="https://github.com/jdemetra/jwsacruncher/releases">https://github.com/jdemetra/jwsacruncher/releases</a> >) is a console tool that re-estimates all the multi-processing defined in a workspace and to export the result. 'rjwsacruncher' allows to launch easily the 'JWSACruncher'. / GPL-3	noarch
r-rjython	0.0_4	R interface to Python via Jython allowing R to call python code. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-rkeajars	5.0_3	External jars required for package RKEA. / GPL-2	noarch
r-rkeedata	1.0.5	'KEEL' is a popular Java software for a large number of different knowledge data discovery tasks. Furthermore, 'RKEEL' is a package with a R code layer between R and 'KEEL', for using 'KEEL' in R code. This package includes the datasets from 'KEEL' in .dat format for its use in 'RKEEL' package. For more information about 'KEEL', see < <a href="http://www.keel.es/">http://www.keel.es/</a> >. / GPL-3	noarch
r-rkeeljars	1.0.19	'KEEL' is a popular Java software for a large number of different knowledge data discovery tasks. Furthermore, 'RKEEL' is a package with a R code layer between R and 'KEEL', for using 'KEEL' in R code. This package downloads and install the .jar files necessary for 'RKEEL' algorithms execution. For more information about 'KEEL', see < <a href="http://www.keel.es/">http://www.keel.es/</a> >. / GPL-3	noarch
r-rkelly	1.0	Calculates the Kelly criterion (Kelly, J.L. (1956) <doi:10.1002/j.1538-7305.1956.tb03809.x>) for bets given quoted prices, model predictions and commissions. Additionally it contains helper functions to calculate the probabilities for wins and draws in multi-leg games. / MIT	noarch
r-rklout	1.0	An interface of R to Klout API v2. It fetches Klout Score for a Twitter Username/handle in real time. Klout is a website and mobile app that uses social media analytics to rank its users according to online social influence via the Klout Score, which is a numerical value between 1 and 100. In determining the user score, Klout measures the size of a user's social media network and correlates the content created to measure how other users interact with that content. / GPL-2	noarch
r-rkmetrics	1.3	Hybrid Mortality Modelling (HMM) provides a framework in which mortality around the accident hump and at very old ages can be modelled under a single model. The graphics' codes necessary for visualization of the models' output are included here. Specifically, the graphics are based on the assumption that, the mortality rates can be expressed as a function of the area under the curve between the crude mortality rates plots and the tangential transform of the force of mortality. / GPL-3	noarch
r-rknn	1.2_1	Random knn classification and regression are implemented. Random knn based feature selection methods are also included. The approaches are mainly developed for high-dimensional data with small sample size. / GPL-2	linux-64, osx-64, win-64
r-rkt	1.5	Contains function rkt which computes the Mann-Kendall test (MK) and the Seasonal and the Regional Kendall Tests for trend (SKT and RKT) and Theil-Sen's slope estimator. / GPL-2	noarch
r-rkum	0.1.1	Robust kernel center matrix, robust kernel cross-covariance operator for kernel unsupervised methods, kernel canonical correlation analysis, influence function of identifying significant outliers or atypical objects from multimodal datasets. Alam, M. A, Fukumizu, K., Wang Y.-P. (2018) <doi:10.1016/j.neucom.2018.04.008>. Alam, M. A, Calhoun, C. D., Wang Y.-P. (2018) <doi:10.1016/j.csda.2018.03.013>. / GPL-3	noarch
r-rkvo	0.1	This package provides functionality to read files containing observations which consist of arbitrary key/value pairs. / GPL-3	linux-64, osx-64, win-64
r-rlab	2.15.1	Functions and Datasets Required for ST370 class / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-rlabkey</a>	2.3.1	The ‘LabKey’ client library for R makes it easy for R users to load live data from a ‘LabKey’ Server, < <a href="http://www.labkey.com/">http://www.labkey.com/</a> >, into the R environment for analysis, provided users have permissions to read the data. It also enables R users to insert, update, and delete records stored on a ‘LabKey’ Server, provided they have appropriate permissions to do so. / Apache License 2.0	linux-64, osx-64, win-64
<a href="#">r-rlakeanalyzer</a>	1.11.4	Standardized methods for calculating common important derived physical features of lakes including water density based on temperature, thermal layers, thermocline depth, lake number, Wedderburn number, Schmidt stability and others. / GPL-2	noarch
<a href="#">r-rlang</a>	0.3.4	A toolbox for working with base types, core R features like the condition system, and core ‘Tidyverse’ features like tidy evaluation. / GPL-3	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-rlas</a>	1.3.3	Read and write ‘las’ and ‘laz’ binary file formats. The LAS file format is a public file format for the interchange of 3-dimensional point cloud data between data users. The LAS specifications are approved by the American Society for Photogrammetry and Remote Sensing < <a href="https://www.asprs.org/committee-general/laser-las-file-format-exchange-activities.html">https://www.asprs.org/committee-general/laser-las-file-format-exchange-activities.html</a> >. The LAZ file format is an open and lossless compression scheme for binary LAS format versions 1.0 to 1.3 < <a href="https://www.laszip.org/">https://www.laszip.org/</a> >. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-rld</a>	1.0	Analyzes data from repeated low-dose challenge experiments and provide vaccine efficacy estimates. In addition, this package can provide guidance to design repeated low-dose challenge studies. / GPL-2	noarch
<a href="#">r-rlda</a>	0.2.6	Estimates the Bayesian LDA model for mixed-membership clustering based on different types of data (i.e., Multinomial, Bernoulli, and Binomial entries). Albuquerque, Valle and Li (2019) <doi:10.1016/j.knosys.2018.10.024>. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-rldcp</a>	1.0.2	Linguistic Descriptions of Complex Phenomena (LDCP) is an architecture and methodology that allows us to model complex phenomena, interpreting input data, and generating automatic text reports customized to the user needs (see <doi:10.1016/j.ins.2016.11.002> and <doi:10.1007/s00500-016-2430-5>). The proposed package contains a set of methods that facilitates the development of LDCP systems. Its main goal is increasing the visibility and practical use of this research line. / GPL-2	noarch
<a href="#">r-rleafangle</a>	1.0	Leaf angle distribution is described by a number of functions (e.g. ellipsoidal, Beta and rotated ellipsoidal). The parameters of leaf angle distributions functions are estimated through different empirical relationship. This package includes estimations of parameters of different leaf angle distribution function, plots and evaluates leaf angle distribution functions, calculates extinction coefficients given leaf angle distribution. Reference: Wang(2007)<doi:10.1016/j.agrformet.2006.12.003>. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-rleafmap</a>	0.2	Display spatial data with interactive maps powered by the open-source JavaScript library ‘Leaflet’ (see < <a href="http://leafletjs.com/">http://leafletjs.com/</a> >). Maps can be rendered in a web browser or displayed in the HTML viewer pane of ‘RStudio’. This package is designed to be easy to use and can create complex maps with vector and raster data, web served map tiles and interface elements. / GPL-3	noarch
<a href="#">r-rlecuyer</a>	0.3.4	Provides an interface to the C implementation of the random number generator with multiple independent streams developed by L’Ecuyer et al (2002). The main purpose of this package is to enable the use of this random number generator in parallel R applications. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-rlibeemd</a>	1.4.1	An R interface for libeemd (Luukko, Helske, Räsänen, 2016) <doi:10.1007/s00180-015-0603-9>, a C library of highly efficient parallelizable functions for performing the ensemble empirical mode decomposition (EEMD), its complete variant (CEEMDAN), the regular empirical mode decomposition (EMD), and bivariate EMD (BEMD). Due to the possible portability issues CRAN version no longer supports OpenMP, you can install OpenMP-supported version from GitHub: < <a href="https://github.com/helske/Rlibeemd/">https://github.com/helske/Rlibeemd/</a> >. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-rlinkedin</a>	0.2	A series of functions that allow users to access the ‘LinkedIn’ API to get information about connections, search for people and jobs, share updates with their network, and create group discussions. For more information about using the API please visit < <a href="https://developer.linkedin.com/">https://developer.linkedin.com/</a> >. / GPL-2	noarch
<a href="#">r-rlist</a>	0.4.6	Provides a set of functions for data manipulation with list objects, including mapping, filtering, grouping, sorting, updating, searching, and other useful functions. Most functions are designed to be pipeline friendly so that data processing with lists can be chained. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-rlm</a>	1.2	Robust fitting of linear model which can take response in matrix form. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-rlmdatadriven</a>	0.3.0	Data driven approach for robust regression estimation in homoscedastic and heteroscedastic context. See Wang et al. (2007), <doi:10.1198/106186007X180156> regarding homoscedastic framework. / GPL (>= 2.0)	noarch
<a href="#">r-rlme</a>	0.5	Estimates robust rank-based fixed effects and predicts robust random effects in two- and three- level random effects nested models. The methodology is described in Bilgic & Susmann (2013) < <a href="https://journal.r-project.org/archive/2013/RJ-2013-027/">https://journal.r-project.org/archive/2013/RJ-2013-027/</a> >. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-rlof</a>	1.1.1	R parallel implementation of Local Outlier Factor(LOF) which uses multiple CPUs to significantly speed up the LOF computation for large datasets. (Note: The overall performance depends on the computers especially the number of the cores).It also supports multiple k values to be calculated in parallel, as well as various distance measures in addition to the default Euclidean distance. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-rlrsim</a>	3.1.3	Rapid, simulation-based exact (restricted) likelihood ratio tests for testing the presence of variance components/nonparametric terms for models fit with nlme::lme(), lme4::lmer(), lmeTest::lmer(), gamm4::gamm4(), mgcv::gamm() and SemiPar::spm(). / GPL-3	linux-64, osx-64, win-64
<a href="#">r-rlt</a>	3.2.2	Random forest with a variety of additional features for regression, classification and survival analysis. The features include: parallel computing with OpenMP, embedded model for selecting the splitting variable (based on Zhu, Zeng & Kosorok, 2015), subject weight, variable weight, tracking subjects used in each tree, etc. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-rltp</a>	0.1.4	R interface to the ‘LTP’-Cloud service for Natural Language Processing in Chinese ( <a href="http://www.ltp-cloud.com/">http://www.ltp-cloud.com/</a> ). / LGPL-3	linux-64, osx-64, win-64
<a href="#">r-rm2006</a>	0.1.0	Estimation the conditional covariance matrix using the RiskMetrics 2006 methodology of Zumbach (2007) <doi:10.2139/ssrn.1420185>. / GPL-2	noarch
<a href="#">r-rmaf</a>	3.0.1	Uses refined moving average filter based on the optimal and data-driven moving average lag q or smoothing spline to estimate trend and seasonal components, as well as irregularity (residuals) for univariate time series or data. / GPL-2	noarch
<a href="#">r-rmake</a>	1.1.0	Creates and maintains a build process for complex analytic tasks in R. Package allows to easily generate Makefile for the (GNU) ‘make’ tool, which drives the build process by (in parallel) executing build commands in order to update results accordingly to given dependencies on changed data or updated source files. / GPL (>= 3.0)	noarch
<a href="#">r-rmallow</a>	1.0	An EM algorithm to fit Mallows’ Models to full or partial rankings, with or without ties. / GPL-2	noarch
<a href="#">r-rmalschains</a>	0.2.5	An implementation of an algorithm family for continuous optimization called memetic algorithms with local search chains (MA-LS-Chains). Memetic algorithms are hybridizations of genetic algorithms with local search methods. They are especially suited for continuous optimization. / GPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-rmargint</a>	1.0.2	Three robust marginal integration procedures for additive models based on local polynomial kernel smoothers. As a preliminary estimator of the multivariate function for the marginal integration procedure, a first approach uses local constant M-estimators, a second one uses local polynomials of order 1 over all the components of covariates, and the third one uses M-estimators based on local polynomials but only in the direction of interest. For this last approach, estimators of the derivatives of the additive functions can be obtained. All three procedures can compute predictions for points outside the training set if desired. See Boente and Martinez (2017) <doi:10.1007/s11749-016-0508-0> for details. / GPL (>= 3.0)	linux-64, osx-64, win-64
<a href="#">r-rmariadb</a>	1.0.6	Implements a 'DBI'-compliant interface to 'MariaDB' (< <a href="https://mariadb.org/">https://mariadb.org/</a> >) and 'MySQL' (< <a href="https://www.mysql.com/">https://www.mysql.com/</a> >) databases. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-rmarkdown</a>	1.12	Convert R Markdown documents into a variety of formats. / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-rmatio</a>	0.14.0	Read and write 'Matlab' MAT files from R. The 'rmatio' package supports reading MAT version 4, MAT version 5 and MAT compressed version 5. The 'rmatio' package can write version 5 MAT files and version 5 files with variable compression. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-rmawgen</a>	1.3.3	S3 and S4 functions are implemented for spatial multi-site stochastic generation of daily time series of temperature and precipitation. These tools make use of Vector AutoRegressive models (VARs). The weather generator model is then saved as an object and is calibrated by daily instrumental Gaussianized time series through the 'vars' package tools. Once obtained this model, it can be used for weather generations and be adapted to work with several climatic monthly time series. / GPL-2	noarch
<a href="#">r-rmcorr</a>	0.3.0	Compute the repeated measures correlation, a statistical technique for determining the overall within-individual relationship among paired measures assessed on two or more occasions, first introduced by Bland and Altman (1995). Includes functions for diagnostics, p-value, effect size with confidence interval including optional bootstrapping, as well as graphing. Also includes several example datasets. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-rmdfiltr</a>	0.1.0	A collection of ‘Lua’ filters that extend the functionality of R Markdown templates (e.g., count words or post-process ‘pandoc-citeproc’- citations). / MIT	noarch
<a href="#">r-rmdplgr</a>	0.4.0	Formats for R Markdown that undo modifications by ‘pandoc’ and ‘rmarkdown’ to original ‘latex’ templates, such as smaller margins, paragraph spacing, and compact titles. In addition, enhancements such as author blocks with affiliations and headers and footers are introduced. All of this functionality is built around plugins that modify the default ‘pandoc’ template without relying on custom templates. / GPL-3	noarch
<a href="#">r-rmdshower</a>	2.1.1	‘R’ ‘Markdown’ format for ‘shower’ presentations, see < <a href="https://github.com/shower/shower">https://github.com/shower/shower</a> >. / MIT	noarch
<a href="#">r-rmea</a>	1.1.0	A suite of tools useful to read, visualize and export bivariate motion energy time-series. Lagged synchrony between subjects can be analyzed through windowed cross-correlation. Surrogate data generation allows an estimation of pseudosynchrony that helps to estimate the effect size of the observed synchronization. Ramseyer & Tschacher (2011) <doi:10.1037/a0023419>. / GPL-3	noarch
<a href="#">r-rmecabko</a>	0.1.6.2	An ‘Rcpp’ interface for Eunjeon project < <a href="http://eunjeon.blogspot.com/">http://eunjeon.blogspot.com/</a> >. The ‘mecab-ko’ and ‘mecab-ko-dic’ is based on a C library, and part-of-speech tagging with them is useful when the spacing of source Korean text is not correct. This package provides part-of-speech tagging and tokenization function for Korean text. / GPL-2	win-64
<a href="#">r-rmediation</a>	1.1.4	We provide functions to compute confidence intervals (CIs) for a well-defined nonlinear function of the model parameters (e.g., product of k coefficients) in single-level and multilevel structural equation models. / GPL-2	noarch
<a href="#">r-rmeta</a>	3.0	Functions for simple fixed and random effects meta-analysis for two-sample comparisons and cumulative meta-analyses. Draws standard summary plots, funnel plots, and computes summaries and tests for association and heterogeneity. / GPL-2	noarch
<a href="#">r-rmi</a>	0.1.1	Provides mutual information estimators based on k-nearest neighbor estimators by A. Kraskov, et al. (2004) <doi:10.1103/PhysRevE.69.066138>, S. Gao, et al. (2015) < <a href="http://proceedings.mlr.press/v38/gao15.pdf">http://proceedings.mlr.press/v38/gao15.pdf</a> > and local density estimators by W. Gao, et al. (2017) <doi:10.1109/ISIT.2017.8006749>. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-rmio</a>	0.1.2	Provides header files of ‘mio’, a cross-platform C11 header-only library for memory mapped file IO < <a href="https://github.com/mandreyel/mio">https://github.com/mandreyel/mio</a> >. / GPL-3	noarch
<a href="#">r-rmisc</a>	1.5	The Rmisc library contains many functions useful for data analysis and utility operations. / GPL-3	noarch
<a href="#">r-rmixmod</a>	2.1.2	Interface of ‘MIXMOD’ software for supervised, unsupervised and semi-supervised classification with mixture modelling. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-rmixpanel</a>	0.7.1	Provides an interface to many endpoints of Mixpanel’s Data Export, Engage and JQL API. The R functions allow for event and profile data export as well as for segmentation, retention, funnel and addiction analysis. Results are always parsed into convenient R objects. Furthermore it is possible to load and update profiles. / MIT	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-rmxtcompio</a>	4.0.1	Mixture Composer < <a href="https://github.com/modal-inria/MixtComp">https://github.com/modal-inria/MixtComp</a> > is a project to build mixture models with heterogeneous data sets and partially missing data management. It includes models for real, categorical, counting, functional and ranking data. This package contains the minimal R interface of the C ‘MixtComp’ library. / AGPL-3	linux-64, osx-64, win-64
<a href="#">r-rmkdiscrete</a>	0.1	Sundry discrete probability distributions and helper functions. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-rmoajars</a>	1.0.1	External jars required for package RMOA. RMOA is a framework to build data stream models on top of MOA (Massive Online Analysis - < <a href="http://moa.cms.waikato.ac.nz">http://moa.cms.waikato.ac.nz</a> >). The jar files are put in this R package, the modelling logic can be found in the RMOA package. / GPL-3	noarch
<a href="#">r-rmonad</a>	0.5.0	A monadic solution to pipeline analysis. All operations – and the errors, warnings and messages they emit – are merged into a directed graph. Infix binary operators mediate when values are stored, how exceptions are handled, and where pipelines branch and merge. The resulting structure may be queried for debugging or report generation. ‘rmonad’ complements, rather than competes with, non-monadic pipeline packages like ‘magrittr’ or ‘pipeR’. This work is funded by the NSF (award number 1546858). / GPL-3	noarch
<a href="#">r-rmosek</a>	1.3.5	This is a meta-package designed to support the installation of Rmosek (>= 6.0) and bring the optimization facilities of MOSEK (>= 6.0) to the R-language. The interface supports large-scale optimization of many kinds: Mixed-integer and continuous linear, second-order cone, exponential cone and power cone optimization, as well as continuous semidefinite optimization. Rmosek and the R-language are open-source projects. MOSEK is a proprietary product, but unrestricted trial and academic licenses are available. / LGPL-2.1	noarch
<a href="#">r-rmpfr</a>	0.7_2	Arithmetic (via S4 classes and methods) for arbitrary precision floating point numbers, including transcendental (special) functions. To this end, the package interfaces to the ‘LGPL’ licensed ‘MPFR’ (Multiple Precision Floating-Point Reliable) Library which itself is based on the ‘GMP’ (GNU Multiple Precision) Library. / GPL-2	linux-64, osx-64
<a href="#">r-rmpw</a>	0.0.4	We implement causal mediation analysis using the methods proposed by Hong (2010) and Hong, Deutsch & Hill (2015) <doi:10.3102/1076998615583902>. It allows the estimation and hypothesis testing of causal mediation effects through ratio of mediator probability weights (RMPW). This strategy conveniently relaxes the assumption of no treatment-by-mediator interaction while greatly simplifying the outcome model specification without invoking strong distributional assumptions. We also implement a sensitivity analysis by extending the RMPW method to assess potential bias in the presence of omitted pretreatment or posttreatment covariates. The sensitivity analysis strategy was proposed by Hong, Qin, and Yang (2018) <doi:10.3102/1076998617749561>. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<code>r-rmr</code>	1.1.0	Analysis of oxygen consumption data generated by Loligo (R) Systems respirometry equipment. The package includes a function for loading data output by Loligo's 'AutoResp' software ( <code>get.witrox.data()</code> ), functions for calculating metabolic rates over user-specified time intervals, extracting critical points from data using broken stick regressions based on Yeager and Ultsch (<DOI:10.1086/physzool.62.4.30157935>), and easy functions for converting between different units of barometric pressure. / GPL-3	noarch
<code>r-rmr2</code>	3.3.1	Supports the map reduce programming model on top of hadoop streaming / Apache 2.0	linux-32, linux-64, osx-64, win-32, win-64
<code>r-rms</code>	5.1_3	Regression modeling, testing, estimation, validation, graphics, prediction, and typesetting by storing enhanced model design attributes in the fit. 'rms' is a collection of functions that assist with and streamline modeling. It also contains functions for binary and ordinal logistic regression models, ordinal models for continuous Y with a variety of distribution families, and the Buckley-James multiple regression model for right-censored responses, and implements penalized maximum likelihood estimation for logistic and ordinary linear models. 'rms' works with almost any regression model, but it was especially written to work with binary or ordinal regression models, Cox regression, accelerated failure time models, ordinary linear models, the Buckley-James model, generalized least squares for serially or spatially correlated observations, generalized linear models, and quantile regression. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<code>r-rms.gof</code>	1.0	This package can be used to test any simple null hypothesis using the root-mean-square goodness of fit test. Monte Carlo estimation is used to calculate the associated P-value. / GPL-3	noarch
<code>r-rmsfact</code>	0.0.3	Display a randomly selected quote about Richard M. Stallman based on the collection in the 'GNU Octave' function 'fact()' which was aggregated by Jordi Guti��rrez Hermoso based on the (now defunct) site stallmanfacts.com (which is accessible only via < <a href="http://archive.org">http://archive.org</a> >). / GPL-3	noarch
<code>r-rmthreshold</code>	1.1	An algorithm which can be used to determine an objective threshold for signal-noise separation in large random matrices (correlation matrices, mutual information matrices, network adjacency matrices) is provided. The package makes use of the results of Random Matrix Theory (RMT). The algorithm increments a suppositional threshold monotonically, thereby recording the eigenvalue spacing distribution of the matrix. According to RMT, that distribution undergoes a characteristic change when the threshold properly separates signal from noise. By using the algorithm, the modular structure of a matrix - or of the corresponding network - can be unraveled. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-rmtl</a>	0.9	Efficient solvers for 10 regularized multi-task learning algorithms applicable for regression, classification, joint feature selection, task clustering, low-rank learning, sparse learning and network incorporation. Based on the accelerated gradient descent method, the algorithms feature a state-of-art computational complexity $O(1/k^2)$ . Sparse model structure is induced by the solving the proximal operator. The detail of the package is described in the paper of Han Cao and Emanuel Schwarz (2018) <doi:10.1093/bioinformatics/bty831>. / GPL-3	noarch
<a href="#">r-rmtstat</a>	0.3	Functions for working with the Tracy-Widom laws and other distributions related to the eigenvalues of large Wishart matrices. The tables for computing the Tracy-Widom densities and distribution functions were computed by Momar Dieng's MATLAB package RMLab (formerly available on his homepage at <a href="http://math.arizona.edu/~momar/research.htm">http://math.arizona.edu/~momar/research.htm</a> ). This package is part of a collaboration between Iain Johnstone, Zongming Ma, Patrick Perry, and Morteza Shahram. It will soon be replaced by a package with more accuracy and built-in support for relevant statistical tests. / BSD_3_clause	noarch
<a href="#">r-rmumps</a>	5.2.1	Some basic features of MUMPS (Multifrontal Massively Parallel sparse direct Solver) are wrapped in a class whose methods can be used for sequentially solving a sparse linear system (symmetric or not) with one or many right hand sides (dense or sparse). There is a possibility to do separately symbolic analysis, LU (or $LDL^t$ ) factorization and system solving. Third part ordering libraries are included and can be used: PORD, METIS, SCOTCH. MUMPS method was first described in Amestoy et al. (2001) <doi:10.1137/S0895479899358194> and Amestoy et al. (2006) <doi:10.1016/j.parco.2005.07.004>. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-rmutil</a>	1.1.3	A toolkit of functions for nonlinear regression and repeated measurements not to be used by itself but called by other Lindsey packages such as 'gnlm', 'stable', 'growth', 'repeated', and 'event' (available at < <a href="http://www.commanster.eu/rcode.html">http://www.commanster.eu/rcode.html</a> >). / GPL-2	linux-64, osx-64, win-64
<a href="#">r-rmvp</a>	0.99.1A	A memory-efficient, visualize-enhanced, parallel-accelerated Genome-Wide Association Study (GWAS) tool. It can (1) effectively process large data, (2) rapidly evaluate population structure, (3) efficiently estimate variance components several algorithms, (4) implement parallel-accelerated association tests of markers three methods, (5) globally efficient design on GWAS process computing, (6) enhance visualization of related information. 'rMVP' contains three models GLM (Alkes Price (2006) <DOI:10.1038/ng1847>), MLM (Jianming Yu (2006) <DOI:10.1038/ng1702>) and FarmCPU (Xiaolei Liu (2016) <doi:10.1371/journal.pgen.1005767>); variance components estimation methods EMMAX (Hyunmin Kang (2008) <DOI:10.1534/genetics.107.080101>), FaSTLMM (method: Christoph Lippert (2011) <DOI:10.1038/nmeth.1681>, R implementation from 'GAPIT2': You Tang and Xiaolei Liu (2016) <DOI:10.1371/journal.pone.0107684> and 'SUPER': Qishan Wang and Feng Tian (2014) <DOI:10.1371/journal.pone.0107684>), and HE regression (Xiang Zhou (2017) <DOI:10.1214/17-AOAS1052>). / Apache License 2.0	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-rmysql</a>	0.10.1	A ‘DBI’ interface to ‘MySQL’ / ‘MariaDB’. The ‘RMySQL’ package contains an old implementation based on legacy code from S-PLUS which being phased out. A modern ‘MySQL’ client based on ‘Rcpp’ is available from the ‘RMariaDB’ package. / GPL-2	linux-32, linux-64, osx-64, win-64
<a href="#">r-rnaseqwrapper</a>	1.0.1	This package is designed to streamline several of the common steps for RNA-seq analysis, including differential expression and variant discovery. For the development build, or to contribute changes to this package, please see our repository at <a href="https://bitbucket.org/petersmp/rnaseqwrapper/">https://bitbucket.org/petersmp/rnaseqwrapper/</a> / GPL-3	noarch
<a href="#">r-rnassqs</a>	0.5.0	Interface to access data via the United States Department of Agriculture’s National Agricultural Statistical Service (NASS) ‘Quick Stats’ web API < <a href="https://quickstats.nass.usda.gov/api">https://quickstats.nass.usda.gov/api</a> >. Convenience functions facilitate building queries based on available parameters and valid parameter values. / MIT	noarch
<a href="#">r-rnaturalearthdata</a>	0.1.0	Vector map data from < <a href="http://www.naturalearthdata.com/">http://www.naturalearthdata.com/</a> >. Access functions are provided in the accompanying package ‘rnaturalearth’. / CC0	noarch
<a href="#">r-rnavgraphimagedata</a>	0.0.4	Image data used as examples in the loon R package. / GPL-2	noarch
<a href="#">r-rnavicell</a>	0.2	Provides a set of functions to access a data visualization web service. For more information and a tutorial on how to use it, see <a href="https://navicell.curie.fr/pages/nav_web_service.html">https://navicell.curie.fr/pages/nav_web_service.html</a> and <a href="https://github.com/sysbio-curie/RNaviCell">https://github.com/sysbio-curie/RNaviCell</a> . / LGPL-2.1	noarch
<a href="#">r-rnbp</a>	0.1.0	Use the < <a href="http://api.nbp.pl/">http://api.nbp.pl/</a> > API through R. Retrieve currency exchange rates and gold prices data published by the National Bank of Poland in form of convenient R objects. / GPL-3	noarch
<a href="#">r-rncbieutillslibs</a>	0.9	Provides the libraries of the EUtils operations for the RNCBI package. / GPL-3	noarch
<a href="#">r-rnd</a>	1.2	Extract the implied risk neutral density from options using various methods. / GPL-2	noarch
<a href="#">r-rndtexexams</a>	1.5	Using as input a ‘LaTeX’ file with a multiple choice exam, this package will produce several versions with randomized contents of the same exam. Functions for grading are also available. / GPL-2	noarch
<a href="#">r-rnentropy</a>	1.2.2	An implementation of a method based on information theory devised for the identification of genes showing a significant variation of expression across multiple conditions. Given expression estimates from any number of RNA-Seq samples and conditions it identifies genes or transcripts with a significant variation of expression across all the conditions studied, together with the samples in which they are over- or under-expressed. Zambelli et al. (2018) <doi:10.1093/nar/gky055>. / GPL-3	noarch
<a href="#">r-rneos</a>	0.3.2	Within this package the XML-RPC API to NEOS < <a href="https://neos-server.org/neos/">https://neos-server.org/neos/</a> > is implemented. This enables the user to pass optimization problems to NEOS and retrieve results within R. / GPL-2	noarch
<a href="#">r-rnetcarto</a>	0.2.4	It provides functions to compute the modularity and modularity-related roles in networks. It is a wrapper around the rgraph library (Guimera & Amaral, 2005, doi:10.1038/nature03288). / GPL-2	linux-64, osx-64

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Name	Version	Summary/License	Platforms
<a href="#">r-rnetcdf</a>	1.9_1	An interface to the NetCDF file format designed by Unidata for efficient storage of array-oriented scientific data and descriptions. The R interface is closely based on the C API of the NetCDF library, and it includes calendar conversions from the Unidata UDUNITS library. The current implementation supports all operations on NetCDF datasets in classic and 64-bit offset file formats, and NetCDF4-classic format is supported for reading and modification of existing files. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-rnetlogo</a>	1.0_4	Interface to use and access Wilensky's 'NetLogo' (Wilensky 1999) from R using either headless (no GUI) or interactive GUI mode. Provides functions to load models, execute commands, and get values from reporters. Mostly analogous to the 'NetLogo' 'Mathematica' Link < <a href="https://github.com/NetLogo/Mathematica-Link">https://github.com/NetLogo/Mathematica-Link</a> >. / GPL-2	noarch
<a href="#">r-rngforgpd</a>	1.0_2	Generation of univariate and multivariate data that follow the generalized Poisson distribution. The details of the univariate part are explained in Demirtas (2017), and the multivariate part is an extension of the correlated Poisson data generation routine that was introduced in Yahav and Shmueli (2012). / GPL-2   GPL-3	noarch
<a href="#">r-rngsetseed</a>	0.3_2	A function <code>setVectorSeed()</code> is provided. Its argument is a numeric vector of an arbitrary nonzero length, whose components have integer values from $[0, 2^{32}-1]$ . The input vector is transformed using AES (Advanced Encryption Standard) algorithm into an initial state of Mersenne-Twister random number generator. The function provides a better alternative to the R base function <code>set.seed()</code> , if the input vector is a single integer. Initializing a stream of random numbers with a vector is a convenient way to obtain several streams, each of which is identified by several integer indices. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-rngtools</a>	1.3.1	Provides a set of functions for working with Random Number Generators (RNGs). In particular, a generic S4 framework is defined for getting/setting the current RNG, or RNG data that are embedded into objects for reproducibility. Notably, convenient default methods greatly facilitate the way current RNG settings can be changed. / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-rngwell</a>	0.10_5	It is a dedicated package to WELL pseudo random generators, which were introduced in Panneton et al. (2006), "Improved Long-Period Generators Based on Linear Recurrences Modulo 2", ACM Transactions on Mathematical Software. But this package is not intended to be used directly, you are strongly __encouraged__ to use the 'randtoolbox' package, which depends on this package. / BSD_3_clause	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-rngwell19937</a>	0.6_0	Long period linear random number generator WELL19937a by F. Panneton, P. L'Ecuyer and M. Matsumoto. The initialization algorithm allows to seed the generator with a numeric vector of an arbitrary length and uses MRG32k5a by P. L'Ecuyer to achieve good quality of the initialization. The output function may be set to provide numbers from the interval (0,1) with 53 (the default) or 32 random bits. WELL19937a is of similar type as Mersenne Twister and has the same period. WELL19937a is slightly slower than Mersenne Twister, but has better equidistribution and bit-mixing properties and faster recovery from states with prevailing zeros than Mersenne Twister. All WELL generators with orders 512, 1024, 19937 and 44497 can be found in randtoolbox package. / file LICENSE (Restricts use)	linux-64, osx-64, win-64
<a href="#">r-rnifti</a>	0.11	Provides very fast read and write access to images stored in the NIFTI-1 and ANALYZE-7.5 formats, with seamless synchronisation between compiled C and interpreted R code. Also provides a C/C API that can be used by other packages. Not to be confused with 'RNiftyReg', which performs image registration. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-rnomni</a>	0.7.1	Genetic association tests that use the rank-based inverse normal transformation (INT). These tests are recommend for continuous traits with non-normally distributed residuals. INT-based tests robustly control the type I error in settings where standard linear regression does not. Moreover, INT-based tests dominate standard linear regression in terms of power. INT-based tests may be classified into two types: tests that directly transform the phenotype (D-INT) and tests that transform phenotypic residuals (I-INT). Our omnibus test (O-INT) adaptively combines D-INT and I-INT into a single robust and statistically powerful approach. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-rnpn</a>	0.1.0	Programmatic interface to the Web Service methods provided by the National 'Phenology' Network (< <a href="https://usanpn.org/">https://usanpn.org/</a> >), which includes data on various life history events that occur at specific times. / MIT	noarch
<a href="#">r-rnr</a>	0.2.1	Apply sensitivity analysis for offline policy evaluation, as implemented in Jung et al. (2017) <arXiv:1702.04690> based on Rosenbaum and Rubin (1983) < <a href="http://www.jstor.org/stable/2345524">http://www.jstor.org/stable/2345524</a> >. / GPL-3	noarch
<a href="#">r-rnumeraai</a>	0.3	Routines to interact with the Numerai Machine Learning Tournament API < <a href="https://numer.ai">https://numer.ai</a> >. The functionality includes the ability to automatically download the current tournament data, submit predictions, and to get information for your user. General 'GraphQL' queries can also be executed. / GPL-3	noarch
<a href="#">r-roauth</a>	0.9.6	Provides an interface to the OAuth 1.0 specification allowing users to authenticate via OAuth to the server of their choice. / Artistic-2.0	noarch
<a href="#">r-robastrda</a>	1.2.0	Includes 'sysdata.rda' file for packages of the 'RobAST' - family of packages; is currently used by package 'RobExtremes' only. / LGPL-3	noarch
<a href="#">r-robcor</a>	0.1_6	Robust pairwise correlations based on estimates of scale, particularly on FastQn one-step M-estimate. / GPL-2	noarch
<a href="#">r-robcp</a>	0.2.4	Provides robust methods to detect change-points in uni- or multivariate time series. They can cope with corrupted data and heavy tails. One can detect changes in location, scale and dependence structure of a possibly multivariate time series. Procedures are based on Huberized versions of CUSUM tests proposed in Duerre and Fried (2019) <arXiv:1905.06201>. / GPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-robeth</a>	2.7.5	Locations problems, M-estimates of coefficients and scale in linear regression, Weights for bounded influence regression, Covariance matrix of the coefficient estimates, Asymptotic relative efficiency of regression M-estimates, Robust testing in linear models, High breakdown point regression, M-estimates of covariance matrices, M-estimates for discrete generalized linear models. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-robfilter</a>	4.1.1	A set of functions to filter time series based on concepts from robust statistics. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-robfitcongraph</a>	0.1.0	Contains a single function named robFitConGraph() which includes two algorithms for robust estimation of scatter matrices subject to zero-constraints in its inverse. The methodology is described in Vogel & Tyler (2014) <doi:10.1093/biomet/asu041>. See robFitConGraph() function documentation for further details. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-robrsvd</a>	1.0	This package provides the function to calculate SVD, regularized SVD, robust SVD and robust regularized SVD method. The robust SVD methods use alternating iteratively reweighted least squares methods. The regularized SVD uses generalized cross validation to choose the optimal smoothing parameters. / GPL-3	noarch
<a href="#">r-robumeta</a>	2.0	Functions for conducting robust variance estimation (RVE) meta-regression using both large and small sample RVE estimators under various weighting schemes. These methods are distribution free and provide valid point estimates, standard errors and hypothesis tests even when the degree and structure of dependence between effect sizes is unknown. Also included are functions for conducting sensitivity analyses under correlated effects weighting and producing RVE-based forest plots. / GPL-2	noarch
<a href="#">r-robustaft</a>	1.4.4	R functions for the computation of the truncated maximum likelihood and the robust accelerated failure time regression for gaussian and log-Weibull case. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-robustbase</a>	0.93	Essential Robust Statistics. Tools allowing to analyze data with robust methods. This includes regression methodology including model selections and multivariate statistics where we strive to cover the book Robust Statistics, Theory and Methods by ‘Maronna, Martin and Yohai’; Wiley 2006. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-robustblme</a>	0.1.3	Bayesian robust fitting of linear mixed effects models through weighted likelihood equations and approximate Bayesian computation as proposed by Ruli et al. (2017) <arXiv:1706.01752>. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-robustetm</a>	1.0	Testing homogeneity for generalized exponential tilt model. This package includes a collection of functions for (1) implementing methods for testing homogeneity for generalized exponential tilt model; and (2) implementing existing methods under comparison. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-robustgam</a>	0.1.7	This package provides robust estimation for generalized additive models. It implements a fast and stable algorithm in Wong, Yao and Lee (2013). The implementation also contains three automatic selection methods for smoothing parameter. They are designed to be robust to outliers. For more details, see Wong, Yao and Lee (2013). / GPL-2	linux-64, osx-64, win-64
<a href="#">r-robustgasp</a>	0.5.7	Robust parameter estimation and prediction of Gaussian stochastic process emulators. It allows for robust parameter estimation and prediction using Gaussian stochastic process emulator. It also implements the parallel partial Gaussian stochastic process emulator for computer model with massive outputs See the reference: Mengyang Gu and Jim Berger, 2016, Annals of Applied Statistics; Mengyang Gu, Xiaojing Wang and Jim Berger, 2018, Annals of Statistics. / GPL-2   GPL-3	linux-64, osx-64, win-64
<a href="#">r-robustrankagggreg</a>	1.1	Methods for aggregating ranked lists, especially lists of genes. It implements the Robust Rank Aggregation (Kolde et. al in preparation) and some other simple algorithms for the task. RRA method uses a probabilistic model for aggregation that is robust to noise and also facilitates the calculation of significance probabilities for all the elements in the final ranking. / GPL-2	noarch
<a href="#">r-robustreg</a>	0.1.1	Linear regression functions using Huber and bisquare psi functions. Optimal weights are calculated using IRLS algorithm. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-robustx</a>	1.2.4	Robustness – ‘eXperimental’, ‘eXtraneous’, or ‘eXtraordinary’ Functionality for Robust Statistics. In other words, methods which are not yet well established, often related to methods in package ‘robustbase’. / GPL-2	noarch
<a href="#">r-rocc</a>	1.2	Functions for a classification method based on receiver operating characteristics (ROC). Briefly, features are selected according to their ranked AUC value in the training set. The selected features are merged by the mean value to form a metagene. The samples are ranked by their metagene value and the metagene threshold that has the highest accuracy in splitting the training samples is determined. A new sample is classified by its metagene value relative to the threshold. In the first place, the package is aimed at two class problems in gene expression data, but might also apply to other problems. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<code>r-roccv</code>	1.2	Cross validate large genetic data while specifying clinical variables that should always be in the model using the function <code>cv()</code> . An ROC plot from the cross validation data with AUC can be obtained using <code>rocplot()</code> , which also can be used to compare different models. Framework was built to handle genetic data, but works for any data. / MIT	noarch
<code>r-rocit</code>	1.1.1	Sensitivity (or recall or true positive rate), false positive rate, specificity, precision (or positive predictive value), negative predictive value, misclassification rate, accuracy, F-score- these are popular metrics for assessing performance of binary classifier for certain threshold. These metrics are calculated at certain threshold values. Receiver operating characteristic (ROC) curve is a common tool for assessing overall diagnostic ability of the binary classifier. Unlike depending on a certain threshold, area under ROC curve (also known as AUC), is a summary statistic about how well a binary classifier performs overall for the classification task. ROCit package provides flexibility to easily evaluate threshold-bound metrics. Also, ROC curve, along with AUC, can be obtained using different methods, such as empirical, binormal and non-parametric. ROCit encompasses a wide variety of methods for constructing confidence interval of ROC curve and AUC. ROCit also features the option of constructing empirical gains table, which is a handy tool for direct marketing. The package offers options for commonly used visualization, such as, ROC curve, KS plot, lift plot. Along with in-built default graphics setting, there are rooms for manual tweak by providing the necessary values as function arguments. ROCit is a powerful tool offering a range of things, yet it is very easy to use. / GPL-3	noarch
<code>r-rocnit</code>	1.0	Non-inferiority test and diagnostic test are very important in clinical trials. This package is to get a p value from the non-inferiority test for ROC curves from diagnostic test. / GPL-3	noarch
<code>r-rococo</code>	1.1.7	Provides the robust gamma rank correlation coefficient as introduced by Bodenhofer, Krone, and Klawonn (2013) <DOI:10.1016/j.ins.2012.11.026> along with a permutation-based rank correlation test. The rank correlation coefficient and the test are explicitly designed for dealing with noisy numerical data. / GPL-2	linux-64, osx-64, win-64
<code>r-rocr</code>	1.0.7	ROC graphs, sensitivity/specificity curves, lift charts, and precision/recall plots are popular examples of trade-off visualizations for specific pairs of performance measures. ROCR is a flexible tool for creating cutoff-parameterized 2D performance curves by freely combining two from over 25 performance measures (new performance measures can be added using a standard interface). Curves from different cross-validation or bootstrapping runs can be averaged by different methods, and standard deviations, standard errors or box plots can be used to visualize the variability across the runs. The parameterization can be visualized by printing cutoff values at the corresponding curve positions, or by coloring the curve according to cutoff. All components of a performance plot can be quickly adjusted using a flexible parameter dispatching mechanism. Despite its flexibility, ROCR is easy to use, with only three commands and reasonable default values for all optional parameters. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<code>r-rocwogs</code>	1.0	Function to estimate the ROC Curve of a continuous-scaled diagnostic test with the help of a second imperfect diagnostic test with binary responses. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-rodam</a>	0.1.6	‘ODAM’ (Open Data for Access and Mining) is a framework that implements a simple way to make research data broadly accessible and fully available for reuse, including by a script language such as R. The main purpose is to make a data set accessible online with a minimal effort from the data provider, and to allow any scientists or bioinformaticians to be able to explore the data set and then extract a subpart or the totality of the data according to their needs. The Rodam package has only one class, ‘odamws’, that provides methods to allow you to retrieve online data using ‘ODAM’ Web Services. This obviously requires that data are implemented according the ‘ODAM’ approach, namely that the data subsets were deposited in the suitable data repository in the form of TSV files associated with their metadata also described in TSV files. See < <a href="http://www.slideshare.net/danieljacob771282/odam-open-data-access-and-mining">http://www.slideshare.net/danieljacob771282/odam-open-data-access-and-mining</a> >. / LGPL-3	noarch
<a href="#">r-rodbc</a>	1.3.1	An ODBC database interface. / GPL-2   GPL-3	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-rodcbdbi</a>	0.1.1	An implementation of R’s DBI interface using ODBC package as a back-end. This allows R to connect to any DBMS that has a ODBC driver. / MIT	noarch
<a href="#">r-rodcbext</a>	0.3.1	An extension for RODBC package adding support for parameterized queries. / GPL-2   GPL-3	linux-64, osx-64, win-64
<a href="#">r-rode</a>	0.99.6	Show physics, math and engineering students how an ODE solver is made and how effective R classes can be for the construction of the equations that describe natural phenomena. Inspiration for this work comes from the book on Computer Simulations in Physics by Harvey Gould, Jan Tobochnik, and Wolfgang Christian. Book link: < <a href="http://www.compadre.org/osp/items/detail.cfm?ID=7375">http://www.compadre.org/osp/items/detail.cfm?ID=7375</a> >. / GPL-2	noarch
<a href="#">r-rodeo</a>	0.7.4	Provides an R6 class and several utility methods to facilitate the implementation of models based on ordinary differential equations. The heart of the package is a code generator that creates compiled ‘Fortran’ (or ‘R’) code which can be passed to a numerical solver. There is direct support for solvers contained in packages ‘deSolve’ and ‘rootSolve’. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-rodmm</a>	1.1	This package implements an interface to Oracle Data Mining (ODM). It provides an ideal environment for rapid development of demos and proof of concept data mining studies. It facilitates the prototyping of vertical applications and makes ODM and the RDBMS environment easily accessible to statisticians and data analysts familiar with R but not fluent in SQL or familiar with the database environment. It also facilitates the benchmarking and testing of ODM functionality including the production of summary statistics, performance metrics and graphics. It enables the scripting and control of production data mining methodologies from a high-level environment. Oracle Data Mining (ODM) is an option of Oracle Relational Database Management System (RDBMS) Enterprise Edition (EE). It contains several data mining and data analysis algorithms for classification, prediction, regression, clustering, associations, feature selection, anomaly detection, feature extraction, and specialized analytics. It provides means for the creation, management and operational deployment of data mining models inside the database environment. For more information consult the entry for Oracle Data Mining in Wikipedia ( <a href="http://en.wikipedia.org">en.wikipedia.org</a> ). / LGPL-2	noarch
<a href="#">r-roi</a>	0.3_2	The R Optimization Infrastructure ('ROI') is a sophisticated framework for handling optimization problems in R. More information can be found on the 'ROI' homepage < <a href="http://roi.r-forge.r-project.org/">http://roi.r-forge.r-project.org/</a> >. / GPL-3	noarch
<a href="#">r-rollbar</a>	0.1.0	Reports errors and messages to Rollbar, the error tracking platform < <a href="https://rollbar.com">https://rollbar.com</a> >. / MIT	noarch
<a href="#">r-rolldown</a>	0.1	R Markdown output formats based on JavaScript libraries such as 'Scrollama' (< <a href="https://github.com/russellgoldenbergs/scrollama">https://github.com/russellgoldenbergs/scrollama</a> >) for storytelling. / MIT	noarch
<a href="#">r-rollregres</a>	0.1.2	Methods for fast rolling and expanding linear regression models. That is, series of linear regression models estimated on either an expanding window of data or a moving window of data. The methods use rank-one updates and downdates of the upper triangular matrix from a QR decomposition (see Dongarra, Moler, Bunch, and Stewart (1979) <doi:10.1137/1.9781611971811>). / GPL-2	linux-64, osx-64, win-64
<a href="#">r-roloc</a>	0.1_1	Functions to convert an R colour specification to a colour name. The user can select and create different lists of colour names and different colour metrics for the conversion. / GPL-2   GPL-3	noarch
<a href="#">r-rolr</a>	1.0.0	Provides fast procedures for exploring all pairs of cutpoints of a single covariate with respect to survival and determining optimal cutpoints using a hierarchical method and various ordered logrank tests. / GPL-3	noarch
<a href="#">r-ronfhir</a>	0.3.1	R on FHIR is an easy to use wrapper around the 'HL7 FHIR' REST API (STU 3). It provides tools to easily read and search resources on a FHIR server and brings the results into the R environment. R on FHIR is based on the FhirClient of the official 'HL7 FHIR .NET API', also made by Firely. / BSD_3_clause	noarch
<a href="#">r-rook</a>	1.1_1	This package contains the Rook specification and convenience software for building and running Rook applications. To get started, be sure and read the 'Rook' help file first. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
r-rootsolve	1.7	Routines to find the root of nonlinear functions, and to perform steady-state and equilibrium analysis of ordinary differential equations (ODE). Includes routines that: (1) generate gradient and jacobian matrices (full and banded), (2) find roots of non-linear equations by the ‘Newton-Raphson’ method, (3) estimate steady-state conditions of a system of (differential) equations in full, banded or sparse form, using the ‘Newton-Raphson’ method, or by dynamically running, (4) solve the steady-state conditions for uni-and multicomponent 1-D, 2-D, and 3-D partial differential equations, that have been converted to ordinary differential equations by numerical differencing (using the method-of-lines approach). Includes fortran code. / GPL-2	linux-64, osx-64, win-64
r-rootwishart	0.4.1	Functions for hypothesis testing in single and double Wishart settings, based on Roy’s largest root. This test statistic is especially useful in multivariate analysis. The computations are based on results by Chiani (2014) <DOI:10.1016/j.jmva.2014.04.002> and Chiani (2016) <DOI:10.1016/j.jmva.2015.10.007>. They use the fact that the CDF is related to the Pfaffian of a matrix that can be computed in a finite number of iterations. This package takes advantage of the Boost and Eigen C libraries to perform multi-precision linear algebra. / GPL-2	linux-64, osx-64, win-64
r-rop	1.0	Trees Classification and Regression using multivariate nodes calculated by an exhaustive numerical approach. We propose a new concept of decision tree, including multivariate knots and non hierarchical pathway. This package’s model uses a multivariate nodes tree that calculates directly a risk score for each observation for the state Y observed. Nguyen JM, Gaultier A, Antonioli D (2015) <doi:10.1016/j.respe.2018.03.088> Castillo JM, Knol AC, Nguyen JM, Khammari A, Saint Jean M, Dreno B (2016) <doi:10.1684/ejd.2016.2826> Vildy S, Nguyen JM, Gaultier A, Khammari A, Dreno B (2017) <doi:10.1684/ejd.2016.2955> Nguyen JM, Gaultier A, Antonioli D (2018) <doi:10.1016/j.respe.2018.03.088>. / GPL (>= 2.0)	noarch
r-rope	1.0	Selects one model with variable selection FDR controlled at a specified level. A q-value for each potential variable is also returned. The input, variable selection counts over many bootstraps for several levels of penalization, is modeled as coming from a beta-binomial mixture distribution. / GPL-3	noarch
r-ropendata	0.1.0	‘Rapid7’ collects ‘cybersecurity’ data and makes it available via their ‘Open Data’ < <a href="http://opendata.rapid7.com">http://opendata.rapid7.com</a> > portal which has an API. Tools are provided to assist in querying for available data sets and downloading any data set authorized to a free, registered account. / MIT	noarch
r-ropendota	0.1.2	Provides a client for the API of OpenDota. OpenDota is a web service which is provide DOTA2 real time data. Data is collected through the Steam WebAPI. With ROpenDota you can easily grab the latest DOTA2 statistics in R programming such as latest match on official international competition, analyzing your or enemy performance to learn their strategies,etc. Please see < <a href="https://github.com/rosdyana/ROpenDota">https://github.com/rosdyana/ROpenDota</a> > for more information. / MIT	noarch
r-ropenfigi	0.2.8	Provide a simple interface to Bloomberg’s OpenFIGI API. Please see < <a href="https://openfigi.com">https://openfigi.com</a> > for API details and registration. You may be eligible to have an API key to accelerate your loading process. / GPL-3	noarch
r-ropensecretsapi	1.0.1	An R package for the OpenSecrets.org web services API. / LGPL-3	noarch
r-ropenweathermap	1.1	OpenWeatherMap (OWM) < <a href="http://openweathermap.org/api">http://openweathermap.org/api</a> > is a service providing weather related data. This package can be used to access current weather data for one location or several locations. It can also be used to forecast weather for 5 days with data for every 3 hours. / MIT	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-roperators</a>	1.1.0	Provides string arithmetic, reassignment operators, logical operators that handle missing values, and extra logical operators such as floating point equality and all or nothing. The intent is to allow R users to write code that is easier to read, write, and maintain while providing a friendlier experience to new R users from other language backgrounds (such as ‘Python’) who are used to concepts such as <code>x = 1</code> and <code>‘foo’ ‘bar’</code> . / MIT	noarch
<a href="#">r-roptimizely</a>	0.2.0	R package extracts optimizely test results and test information using Optimizely REST API. Only read functionality is supported for analysis and reporting. / GPL-2	noarch
<a href="#">r-rose</a>	0.0.3	The package provides functions to deal with binary classification problems in the presence of imbalanced classes. Synthetic balanced samples are generated according to ROSE (Menardi and Torelli, 2013). Functions that implement more traditional remedies to the class imbalance are also provided, as well as different metrics to evaluate a learner accuracy. These are estimated by holdout, bootstrap or cross-validation methods. / GPL-2	noarch
<a href="#">r-rosetteapi</a>	1.12.1	‘Rosette’ is an API for multilingual text analysis and information extraction. More information can be found at < <a href="https://developer.rosette.com">https://developer.rosette.com</a> >. / Apache License 2.0   file LICENSE	noarch
<a href="#">r-rotationforest</a>	0.1.3	Fit and deploy rotation forest models (Rodriguez, J.J., Kuncheva, L.I., 2006. Rotation forest: A new classifier ensemble method. IEEE Trans. Pattern Anal. Mach. Intell. 28, 1619-1630 <doi:10.1109/TPAMI.2006.211>) for binary classification. Rotation forest is an ensemble method where each base classifier (tree) is fit on the principal components of the variables of random partitions of the feature set. / GPL-2	noarch
<a href="#">r-rotor</a>	0.2.3	Conditionally rotate or back-up files based on their size or the date of the last backup; inspired by the ‘Linux’ utility ‘logrotate’. / MIT	noarch
<a href="#">r-roughsetknowledge reduction</a>	0.1	Rough Sets were introduced by Zdzislaw Pawlak on his book Rough Sets: Theoretical Aspects of Reasoning About Data. Rough Sets provide a formal method to approximate crisp sets when the set-element belonging relationship is either known or undetermined. This enables the use of Rough Sets for reasoning about incomplete or contradictory knowledge. A decision table is a prescription of the decisions to make given some conditions. Such decision tables can be reduced without losing prescription ability. This package provides the classes and methods for knowledge reduction from decision tables as presented in the chapter 7 of the aforementioned book. This package provides functions for calculating the both the discernibility matrix and the essential parts of decision tables. / MIT	noarch
<a href="#">r-roundhouse</a>	0.0.1	An R wrapper to the ‘Internet Chuck Norris database’ (‘ICNDb’) API for generating random Chuck Norris facts. / GPL-2	noarch
<a href="#">r-rowt</a>	1.1.3	Provides utilities which interact with all R objects as if they were arranged in rows. It allows more consistent and predictable output to common functions, and generalizes a number of utility functions to to be failsafe with any number and type of input objects. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-roxygen2	6.1.1	Generate your Rd documentation, 'NAMESPACE' file, and collation field using specially formatted comments. Writing documentation in-line with code makes it easier to keep your documentation up-to-date as your requirements change. 'Roxygen2' is inspired by the 'Doxygen' system for C. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
r-rpaci	0.1.1	Analysis of corneal data obtained from a Placido disk corneal topographer with calculation of irregularity indices. A corneal topographer is an ophthalmic clinical device that obtains measurements in the cornea (the anterior part of the eye). A Placido disk corneal topographer makes use of the Placido disk (Rowsey et al. (1981), <doi:10.1001/archopht.1981.03930011093022>, Rand et al. (1997), <doi:10.1016/S0886-3350(99)00355-7>), which produce a circular pattern of measurement nodes. The raw information measured by such a topographer is used by practitioners to analyze curvatures, to study optical aberrations, or to diagnose specific conditions of the eye. The rPACI package allows the calculation of the corneal irregularity indices described in Ramos-Lopez et al. (2013), <doi:10.1097/OPX.0b013e3182843f2a>, and that were firstly introduced in Ramos-Lopez et al. (2011), <doi:10.1097/OPX.0b013e3182843f2a>. It provides a simple interface to read corneal topography data files as exported by a typical Placido disk topographer, to compute the irregularity indices mentioned before, and to display summary plots that are easy to interpret for a clinician. / GPL-3	noarch
r-rpanel	1.1_4	A set of functions to build simple GUI controls for R functions. These are built on the 'tcltk' package. Uses could include changing a parameter on a graph by animating it with a slider or a doublebutton, up to more sophisticated control panels. Some functions for specific graphical tasks, referred to as 'cartoons', are provided. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-rpart	4.1_1	Recursive partitioning for classification, regression and survival trees. An implementation of most of the functionality of the 1984 book by Breiman, Friedman, Olshen and Stone. / GPL-2   GPL-3	linux-32, linux-64, osx-64, win-32, win-64
r-rpart.plot	3.0.8	Plot 'rpart' models. Extends plot.rpart() and text.rpart() in the 'rpart' package. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-rpart.utils</a>	0.5	This package contains additional tools for working with <code>rpart</code> objects. Most importantly, it includes methods for converting <code>rpart</code> rules into a series of structured tables sufficient for executing the decision tree completely in SQL. / GPL-3	noarch
<a href="#">r-rpartscore</a>	1.0.1	This package contains functions that allow to build classification trees for ordinal responses within the CART framework. The trees are grown using the Generalized Gini impurity function, where the misclassification costs are given by the absolute or squared differences in scores assigned to the categories of the response. Pruning is based on the total misclassification rate or on the total misclassification cost. / GPL-2	noarch
<a href="#">r-rpca</a>	0.2.3	Suppose we have a data matrix, which is the superposition of a low-rank component and a sparse component. Candes, E. J., Li, X., Ma, Y., & Wright, J. (2011). Robust principal component analysis?. Journal of the ACM (JACM), 58(3), 11. prove that we can recover each component individually under some suitable assumptions. It is possible to recover both the low-rank and the sparse components exactly by solving a very convenient convex program called Principal Component Pursuit; among all feasible decompositions, simply minimize a weighted combination of the nuclear norm and of the L1 norm. This package implements this decomposition algorithm resulting with Robust PCA approach. / GPL-2   GPL-3	noarch
<a href="#">r-rpclr</a>	1.0	This package implements the R-PCLR (Random-Penalized Conditional Logistic Regression) algorithm for obtaining variable importance. The algorithm is applicable for the analysis of high dimensional data from matched case-control studies. / GPL-2	noarch
<a href="#">r-rpensemble</a>	0.4	Implements the methodology of Cannings, T. I. and Samworth, R. J. (2017) Random-projection ensemble classification, J. Roy. Stat. Soc., Ser. B. (with discussion), 79, 959–1035. The random projection ensemble classifier is a general method for classification of high-dimensional data, based on careful combination of the results of applying an arbitrary base classifier to random projections of the feature vectors into a lower-dimensional space. The random projections are divided into non-overlapping blocks, and within each block the projection yielding the smallest estimate of the test error is selected. The random projection ensemble classifier then aggregates the results of applying the base classifier on the selected projections, with a data-driven voting threshold to determine the final assignment. / GPL-3	noarch
<a href="#">r-rpexe.rpext</a>	0.0.1	This reduced piecewise exponential survival software implements the likelihood ratio test and backward elimination procedure in Han, Schell, and Kim (2012 <doi:10.1080/19466315.2012.698945>, 2014 <doi:10.1002/sim.5915>), and Han et al. (2016 <doi:10.1111/biom.12590>). Inputs to the program can be either times when events/censoring occur or the vectors of total time on test and the number of events. Outputs of the programs are times and the corresponding p-values in the backward elimination. Details about the model and implementation are given in Han et al. 2014. This program can run in R version 3.2.2 and above. / GPL-3	noarch
<a href="#">r-rphylic</a>	0.1.2	Rphylic provides an R interface for the PHYLIP package. All users of Rphylic will thus first have to install the PHYLIP phylogeny methods program package (Felsenstein 2013). See <a href="http://www.phylip.com">http://www.phylip.com</a> for more information about installing PHYLIP. / GPL-2	noarch
<a href="#">r-rpinterest</a>	0.3.1	Get information (boards, pins and users) from the Pinterest < <a href="http://www.pinterest.com">http://www.pinterest.com</a> > API. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-rpipedrive	0.1.1	R interaction with ‘pipedrive.com API’. All functions were created and documented according to < <a href="https://developers.pipedrive.com/docs/api/v1/">https://developers.pipedrive.com/docs/api/v1/</a> >. Created with the objective of offering integration and even the development of ‘APIs’. Making possible to create workflows and easily downloading databases for analysis. / GPL-2	noarch
r-rpivottable	0.3.0	Build powerful pivot tables (aka Pivot Grid, Pivot Chart, Cross-Tab) and dynamically slice & dice / drag ‘n’ drop your data. ‘rpivotTable’ is a wrapper of ‘pivottable’, a powerful open-source Pivot Table library implemented in ‘JavaScript’ by Nicolas Kruchten. Aligned to ‘pivottable’ v2.19.0. / MIT	noarch
r-rplotengine	1.0.7	Generate basic charts either by custom applications, or from a small script launched from the system console, or within the R console. Two ASCII text files are necessary: (1) The graph parameters file, which name is passed to the function ‘rplotengine()’. The user can specify the titles, choose the type of the graph, graph output formats (e.g. png, eps), proportion of the X-axis and Y-axis, position of the legend, whether to show or not a grid at the background, etc. (2) The data to be plotted, which name is specified as a parameter (‘data_filename’) in the previous file. This data file has a tabulated format, with a single character (e.g. tab) between each column, and a headers line located in the first row. Optionally, the file could include data columns for showing confidence intervals. / GPL-2	noarch
r-rpmg	2.2.2	Really Poor Man’s Graphical User Interface, used to create interactive R analysis sessions with simple R commands. / GPL-2	noarch
r-rpmm	1.25	Recursively Partitioned Mixture Model for Beta and Gaussian Mixtures. This is a model-based clustering algorithm that returns a hierarchy of classes, similar to hierarchical clustering, but also similar to finite mixture models. / GPL-2	noarch
r-rpnf	1.0.5	A set of functions to analyze and print the development of a commodity using the Point and Figure (P&F) approach. A P&F processor can be used to calculate daily statistics for the time series. These statistics can be used for deeper investigations as well as to create plots. Plots can be generated as well known X/O Plots in plain text format, and additionally in a more graphical format. / GPL-3	noarch
r-rpoet	1.1.0	Wrapper for the ‘PoetryDB’ API < <a href="http://poetrydb.org">http://poetrydb.org</a> > that allows for interaction and data extraction from the database in an R interface. The ‘PoetryDB’ API is a database of poetry and poets implemented with ‘MongoDB’ to enable developers and poets to easily access one of the most comprehensive poetry databases currently available. / GPL-2	noarch
r-rppairwisdesign	1.0	Using some association schemes to obtain a new series of resolvable partially pairwise balanced designs (RPPBD) and space-filling designs. / GPL-3	noarch
r-rprime	0.1.0	‘Eprime’ is a set of programs for administering psychological experiments by computer. This package provides functions for loading, parsing, filtering and exporting data in the text files produced by ‘Eprime’ experiments. / GPL-2	noarch
r-rprintf	0.2.1	Provides a set of functions to facilitate building formatted strings under various replacement rules: C-style formatting, variable-based formatting, and number-based formatting. C-style formatting is basically identical to built-in function ‘sprintf’. Variable-based formatting allows users to put variable names in a formatted string which will be replaced by variable values. Number-based formatting allows users to use index numbers to represent the corresponding argument value to appear in the string. / MIT	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-rprobsup</a>	2.1	The A() function calculates the A statistic, a nonparametric measure of effect size for two independent groups thatâ€™s also known as the probability of superiority (Ruscio, 2008), along with its standard error and a confidence interval constructed using bootstrap methods (Ruscio & Mullen, 2012). Optional arguments can be specified to calculate variants of the A statistic developed for other research designs (e.g., related samples, more than two independent groups or related samples; Ruscio & Gera, 2013). <DOI: 10.1037/1082-989X.13.1.19>. <DOI: 10.1080/00273171.2012.658329>. <DOI: 10.1080/00273171.2012.738184>. / MIT	noarch
<a href="#">r-rprojroot</a>	1.3.2	Robust, reliable and flexible paths to files below a project root. The ‘root’ of a project is defined as a directory that matches a certain criterion, e.g., it contains a certain regular file. / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-rpsychi</a>	0.8	The rpsychi offers a number of functions for psychiatry, psychiatric nursing, clinical psychology. Functions are primarily for statistical significance testing using published work. For example, you can conduct a factorial analysis of variance (ANOVA), which requires only the mean, standard deviation, and sample size for each cell, rather than the individual data. This package covers fundamental statistical tests such as t-test, chi-square test, analysis of variance, and multiple regression analysis. With some exceptions, you can obtain effect size and its confidence interval. These functions help you to obtain effect size from published work, and then to conduct a priori power analysis or meta-analysis, even if a researcher do not report effect size in a published work. / GPL-2	noarch
<a href="#">r-rpublica</a>	0.1.3	Client for accessing data journalism APIs from ProPublica < <a href="http://www.propublica.org/">http://www.propublica.org/</a> >. / GPL-2	noarch
<a href="#">r-rpushbullet</a>	0.3.2	An R interface to the Pushbullet messaging service which provides fast and efficient notifications (and file transfer) between computers, phones and tablets. An account has to be registered at the site < <a href="http://www.pushbullet.com">http://www.pushbullet.com</a> > site to obtain a (free) API key. / GPL-2	noarch
<a href="#">r-rqcc</a>	0.19.8	Constructs robust quality control chart based on the median and Hodges-Lehmann estimators (location) and the median absolute deviation (MAD) and Shamos estimators (scale) which are unbiased with a sample of finite size. For more details, see Park, Kim and Wang (2019)<arXiv:1908.00462>. This work was partially supported by the National Research Foundation of Korea (NRF) grant funded by the Korea government (No. NRF-2017R1A2B4004169). / GPL-2   GPL-3	noarch
<a href="#">r-rrate</a>	1.0	Replication Rate (RR) is the probability of replicating a statistically significant association in genome-wide association studies. This R-package provide the estimation method for replication rate which makes use of the summary statistics from the primary study. We can use the estimated RR to determine the sample size of the replication study, and to check the consistency between the results of the primary study and those of the replication study. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-rrblup</a>	4.6	Software for genomic prediction with the RR-BLUP mixed model (Endelman 2011, <doi:10.3835/plantgenome2011.08.0024>). One application is to estimate marker effects by ridge regression; alternatively, BLUPs can be calculated based on an additive relationship matrix or a Gaussian kernel. / GPL-3	noarch
<a href="#">r-rtna</a>	1.0	Functions for creating and manipulating RNA secondary structure plots. / GPL-3	noarch
<a href="#">r-rrroad</a>	0.0.5	Computation of the International Roughness Index (IRI) given a longitudinal road profile. The IRI can be calculated for a single road segment or for a sequence of segments with a fixed length (e. g. 100m). For the latter, an overlap of the segments can be selected. The IRI and likewise the algorithms for its determination are defined in Sayers, Michael W; Gillespie, Thomas D; Queiroz, Cesar A.V. 1986. The International Road Roughness Experiment (IRRE) : establishing correlation and a calibration standard for measurements. World Bank technical paper; no. WTP 45. Washington, DC : The World Bank. (ISBN 0-8213-0589-1) available from < <a href="http://documents.worldbank.org/curated/en/326081468740204115">http://documents.worldbank.org/curated/en/326081468740204115</a> >. / MIT	noarch
<a href="#">r-rrromeo</a>	0.1.0	Fetches information from the ‘SHERPA/RoMEO’ API < <a href="http://www.sherpa.ac.uk/romeo/apimanual.php">http://www.sherpa.ac.uk/romeo/apimanual.php</a> > which indexes policies of journal regarding the archival of scientific manuscripts before and/or after peer-review as well as formatted manuscripts. / GPL-3	noarch
<a href="#">r-rrpp</a>	0.4.2	Linear model calculations are made for many random versions of data. Using residual randomization in a permutation procedure, sums of squares are calculated over many permutations to generate empirical probability distributions for evaluating model effects. This packaged is described by Collyer & Adams (2018) <doi:10.1111/2041-210X.13029>. Additionally, coefficients, statistics, fitted values, and residuals generated over many permutations can be used for various procedures including pairwise tests, prediction, classification, and model comparison. This package should provide most tools one could need for the analysis of high-dimensional data, especially in ecology and evolutionary biology, but certainly other fields, as well. / GPL-2	noarch
<a href="#">r-rrreg</a>	0.7.0	Univariate and multivariate methods to analyze randomized response (RR) survey designs (e.g., Warner, S. L. (1965). Randomized response: A survey technique for eliminating evasive answer bias. Journal of the American Statistical Association, 60, 63–69, <doi:10.2307/2283137>). Besides univariate estimates of true proportions, RR variables can be used for correlations, as dependent variable in a logistic regression (with or without random effects), or as predictors in a linear regression (Heck, D. W., & Moshagen, M. (2018). RRreg: An R package for correlation and regression analyses of randomized response data. Journal of Statistical Software, 85(2), 1–29, <doi:10.18637/jss.v085.i02>). For simulations and the estimation of statistical power, RR data can be generated according to several models. The implemented methods also allow to test the link between continuous covariates and dishonesty in cheating paradigms such as the coin-toss or dice-roll task (Moshagen, M., & Hilbig, B. E. (2017). The statistical analysis of cheating paradigms. Behavior Research Methods, 49, 724–732, <doi:10.3758/s13428-016-0729-x>). / GPL-3	noarch
<a href="#">r-rrscale</a>	0.1.3	Non-linear transformations of data to better discover latent effects. Applies a sequence of three transformations (1) a Gaussianizing transformation, (2) a Z-score transformation, and (3) an outlier removal transformation. / GPL-3	noarch
<a href="#">r-rsadbe</a>	1.0	The package contains all the data sets related to the book written by the maintainer of the package. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-rsampling</a>	0.1.1	Resampling Stats ( <a href="http://www.resample.com">http://www.resample.com</a> ) is an add-in for running randomization tests in Excel worksheets. The workflow is (1) to define a statistic of interest that can be calculated from a data table, (2) to randomize rows and/or columns of a data table to simulate a null hypothesis and (3) to score the value of the statistic from many randomizations. The relative frequency distribution of the statistic in the simulations is then used to infer the probability of the observed value being generated by the null process (probability of Type I error). This package intends to translate this logic for R for teaching purposes. Keeping the original workflow is favored over performance. / GPL-2	noarch
<a href="#">r-rsrules</a>	1.0	Implements the Gibbs sampling algorithm to randomly sample association rules with one pre-chosen item as the consequent from a transaction dataset. The Gibbs sampling algorithm was proposed in G. Qian, C.R. Rao, X. Sun and Y. Wu (2016) <DOI:10.1073/pnas.1604553113>. / GPL-3	noarch
<a href="#">r-rsatscan</a>	0.3.92	SaTScan(TM) ( <a href="http://www.satscan.org">http://www.satscan.org</a> ) is software for finding regions in Time, Space, or Time-Space that have excess risk, based on scan statistics, and uses Monte Carlo hypothesis testing to generate P-values for these regions. The rsatscan package provides functions for writing R data frames in SaTScan-readable formats, for setting SaTScan parameters, for running SaTScan in the OS, and for reading the files that SaTScan creates. / GPL-3	noarch
<a href="#">r-saucelabs</a>	0.1.6	Retrieve, update, delete job information from < <a href="https://saucelabs.com/">https://saucelabs.com/</a> >. Poll the 'SauceLabs' services current status and access supported platforms. Send and retrieve files from 'SauceLabs' and manage tunnels associated with 'SauceConnect'. / GPL-3	noarch
<a href="#">r-rsca</a>	3.0	A statistical tool for multivariate modeling and clustering using stepwise cluster analysis. The modeling output of rSCA is constructed as a cluster tree to represent the complicated relationships between multiple dependent and independent variables. A free tool (named rSCA Tree Generator) for visualizing the cluster tree from rSCA is also released and it can be downloaded at < <a href="https://rscatree.weebly.com/">https://rscatree.weebly.com/</a> >. / GPL-2	noarch
<a href="#">r-rscala</a>	3.2.15	'Scala' < <a href="http://www.scala-lang.org/">http://www.scala-lang.org/</a> > is embedded in 'R' and callbacks from 'Scala' to 'R' are available. Support is provided to write 'R' packages that access 'Scala'. After installation, please run 'rscala::scalaConfig()'. / Apache License 2.0   file LICENSE	noarch
<a href="#">r-rsconnect</a>	0.8.13	Programmatic deployment interface for 'RPubs', 'shinyapps.io', and 'RStudio Connect'. Supported content types include R Markdown documents, Shiny applications, Plumber APIs, plots, and static web content. / GPL-2	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-rsdmx</a>	0.5.1	Set of classes and methods to read data and metadata documents exchanged through the Statistical Data and Metadata Exchange (SDMX) framework, currently focusing on the SDMX XML standard format (SDMX-ML). / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-rse	1.3	A Bayesian-weighted estimator and two unweighted estimators are developed to estimate the number of newly found rare species in additional ecological samples. Among these methods, the Bayesian-weighted estimator and an unweighted (Chao-derived) estimator are of high accuracy and recommended for practical applications. Technical details of the proposed estimators have been well described in the following paper: Shen TJ, Chen YH (2018) A Bayesian weighted approach to predicting the number of newly discovered rare species. Conservation Biology, In press. / GPL-3	noarch
r-rseedcalc	1.3	Estimate the percentage of seeds in a seedlot that contain stacks of genetically modified traits. Estimates are calculated using a multinomial group testing model with maximum likelihood estimation of the parameters. / GPL-2	noarch
r-rsem	0.4.6	A robust procedure is implemented to estimate means and covariance matrix of multiple variables with missing data using Huber weight and then to estimate a structural equation model. / GPL-2	noarch
r-rserve	1.7.3	Rserve acts as a socket server (TCP/IP or local sockets) which allows binary requests to be sent to R. Every connection has a separate workspace and working directory. Client-side implementations are available for popular languages such as C/C and Java, allowing any application to use facilities of R without the need of linking to R code. Rserve supports remote connection, user authentication and file transfer. A simple R client is included in this package as well. / GPL-2   file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
r-rsfa	1.04	Slow Feature Analysis in R, ported to R based on the matlab versions SFA toolkit 1.0 by Pietro Berkes and SFA toolkit 2.8 by Wolfgang Konen for matlab. / GPL-2	noarch
r-rsitecatalyst	1.4.15	Functions for interacting with the Adobe Analytics API V1.4 (< <a href="https://api.omniture.com/admin/1.4/rest/">https://api.omniture.com/admin/1.4/rest/</a> >). / MIT	noarch
r-rskey	0.4.1	Create custom keyboard shortcuts to examine code selected in the 'Rstudio' editor. F3 can for example yield 'str(selection)' and F7 open the source code of CRAN and base package functions on 'github'. / GPL-2	noarch
r-rslp	0.1.0	Implements the Stemming Algorithm for the Portuguese Language <DOI:10.1109/SPIRE.2001.10024>. / MIT	noarch
r-rslurm	0.4.0	Functions that simplify submitting R scripts to a Slurm workload manager, in part by automating the division of embarrassingly parallel calculations across cluster nodes. / GPL-3	noarch
r-rsm	2.10	Provides functions to generate response-surface designs, fit first- and second-order response-surface models, make surface plots, obtain the path of steepest ascent, and do canonical analysis. A good reference on these methods is Chapter 10 of Wu, C-F J and Hamada, M (2009) Experiments: Planning, Analysis, and Parameter Design Optimization ISBN 978-0-471-69946-0. / GPL-2	noarch
r-rsmartlyio	0.1.3	Aims at loading Facebook and Instagram advertising data from 'Smartly.io' into R. 'Smartly.io' is an online advertising service that enables advertisers to display commercial ads on social media networks (see < <a href="http://www.smartly.io/">http://www.smartly.io/</a> > for more information). The package offers an interface to query the 'Smartly.io' API and loads data directly into R for further data processing and data analysis. / MIT	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-rsocrata</a>	1.7.9	Provides easier interaction with ‘Socrata’ open data portals < <a href="http://dev.socrata.com">http://dev.socrata.com</a> >. Users can provide a ‘Socrata’ data set resource URL, or a ‘Socrata’ Open Data API (SoDA) web query, or a ‘Socrata’ human-friendly URL, returns an R data frame. Converts dates to ‘POSIX’ format and manages throttling by ‘Socrata’. Users can upload data to ‘Socrata’ portals directly from R. / MIT	noarch
<a href="#">r-rsoi</a>	0.5.0	Downloads Southern Oscillation Index, Oceanic Nino Index, North Pacific Gyre Oscillation data, North Atlantic Oscillation and Arctic Oscillation. Data sources are described in the README file. / GPL-3	noarch
<a href="#">r-rspc</a>	1.2.2	Implementation of Nelson rules for control charts in ‘R’. The ‘Rspc’ implements some Statistical Process Control methods, namely Levey-Jennings type of I (individuals) chart, Shewhart C (count) chart and Nelson rules (as described in Montgomery, D. C. (2013) Introduction to statistical quality control. Hoboken, NJ: Wiley.). Typical workflow is taking the time series, specify the control limits, and list of Nelson rules you want to evaluate. There are several options how to modify the rules (one sided limits, numerical parameters of rules, etc.). Package is also capable of calculating the control limits from the data (so far only for i-chart and c-chart are implemented). / GPL-3	noarch
<a href="#">r-rspde</a>	0.4.6	Functions that compute rational approximations of fractional elliptic stochastic partial differential equations. The package also contains functions for common statistical usage of these approximations. The main reference for the methods is Bolin and Kirchner (2019) <arXiv:1711.04333>, which can be generated by the citation function in R. / GPL-3	noarch
<a href="#">r-rspincalc</a>	1.0.2	Conversion between attitude representations: DCM, Euler angles, Quaternions, and Euler vectors. Plus conversion between 2 Euler angle set types (xyx, yzy, xzx, xzy, yxz, yzx, xzy, yxz, zyx). Fully vectorized code, with warnings/errors for Euler angles (singularity, out of range, invalid angle order), DCM (orthogonality, not proper, exceeded tolerance to unity determinant) and Euler vectors(not unity). Also quaternion and other useful functions. Based on SpinCalc by John Fuller and SpinConv by Paolo de Leva. / GPL-3	noarch
<a href="#">r-rsps</a>	1.0	Provides functions for estimating power or sample size for RNA-Seq studies. Empirical approach is used and the data is assumed to be count in nature. The underlying distribution of data is assumed to be Poisson or negative binomial. The package contains 6 function; 4 functions provide estimates of sample size or power for Poisson and Negative Binomial distribution; 2 functions provide plots of power for given sample size or sample size for given power. / GPL-2	noarch
<a href="#">r-rsq</a>	1.1	Calculate generalized R-squared, partial R-squared, and partial correlation coefficients for generalized linear models (including quasi models with well defined variance functions). / GPL-2	noarch
<a href="#">r-rsqlite</a>	2.1.1	Embeds the ‘SQLite’ database engine in R and provides an interface compliant with the ‘DBI’ package. The source for the ‘SQLite’ engine is included. / LGPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
r-rssop	1.1	Reservoir Systems Standard Operation Policy. A system for simulation of supply reservoirs. It proposes functionalities for plotting and evaluation of supply reservoirs systems. / GPL-2	noarch
r-rstack	1.0.0	An extremely simple stack data type, implemented with ‘R6’ classes. The size of the stack increases as needed, and the amortized time complexity is O(1). The stack may contain arbitrary objects. / MIT	noarch
r-rstackdeque	1.1.1	Provides fast, persistent (side-effect-free) stack, queue and deque (double-ended-queue) data structures. While dequeues include a superset of functionality provided by queues, in these implementations queues are more efficient in some specialized situations. See the documentation for rstack, rdeque, and rqueue for details. / MIT	noarch
r-rstan	2.18.2	User-facing R functions are provided to parse, compile, test, estimate, and analyze Stan models by accessing the header-only Stan library provided by the ‘StanHeaders’ package. The Stan project develops a probabilistic programming language that implements full Bayesian statistical inference via Markov Chain Monte Carlo, rough Bayesian inference via ‘variational’ approximation, and (optionally penalized) maximum likelihood estimation via optimization. In all three cases, automatic differentiation is used to quickly and accurately evaluate gradients without burdening the user with the need to derive the partial derivatives. / GPL (>= 3)	linux-32, linux-64, osx-64, win-32, win-64
r-rstantools	1.5.1	Provides various tools for developers of R packages interfacing with ‘Stan’ < <a href="http://mc-stan.org">http://mc-stan.org</a> >, including functions to set up the required package structure, S3 generics and default methods to unify function naming across ‘Stan’-based R packages, and vignettes with recommendations for developers. / GPL-3	noarch
r-rstata	1.1.1	A simple R -> Stata interface allowing the user to execute Stata commands (both inline and from a .do file) from R. / GPL-3	noarch
r-rstatscn	1.1.3	R interface for china national data < <a href="http://data.stats.gov.cn/">http://data.stats.gov.cn/</a> >, some convenient functions for accessing the national data are provided. / Apache License 2.0	noarch
r-rstorm	1.0	While streaming processing provides opportunities to deal with extremely large and ever growing data sets in (near) real time, the development of streaming algorithms for complex models is often cumbersome: the software packages that facilitate streaming processing in production environments do not provide statisticians with the simulation, estimation, and plotting tools they are used to. Developers of streaming algorithms would thus benefit from the flexibility of [R] to create, plot and compute data while developing streaming algorithms. Package RStorm implements a streaming architecture modeled on Storm for easy development and testing of streaming algorithms in [R]. RStorm is not intended as a production package, but rather a development tool for streaming algorithms. / GPL-2	noarch
r-rstripe	0.1	A convenience interface for communicating with the Stripe payment processor to accept payments online. See < <a href="https://stripe.com">https://stripe.com</a> > for more information. / MIT	noarch

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Name	Version	Summary/License	Platforms
r-rstudioapi	0.10	Access the RStudio API (if available) and provide informative error messages when it's not. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-rsubgroup	0.6	A collection of efficient and effective tools and algorithms for subgroup discovery and analytics. The package integrates an R interface to the org.vikamine.kernel library of the VIKAMINE system ( <a href="http://www.vikamine.org">http://www.vikamine.org</a> ) implementing subgroup discovery, pattern mining and analytics in Java. / GPL-3	noarch
r-rsurfer	0.2	The software suite, 'Freesurfer', is a open-source software suite involving the segmentation of brain MRIs (see < <a href="http://freesurfer.net/">http://freesurfer.net/</a> > for more information). This package provides functionality to import the data generated by 'Freesurfer'; functions to easily manipulate the data; and provides brain specific normalisation commonly used when studying structural brain MRIs. This package has been designed using an installation of and data generated from 'Freesurfer' version 5.3. / MIT	noarch
r-rsurrogate	2.0	Provides functions to estimate the proportion of treatment effect on the primary outcome that is explained by the treatment effect on the surrogate marker. / GPL-3	noarch
r-rsvd	1.0.2	Low-rank matrix decompositions are fundamental tools and widely used for data analysis, dimension reduction, and data compression. Classically, highly accurate deterministic matrix algorithms are used for this task. However, the emergence of large-scale data has severely challenged our computational ability to analyze big data. The concept of randomness has been demonstrated as an effective strategy to quickly produce approximate answers to familiar problems such as the singular value decomposition (SVD). The rsvd package provides several randomized matrix algorithms such as the randomized singular value decomposition (rsvd), randomized principal component analysis (rpca), randomized robust principal component analysis (rrpca), randomized interpolative decomposition (rid), and the randomized CUR decomposition (rcur). In addition several plot functions are provided. The methods are discussed in detail by Erichson et al. (2016) <arXiv:1608.02148>. / GPL-3	noarch
r-rt.test	1.18.7	Performs one-sample t-test based on robustified statistics using median/MAD (TA) and Hodges-Lehmann/Shamos (TB). For more details, see Park and Wang (2018)<arXiv:1807.02215>. This work was partially supported by the National Research Foundation of Korea (NRF) grant funded by the Korea government (No. NRF-2017R1A2B4004169). / GPL-2   GPL-3	noarch
r-rt3	0.1.2	Play the classic game of tic-tac-toe (naughts and crosses). / MIT	noarch

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Name	Version	Summary/License	Platforms
r-rtape	2.2	Storing huge data in RData format causes problems because of the necessity to load the whole file to the memory in order to access and manipulate objects inside such file; rtape is a simple solution to this problem. The package contains several wrappers of R built-in serialize/unserialize mechanism allowing user to quickly append objects to a tape-like file and later iterate over them requiring only one copy of each stored object to reside in memory a time. / GPL-2	noarch
r-rtauchen	1.0	Discretize AR(1) process following Tauchen (1986) < <a href="http://www.sciencedirect.com/science/article/pii/0165176586901680">http://www.sciencedirect.com/science/article/pii/0165176586901680</a> >. A discrete Markov chain that approximates in the sense of weak convergence a continuous-valued univariate Autoregressive process of first order is generated. It is a popular method used in economics and in finance. / GPL-2	noarch
r-rtaxometrics	2.3	We provide functions to perform taxometric analyses. This package contains 44 functions, but only 5 should be called directly by users. CheckData() should be run prior to any taxometric analysis to ensure that the data are appropriate for taxometric analysis. RunTaxometrics() performs taxometric analyses for a sample of data. RunCCFIPProfile() performs a series of taxometric analyses to generate a CCFI profile. CreateData() generates a sample of categorical or dimensional data. ClassifyCases() assigns cases to groups using the base-rate classification method. / MIT	noarch
r-rtconnect	0.1.4	Tools for analyzing sales report files of iTunes Connect. / GPL-3	noarch
r-rtde	0.2_0	Robust tail dependence estimation for bivariate models. This package is based on two papers by the authors: 'Robust and bias-corrected estimation of the coefficient of tail dependence' and 'Robust and bias-corrected estimation of probabilities of extreme failure sets'. This work was supported by a research grant (VKR023480) from VILLUM FONDEN and an international project for scientific cooperation (PICS-6416). / GPL-2	noarch
r-rtematres	0.2	Exploit controlled vocabularies organized on tematres servers. / GPL-3	noarch
r-rtensor	1.4	A set of tools for creation, manipulation, and modeling of tensors with arbitrary number of modes. A tensor in the context of data analysis is a multidimensional array. rTensor does this by providing a S4 class 'Tensor' that wraps around the base 'array' class. rTensor provides common tensor operations as methods, including matrix unfolding, summing/averaging across modes, calculating the Frobenius norm, and taking the inner product between two tensors. Familiar array operations are overloaded, such as index subsetting via '[' and element-wise operations. rTensor also implements various tensor decomposition, including CP, GLRAM, MPCA, PVD, and Tucker. For tensors with 3 modes, rTensor also implements transpose, t-product, and t-SVD, as defined in Kilmer et al. (2013). Some auxiliary functions include the Khatri-Rao product, Kronecker product, and the Hamadard product for a list of matrices. / GPL-2	noarch
r-rtephra	0.1	Models and displays tephra transport through custom (windy, turbulent, heterogeneous) atmosphere over custom topography. Includes a Lagrangian (particle-tracking) tephra transport model and a function to save snapshots of model as png files. / GPL-3	noarch
r-rttexturemetrics	1.1	This package contains several functions for calculation of texture metrics for Grey Level Co-occurrence matrices / GPL-2	noarch
r-rtf	0.4_14	A set of R functions to output Rich Text Format (RTF) files with high resolution tables and graphics that may be edited with a standard word processor such as Microsoft Word. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-rticles	0.10	A suite of custom R Markdown formats and templates for authoring journal articles and conference submissions. / GPL-3	noarch
r-rtika	1.22	Extract text or metadata from over a thousand file types, using Apache Tika < <a href="https://tika.apache.org/">https://tika.apache.org/</a> >. Get either plain text or structured XHTML content. / Apache License 2.0   file LICENSE	noarch
r-rtnmin	2016_7	Truncated Newton function minimization with bounds constraints based on the ‘Matlab’/‘Octave’ codes of Stephen Nash. / GPL-2	noarch
r-rtorch	0.0.3	‘R’ implementation and interface of the Machine Learning platform ‘PyTorch’ < <a href="https://pytorch.org/">https://pytorch.org/</a> > developed in ‘Python’. It requires a ‘conda’ environment with ‘torch’ and ‘torchvision’ to provide ‘PyTorch’ functions, methods and classes. The key object in ‘PyTorch’ is the tensor which is in essence a multidimensional array. These tensors are fairly flexible to perform calculations in CPUs as well as ‘GPUs’ to accelerate the process. / MIT	noarch
r-trim	2.0.6	The TRIM model is widely used for estimating growth and decline of animal populations based on (possibly sparsely available) count data. The current package is a reimplement of the original TRIM software developed at Statistics Netherlands by Jeroen Pannekoek. See < <a href="https://www.cbs.nl/en-gb/society/nature-and-environment/indices-and-trends%2d%2dtrim%2d%2d">https://www.cbs.nl/en-gb/society/nature-and-environment/indices-and-trends%2d%2dtrim%2d%2d</a> > for more information about TRIM. / EUPL	noarch
r-rts	1.0_49	This framework aims to provide classes and methods for manipulating and processing of raster time series data (e.g. a time series of satellite images). / GPL-3	noarch
r-rtson	1.3	TSON, short for Typed JSON, is a binary-encoded serialization of JSON like document that support JavaScript typed data ( <a href="https://github.com/tercen/TSON">https://github.com/tercen/TSON</a> ). / Apache License Version 2.0	noarch
r-rtspplot	0.1.1	A fast and elegant time series visualization package. In addition to the standard R plot types, this package supports candle sticks, open-high-low-close, and volume plots. Useful for visualizing any time series data, e.g., stock prices and technical indicators. / MIT	noarch
r-rtwalk	1.8.0	The ‘t-walk’ is a general-purpose MCMC sampler for arbitrary continuous distributions that requires no tuning. / GPL-3	noarch
r-rtype	0.1_1	A strong type system for R which supports symbol declaration and assignment with type checking and condition checking. / MIT	noarch
r-runit	0.4.32	R functions implementing a standard Unit Testing framework, with additional code inspection and report generation tools. / GPL-2	linux-64, noarch, osx-64, win-64
r-runiversal	1.0.2	This package contains some functions for converting R objects to Java style variables and XML. Generated Java code is interpretable by dynamic Java libraries such as Beanshell. Calling R externally and handling the Java or XML output is an other way to call R from other languages without native interfaces. For a Java implementation of this approach visit <a href="http://www.mhsatman.com/rcaller.php">http://www.mhsatman.com/rcaller.php</a> and <a href="http://stdioe.blogspot.com/search/label/rcaller">http://stdioe.blogspot.com/search/label/rcaller</a> / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-runstats</a>	1.0.1	Provides methods for fast computation of running sample statistics for time series. These include: (1) mean, (2) standard deviation, and (3) variance over a fixed-length window of time-series, (4) correlation, (5) covariance, and (6) Euclidean distance (L2 norm) between short-time pattern and time-series. Implemented methods utilize Convolution Theorem to compute convolutions via Fast Fourier Transform (FFT). / GPL-3	noarch
<a href="#">r-ruta</a>	1.1.0	Implementation of several unsupervised neural networks, from building their architecture to their training and evaluation. Available networks are auto-encoders including their main variants: sparse, contractive, denoising, robust and variational, as described in Charte et al. (2018) <doi:10.1016/j.inffus.2017.12.007>. / GPL-3	noarch
<a href="#">r-rv</a>	2.3.3	Implements a simulation-based random variable class and a suite of methods for extracting parts of random vectors, calculating extremes of random vectors, and generating random vectors under a variety of distributions following Kerman and Gelman (2007) <doi:10.1007/s11222-007-9020-4>. / GPL-2	noarch
<a href="#">r-rvcheck</a>	0.1.3	Check latest release version of R and R package (both in ‘CRAN’, ‘Bioconductor’ or ‘Github’). / Artistic-2.0	noarch
<a href="#">r-rversions</a>	1.1.0	Query the main ‘R’ ‘SVN’ repository to find the versions ‘r-release’ and ‘r-oldrel’ refer to, and also all previous ‘R’ versions and their release dates. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-rvest</a>	0.3.3	Wrappers around the ‘xml2’ and ‘httr’ packages to make it easy to download, then manipulate, HTML and XML. / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-rvhpd</a>	3.0	To detecting rare variants for binary traits using general pedigrees, the pedigree disequilibrium tests are proposed by collapsing rare haplotypes/variants with/without weights. To run the test, MERLIN is needed in Linux for haplotyping. / GPL-2	noarch
<a href="#">r-rviennacl</a>	1.7.1	‘ViennaCL’ is a free open-source linear algebra library for computations on many-core architectures (GPUs, MIC) and multi-core CPUs. The library is written in C and supports ‘CUDA’, ‘OpenCL’, and ‘OpenMP’ (including switches at runtime). I have placed these libraries in this package as a more efficient distribution system for CRAN. The idea is that you can write a package that depends on the ‘ViennaCL’ library and yet you do not need to distribute a copy of this code with your package. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-rviewgraph</a>	1.2	This is an ‘R’ interface to Alun Thomas’s ‘ViewGraph’ ‘Java’ graph viewing program. It takes a graph specified as an incidence matrix, list of edges, or in ‘igraph’ format and runs a graphical user interface that shows an animation of a force directed algorithm positioning the vertices in two dimensions. It works well for graphs of various structure of up to a few thousand vertices. It’s not fazed by graphs that comprise several components. The coordinates can be read as an ‘igraph’ style layout matrix at any time. The user can mess with the layout using a mouse, preferably one with 3 buttons, and some keyed commands. The ‘Java’ program ‘ViewGraph’ is contained in Alun Thomas’s ‘JPS-GCS’ collection of ‘Java’ programs for statistical genetics and computational statistics. The homepage for ‘JPSGCS’ is < <a href="http://www-genepi.med.utah.edu/~alun/software/index.html">http://www-genepi.med.utah.edu/~alun/software/index.html</a> >. The documentation page for ‘ViewGraph’ is at < <a href="http://www-genepi.med.utah.edu/~alun/software/docs/ViewGraph.html">http://www-genepi.med.utah.edu/~alun/software/docs/ViewGraph.html</a> >. / GPL-2	noarch
<a href="#">r-rvtdt</a>	1.0	Used to compute population controls weighted rare variants transmission distortion test / GPL-3	noarch
<a href="#">r-rwars</a>	1.0.0	Provides functions to retrieve and reformat data from the ‘Star Wars’ API (SWAPI) < <a href="https://swapi.co/">https://swapi.co/</a> >. / MIT	noarch
<a href="#">r-rwc</a>	1.11	Code to facilitate simulation and inference when connectivity is defined by underlying random walks. Methods for spatially-correlated pairwise distance data are especially considered. This provides core code to conduct analyses similar to that in Hanks and Hooten (2013) <doi:10.1080/01621459.2012.724647>. / GPL-2	noarch
<a href="#">r-rweblogo</a>	1.0.3	RWebLogo is a wrapper for the WebLogo python package that allows generating of customised sequence logos. Sequence logos are graphical representations of the sequence conservation of nucleotides (in a strand of DNA/RNA) or amino acids (in protein sequences). Each logo consists of stacks of symbols, one stack for each position in the sequence. The overall height of the stack indicates the sequence conservation at that position, while the height of symbols within the stack indicates the relative frequency of each amino or nucleic acid at that position. In general, a sequence logo provides a richer and more precise description of, for example, a binding site, than would a consensus sequence. / BSD_3_clause	noarch
<a href="#">r-rwekajars</a>	3.9.3	External jars required for package ‘RWeka’. / GPL-2	noarch
<a href="#">r-rwhois</a>	1.0.3	Queries data from WHOIS servers. / MIT	noarch
<a href="#">r-rwinsteps</a>	1.0_1	Facilitates communication between R and the Rasch modeling software Winsteps. Currently includes functions for reading and writing command files, sending them to Winsteps, reading and writing data according to command file specifications, reading output into R, and plotting various results. / GPL-2	noarch
<a href="#">r-rwishart</a>	0.1.1	An expansion of R’s ‘stats’ random wishart matrix generation. This package allows the user to generate singular, Uhlig and Harald (1994) <doi:10.1214/aos/1176325375>, and pseudo wishart, Diaz-Garcia, et al.(1997) <doi:10.1006/jmva.1997.1689>, matrices. In addition the user can generate wishart matrices with fractional degrees of freedom, Adhikari (2008) <doi:10.1061/(ASCE)0733-9399(2008)134:12(1029)>, commonly used in volatility modeling. Users can also use this package to create random covariance matrices. / GPL-2	noarch
<a href="#">r-rworldxtra</a>	1.01	High resolution vector country boundaries derived from Natural Earth data, can be plotted in rworldmap. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-rxkcd	1.8.2	Visualize your favorite XKCD comic strip directly from R. XKCD < <a href="https://xkcd.com">https://xkcd.com</a> > web comic content is provided under the Creative Commons Attribution-NonCommercial 2.5 License. / GPL-2	noarch
r-rxnat	1.0.6	Allows communication with Extensible Neuroimaging Archive Toolkit < <a href="https://www.xnat.org">https://www.xnat.org</a> >. 'Rxnat' is using the 'XNAT' REST API to perform data queries and download images. / GPL-2	noarch
r-rxseq	0.99.3	Analysis of combined total and allele specific reads from the reciprocal cross study with RNA-seq data. / GPL-2	noarch
r-rxshrink	1.1	Identify and display TRACES for a specified shrinkage path and determine the extent of shrinkage most likely, under normal distribution theory, to produce an optimal reduction in MSE Risk in estimates of regression (beta) coefficients. Alternative estimates are also provided when ill-conditioned (nearly multicollinear) models yield OLS estimates with wrong numerical signs. / GPL-3	noarch
r-ryandextranslate	1.0	'Yandex Translate' ( <a href="https://translate.yandex.com/">https://translate.yandex.com/</a> ) is a statistical machine translation system. The system translates separate words, complete texts, and webpages. This package can be used to detect language from text and to translate it to supported target language. For more info: <a href="https://tech.yandex.com/translate/doc/dg/concepts/About-docpage/">https://tech.yandex.com/translate/doc/dg/concepts/About-docpage/</a> . / MIT	noarch
r-rym	0.5.2	Allows work with 'Management API' for load counters, segments, filters, user permissions and goals list from Yandex Metrika, 'Reporting API' allows you to get information about the statistics of site visits and other data without using the web interface, 'Logs API' allows to receive non-aggregated data and 'Compatible with Google Analytics Core Reporting API v3' allows receive information about site traffic and other data using field names from Google Analytics Core API. For more information see official documents < <a href="https://tech.yandex.ru/metrika/doc/api2/concept/about-docpage/">https://tech.yandex.ru/metrika/doc/api2/concept/about-docpage/</a> >. / GPL-2	noarch
r-ryoudaotranslate	1.0	You can use this package to translate thousands of words. The Youdao translation open API is applied in this package. But, it just translates less than 1000 English words into Chinese. / GPL-2	noarch
r-ryotheria	1.0.3	A programmatic interface to web-services of YouTheria. YouTheria is an online database of mammalian trait data < <a href="http://www.utheria.org/">http://www.utheria.org/</a> >. / MIT	noarch
r-rzabbix	0.1.0	R interface to the 'Zabbix API' data < <a href="https://www.zabbix.com/documentation/3.0/manual/api/reference">https://www.zabbix.com/documentation/3.0/manual/api/reference</a> >. Enables easy and direct communication with 'Zabbix API' from 'R'. / GPL-2	noarch
r-rzeit2	0.2.3	Interface to gather newspaper articles from 'DIE ZEIT' and 'ZEIT ONLINE', based on a multilevel query < <a href="http://developer.zeit.de/">http://developer.zeit.de/</a> >. A personal API key is required for usage. / MIT	noarch
r-rzmq	0.9.6	Interface to the 'ZeroMQ' lightweight messaging kernel (see < <a href="http://www.zeromq.org/">http://www.zeromq.org/</a> > for more information). / GPL-3	linux-32, linux-64, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
r-s20x	3.1.28	A set of functions used in teaching STATS 201/208 Data Analysis at the University of Auckland. The functions are designed to make parts of R more accessible to a large undergraduate population who are mostly not statistics majors. / GPL-2	noarch
r-sabarsi	0.1.0	Implements a new approach ‘SABARSI’ described in Wang et al., A Statistical Approach of Background Removal and Spectrum Identification for SERS Data (Unpublished). Sabarsi forms a pipeline for SERS (surface-enhanced Raman scattering) data analysis including background removal, signal detection, signal integration, and cross-experiment comparison. The background removal algorithm, the very first step of SERS data analysis, takes into account the change of background shape. / GPL-3	noarch
r-sac	1.0.1	Semiparametric empirical likelihood ratio based test of changepoint with one-change or epidemic alternatives with data-based model diagnostic / GPL-2	noarch
r-sacobra	1.1	Performs surrogate-assisted optimization for expensive black-box constrained problems. / GPL-2	noarch
r-sadeg	1.0.0	We analyzed the nucleotide composition of genes with a special emphasis on stability of DNA sequences. Besides, in a variety of different organisms unequal use of synonymous codons, or codon usage bias, occurs which also show variation among genes in the same genome. Seemingly, codon usage bias is affected by both selective constraints and mutation bias which allows and enables us to examine and detect changes in these two evolutionary forces between genomes or along one genome. Therefore, we determined the codon adaptation index (CAI), effective number of codons (ENC) and codon usage analysis with calculation of the relative synonymous codon usage (RSCU), and subsequently predicted the translation efficiency and accuracy through GC-rich codon usages. Furthermore, we estimated the relative stability of the DNA sequence following calculation of the average free energy (Delta G) and Dimer base-stacking energy level. / GPL-3	noarch
r-sae	1.2	Functions for small area estimation. / GPL-2	noarch
r-saemix	2.2	The SAEMIX package implements the Stochastic Approximation EM algorithm for parameter estimation in (non)linear mixed effects models. The SAEM algorithm: - computes the maximum likelihood estimator of the population parameters, without any approximation of the model (linearisation, quadrature approximation,...), using the Stochastic Approximation Expectation Maximization (SAEM) algorithm, - provides standard errors for the maximum likelihood estimator - estimates the conditional modes, the conditional means and the conditional standard deviations of the individual parameters, using the Hastings-Metropolis algorithm. Several applications of SAEM in agronomy, animal breeding and PKPD analysis have been published by members of the Monolix group (< <a href="http://group.monolix.org/">http://group.monolix.org/</a> >). / GPL-2	noarch
r-saery	1.0	A complete set of functions to calculate several EBLUP (Empirical Best Linear Unbiased Predictor) estimators and their mean squared errors. All estimators are based on an area-level linear mixed model introduced by Rao and Yu in 1994 (see documentation). The REML method is used for fitting this model. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-safd</a>	2.1	The aim of the package is to provide some basic functions for doing statistics with one dimensional Fuzzy Data (in the form of polygonal fuzzy numbers). In particular, the package contains functions for the basic operations on the class of fuzzy numbers (sum, scalar product, mean, median, Hukuhara difference) as well as for calculating (Bertoluzza) distance and sample variance. Moreover a function to simulate fuzzy random variables and bootstrap tests for the equality of means is included. Version 2.1 fixes some bugs of previous versions. / GPL-2	noarch
<a href="#">r-saic</a>	1.0	Computes the Akaike information criterion for the generalized linear models (logistic regression, Poisson regression, and Gaussian graphical models) estimated by the lasso. / GPL-2	noarch
<a href="#">r-saltsampler</a>	1.1.0	The SALTSampler package facilitates Monte Carlo Markov Chain (MCMC) sampling of random variables on a simplex. A Self-Adjusting Logit Transform (SALT) proposal is used so that sampling is still efficient even in difficult cases, such as those in high dimensions or with parameters that differ by orders of magnitude. Special care is also taken to maintain accuracy even when some coordinates approach 0 or 1 numerically. Diagnostic and graphic functions are included in the package, enabling easy assessment of the convergence and mixing of the chain within the constrained space. / BSD_3_clause	noarch
<a href="#">r-salty</a>	0.1.0	Take real or simulated data and salt it with errors commonly found in the wild, such as pseudo-OCR errors, Unicode problems, numeric fields with nonsensical punctuation, bad dates, etc. / MIT	noarch
<a href="#">r-sample.size</a>	1.0	Computes the required sample size using the optimal designs with multiple constraints proposed in Mayo et al.(2010). This optimal method is designed for two-arm, randomized phase II clinical trials, and the required sample size can be optimized either using fixed or flexible randomization allocation ratios. / GPL-2	noarch
<a href="#">r-samplesize</a>	0.2_4	Computes sample size for Student's t-test and for the Wilcoxon-Mann-Whitney test for categorical data. The t-test function allows paired and unpaired (balanced / unbalanced) designs as well as homogeneous and heterogeneous variances. The Wilcoxon function allows for ties. / GPL-2	noarch
<a href="#">r-samplesize4clinicaltrials</a>	0.1.0	The design of phase 3 clinical trials can be classified into 4 types: (1) Testing for equality;(2) Superiority trial;(3) Non-inferiority trial; and (4) Equivalence trial according to the goals. Given that none of the available packages combines these designs in a single package, this package has made it possible for researchers to calculate sample size when comparing means or proportions in phase 3 clinical trials with different designs. The ssc function can calculate the sample size with pre-specified type 1 error rate,statistical power and effect size according to the hypothesis testing framework. Furthermore, effect size is comprised of true treatment difference and non-inferiority or equivalence margins which can be set in ssc function. (Reference: Yin, G. (2012). Clinical Trial Design: Bayesian and Frequentist Adaptive Methods. John Wiley & Sons.) / GPL-2	noarch
<a href="#">r-samplesizecmh</a>	0.0.0	Calculates the power and sample size for Cochran-Mantel-Haenszel tests. There are also several helper functions for working with probability, odds, relative risk, and odds ratio values. / GPL-2   GPL-3	noarch
<a href="#">r-samplesizelogisticcasecontrol</a>	0.0.6	To determine sample size for case-control studies to be analyzed using logistic regression. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-samplesizemeans</a>	1.1	A set of R functions for calculating sample size requirements using three different Bayesian criteria in the context of designing an experiment to estimate a normal mean or the difference between two normal means. Functions for calculation of required sample sizes for the Average Length Criterion, the Average Coverage Criterion and the Worst Outcome Criterion in the context of normal means are provided. Functions for both the fully Bayesian and the mixed Bayesian/likelihood approaches are provided. / GPL-2	noarch
<a href="#">r-samplesizeproportions</a>	1.0	A set of R functions for calculating sample size requirements using three different Bayesian criteria in the context of designing an experiment to estimate the difference between two binomial proportions. Functions for calculation of required sample sizes for the Average Length Criterion, the Average Coverage Criterion and the Worst Outcome Criterion in the context of binomial observations are provided. In all cases, estimation of the difference between two binomial proportions is considered. Functions for both the fully Bayesian and the mixed Bayesian/likelihood approaches are provided. / GPL-2	noarch
<a href="#">r-samplingdatacrt</a>	1.0	Package provides the possibility to sampling complete datasets from a normal distribution to simulate cluster randomized trials for different study designs. / GPL-3	noarch
<a href="#">r-sandwich</a>	2.5.1	Model-robust standard error estimators for cross-sectional, time series, clustered, panel, and longitudinal data. / GPL-2   GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-sanon</a>	1.5	There are several functions to implement the method for analysis in a randomized clinical trial with strata with following key features. A stratified Mann-Whitney estimator addresses the comparison between two randomized groups for a strictly ordinal response variable. The multivariate vector of such stratified Mann-Whitney estimators for multivariate response variables can be considered for one or more response variables such as in repeated measurements and these can have missing completely at random (MCAR) data. Non-parametric covariance adjustment is also considered with the minimal assumption of randomization. The p-value for hypothesis test and confidence interval are provided. / GPL-2	noarch
<a href="#">r-sarp.moodle</a>	0.3.10	Provides a set of basic functions for creating Moodle XML output files suited for importing questions in Moodle (a learning management system, see < <a href="https://moodle.org/">https://moodle.org/</a> > for more information). / Artistic-2.0	noarch
<a href="#">r-sas7bdat</a>	0.5	Read SAS files in the sas7bdat data format. / GPL-2	noarch
<a href="#">r-sascii</a>	1.0	Using any importation code designed for SAS users to read ASCII files into sas7bdat files, the SAScii package parses through the INPUT block of a (.sas) syntax file to design the parameters needed for a read.fwf function call. This allows the user to specify the location of the ASCII (often a .dat) file and the location of the .sas syntax file, and then load the data frame directly into R in just one step. / GPL-2	noarch
<a href="#">r-sasmarkdown</a>	0.4.3	Settings and functions to extend the ‘knitr’ ‘SAS’ engine. / MIT	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-sasmixed</a>	1.0_4	Data sets and sample lmer analyses corresponding to the examples in Littell, Milliken, Stroup and Wolfinger (1996), SAS System for Mixed Models, SAS Institute. / GPL-2	noarch
<a href="#">r-saspect</a>	0.1_1	A statistical method for significant analysis of comparative proteomics based on LC-MS/MS Experiments / GPL-2	noarch
<a href="#">r-sautomata</a>	0.1.0	Machine learning provides algorithms that can learn from data and make inferences or predictions. Stochastic automata is a class of input/output devices which can model components. This work provides implementation an inference algorithm for stochastic automata which is similar to the Viterbi algorithm. Moreover, we specify a learning algorithm using the expectation-maximization technique and provide a more efficient implementation of the Baum-Welch algorithm for stochastic automata. This work is based on Inference and learning in stochastic automata was by Karl-Heinz Zimmermann(2017) <doi:10.12732/ijpam.v11i5i3.15>. / GPL-3	noarch
<a href="#">r-saver</a>	1.1.1	An implementation of a regularized regression prediction and empirical Bayes method to recover the true gene expression profile in noisy and sparse single-cell RNA-seq data. See Huang M, et al (2018) <doi:10.1038/s41592-018-0033-z> for more details. / GPL-2	noarch
<a href="#">r-saves</a>	0.5	The purpose of this package is to be able to save and load only the needed variables/columns of a dataframe in special binary files (tar archives) - which seems to be a lot faster method than loading the whole binary object (RData files) via load() function, or than loading columns from SQLite/MySQL databases via SQL commands (see vignettes). Performance gain on SSD drives is a lot more sensible compared to basic load() function. The performance improvement gained by loading only the chosen variables in binary format can be useful in some special cases (e.g. where merging data tables is not an option and very different datasets are needed for reporting), but be sure if using this package that you really need this, as non-standard file formats are used! / AGPL-3	noarch
<a href="#">r-sbf</a>	1.1.1	Smooth Backfitting for additive models using Nadaraya-Watson estimator / GPL-2	noarch
<a href="#">r-sbgcop</a>	0.980	Estimation and inference for parameters in a Gaussian copula model, treating the univariate marginal distributions as nuisance parameters as described in Hoff (2007) <doi:10.1214/07-AOAS107>. This package also provides a semi-parametric imputation procedure for missing multivariate data. / GPL-2	noarch
<a href="#">r-sbl</a>	0.1.0	Implements sparse Bayesian learning method for QTL mapping and genome-wide association studies. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-sbrect</a>	0.26	The package uses fitting axes-aligned rectangles to a time series in order to find structural breaks. The algorithm enclose the time series in a number of axes-aligned rectangles and tries to minimize their area and number. As these are conflicting aims, the user has to specify a parameter alpha in [0.0,1.0]. Values close to 0 result in more breakpoints, values close to 1 in fewer. The left edges of the rectangles are the breakpoints. The package supplies two methods, <code>computeBreakPoints(series,alpha)</code> which returns the indices of the break points and <code>computeRectangles(series,alpha)</code> which returns the rectangles. The algorithm is randomised; it uses a genetic algorithm. Therefore, the break point sequence found can be different in different executions of the method on the same data, especially when used on longer series of some thousand observations. The algorithm uses a range-tree as background data structure which makes it very fast and suited to analyse series with millions of observations. A detailed description can be found in Paul Fischer, Astrid Hilbert, Fast detection of structural breaks, Proceedings of Compstat 2014. / GPL-2	noarch
<a href="#">r-sbsdif</a>	0.1.0	Calculates a Satorra-Bentler scaled chi-squared difference test between nested models that were estimated using maximum likelihood (ML) with robust standard errors, which cannot be calculated the traditional way. For details see Satorra & Bentler (2001) <doi:10.1007/bf02296192> and Satorra & Bentler (2010) <doi:10.1007/s11336-009-9135-y>. This package may be particularly helpful when used in conjunction with ‘Mplus’ software, specifically when implementing the complex survey option. In such cases, the model estimator in ‘Mplus’ defaults to ML with robust standard errors. / MIT	noarch
<a href="#">r-scagnostics</a>	0.2.4	Calculates graph theoretic scagnostics. Scagnostics describe various measures of interest for pairs of variables, based on their appearance on a scatterplot. They are useful tool for discovering interesting or unusual scatterplots from a scatterplot matrix, without having to look at every individual plot. / file LICENSE (FOSS)	noarch
<a href="#">r-scales</a>	1.0.0	Graphical scales map data to aesthetics, and provide methods for automatically determining breaks and labels for axes and legends. / MIT file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-scalreg</a>	1.0.1	Algorithms for fitting scaled sparse linear regression and estimating precision matrices. / GPL-2	noarch
<a href="#">r-scaml</a>	1.2.5	Routines for generalized additive modelling under shape constraints on the component functions of the linear predictor (Pya and Wood, 2015) <doi:10.1007/s11222-013-9448-7>. Models can contain multiple shape constrained (univariate and/or bivariate) and unconstrained terms. The routines of <code>gam()</code> in package ‘mgcv’ are used for setting up the model matrix, printing and plotting the results. Penalized likelihood maximization based on Newton-Raphson method is used to fit a model with multiple smoothing parameter selection by GCV or UBRE/AIC. / GPL-2	noarch
<a href="#">r-scatterd3</a>	0.9	Creates ‘D3’ ‘JavaScript’ scatterplots from ‘R’ with interactive features : panning, zooming, tooltips, etc. / GPL-3	noarch
<a href="#">r-scatterplot3d</a>	0.3.4	Plots a three dimensional (3D) point cloud. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-scbmeanfd</a>	1.2.2	Statistical methods for estimating and inferring the mean of functional data. The methods include simultaneous confidence bands, local polynomial fitting, bandwidth selection by plug-in and cross-validation, goodness-of-fit tests for parametric models, equality tests for two-sample problems, and plotting functions. / GPL-3	noarch
<a href="#">r-scdensity</a>	1.0.2	Implements methods for obtaining kernel density estimates subject to a variety of shape constraints (unimodality, bimodality, symmetry, tail monotonicity, bounds, and constraints on the number of inflection points). Enforcing constraints can eliminate unwanted waves or kinks in the estimate, which improves its subjective appearance and can also improve statistical performance. The main function <code>scdensity()</code> is very similar to the <code>density()</code> function in ‘stats’, allowing shape-restricted estimates to be obtained with little effort. The methods implemented in this package are described in Wolters and Braun (2017) <doi:10.1080/03610918.2017.1288247>, Wolters (2012) <doi:10.18637/jss.v047.i06>, and Hall and Huang (2002) <http://www3.stat.sinica.edu.tw/statistica/j12n4/j12n41/j12n41.htm>. See the <code>scdensity()</code> help for full citations. / GPL-2	noarch
<a href="#">r-scdhlm</a>	0.3.1	Provides a set of tools for estimating hierarchical linear models and effect sizes based on data from single-case designs. Functions are provided for calculating standardized mean difference effect sizes that are directly comparable to standardized mean differences estimated from between-subjects randomized experiments, as described in Hedges, Pustejovsky, and Shadish (2012) <DOI:10.1002/jrsm.1052>; Hedges, Pustejovsky, and Shadish (2013) <DOI:10.1002/jrsm.1086>; and Pustejovsky, Hedges, and Shadish (2014) <DOI:10.3102/1076998614547577>. Includes an interactive web interface. / GPL-3	noarch
<a href="#">r-scenario</a>	1.0	Uses the neural gas algorithm to construct a scenario tree for use in multi-stage stochastic programming. The primary input is a set of initial scenarios or realizations of a disturbance. The scenario tree nodal structure must be predefined using a scenario tree nodal partition matrix. / GPL-2	noarch
<a href="#">r-schoenberg</a>	2.0.2	Functions for creating and manipulating 12-tone (i.e., dodecaphonic) musical matrices using Arnold Schoenberg’s (1923) serialism technique. This package can generate random 12-tone matrices and can generate matrices using a pre-determined sequence of notes. / GPL-3	noarch
<a href="#">r-schoolmath</a>	0.4	This package contains functions and datasets for math taught in school. A main focus is set to prime-calculation / GPL-2	noarch
<a href="#">r-schorsch</a>	1.6	Offers a helping hand to psychologists and other behavioral scientists who routinely deal with experimental data from factorial experiments. It includes several functions to format output from other R functions according to the style guidelines of the APA (American Psychological Association). This formatted output can be copied directly into manuscripts to facilitate data reporting. These features are backed up by a toolkit of several small helper functions, e.g., offering out-of-the-box outlier removal. The package lends its name to Georg Schorsch Schuessler, ingenious technician at the Department of Psychology III, University of Wuerzburg. For details on the implemented methods, see Roland Pfister and Markus Janczyk (2016) <doi: 10.20982/tqmp.12.2.p147>. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-schumaker</a>	1.1	This is a shape preserving spline <doi:10.1137/0720057> which is guaranteed to be monotonic and concave or convex if the data is monotonic and concave or convex. It does not use any optimisation and is therefore quick and smoothly converges to a fixed point in economic dynamics problems including value function iteration. It also automatically gives the first two derivatives of the spline and options for determining behaviour when evaluated outside the interpolation domain. / MIT	noarch
<a href="#">r-scico</a>	1.1.0	Colour choice in information visualisation is important in order to avoid being misled by inherent bias in the used colour palette. The ‘scico’ package provides access to the perceptually uniform and colour-blindness friendly palettes developed by Fabio Crameri and released under the Scientific Colour-Maps moniker. The package contains 24 different palettes and includes both diverging and sequential types. / MIT	noarch
<a href="#">r-scientotext</a>	0.1	It involves bibliometric indicators calculation from bibliometric data. It also deals pattern analysis using the text part of bibliometric data. The bibliometric data are obtained from mainly Web of Science and Scopus. / GPL-3	noarch
<a href="#">r-scifigure</a>	0.2	Users may specify what fundamental qualities of a new study have or have not changed in an attempt to reproduce or replicate an original study. A comparison of the differences is visualized. Visualization approach follows ‘Patil’, ‘Peng’, and ‘Leek’ (2016) <doi:10.1101/066803>. / MIT	noarch
<a href="#">r-scina</a>	1.2.0	An automatic cell type detection and assignment algorithm for single cell RNA-Seq and Cytof/FACS data. ‘SCINA’ is capable of assigning cell type identities to a pool of cells profiled by scRNA-Seq or Cytof/FACS data with prior knowledge of markers, such as genes and protein symbols that are highly or lowly expressed in each category. See Zhang Z, et al (2019) <doi:10.3390/genes10070531> for more details. / GPL-2	noarch
<a href="#">r-sciplot</a>	1.1_1	A collection of functions that creates graphs with error bars for data collected from one-way or higher factorial designs. / GPL-2	noarch
<a href="#">r-sciviews</a>	0.9_1	Functions to install SciViews additions to R, and more tools. / GPL-2	noarch
<a href="#">r-scma</a>	1.3.0	Perform meta-analysis of single-case experiments, including calculating various effect size measures (SMD, PND, PEM and NAP) and probability combining (additive and multiplicative method), as discussed in Bulte and Onghena (2013) <doi:10.22237/jmasm/1383280020>. / GPL-2	noarch
<a href="#">r-scoreggum</a>	1.0	Estimate GGUM Person Parameters Using Pre-Calibrated Item Parameters and Binary or Graded Disagree-Agree Responses / GPL-2	noarch
<a href="#">r-scorer2</a>	0.99.0	This package contains the functions necessary to run the SCORER 2.0 algorithm. SCORER 2.0 can be used to differentiate between parallel dimeric and trimeric coiled-coil sequence, which are the two most more frequent coiled-coil structures observed naturally. As such, SCORER 2.0 is particularly useful for researchers looking to characterize novel coiled-coil sequences. It may also be used to assist in the structural characterization of synthetic coiled-coil sequences. Also included in this package are functions that allows the user to retrain the SCORER 2.0 algorithm using user-defined training data. / GPL-2	noarch
<a href="#">r-scoring</a>	0.6	Evaluating probabilistic forecasts via proper scoring rules. scoring implements the beta, power, and pseudospherical families of proper scoring rules, along with ordered versions of the latter two families. Included among these families are popular rules like the Brier (quadratic) score, logarithmic score, and spherical score. For two-alternative forecasts, also includes functionality for plotting scores that one would obtain under specific scoring rules. / GPL-2	noarch
<a href="#">r-scottknott</a>	1.2_7	Division of an ANOVA experiment treatment means into homogeneous distinct groups using the clustering method of Scott & Knott. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-scperf	1.1.1	Implements different inventory models, the bullwhip effect and other supply chain performance variables. Marchena Marlene (2010) <arXiv:1009.3977>. / GPL-3	noarch
r-scrabble	1.0	Given a word will produce that word's scrabble score. Unlike many naive implementations this package takes into consideration the distribution of letter in scrabble. So a word like 'zzz' will be scored '10' rather than '30'. / MIT License	noarch
r-scrap	1.1	A utility to webscrape the in-house careers of members of the European parliament, from its website < <a href="http://www.europarl.europa.eu">http://www.europarl.europa.eu</a> >. / GPL-3	noarch
r-scrap	0.1.6	Tools for Scraping Data from Web-Based Documents / GPL-2	noarch
r-screenclean	1.0.1	Routines for a collection of screen-and-clean type variable selection procedures, including UPS and GS. / GPL-2	noarch
r-scrime	1.3.5	Tools for the analysis of high-dimensional data developed/implemented at the group Statistical Complexity Reduction In Molecular Epidemiology (SCRIME). Main focus is on SNP data. But most of the functions can also be applied to other types of categorical data. / GPL-2	noarch
r-scriptests	1.0.1	Support for using .Rt (transcript) tests in the tests directory of a package. Provides more convenience and features than the standard .R/Rout.save tests. Tests can be run under R CMD check and also interactively. Provides source.pkg() for quickly loading code, DLLs, and data from a package for use in an edit/compile/test development cycle. / GPL-3	noarch
r-scriptexec	0.3.1	Run complex native scripts with a single command, similar to system commands. / Apache License 2.0	noarch
r-scriptname	1.0.1	A small set of functions wrapping up the call stack and command line inspection needed to determine a running script's filename from within the script itself. / MIT	noarch
r-scripturs	0.1.0	Full text, in data frames containing one row per verse, of the Standard Works of The Church of Jesus Christ of Latter-day Saints (LDS). These are the Old Testament, (KJV), the New Testament (KJV), the Book of Mormon, the Doctrine and Covenants, and the Pearl of Great Price. / MIT	noarch
r-scrobber	0.1.0	'Last.fm' < <a href="https://www.last.fm">https://www.last.fm</a> > is a music platform focussed on building a detailed profile of a users listening habits. It does this by 'scrobbling' (recording) every track you listen to on other platforms ('spotify', 'youtube', 'soundcloud' etc) and transferring them to your 'Last.fm' database. This allows 'Last.fm' to act as a complete record of your entire listening history. 'scrobber' provides helper functions to download and analyse your listening history in R. / GPL-3	noarch
r-scrselect	1.3.3	Contains four functions used in the DIC-tau_g procedure. SCRSELECT() and SCRSELECTRUN() uses Stochastic Search Variable Selection to select important covariates in the three hazard functions of a semi-competing risks model. These functions perform the Gibbs sampler for variable selection and a Metropolis-Hastings-Green sampler for the number of split points and parameters for the three baseline hazard function. The function SCRSELECT() returns the posterior sample of all quantities sampled in the Gibbs sampler after a burn-in period to a desired file location, while the function SCRSELECTRUN() returns posterior values of important quantities to the DIC-Tau_g procedure in a list. The function DICTAUG() returns a list containing the DIC values for the unique models visited by the DIC-Tau_g grid search. The function ReturnModel() uses SCRSELECTRUN() and DICTAUG() to return a summary of the posterior coefficient vectors for the optimal model along with saving this posterior sample to a desired path location. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-scrt	1.3.0	Design single-case phase, alternation and multiple-baseline experiments, and conduct randomization tests on data gathered by means of such designs, as discussed in Bulte and Onghena (2013) <doi:10.22237/jmasm/1383280020>. / GPL-2	noarch
r-sdaa	0.1_3	Functions and Datasets from Lohr, S. (1999), Sampling: Design and Analysis, Duxbury. / GPL-3	noarch
r-sdat	1.1	Test the global null in linear models using marginal approach. / GPL-2	linux-64, osx-64, win-64
r-sdcspatial	0.1.1	Privacy protected raster maps can be created from spatial point data. Protection methods include smoothing of dichotomous variables by de Jonge and de Wolf (2016) <doi:10.1007/978-3-319-45381-1_9>, continuous variables by de Wolf and de Jonge (2018) <doi:10.1007/978-3-319-99771-1_23>, suppressing revealing values and a generalization of the quad tree method by Suñé, Rovira, Ibáñez and Farré (2017) <doi:10.2901/EUROSTAT.C2017.001>. / GPL-2	noarch
r-sdde	1.0.1	Compares the evolution of an original network X to an augmented network Y by counting the number of Shortcuts, Detours, Dead Ends (SDDE), equal paths and disconnected nodes. / GPL-3	linux-64, osx-64, win-64
r-sddpack	0.9	The semidiscrete decomposition (SDD) approximates a matrix as a weighted sum of outer products formed by vectors with entries constrained to be in the set $\{-1, 0, 1\}$ . / GPL-2	noarch
r-sdef	1.7	Performs two tests to evaluate if the experiments are associated and returns a list of interesting features common to all the experiments. / GPL-2	noarch
r-sdm	1.0_67	An extensible framework for developing species distribution models using individual and community-based approaches, generate ensembles of models, evaluate the models, and predict species potential distributions in space and time. For more information, please check the following paper: Naimi, B., Araujo, M.B. (2016) <doi:10.1111/ecog.01881>. / GPL-3	noarch
r-sdmttools	1.1_22	This packages provides a set of tools for post processing the outcomes of species distribution modeling exercises. It includes novel methods for comparing models and tracking changes in distributions through time. It further includes methods for visualizing outcomes, selecting thresholds, calculating measures of accuracy and landscape fragmentation statistics, etc.. This package was made possible in part by financial support from the Australian Research Council & ARC Research Network for Earth System Science. / GPL-3	osx-64, win-64
r-sdmvspecies	0.3.2	A software package help user to create virtual species for species distribution modelling. It includes several methods to help user to create virtual species distribution map. Those maps can be used for Species Distribution Modelling (SDM) study. SDM use environmental data for sites of occurrence of a species to predict all the sites where the environmental conditions are suitable for the species to persist, and may be expected to occur. / AGPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-sdnet</a>	2.4.1	Fitting discrete Bayesian networks using soft-discretized data. Soft-discretization is based on mixture of normal distributions. Also implemented is a supervised Bayesian network learning employing Kullback-Leibler divergence. For more information see Balov (2013) <DOI:10.1186/1755-8794-6-S3-S1>. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-sdpt3r</a>	0.3	Solves the general Semi-Definite Linear Programming formulation using an R implementation of SDPT3 (K.C. Toh, M.J. Todd, and R.H. Tutuncu (1999) <doi:10.1080/10556789908805762>). This includes problems such as the nearest correlation matrix problem (Higham (2002) <doi:10.1093/imanum/22.3.329>), D-optimal experimental design (Smith (1918) <doi:10.2307/2331929>), Distance Weighted Discrimination (Marron and Todd (2012) <doi:10.1198/016214507000001120>), as well as graph theory problems including the maximum cut problem. Technical details surrounding SDPT3 can be found in R.H Tutuncu, K.C. Toh, and M.J. Todd (2003) <doi:10.1007/s10107-002-0347-5>. / GPL-2   GPL-3	linux-64, osx-64, win-64
<a href="#">r-sdt</a>	1.0.0	Functions for self-determination motivation theory (SDT) to compute measures of motivation internalization, motivation simplex structure, and of the original and adjusted self-determination or relative autonomy index. SDT was introduced by Deci and Ryan (1985) <doi:10.1007/978-1-4899-2271-7>. See package?SDT for an overview. / GPL-2	noarch
<a href="#">r-sdtoolkit</a>	2.33	Implements algorithms to help with scenario discovery - currently only modified version of the the Patient Rule Induction Method. / GPL-3	noarch
<a href="#">r-sdwd</a>	1.0.2	Formulates a sparse distance weighted discrimination (SDWD) for high-dimensional classification and implements a very fast algorithm for computing its solution path with the L1, the elastic-net, and the adaptive elastic-net penalties. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-seacarb</a>	3.2.12	Calculates parameters of the seawater carbonate system and assists the design of ocean acidification perturbation experiments. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-sealasso</a>	0.1_2	Standard error adjusted adaptive lasso (SEA-lasso) is a version of the adaptive lasso, which incorporates OLS standard error to the L1 penalty weight. This method is intended for variable selection under linear regression settings ( $n > p$ ). This new weight assignment strategy is especially useful when the collinearity of the design matrix is a concern. / GPL-2	noarch
<a href="#">r-searchable</a>	0.3.3	Provides functionality for searching / subsetting and slicing named objects using 'stringr/i'-style modifiers by case (in)sensitivity, regular expressions or fixed expressions; searches uses the standard '[' operator and allows specification of default search behavior to either the search target (named object) and/or the search pattern. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<code>r-searcher</code>	0.0.4	Provides a search interface to look up terms on ‘Google’, ‘Bing’, ‘DuckDuckGo’, ‘Startpage’, ‘StackOverflow’, ‘RStudio Community’, ‘GitHub’, and ‘BitBucket’. Upon searching, a browser window will open with the aforementioned search results. / GPL-2	noarch
<code>r-searchtrees</code>	0.5.2	This package provides an implementation of the QuadTree data structure. It uses this to implement fast k-Nearest Neighbor and Rectangular range lookups in 2 dimensions. The primary target is high performance interactive graphics. / LGPL-3	linux-64, osx-64, win-64
<code>r-seas</code>	0.5.2	Capable of deriving seasonal statistics, such as normals, and analysis of seasonal data, such as departures. This package also has graphics capabilities for representing seasonal data, including boxplots for seasonal parameters, and bars for summed normals. There are many specific functions related to climatology, including precipitation normals, temperature normals, cumulative precipitation departures and precipitation interarrivals. However, this package is designed to represent any time-varying parameter with a discernible seasonal signal, such as found in hydrology and ecology. / GPL-2	linux-64, osx-64, win-64
<code>r-seasic</code>	0.1	This package conducts Score Equity Assessment (SEA; Dorans, 2004) by calculating and plotting multiple SEA indices as introduced by a variety of authors and summarized by Huggins and Penfield (2012). / GPL-3	noarch
<code>r-seasonal</code>	1.7.0	Easy-to-use interface to X-13-ARIMA-SEATS, the seasonal adjustment software by the US Census Bureau. It offers full access to almost all options and outputs of X-13, including X-11 and SEATS, automatic ARIMA model search, outlier detection and support for user defined holiday variables, such as Chinese New Year or Indian Diwali. A graphical user interface can be used through the ‘seasonalview’ package. Uses the X-13-binaries from the ‘x13binary’ package. / GPL-3	noarch
<code>r-secr</code>	3.2.1	Functions to estimate the density and size of a spatially distributed animal population sampled with an array of passive detectors, such as traps, or by searching polygons or transects. Models incorporating distance-dependent detection are fitted by maximizing the likelihood. Tools are included for data manipulation and model selection. / GPL-2	linux-64, osx-64, win-64
<code>r-secret</code>	1.0.0	Allow sharing sensitive information, for example passwords, ‘API’ keys, etc., in R packages, using public key cryptography. / MIT	noarch
<code>r-secure</code>	0.5	Sequential factor extraction via co-sparse unit-rank estimation (SeCURE). / GPL (>= 3.0)	linux-64, osx-64, win-64
<code>r-securitytxt</code>	0.1.1	When security risks in web services are discovered by independent security researchers who understand the severity of the risk, they often lack the channels to properly disclose them. As a result, security issues may be left unreported. The ‘security.txt’ ‘Web Security Policies’ specification defines an ‘IETF’ draft standard < <a href="https://tools.ietf.org/html/draft-foudil-securitytxt-00">https://tools.ietf.org/html/draft-foudil-securitytxt-00</a> > to help organizations define the process for security researchers to securely disclose security vulnerabilities. Tools are provided to help identify and parse ‘security.txt’ files to enable analysis of the usage and adoption of these policies. / MIT	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-seeclickfixr	1.1.0	Provides a wrapper to access data from the SeeClickFix web API for R. SeeClickFix is a central platform employed by many cities that allows citizens to request their city's services. This package creates several functions to work with all the built-in calls to the SeeClickFix API. Allows users to download service request data from numerous locations in easy-to-use dataframe format manipulable in standard R functions. / GPL-3	noarch
r-seedcalc	1.0.0	Functions to calculate seed germination and seedling emergence and growth indexes. The main indexes for germination and seedling emergence, considering the time for seed germinate are: T10, T50 and T90, in Farooq et al. (2005) <10.1111/j.1744-7909.2005.00031.x>; and MGT, in Labouriau (1983). Considering the germination speed are: Germination Speed Index, in Maguire (1962), Mean Germination Rate, in Labouriau (1983); considering the homogeneity of germination are: Coefficient of Variation of the Germination Time, in Carvalho et al. (2005) <10.1590/S0100-84042005000300018>, and Variance of Germination, in Labouriau (1983); Uncertainty, in Labouriau and Valadares (1976) <ISSN:0001-3765>; and Synchrony, in Primack (1980). The main seedling indexes are Growth, in Sako (2001), Uniformity, in Sako (2001) and Castan et al. (2018) <doi:10.1590/1678-992x-2016-0401>; and Vigour, in Medeiros and Pereira (2018) <doi:10.1590/1983-40632018v4852340>. / GPL-2	noarch
r-seedwater	1.0	Bringing together tools for modeling drying and soaking (rehydration) kinetics of seeds. This package contains several widely used predictive models (e.g.: da Silva et al., 2018). As these are nonlinear, the functions are interactive-based and easy-to-use. Least squares estimates are obtained with just a few visual adjustments of the initial parameter values. Reference: da Silva AR et al. (2018) <doi:10.2134/agronj2017.07.0373>. / GPL-2	noarch
r-seer2r	1.0	read and write SEER*STAT data files / GPL-2	noarch
r-seermapper2010east	1.2.0	Provides supplemental 2010 census tract boundary package for 23 states without Seer Registries that are east of the Mississippi river for use with the 'SeerMapper' package. The data contained in this package is derived from U. S. Census data and is in public domain. / GPL-2	noarch
r-seermapper2010regs	1.2.0	Provides supplemental 2010 census tract boundaries of the 15 states containing Seer Registries for use with the 'SeerMapper' package. The data contained in this package is derived from U. S. 2010 Census data and is in public domain. / GPL-2	noarch
r-seermapper2010west	1.2.0	Provides supplemental 2010 census tract boundaries for the 14 states without Seer Registries that are west of the Mississippi river for use with the 'SeerMapper' package. The data contained in this package is derived from U. S. 2010 Census data and is in public domain. / GPL-2	noarch
r-seermappereast	1.2.0	Provides supplemental 2000 census tract boundaries for the 23 states without Seer Registries that are east of the Mississippi river for use with the 'SeerMapper' package. The data contained in this package is derived from U. S. Census data and is in the public domain. / GPL-2	noarch
r-seermapperregs	1.2.0	Provides supplemental 2000 census tract boundaries for the 15 states containing Seer Registries for use with the 'SeerMapper' package. The data contained in this package is derived from U. S. Census data and is in the public domain. / GPL-2	noarch
r-seermapperwest	1.2.0	Provides supplemental 2000 census tract boundaries for the 14 states without Seer Registries that are west of the Mississippi river for use with the 'SeerMapper' package. The data contained in this package is derived from U. S. Census data and is in the public domain. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-segmag	1.2.4	Contains functions that help to determine event boundaries in event segmentation experiments by bootstrapping a critical segmentation magnitude under the null hypothesis that all key presses were randomly distributed across the experiment. Segmentation magnitude is defined as the sum of Gaussians centered at the times of the segmentation key presses performed by the participants. Within a participant, the maximum of the overlaid Gaussians is used to prevent an excessive influence of a single participant on the overall outcome (e.g. if a participant is pressing the key multiple times in succession). Further functions are included, such as plotting the results. / GPL-3	linux-64, osx-64, win-64
r-segmented	1.0_0	Given a regression model, segmented ‘updates’ it by adding one or more segmented (i.e., piece-wise linear) relationships. Several variables with multiple breakpoints are allowed. The estimation method is discussed in Muggeo (2003, <doi:10.1002/sim.1545>) and illustrated in Muggeo (2008, < <a href="https://www.r-project.org/doc/Rnews/Rnews_2008-1.pdf">https://www.r-project.org/doc/Rnews/Rnews_2008-1.pdf</a> >). An approach for hypothesis testing is presented in Muggeo (2016, <doi:10.1080/00949655.2016.1149855>), and interval estimation for the breakpoint is discussed in Muggeo (2017, <doi:10.1111/anzs.12200>). / GPL-3	noarch
r-segmentier	0.1.2	A dynamic programming solution to segmentation based on maximization of arbitrary similarity measures within segments. The general idea, theory and this implementation are described in Machne, Murray & Stadler (2017) <doi:10.1038/s41598-017-12401-8>. In addition to the core algorithm, the package provides time-series processing and clustering functions as described in the publication. These are generally applicable where a <i>k-means</i> clustering yields meaningful results, and have been specifically developed for clustering of the Discrete Fourier Transform of periodic gene expression data (‘circadian’ or ‘yeast metabolic oscillations’). This clustering approach is outlined in the supplemental material of Machne & Murray (2012) <doi:10.1371/journal.pone.0037906>), and here is used as a basis of segment similarity measures. Notably, the time-series processing and clustering functions can also be used as stand-alone tools, independent of segmentation, e.g., for transcriptome data already mapped to genes. / GPL-2	linux-64, osx-64, win-64
r-segmentor3isback	2.0	Performs a fast exact segmentation on data and allows for use of various cost functions. / GPL-2	linux-64, osx-64, win-64
r-segmentr	0.2.0	Given a likelihood provided by the user, this package applies it to a given matrix dataset in order to find change points in the data that maximize the sum of the likelihoods of all the segments. This package provides a handful of algorithms with different time complexities and assumption compromises so the user is able to choose the best one for the problem at hand. The implementation of the segmentation algorithms in this package are based on the paper by Bruno M. de Castro, Florencia Leonardi (2018) <arXiv:1501.01756>. The Berlin weather sample dataset was provided by Deutscher Wetterdienst < <a href="https://dwd.de/">https://dwd.de/</a> >. You can find all the references in the Acknowledgments section of this package’s repository via the URL below. / MIT	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-segmarch</a>	1.2	Implements a segmentation algorithm for multiple change-point detection in high-dimensional GARCH processes. It simultaneously segments GARCH processes by identifying ‘common’ change-points, each of which can be shared by a subset or all of the component time series as a change-point in their within-series and/or cross-sectional correlation structure. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-segregation</a>	0.2.0	Computes entropy-based segregation indices, as developed by Theil (1971) <isbn:978-0471858454>, with a focus on the Mutual Information Index (M) and Theil’s Information Index (H). The M, further described by Mora and Ruiz-Castillo (2011) <doi:10.1111/j.1467-9531.2011.01237.x> and Frankel and Volij (2011) <doi:10.1016/j.jet.2010.10.008>, is a measure of segregation that is highly decomposable. The package provides tools to decompose the index by units and groups (local segregation), and by within and between terms. Includes standard error estimation by bootstrapping. / MIT	noarch
<a href="#">r-seismic</a>	1.0	An implementation of self-exciting point process model for information cascades, which occurs when many people engage in the same acts after observing the actions of others (e.g. post resharings on Facebook or Twitter). It provides functions to estimate the infectiousness of an information cascade and predict its popularity given the observed history. See <a href="http://snap.stanford.edu/seismic/">http://snap.stanford.edu/seismic/</a> for more information and datasets. / GPL-3	noarch
<a href="#">r-seismicroll</a>	1.1.3	Fast versions of seismic analysis functions that ‘roll’ over a vector of values. See the ‘RcppRoll’ package for alternative versions of basic statistical functions such as rolling mean, median, etc. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-sejong</a>	0.01	Sejong( <a href="http://www.sejong.or.kr/">http://www.sejong.or.kr/</a> ) corpus and Hannanum( <a href="http://semanticweb.kaist.ac.kr/home/index.php/HanNanum">http://semanticweb.kaist.ac.kr/home/index.php/HanNanum</a> ) dictionaries for KoNLP / GPL-3	noarch
<a href="#">r-sel</a>	1.0_2	This package implements a novel method for fitting a bounded probability distribution to quantiles (for example stated by an expert), see Bornkamp and Ickstadt (2009) for details. For this purpose B-splines are used, and the density is obtained by penalized least squares based on a Brier entropy penalty. The package provides methods for fitting the distribution as well as methods for evaluating the underlying density and cdf. In addition methods for plotting the distribution, drawing random numbers and calculating quantiles of the obtained distribution are provided. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-selectapref</a>	0.1.1	Provides indices such as Manly’s alpha, foraging ratio, and Ivlev’s selectivity to allow for analysis of dietary selectivity and preference. Can accommodate multiple experimental designs such as constant prey number of prey depletion. Please contact the package maintainer with any publications making use of this package in an effort to maintain a repository of dietary selections studies. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-selectiongain	2.0.59	Multi-stage selection is practiced in numerous fields of life and social sciences and particularly in breeding. A special characteristic of multi-stage selection is that candidates are evaluated in successive stages with increasing intensity and effort, and only a fraction of the superior candidates is selected and promoted to the next stage. For the optimum design of such selection programs, the selection gain plays a crucial role. It can be calculated by integration of a truncated multivariate normal (MVN) distribution. While mathematical formulas for calculating the selection gain and the variance among selected candidates were developed long time ago, solutions for numerical calculation were not available. This package can also be used for optimizing multi-stage selection programs for a given total budget and different costs of evaluating the candidates in each stage. / GPL-2	noarch
r-selectmeta	1.0.8	Publication bias, the fact that studies identified for inclusion in a meta analysis do not represent all studies on the topic of interest, is commonly recognized as a threat to the validity of the results of a meta analysis. One way to explicitly model publication bias is via selection models or weighted probability distributions. In this package we provide implementations of several parametric and nonparametric weight functions. The novelty in Rufibach (2011) is the proposal of a non-increasing variant of the nonparametric weight function of Dear & Begg (1992). The new approach potentially offers more insight in the selection process than other methods, but is more flexible than parametric approaches. To maximize the log-likelihood function proposed by Dear & Begg (1992) under a monotonicity constraint we use a differential evolution algorithm proposed by Ardia et al (2010a, b) and implemented in Mullen et al (2009). In addition, we offer a method to compute a confidence interval for the overall effect size theta, adjusted for selection bias as well as a function that computes the simulation-based p-value to assess the null hypothesis of no selection as described in Rufibach (2011, Section 6). / GPL-2	noarch
r-selectr	0.4.1	Translates a CSS3 selector into an equivalent XPath expression. This allows us to use CSS selectors when working with the XML package as it can only evaluate XPath expressions. Also provided are convenience functions useful for using CSS selectors on XML nodes. This package is a port of the Python package 'cssselect' (< <a href="https://cssselect.readthedocs.io/">https://cssselect.readthedocs.io/</a> >). / BSD_3_clause file LICENCE	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-selemix	1.0.1	Detection of outliers and influential errors using a latent variable model. / EUPL	noarch
r-seleniumpipes	0.3.7	The W3C WebDriver specification defines a way for out-of-process programs to remotely instruct the behaviour of web browsers. It is detailed at < <a href="https://w3c.github.io/webdriver/webdriver-spec.html">https://w3c.github.io/webdriver/webdriver-spec.html</a> >. This package provides an R client implementing the W3C specification. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-selfingtree</a>	0.2	A probability tree allows to compute probabilities of complex events, such as genotype probabilities in intermediate generations of inbreeding through recurrent self-fertilization (selfing). This package implements functionality to compute probability trees for two- and three-marker genotypes in the F2 to F7 selfing generations. The conditional probabilities are derived automatically and in symbolic form. The package also provides functionality to extract and evaluate the relevant probabilities. / BSD_3_clause	noarch
<a href="#">r-semicomprisks</a>	3.3	Hierarchical multistate models are considered to perform the analysis of independent/clustered semi-competing risks data. The package allows to choose the specification for model components from a range of options giving users substantial flexibility, including: accelerated failure time or proportional hazards regression models; parametric or non-parametric specifications for baseline survival functions and cluster-specific random effects distribution; a Markov or semi-Markov specification for terminal event following non-terminal event. While estimation is mainly performed within the Bayesian paradigm, the package also provides the maximum likelihood estimation approach for several parametric models. The package also includes functions for univariate survival analysis as complementary analysis tools. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-semid</a>	0.3.2	Provides routines to check identifiability or non-identifiability of linear structural equation models as described in Drton, Foygel, and Sullivant (2011) <DOI:10.1214/10-AOS859>, Foygel, Draisma, and Drton (2012) <DOI:10.1214/12-AOS1012>, and other works. The routines are based on the graphical representation of structural equation models by a path diagram/mixed graph. / GPL-2	noarch
<a href="#">r-semplr</a>	0.7.0	A powerful, easy to write and easy to modify syntax for specifying and estimating Partial Least Squares (PLS) path models allowing for the latest estimation methods for Consistent PLS as per Dijkstra & Henseler (2015, MISQ 39(2): 297-316), adjusted interactions as per Henseler & Chin (2010) <doi:10.1080/10705510903439003> and bootstrapping utilizing parallel processing as per Hair et al. (2017, ISBN:978-1483377445). / GPL-3	noarch
<a href="#">r-semipar</a>	1.0_4	Functions for semiparametric regression analysis, to complement the book: Ruppert, D., Wand, M.P. and Carroll, R.J. (2003). Semiparametric Regression. Cambridge University Press. / GPL-2	noarch
<a href="#">r-semmodcomp</a>	1.0	Conduct tests of difference in fit for mean and covariance structure models as in structural equation modeling (SEM) / GPL-3	noarch
<a href="#">r-semnetdictionaries</a>	0.1.3	Implements dictionaries that can be used in the ‘SemNetCleaner’ package. Also includes several functions aimed at facilitating the text cleaning analysis in the ‘SemNetCleaner’ package. This package is designed to integrate and update word lists and dictionaries based on each user’s individual needs by allowing users to store and save their own dictionaries. Dictionaries can be added to the ‘SemNetDictionaries’ package by submitting user-defined dictionaries to < <a href="https://github.com/AlexChristensen/SemNetDictionaries">https://github.com/AlexChristensen/SemNetDictionaries</a> >. / GPL (>= 3.0)	noarch
<a href="#">r-sempls</a>	1.0_10	Fits structural equation models using partial least squares (PLS). The PLS approach is referred to as ‘soft-modeling’ technique requiring no distributional assumptions on the observed data. / GPL-2	noarch
<a href="#">r-sempower</a>	1.0.0	Provides a-priori, post-hoc, and compromise power-analyses for structural equation models (SEM). Moshagen & Erdfelder (2016) <doi:10.1080/10705511.2014.950896>. / LGPL-3	noarch

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Name	Version	Summary/License	Platforms
r-semver	0.2.0	Tools and functions for parsing, rendering and operating on semantic version strings. Semantic versioning is a simple set of rules and requirements that dictate how version numbers are assigned and incremented as outlined at < <a href="http://semver.org">http://semver.org</a> >. / MIT	linux-64, osx-64, win-64
r-sendmailr	1.2_1	Package contains a simple SMTP client which provides a portable solution for sending email, including attachment, from within R. / GPL-2	noarch
r-sensemakr	0.1.2	Implements a suite of sensitivity analysis tools that extends the traditional omitted variable bias framework and makes it easier to understand the impact of omitted variables in regression models, as discussed in Cinelli and Hazlett (2018) < <a href="https://www.researchgate.net/publication/322509816_Making_Sense_of_Sensitivity_Extending_Omitted_Variable_Bias">https://www.researchgate.net/publication/322509816_Making_Sense_of_Sensitivity_Extending_Omitted_Variable_Bias</a> >. / GPL-3	noarch
r-sensibo.sky	1.0.0	Provides an interface to the ‘Sensibo Sky’ API which allows to remotely control non-smart air conditioning units. See < <a href="https://sensibo.com">https://sensibo.com</a> > for more informations. / MIT	noarch
r-sensitivity2x2xk	1.01	Performs exact or approximate adaptive or nonadaptive Cochran-Mantel-Haenszel-Birch tests and sensitivity analyses for one or two 2x2xk tables in observational studies. / GPL-2	noarch
r-sensitivitycasecontrol	2.1	This package performs sensitivity analysis for case-control studies in which some cases may meet a more narrow definition of being a case compared to other cases which only meet a broad definition. The sensitivity analyses are described in Small, Cheng, Halloran and Rosenbaum (2013, Case Definition and Sensitivity Analysis, Journal of the American Statistical Association, 1457-1468). The functions sens.analysis.mh and sens.analysis.aberrant.rank provide sensitivity analyses based on the Mantel-Haenszel test statistic and aberrant rank test statistic as described in Rosenbaum (1991, Sensitivity Analysis for Matched Case Control Studies, Biometrics); see also Section 1 of Small et al. The function adaptive.case.test provides adaptive inferences as described in Section 5 of Small et al. The function adaptive.noether.brown provides a sensitivity analysis for a matched cohort study based on an adaptive test. The other functions in the package are internal functions. / GPL-2	noarch
r-sensitivityfull	1.5.6	Sensitivity to unmeasured biases in an observational study that is a full match. Function senfm() performs tests and function senfmCI() creates confidence intervals. The method uses Huber’s M-statistics, including least squares, and is described in Rosenbaum (2007, Biometrics) <DOI:10.1111/j.1541-0420.2006.00717.x>. / GPL-2	noarch
r-sensitivitymult	1.0.2	Sensitivity analysis for multiple outcomes in observational studies. For instance, all linear combinations of several outcomes may be explored using Scheffe projections in the comparison() function; see Rosenbaum (2016, Annals of Applied Statistics) <doi:10.1214/16-AOAS942>. Alternatively, attention may focus on a few principal components in the principal() function. The package includes parallel methods for individual outcomes, including tests in the senm() function and confidence intervals in the senmCI() function. / GPL-2	noarch
r-sensitivitymv	1.4.3	The package performs a sensitivity analysis in an observational study using an M-statistic, for instance, the mean. The main function in the package is senmv(), but amplify() and truncatedP() are also useful. The method is developed in Rosenbaum Biometrics, 2007, 63, 456-464, <doi:10.1111/j.1541-0420.2006.00717.x>. / GPL-2	noarch
r-sensitivitymw	1.1	Sensitivity analysis analysis in matched observational studies with multiple controls using weighted M-statistics to increase design sensitivity. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-sensitivypstrat</a>	1.0_6	This package provides functions to perform principal stratification sensitivity analyses on datasets. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-sensmediation</a>	0.3.0	We implement functions to estimate and perform sensitivity analysis to unobserved confounding of direct and indirect effects introduced in Lindmark, de Luna and Eriksson (2018) <doi:10.1002/sim.7620>. The estimation and sensitivity analysis are parametric, based on probit and/or linear regression models. Sensitivity analysis is implemented for unobserved confounding of the exposure-mediator, mediator-outcome and exposure-outcome relationships. / GPL-2	noarch
<a href="#">r-sensory</a>	1.1	Contains the function CUUimpute() which performs model-based clustering and imputation simultaneously. / GPL-2	noarch
<a href="#">r-sensr</a>	1.5_1	Provides methods for sensory discrimination methods; duotrio, tetrad, triangle, 2-AFC, 3-AFC, A-not A, same-different, 2-AC and degree-of-difference. This enables the calculation of d-primes, standard errors of d-primes, sample size and power computations, and comparisons of different d-primes. Methods for profile likelihood confidence intervals and plotting are included. / GPL-2   GPL-3	noarch
<a href="#">r-sensrivastava</a>	2015.02.01	Collection of datasets from Sen & Srivastava: Regression Analysis, Theory, Methods and Applications, Springer. Sources for individual data files are more fully documented in the book. / GPL-2	noarch
<a href="#">r-senstrat</a>	1.0.3	Sensitivity analysis in unmatched observational studies, with or without strata. The main functions are sen2sample() and senstrat(). See Rosenbaum, P. R. and Krieger, A. M. (1990), JASA, 85, 493-498, <doi:10.1080/01621459.1990.10476226> and Gastwirth, Krieger and Rosenbaum (2000), JRSS-B, 62, 545-555 <doi:10.1111/1467-9868.00249> . / GPL-2	noarch
<a href="#">r-separate</a>	0.2.1	It combines maximum likelihood estimation of the parameters of matrix and 3rd-order tensor normal distributions with unstructured factor variance-covariance matrices, two procedures, and unbiased modified likelihood ratio testing of simple and double separability for variance-covariance structures, two procedures. / MIT	noarch
<a href="#">r-separationplot</a>	1.1	Functions to generate separation plots for evaluation of model fit. / Artistic-2.0	noarch
<a href="#">r-seqalloc</a>	1.0	Potential randomization schemes are prospectively evaluated when units are assigned to treatment arms upon entry into the experiment. The schemes are evaluated for balance on covariates and on predictability (i.e., how well could a site worker guess the treatment of the next unit enrolled). / GPL-2	noarch
<a href="#">r-seqcbcs</a>	1.2.1	This is a method for DNA Copy Number Profiling using Next-Generation Sequencing. It has new model and test statistics based on non-homogeneous Poisson Processes with change point models. It uses an adaptation of Circular Binary Segmentation. Also included are methods for point-wise Bayesian Confidence Interval and model selection method for the change-point model. A case and a control sample reads (normal and tumor) are required. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-seqdesign</a>	1.2	A modification of the preventive vaccine efficacy trial design of Gilbert, Grove et al. (2011, Statistical Communications in Infectious Diseases) is implemented, with application generally to individual-randomized clinical trials with multiple active treatment groups and a shared control group, and a study endpoint that is a time-to-event endpoint subject to right-censoring. The design accounts for the issues that the efficacy of the treatment/vaccine groups may take time to accrue while the multiple treatment administrations/vaccinations are given; there is interest in assessing the durability of treatment efficacy over time; and group sequential monitoring of each treatment group for potential harm, non-efficacy/efficacy futility, and high efficacy is warranted. The design divides the trial into two stages of time periods, where each treatment is first evaluated for efficacy in the first stage of follow-up, and, if and only if it shows significant treatment efficacy in stage one, it is evaluated for longer-term durability of efficacy in stage two. The package produces plots and tables describing operating characteristics of a specified design including an unconditional power for intention-to-treat and per-protocol/as-treated analyses; trial duration; probabilities of the different possible trial monitoring outcomes (e.g., stopping early for non-efficacy); unconditional power for comparing treatment efficacies; and distributions of numbers of endpoint events occurring after the treatments/vaccinations are given, useful as input parameters for the design of studies of the association of biomarkers with a clinical outcome (surrogate endpoint problem). The code can be used for a single active treatment versus control design and for a single-stage design. / GPL-2	noarch
<a href="#">r-seqicp</a>	1.1	Contains an implementation of invariant causal prediction for sequential data. The main function in the package is 'seqICP', which performs linear sequential invariant causal prediction and has guaranteed type I error control. For non-linear dependencies the package also contains a non-linear method 'seqICPnl', which allows to input any regression procedure and performs tests based on a permutation approach that is only approximately correct. In order to test whether an individual set S is invariant the package contains the subroutines 'seqICP.s' and 'seqICPnl.s' corresponding to the respective main methods. / GPL-3	noarch
<a href="#">r-seqmade</a>	1.0	A network module-based generalized linear model for differential expression analysis with the count-based sequence data from RNA-Seq. / GPL-2	noarch
<a href="#">r-seqmeta</a>	1.6.7	Computes necessary information to meta analyze region-based tests for rare genetic variants (e.g. SKAT, T1) in individual studies, and performs meta analysis. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-seqminer</a>	7.1	Integrate sequencing data (Variant call format, e.g. VCF or BCF) or meta-analysis results in R. This package can help you (1) read VCF/BCF/BGEN files by chromosomal ranges (e.g. 1:100-200); (2) read RareMETAL summary statistics files; (3) read tables from a tabix-indexed files; (4) annotate VCF/BCF files; (5) create customized workflow based on Makefile. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-seqmon</a>	2.3	S4 class object for creating and managing group sequential designs. It calculates the efficacy and futility boundaries at each look. It allows modifying the design and tracking the design update history. / MIT	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-seqrfnp</a>	1.0.1	This package includes functions for handling DNA sequences, especially simulated RFLP and TRFLP pattern based on selected restriction enzyme and DNA sequences. / GPL-2	noarch
<a href="#">r-seqtest</a>	0.1_0	Sequential triangular test for the arithmetic mean in one- and two- samples, proportions in one- and two-samples, and the Pearson's correlation coefficient. / GPL-3	noarch
<a href="#">r-sequences</a>	0.5.9	Educational package used in R courses to illustrate object-oriented programming and package development. Using biological sequences (DNA and RNA) as a working example. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-sequential</a>	3.0.1	Functions to calculate exact critical values, statistical power, expected time to signal, and required sample sizes for performing exact sequential analysis. All these calculations can be done for either Poisson or binomial data, for continuous or group sequential analyses, and for different types of rejection boundaries. In case of group sequential analyses, the group sizes do not have to be specified in advance and the alpha spending can be arbitrarily settled. / GPL-2	noarch
<a href="#">r-sequoia</a>	1.3.3	Fast multi-generational pedigree inference from incomplete data on hundreds of SNPs, including parentage assignment and sibship clustering. See Huisman (2017) (DOI:10.1111/1755-0998.12665, citation('sequoia')) for more information. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-serial</a>	2.1.4	Enables reading and writing binary and ASCII data to RS232/RS422/RS485 or any other virtual serial interfaces of the computer. / GPL-2	noarch
<a href="#">r-serieslcb</a>	0.4.0	Calculate and compare lower confidence bounds for binomial series system reliability. The R 'shiny' application, launched by the function launch_app(), weaves together a workflow of customized simulations and delta coverage calculations to output recommended lower confidence bound methods. / GPL-3	noarch
<a href="#">r-seroincidence</a>	2.0.0	Translates antibody levels measured in a (cross-sectional) population sample into an estimate of the frequency with which seroconversions (infections) occur in the sampled population. / GPL-3	noarch
<a href="#">r-servr</a>	0.15	Start an HTTP server in R to serve static files, or dynamic documents that can be converted to HTML files (e.g., R Markdown) under a given directory. / GPL-3	noarch
<a href="#">r-sesem</a>	1.0.2	Structural equation modeling is a powerful statistical approach for the testing of networks of direct and indirect theoretical causal relationships in complex data sets with inter-correlated dependent and independent variables. Here we implement a simple method for spatially explicit structural equation modeling based on the analysis of variance co-variance matrices calculated across a range of lag distances. This method provides readily interpreted plots of the change in path coefficients across scale. / GPL-2	noarch
<a href="#">r-session</a>	1.0.3	Utility functions for interacting with R processes from external programs. This package includes functions to save and restore session information (including loaded packages, and attached data objects), as well as functions to evaluate strings containing R commands and return the printed results or an execution transcript. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-sessioninfo</a>	1.1.1	Query and print information about the current R session. It is similar to 'utils::sessionInfo()', but includes more information about packages, and where they were installed from. / GPL-2	noarch
<a href="#">r-setpath</a>	1.0	Tests gene expression data from a biological pathway for biologically meaningful differences in the eigenstructure between two classes. Specifically, it tests the null hypothesis that the two classes' leading eigenvalues and sums of eigenvalues are equal. A pathway's leading eigenvalue arguably represents the total variability due to variability in pathway activity, while the sum of all its eigenvalues represents the variability due to pathway activity and to other, unregulated causes. Implementation of the method described in Danaher (2015), Covariance-based analyses of biological pathways. / GPL-2	noarch
<a href="#">r-setrank</a>	1.1.0	Implements an algorithm to conduct advanced gene set enrichment analysis on the results of genomics experiments. / GPL-3	noarch
<a href="#">r-setrng</a>	2013.9	SetRNG provides utilities to help set and record the setting of the seed and the uniform and normal generators used when a random experiment is run. The utilities can be used in other functions that do random experiments to simplify recording and/or setting all the necessary information for reproducibility. See the vignette and reference manual for examples. / GPL-2	noarch
<a href="#">r-sets</a>	1.0_1	Data structures and basic operations for ordinary sets, generalizations such as fuzzy sets, multisets, and fuzzy multisets, customizable sets, and intervals. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-setter</a>	0.0_1	Mutators to set attributes of variables, that work well in a pipe (much like stats::setNames()). / Unlimited	noarch
<a href="#">r-settest</a>	0.2.0	It provides cumulative distribution function (CDF), quantile, p-value, statistical power calculator and random number generator for a collection of group-testing procedures, including the Higher Criticism tests, the one-sided Kolmogorov-Smirnov tests, the one-sided Berk-Jones tests, the one-sided phi-divergence tests, etc. The input are a group of p-values. The null hypothesis is that they are i.i.d. Uniform(0,1). In the context of signal detection, the null hypothesis means no signals. In the context of the goodness-of-fit testing, which contrasts a group of i.i.d. random variables to a given continuous distribution, the input p-values can be obtained by the CDF transformation. The null hypothesis means that these random variables follow the given distribution. For reference, see Hong Zhang, Jiashun Jin and Zheyang Wu. Distributions and Statistical Power of Optimal Signal-Detection Methods In Finite Cases, submitted. / GPL-2	noarch
<a href="#">r-settings</a>	0.2.4	Provides option settings management that goes beyond R's default 'options' function. With this package, users can define their own option settings manager holding option names, default values and (if so desired) ranges or sets of allowed option values that will be automatically checked. Settings can then be retrieved, altered and reset to defaults with ease. For R programmers and package developers it offers cloning and merging functionality which allows for conveniently defining global and local options, possibly in a multilevel options hierarchy. See the package vignette for some examples concerning functions, S4 classes, and reference classes. There are convenience functions to reset par() and options() to their 'factory defaults'. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<code>r-severity</code>	2.0	This package contains functions for calculating severity and generating severity curves. Specifically, the simple case of the one-parameter Normal distribution (i.e., with known variance) is considered. / GPL-2	noarch
<code>r-sf</code>	0.6_3	Support for simple features, a standardized way to encode spatial vector data. Binds to 'GDAL' for reading and writing data, to 'GEOS' for geometrical operations, and to 'PROJ' for projection conversions and datum transformations. / GPL-2   MIT file LICENSE	linux-32, linux-64, osx-64, win-64
<code>r-sfa</code>	1.0_1	Stochastic Frontier Analysis introduced by Aigner, Lovell and Schmidt (1976) and Battese and Coelli (1992, 1995). / GPL-2	noarch
<code>r-sfinx</code>	1.7.99	The straightforward filtering index (SFIX) identifies true positive protein interactions in a fast, user-friendly, and highly accurate way. It is not only useful for the filtering of affinity purification - mass spectrometry (AP-MS) data, but also for similar types of data resulting from other co-complex interactomics technologies, such as TAP-MS, Virotrap and BioID. SFIX can also be used via the website interface at <a href="http://sfinx.ugent.be">http://sfinx.ugent.be</a> . / Apache License 2.0	noarch
<code>r-sfs</code>	0.1.4	An implementation of the Similarity-First Search algorithm (SFS), a combinatorial algorithm which can be used to solve the seriation problem and to recognize some structured weighted graphs. The SFS algorithm represents a generalization to weighted graphs of the graph search algorithm Lexicographic Breadth-First Search (Lex-BFS), a variant of Breadth-First Search. The SFS algorithm reduces to Lex-BFS when applied to binary matrices (or, equivalently, unweighted graphs). Hence this library can be also considered for Lex-BFS applications such as recognition of graph classes like chordal or unit interval graphs. In fact, the SFS seriation algorithm implemented in this package is a multisweep algorithm, which consists in repeating a finite number of SFS iterations (at most n sweeps for a matrix of size n). If the data matrix has a Robinsonian structure, then the ranking returned by the multistep SFS algorithm is a Robinson ordering of the input matrix. Otherwise the algorithm can be used as a heuristic to return a ranking partially satisfying the Robinson property. / GPL-3	linux-64, osx-64, win-64
<code>r-sfsmisc</code>	1.1_3	Useful utilities ['goodies'] from Seminar fuer Statistik ETH Zurich, some of which were ported from S-plus in the 1990's. For graphics, have pretty (Log-scale) axes, an enhanced Tukey-Anscombe plot, combining histogram and boxplot, 2d-residual plots, a 'tachoPlot()', pretty arrows, etc. For robustness, have a robust F test and robust range(). For system support, notably on Linux, provides 'Sys.*()' functions with more access to system and CPU information. Finally, miscellaneous utilities such as simple efficient prime numbers, integer codes, Duplicated(), toLatex.numeric() and is.whole(). / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-sgb</a>	1.0	Main properties and regression procedures using a generalization of the Dirichlet distribution called Simplicial Generalized Beta distribution. It is a new distribution on the simplex (i.e. on the space of compositions or positive vectors with sum of components equal to 1). The Dirichlet distribution can be constructed from a random vector of independent Gamma variables divided by their sum. The SGB follows the same construction with generalized Gamma instead of Gamma variables. The Dirichlet exponents are supplemented by an overall shape parameter and a vector of scales. The scale vector is itself a composition and can be modeled with auxiliary variables through a log-ratio transformation. Graf, M. (2017, ISBN: 978-84-947240-0-8). See also the vignette enclosed in the package. / GPL-2	noarch
<a href="#">r-sgee</a>	0.6_0	Stagewise techniques implemented with Generalized Estimating Equations to handle individual, group, bi-level, and interaction selection. Stagewise approaches start with an empty model and slowly build the model over several iterations, which yields a ‘path’ of candidate models from which model selection can be performed. This ‘slow brewing’ approach gives stagewise techniques a unique flexibility that allows simple incorporation of Generalized Estimating Equations; see Vaughan, G., Aseltine, R., Chen, K., Yan, J., (2017) <doi:10.1111/biom.12669> for details. / GPL-3	noarch
<a href="#">r-sgeostat</a>	1.0_2	An Object-oriented Framework for Geostatistical Modeling in S containing functions for variogram estimation, variogram fitting and kriging as well as some plot functions. Written entirely in S, therefore works only for small data sets in acceptable computing time. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-sgl</a>	1.2	Fit a regularized generalized linear model via penalized maximum likelihood. The model is fit for a path of values of the penalty parameter. Fits linear, logistic and Cox models. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-sglasso</a>	1.2.3	RCON(V, E) models are a kind of restriction of the Gaussian Graphical Models defined by a set of equality constraints on the entries of the concentration matrix. ‘sglasso’ package implements the structured graphical lasso (sglasso) estimator proposed in Abbruzzo et al. (2014) for the weighted l1-penalized RCON(V, E) model. Two cyclic coordinate algorithms are implemented to compute the sglasso estimator, i.e. a cyclic coordinate minimization (CCM) and a cyclic coordinate descent (CCD) algorithm. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-sgloptim</a>	1.3.8	Fast generic solver for sparse group lasso optimization problems. The loss (objective) function must be defined in a C module. The optimization problem is solved using a coordinate gradient descent algorithm. Convergence of the algorithm is established (see reference) and the algorithm is applicable to a broad class of loss functions. Use of parallel computing for cross validation and subsampling is supported through the ‘foreach’ and ‘doParallel’ packages. Development version is on GitHub, please report package issues on GitHub. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-sgmcmc</a>	0.2.4	Provides functions that performs popular stochastic gradient Markov chain Monte Carlo (SGMCMC) methods on user specified models. The required gradients are automatically calculated using ‘TensorFlow’ < <a href="https://www.tensorflow.org/">https://www.tensorflow.org/</a> >, an efficient library for numerical computation. This means only the log likelihood and log prior functions need to be specified. The methods implemented include stochastic gradient Langevin dynamics (SGLD), stochastic gradient Hamiltonian Monte Carlo (SGHMC), stochastic gradient Nose-Hoover thermostat (SGNHT) and their respective control variate versions for increased efficiency. References: M. Welling, Y. W. Teh (2011) < <a href="http://www.icml-2011.org/papers/398_icmlpaper.pdf">http://www.icml-2011.org/papers/398_icmlpaper.pdf</a> >; T. Chen, E. B. Fox, C. E. Guestrin (2014) <arXiv:1402.4102>; N. Ding, Y. Fang, R. Babbush, C. Chen, R. D. Skeel, H. Neven (2014) < <a href="https://papers.nips.cc/paper/5592-bayesian-sampling-using-stochastic-gradient-thermostats">https://papers.nips.cc/paper/5592-bayesian-sampling-using-stochastic-gradient-thermostats</a> >; J. Baker, P. Fearnhead, E. B. Fox, C. Nemeth (2017) <arXiv:1706.05439>. / GPL-3	noarch
<a href="#">r-sgpdata</a>	21.0	Data sets utilized by the ‘SGP’ package as exemplars for users to conduct their own student growth percentiles (SGP) analyses. / GPL-3	noarch
<a href="#">r-sgr</a>	1.3	The package for Sample Generation by Replacement simulations (SGR; Lombardi & Pastore, 2014; Pastore & Lombardi, 2014). The package can be used to perform fake data analysis according to the sample generation by replacement approach. It includes functions for making simple inferences about discrete/ordinal fake data. The package allows to study the implications of fake data for empirical results. / GPL-2	noarch
<a href="#">r-sgrsea</a>	0.1	Provides functions to implement sgRSEA (single-guide RNA Set Enrichment Analysis), which is a robust test for identification of essential genes from genetic screening data using CRISPR (clustered regularly interspaced short palindromic repeats) and Cas9 (CRISPR-associated nuclease 9) system. / GPL-2	noarch
<a href="#">r-shades</a>	1.4.0	Functions for easily manipulating colours, creating colour scales and calculating colour distances. / BSD_3_clause	noarch
<a href="#">r-shape</a>	1.4.4	Functions for plotting graphical shapes such as ellipses, circles, cylinders, arrows, ... / GPL-3	noarch
<a href="#">r-shapechange</a>	1.4	In a scatterplot where the response variable is Gaussian, Poisson or binomial, we consider the case in which the mean function is smooth with a change-point, which is a mode, an inflection point or a jump point. The main routine estimates the mean curve and the change-point as well using shape-restricted B-splines. An optional subroutine delivering a bootstrap confidence interval for the change-point is incorporated in the main routine. / GPL-2	noarch
<a href="#">r-shapefiles</a>	0.7	Functions to read and write ESRI shapefiles / GPL-3	noarch
<a href="#">r-sharpdata</a>	1.2	Functions and data sets inspired by data sharpening - data perturbation to achieve improved performance in nonparametric estimation, as described in Choi, E., Hall, P. and Rousson, V. (2000) <doi:10.1214/aos/1015957396>. Capabilities for enhanced local linear regression function and derivative estimation are included, as well as an asymptotically correct iterated data sharpening estimator for any degree of local polynomial regression estimation. A cross-validation-based bandwidth selector is included which, in concert with the iterated sharpener, will often provide superior performance, according to a median integrated squared error criterion. Sample data sets are provided to illustrate function usage. / Unlimited	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-sharpr2	1.1.1.0	An algorithm for identifying high-resolution driver elements for datasets from a high-definition reporter assay library. Xincheng Wang, Liang He, Sarah Goggin, Alham Saadat, Li Wang, Melina Claussnitzer, Manolis Kellis (2017) <doi:10.1101/193136>. / GPL-2	noarch
r-shiftr	1.5	Fast enrichment analysis for locally correlated statistics via circular permutations. The analysis can be performed at multiple significance thresholds for both primary and auxiliary data sets with efficient correction for multiple testing. / LGPL-3	linux-64, osx-64, win-64
r-shiftsharese	1.0.0	Provides confidence intervals in least-squares regressions when the variable of interest has a shift-share structure, and in instrumental variables regressions when the instrument has a shift-share structure. The confidence intervals implement the AKM and AKM0 methods developed in Adão, Kolesár, and Morales (2019) <doi:10.1093/qje/qjz025>. / GPL-3	noarch
r-shiny	1.3.2	Makes it incredibly easy to build interactive web applications with R. Automatic reactive binding between inputs and outputs and extensive prebuilt widgets make it possible to build beautiful, responsive, and powerful applications with minimal effort. / GPL-3   file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-shiny.i18n	0.1.0	It provides easy internationalization of Shiny applications. It can be used as standalone translation package to translate reports, interactive visualizations or graphical elements as well. / MIT	noarch
r-shiny.router	0.1.1	The minimal router for your Shiny apps. It allows you to create dynamic web applications with real-time user interface and easily share URLs to pages within your Shiny apps. / MIT	noarch
r-shiny.semantic	0.2.1	Creating a great user interface for your Shiny apps can be a hassle, especially if you want to work purely in R and don't want to use, for instance HTML templates. This package adds support for a powerful UI library Semantic UI - < <a href="http://semantic-ui.com/">http://semantic-ui.com/</a> >. It also supports universal UI input binding that works with various DOM elements. / MIT	noarch
r-shinyace	0.4.0	Ace editor bindings to enable a rich text editing environment within Shiny. / MIT	noarch
r-shinyiframe	1.0.1	Make R data available in Web-based virtual reality experiences for immersive, cross-platform data visualizations. Includes the 'gg-iframe' JavaScript package for a Grammar of Graphics declarative HTML syntax to create 3-dimensional data visualizations with 'Mozilla A-Frame' < <a href="https://aframe.io/">https://aframe.io/</a> >. / AGPL-3	noarch
r-shinyalert	1.0	Easily create pretty popup messages (modals) in 'Shiny'. A modal can contain text, images, OK/Cancel buttons, an input to get a response from the user, and many more customizable options. / MIT	noarch
r-shinyanimate	0.3.0	An extension of 'animate.css' that allows user to easily add animations to any UI element in 'shiny' app using the elements id. / MIT	noarch

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Name	Version	Summary/License	Platforms
r-shinybootstrap2	0.2.1	Provides Bootstrap 2 web components for use with the Shiny package. With versions of Shiny prior to 0.11, these Bootstrap 2 components were included as part of the package. Later versions of Shiny include Bootstrap 3, so the Bootstrap 2 components have been moved into this package for those uses who rely on features specific to Bootstrap 2. / GPL-3	noarch
r-shinybs	0.61	Adds additional Twitter Bootstrap components to Shiny. / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-shinybusy	0.1.3	Add a global indicator (spinner, progress bar, gif) in your ‘shiny’ applications to show the user that the server is busy. / GPL-3	noarch
r-shinycssloaders	0.2.0	Create a lightweight Shiny wrapper for the css-loaders created by Luke Hass < <a href="https://github.com/lukehaas/css-loaders">https://github.com/lukehaas/css-loaders</a> >. Wrapping a Shiny output will automatically show a loader when the output is (re)calculating. / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-shinycustomloader	0.9.0	A custom css/html or gif/image file for the loading screen in R ‘shiny’. It also can use the marquee to have custom text loading screen. / GPL-3	noarch
r-shinydashboard	0.7.1	Create dashboards with ‘Shiny’. This package provides a theme on top of ‘Shiny’, making it easy to create attractive dashboards. / GPL (>= 2)   file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-shinydashboardplus	0.7.0	Extend ‘shinydashboard’ with ‘AdminLTE2’ components. ‘AdminLTE2’ is a free ‘Bootstrap 3’ dashboard template available at < <a href="https://adminlte.io">https://adminlte.io</a> >. Customize boxes, add timelines and a lot more. / GPL-2	noarch
r-shinydnd	0.1.0	Add functionality to create drag and drop div elements in shiny. / GPL-3	noarch
r-shinyeffects	0.1.0	Add fancy CSS effects to your ‘shinydashboards’ or ‘shiny’ apps. 100% compatible with ‘shinydashboardPlus’ and ‘bs4Dash’. / GPL-2	noarch
r-shinyfeedback	0.1.0	Easily display user feedback next to Shiny inputs. The feedback message is displayed when the feedback condition evaluates to TRUE. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-shinyglide</a>	0.1.1	Insert Glide JavaScript component into Shiny applications for carousel or assistant-like user interfaces. / GPL-3	noarch
<a href="#">r-shinyhelper</a>	0.3.1	Creates a lightweight way to add markdown helpfiles to ‘shiny’ apps, using modal dialog boxes, with no need to observe each help button separately. / GPL-3	noarch
<a href="#">r-shinyjq</a>	0.3.2	An extension to shiny that brings interactions and animation effects from ‘jQuery UI’ library. / MIT	noarch
<a href="#">r-shinyjs</a>	1.0	Perform common useful JavaScript operations in Shiny apps that will greatly improve your apps without having to know any JavaScript. Examples include: hiding an element, disabling an input, resetting an input back to its original value, delaying code execution by a few seconds, and many more useful functions for both the end user and the developer. ‘shinyjs’ can also be used to easily call your own custom JavaScript functions from R. / AGPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-shinylp</a>	1.1.2	Provides functions that wrap HTML Bootstrap components code to enable the design and layout of informative landing home pages for Shiny applications. This can lead to a better user experience for the users and writing less HTML for the developer. / MIT	noarch
<a href="#">r-shinymaterial</a>	0.5.5	Allows shiny developers to incorporate UI elements based on Google’s Material design. See < <a href="https://material.io/guidelines/">https://material.io/guidelines/</a> > for more information. / GPL-3	noarch
<a href="#">r-shinymatrix</a>	0.2.0	Implements a custom matrix input field. / MIT	noarch
<a href="#">r-shinyshortcut</a>	0.1.0	Provides function shinyShortcut() that, when given the base directory of a shiny application, will produce an executable file that runs the shiny app directly in the user’s default browser. Tested on both windows and unix machines. Inspired by and borrowing from < <a href="http://www.mango-solutions.com/wp/2017/03/shiny-based-tablet-or-desktop-app/">http://www.mango-solutions.com/wp/2017/03/shiny-based-tablet-or-desktop-app/</a> >. / GPL-3	noarch
<a href="#">r-shinysky</a>	2.0.0	A set of Shiny UI components includings alerts and styled buttons / MIT	linux-32, linux-64, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
r-shinythemes	1.1.2	Themes for use with Shiny. Includes several Bootstrap themes from <a href="http://bootswatch.com/">http://bootswatch.com/</a> , which are packaged for use with Shiny applications. / GPL-3   file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-shinytime	1.0.1	Provides a time input widget for Shiny. This widget allows intuitive time input in the '[hh]:[mm]:[ss]' or '[hh]:[mm]' (24H) format by using a separate numeric input for each time component. The interface with R uses date-time objects. See the project page for more information and examples. / GPL-3	noarch
r-shinytoastr	2.1.1	Browser notifications in 'Shiny' apps, using 'toastr': <a href="https://github.com/CodeSeven/toastr#readme">https://github.com/CodeSeven/toastr#readme</a> . / MIT	noarch
r-shinytree	0.2.7	Exposes bindings to jsTree – a JavaScript library that supports interactive trees – to enable a rich, editable trees in Shiny. / MIT	noarch
r-shinywidgets	0.4.9	Collection of custom input controls and user interface components for 'Shiny' applications. Give your applications a unique and colorful style ! / GPL-3	noarch
r-ship	1.0.2	The SHIP-package allows the estimation of various types of shrinkage covariance matrices. These types differ in terms of the so-called covariance target (to be chosen by the user), the highly structured matrix which the standard unbiased sample covariance matrix is shrunk towards and which optionally incorporates prior biological knowledge extracted from the database KEGG. The shrinkage intensity is obtained via an analytical procedure. / GPL-2	noarch
r-shipunov	1.2	A collection of functions for data manipulation, plotting and statistical computing, to use separately or with the book Visual Statistics. Use R!: Shipunov (2019) <a href="http://ashipunov.info/shipunov/software/r/r-en.htm">http://ashipunov.info/shipunov/software/r/r-en.htm</a> . Most useful functions are probably Bclust(), Jclust() and BootA() which bootstrap hierarchical clustering; Recode...() which multiple recode in a fast, flexible and simple way; Misclass() which outputs confusion matrix even if classes are not concerted; Overlap() which calculates overlaps of convex hulls from any projection; and Pleiad() which is fast and flexible correlogram. In fact, there are much more useful functions, please see documentation. / GPL-2	noarch
r-shopifyr	1.0.0	An interface to the Admin API of the E-commerce service Shopify, ( <a href="https://help.shopify.com/en/api/reference">https://help.shopify.com/en/api/reference</a> ). / GPL-3	noarch
r-shotgroups	0.7.5	Analyzes shooting data with respect to group shape, precision, and accuracy. This includes graphical methods, descriptive statistics, and inference tests using standard, but also non-parametric and robust statistical methods. Implements distributions for radial error in bivariate normal variables. Works with files exported by 'OnTarget PC/TDS', 'Silver Mountain' e-target, 'Shot-Marker' e-target, or 'Taran', as well as with custom data files in text format. Supports inference from range statistics like extreme spread. Includes a set of web-based graphical user interfaces. / GPL-2	noarch
r-showimage	1.0.0	Sometimes it is handy to be able to view an image file on an 'R' graphics device. This package just does that. Currently it supports 'PNG' files. / GPL-2   GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-shp2graph</a>	0.5	Functions for converting network data from a <code>SpatialLinesDataFrame</code> object to an 'igraph'-Class object. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-shrinkcovmat</a>	1.4.0	Provides nonparametric Steinian shrinkage estimators of the covariance matrix that are suitable in high dimensional settings, that is when the number of variables is larger than the sample size. / GPL-2   GPL-3	linux-64, osx-64, win-64
<a href="#">r-shuffle</a>	1.0.1	Implementation of the shuffle estimator, a non-parametric estimator for signal and noise variance under mild noise correlations. / GPL (>= 2.0)	noarch
<a href="#">r-shutterstock</a>	0.1.0	Access 'Shutterstock' API from R. The 'Shutterstock' API presents access to search, view, license and download the media and information from the 'Shutterstock's library < <a href="https://api-reference.shutterstock.com/">https://api-reference.shutterstock.com/</a> >. / MIT	noarch
<a href="#">r-si</a>	0.2.0	An implementation of four stochastic methods of integrating in R, including: 1. Stochastic Point Method (or Monte Carlo Method); 2. Mean Value Method; 3. Important Sampling Method; 4. Stratified Sampling Method. It can be used to estimate one-dimension or multi-dimension integration by Monte Carlo methods. And the estimated variance (precision) is given. Reference: Caflisch, R. E. (1998) <doi:10.1017/S0962492900002804>. / GPL-3	noarch
<a href="#">r-siebanxicor</a>	1.0.0	Allows to retrieve time series of all indicators available in the Bank of Mexico's Economic Information System (< <a href="http://www.banxico.org.mx/SieInternet/">http://www.banxico.org.mx/SieInternet/</a> >). / MIT	noarch
<a href="#">r-sier</a>	0.1.0	Methods for regression with high-dimensional predictors and univariate or multivariate response variables. It considers the decomposition of the coefficient matrix that leads to the best approximation to the signal part in the response given any rank, and estimates the decomposition by solving a penalized generalized eigenvalue problem followed by a least squares procedure. Ruiyan Luo and Xin Qi (2017) <doi:10.1016/j.jmva.2016.09.005>. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-sieveph</a>	1.0.0	Implements semiparametric estimation and testing procedures for a continuous, possibly multivariate, mark-specific hazard ratio (treatment/placebo) of an event of interest in a randomized treatment efficacy trial with a time-to-event endpoint, as described in Juraska M and Gilbert PB (2013), Mark-specific hazard ratio model with multivariate continuous marks: an application to vaccine efficacy. <i>Biometrics</i> 69(2):328-337, and in Juraska M and Gilbert PB (2015), Mark-specific hazard ratio model with missing multivariate marks. <i>Lifetime Data Analysis</i> 22(4): 606-25. The former considers continuous multivariate marks fully observed in all subjects who experience the event of interest, whereas the latter extends the previous work to allow multivariate marks that are subject to missingness-at-random. For models with missing marks, two estimators are implemented based on (i) inverse probability weighting (IPW) of complete cases, and (ii) augmentation of the IPW estimating functions by leveraging correlations between the mark and auxiliary data to ‘impute’ the expected profile score vectors for subjects with missing marks. The augmented IPW estimator is doubly robust and recommended for use with incomplete mark data. The methods make two key assumptions: (i) the time-to-event is assumed to be conditionally independent of the mark given treatment, and (ii) the weight function in the semiparametric density ratio/biased sampling model is assumed to be exponential. Diagnostic testing procedures for evaluating validity of both assumptions are implemented. Summary and plotting functions are provided for estimation and inferential results. / GPL-2	noarch
<a href="#">r-sievetest</a>	1.2.3	Functions for making particle-size analysis. Sieve tests are widely used to obtain particle-size distribution of powders or granular materials. / GPL-2	noarch
<a href="#">r-sig</a>	0.0_5	Print function signatures and find overly complicated code. / Unlimited	noarch
<a href="#">r-sigclust</a>	1.1.0	SigClust is a statistical method for testing the significance of clustering results. SigClust can be applied to assess the statistical significance of splitting a data set into two clusters. For more than two clusters, SigClust can be used iteratively. / GPL-2	noarch
<a href="#">r-sightabilitymodel</a>	1.3	Uses logistic regression to model the probability of detection as a function of covariates. This model is then used with observational survey data to estimate population size, while accounting for uncertain detection. See Steinhorst and Samuel (1989). / GPL-2	noarch
<a href="#">r-sigmanet</a>	1.1.0	Create interactive graph visualizations using ‘Sigma.js’ < <a href="http://sigmajs.org/">http://sigmajs.org/</a> >. This package is meant to be used in conjunction with ‘igraph’, replacing the (somewhat underwhelming) plotting features of the package. The idea is to quickly render graphs, regardless of their size, in a way that allows for easy, iterative modification of aesthetics. Because ‘Sigma.js’ is a ‘javascript’ library, the visualizations are inherently interactive and are well suited for integration with ‘Shiny’ apps. While there are several ‘htmlwidgets’ focused on network visualization, they tend to underperform on medium to large sized graphs. ‘Sigma.js’ was designed for larger network visualizations and this package aims to make those strengths available to ‘R’ users. / MIT	noarch
<a href="#">r-sigmoid</a>	0.3.0	Several different sigmoid functions are implemented, including a wrapper function, SoftMax preprocessing and inverse functions. / GPL-3	noarch
<a href="#">r-signal</a>	0.7_6	A set of signal processing functions originally written for ‘Matlab’ and ‘Octave’. Includes filter generation utilities, filtering functions, resampling routines, and visualization of filter models. It also includes interpolation functions. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-signifreg	2.1	Provide consistent significance controlled variable selection procedure with different directions (forward, backward, stepwise) based on diverse criteria (AIC, BIC, adjusted r-square, and p-value). The algorithm selects a final model with only significant variables based on a correction choice of False Discovery Rate, Bonferroni, or no correction. / GPL-2	noarch
r-signmedian.test	1.5.1	Perform sign test on one-sample data, which is one of the oldest non-parametric statistical methods. Assume that X comes from a continuous distribution with median = $v$ ( unknown ). Test the null hypothesis $H_0$ : median of X $v = \mu$ ( $\mu$ is the location parameter and is given in the test ) v.s. the alternative hypothesis $H_1$ : $v > \mu$ ( or $v < \mu$ or $v \neq \mu$ ) and calculate the p-value. When the sample size is large, perform the asymptotic sign test. In both ways, calculate the R-estimate of location of X and the distribution free confidence interval for $\mu$ . / GPL-2	noarch
r-sigopt	0.0.1	Interfaces with the ‘SigOpt’ API. More info at < <a href="https://sigopt.com">https://sigopt.com</a> >. / MIT	noarch
r-sigora	3.0.5	Pathway Analysis is the process of statistically linking observations on the molecular level to biological processes or pathways on the systems(i.e. organism, organ, tissue, cell) level. Traditionally, pathway analysis methods regard pathways as collections of single genes and treat all genes in a pathway as equally informative. This can lead to identification of spurious pathways as statistically significant, since components are often shared amongst pathways. SIGORA seeks to avoid this pitfall by focusing on genes or gene-pairs that are (as a combination) specific to a single pathway. In relying on such pathway gene-pair signatures (Pathway-GPS), SIGORA inherently uses the status of other genes in the experimental context to identify the most relevant pathways. The current version allows for pathway analysis of human and mouse datasets and contains pre-computed Pathway-GPS data for pathways in the KEGG and Reactome pathway repositories as well as mechanisms for extracting GPS for user supplied repositories. / GPL-2	noarch
r-sii	1.0.3	This package calculates ANSI S3.5-1997 Speech Intelligibility Index (SII), a standard method for computing the intelligibility of speech from acoustical measurements of speech, noise, and hearing thresholds. This package includes data frames corresponding to Tables 1 - 4 in the ANSI standard as well as a function utilizing these tables and user-provided hearing threshold and noise level measurements to compute the SII score. The methods implemented here extend the standard computations to allow calculation of SII when the measured frequencies do not match those required by the standard by applying interpolation to obtain values for the required frequencies – Development of this package was funded by the Center for Bioscience Education and Technology (CBET) of the Rochester Institute of Technology (RIT). / GPL-2	noarch
r-sim.diffproc	4.4	It provides users with a wide range of tools to simulate, estimate, analyze, and visualize the dynamics of stochastic differential systems in both forms Ito and Stratonovich. Statistical analysis with parallel Monte Carlo and moment equations methods of SDE’s. Enabled many searchers in different domains to use these equations to modeling practical problems in financial and actuarial modeling and other areas of application, e.g., modeling and simulate of first passage time problem in shallow water using the attractive center (Boukhetala K, 1996) ISBN:1-56252-342-2. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-simboot</a>	0.2.6	Provides estimation of simultaneous bootstrap and asymptotic confidence intervals for diversity indices, namely the Shannon and the Simpson index. Several pre-specified multiple comparison types are available to choose. Further user-defined contrast matrices are applicable. In addition, simboot estimates adjusted as well as unadjusted p-values for two of the three proposed bootstrap methods. Further simboot allows for comparing biological diversities of two or more groups while simultaneously testing a user-defined selection of Hill numbers of orders q, which are considered as appropriate and useful indices for measuring diversity. / GPL-2	noarch
<a href="#">r-simcausal</a>	0.5.5	A flexible tool for simulating complex longitudinal data using structural equations, with emphasis on problems in causal inference. Specify interventions and simulate from intervened data generating distributions. Define and evaluate treatment-specific means, the average treatment effects and coefficients from working marginal structural models. User interface designed to facilitate the conduct of transparent and reproducible simulation studies, and allows concise expression of complex functional dependencies for a large number of time-varying nodes. See the package vignette for more information, documentation and examples. / GPL-2	noarch
<a href="#">r-simcdm</a>	0.1.1	Provides efficient R and 'C' routines to simulate cognitive diagnostic model data for Deterministic Input, Noisy And Gate ('DINA') and reduced Reparameterized Unified Model ('rRUM') from Culpepper and Hudson (2017) <doi: 10.1177/0146621617707511>, Culpepper (2015) <doi:10.3102/1076998615595403>, and de la Torre (2009) <doi:10.3102/1076998607309474>. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-simcop</a>	0.7.0	Provides a framework to generating random variates from arbitrary multivariate copulae, while concentrating on (bivariate) extreme value copulae. Particularly useful if the multivariate copulae are not available in closed form. / GPL-2	noarch
<a href="#">r-simctest</a>	2.5	Algorithms for the implementation and evaluation of Monte Carlo tests, as well as for their use in multiple testing procedures. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-simdistr</a>	1.0.1	Assessment of the distributions of baseline continuous and categorical variables in randomised trials. This method is based on the Carlisle-Stouffer method with Monte Carlo simulations. It calculates p-values for each trial baseline variable, as well as combined p-values for each trial - these p-values measure how compatible are distributions of trials baseline variables with random sampling. This package also allows for graphically plotting the cumulative frequencies of computed p-values. Please note that code was partly adapted from Carlisle JB, Loadman JA. (2017) <doi:10.1111/anae.13650>. / GPL-2	noarch
<a href="#">r-simecol</a>	0.8.1	An object oriented framework to simulate ecological (and other) dynamic systems. It can be used for differential equations, individual-based (or agent-based) and other models as well. It supports structuring of simulation scenarios (to avoid copy and paste) and aims to improve readability and re-usability of code. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-simex</a>	1.8	Implementation of the SIMEX-Algorithm by Cook & Stefanski (1994) <doi:10.1080/01621459.1994.10476871> and MCSIMEX by Küchenhoff, Mwalili & Lesaffre (2006) <doi:10.1111/j.1541-0420.2005.00396.x>. / GPL-3	noarch
<a href="#">r-simexaft</a>	1.0.7	Implement of the Simulation-Extrapolation (SIMEX) algorithm for the accelerated failure time (AFT) with covariates subject to measurement error. / GPL-3	noarch
<a href="#">r-simframe</a>	0.5.3	A general framework for statistical simulation. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-simhaz</a>	0.1	Generate power for the Cox proportional hazards model by simulating survival events data with time dependent exposure status for subjects. A dichotomous exposure variable is considered with a single transition from unexposed to exposed status during the subject's time on study. / GPL-2	noarch
<a href="#">r-similar</a>	1.0.6	An implementation of a novel method to quantify the similarity the code-base of R functions by means of program dependence graphs. Possible use cases include detection of code clones for improving software quality and of plagiarism among students' homework assignments. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-similaritymeasures</a>	1.4	Functions to run and assist four different similarity measures. The similarity measures included are: longest common subsequence (LCSS), Frechet distance, edit distance and dynamic time warping (DTW). Each of these similarity measures can be calculated from two n-dimensional trajectories, both in matrix form. / GPL-3	noarch
<a href="#">r-simile</a>	1.3.3	Allows a Simile model saved as a compiled binary to be loaded, parameterized, executed and interrogated. This version works with Simile v5.97 on. / Unlimited	noarch
<a href="#">r-siminf</a>	6.3.0	Provides an efficient and very flexible framework to conduct data-driven epidemiological modeling in realistic large scale disease spread simulations. The framework integrates infection dynamics in subpopulations as continuous-time Markov chains using the Gillespie stochastic simulation algorithm and incorporates available data such as births, deaths and movements as scheduled events at predefined time-points. Using C code for the numerical solvers and 'OpenMP' (if available) to divide work over multiple processors ensures high performance when simulating a sample outcome. One of our design goals was to make the package extendable and enable usage of the numerical solvers from other R extension packages in order to facilitate complex epidemiological research. The package contains template models and can be extended with user-defined models. / GPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-simmer</a>	4.3.0	A process-oriented and trajectory-based Discrete-Event Simulation (DES) package for R. It is designed as a generic yet powerful framework. The architecture encloses a robust and fast simulation core written in ‘C’ with automatic monitoring capabilities. It provides a rich and flexible R API that revolves around the concept of trajectory, a common path in the simulation model for entities of the same type. Documentation about ‘simmer’ is provided by several vignettes included in this package, via the paper by Ucar, Smeets & Azcorra (2019, <doi:10.18637/jss.v090.i02>), and the paper by Ucar, Hernández, Serrano & Azcorra (2018, <doi:10.1109/MCOM.2018.1700960>); see ‘citation(simmer)’ for details. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-simml</a>	0.1.0	A major challenge in estimating treatment decision rules from a randomized clinical trial dataset with covariates measured at baseline lies in detecting relatively small treatment effect modification-related variability (i.e., the treatment-by-covariates interaction effects on treatment outcomes) against a relatively large non-treatment-related variability (i.e., the main effects of covariates on treatment outcomes). The class of Single-Index Models with Multiple-Links is a novel single-index model specifically designed to estimate a single-index (a linear combination) of the covariates associated with the treatment effect modification-related variability, while allowing a nonlinear association with the treatment outcomes via flexible link functions. The models provide a flexible regression approach to developing treatment decision rules based on patients’ data measured at baseline. We refer to Petkova, Tarpey, Su, and Ogden (2017) <doi: 10.1093/biostatistics/kxw035> and A constrained single-index model for estimating interactions between a treatment and covariates (under review, 2019) for detail. The main function of this package is <code>simml()</code> . / GPL-3	noarch
<a href="#">r-simms</a>	1.2.0	Algorithms to create prognostic biomarkers using biological genesets or networks. / GPL-2	noarch
<a href="#">r-simone</a>	1.0.4	Implements the inference of co-expression networks based on partial correlation coefficients from either steady-state or time-course transcriptomic data. Note that with both type of data this package can deal with samples collected in different experimental conditions and therefore not identically distributed. In this particular case, multiple but related networks are inferred on one <code>simone</code> run. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-simphe</a>	0.2.0	Provides functions to simulate single or multiple, independent or correlated phenotype(s) with additive, dominance effects and their interactions. Also includes functions to generate phenotype(s) with specific heritability. Flexible and user-friendly options for simulation. / GPL-2	noarch
<a href="#">r-simpleboot</a>	1.1.7	Simple bootstrap routines. / GPL-2	noarch
<a href="#">r-simplecache</a>	0.4.1	Provides intuitive functions for caching R objects, encouraging reproducible, restartable, and distributed R analysis. The user selects a location to store caches, and then provides nothing more than a cache name and instructions (R code) for how to produce the R object. Also provides some advanced options like environment assignments, recreating or reloading caches, and cluster compute bindings (using the ‘batchtools’ package) making it flexible enough for use in large-scale data analysis projects. / BSD_2_clause	noarch
<a href="#">r-simplegraph</a>	1.0.0	Simple classic graph algorithms for simple graph classes. Graphs may possess vertex and edge attributes. ‘simplegraph’ has no dependencies and it is written entirely in R, so it is easy to install. / MIT	noarch
<a href="#">r-simpleneural</a>	0.1.1	Trains neural networks (multilayer perceptrons with one hidden layer) for bi- or multi-class classification. / MIT	noarch

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Name	Version	Summary/License	Platforms
r-simplercache	0.3.2	Simple result caching in R based on R.cache. The global environment is not considered when caching results simplifying moving files between multiple instances of R. Relies on more base functions than R.cache (e.g. cached results are saved using saveRDS() and readRDS()). / LGPL-3	noarch
r-simplesetup	0.1.0	When working across multiple machines and, similarly for reproducible research, it can be time consuming to ensure that you have all of the needed packages installed and loaded and that the correct working directory is set. 'simpleSetup' provides simple functions for making these tasks more straightforward. / GPL-3	noarch
r-simplicialcubature	1.2	Provides methods to integrate functions over m-dimensional simplices in n-dimensional Euclidean space. There are exact methods for polynomials and adaptive methods for integrating an arbitrary function. Dirichlet probabilities are calculated in certain cases. / GPL-2	noarch
r-simputation	0.2.3	Easy to use interfaces to a number of imputation methods that fit in the not-a-pipe operator of the 'magrittr' package. / GPL-3	linux-64, osx-64, win-64
r-simsalapar	1.0_1	Tools for setting up (design), conducting, and evaluating large-scale simulation studies with graphics and tables, including parallel computations. / GPL-2   GPL-3	noarch
r-simscrpiecwise	0.1.1	Contains two functions for simulating survival data from piecewise exponential hazards with a proportional hazards adjustment for covariates. The first function SimUNIVPiecwise simulates univariate survival data based on a piecewise exponential hazard, covariate matrix and true regression vector. The second function SimSCRPiecwise semi-competing risks data based on three piecewise exponential hazards, three true regression vectors and three matrices of patient covariates (which can be different or the same). This simulates from the Semi-Markov model of Lee et al (2015) given patient covariates, regression parameters, patient frailties and baseline hazard functions. / GPL-2	noarch
r-simsem	0.5_1	Provides an easy framework for Monte Carlo simulation in structural equation modeling, which can be used for various purposes, such as such as model fit evaluation, power analysis, or missing data handling and planning. / GPL-2	noarch
r-simsv	0.2.3	Simulate survival times from standard parametric survival distributions (exponential, Weibull, Gompertz), 2-component mixture distributions, or a user-defined hazard, log hazard, cumulative hazard, or log cumulative hazard function. Baseline covariates can be included under a proportional hazards assumption. Time dependent effects (i.e. non-proportional hazards) can be included by interacting covariates with linear time or a user-defined function of time. Clustered event times are also accommodated. The 2-component mixture distributions can allow for a variety of flexible baseline hazard functions reflecting those seen in practice. If the user wishes to provide a user-defined hazard or log hazard function then this is possible, and the resulting cumulative hazard function does not need to have a closed-form solution. Note that this package is modelled on the 'survsim' package available in the 'Stata' software (see Crowther and Lambert (2012) < <a href="http://www.stata-journal.com/sjpdf.html?articlenum=st0275">http://www.stata-journal.com/sjpdf.html?articlenum=st0275</a> > or Crowther and Lambert (2013) <doi:10.1002/sim.5823>). / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-simtimer</a>	4.0.0	Handles datetimes as integers for the usage inside Discrete-Event Simulations (DES). The conversion is made using the internally generic function <code>as.numeric()</code> of the base package. DES is described in Simulation Modeling and Analysis by Averill Law and David Kelton (1999) <doi:10.2307/2288169>. / GPL-3	noarch
<a href="#">r-simulator</a>	0.2.0	A framework for performing simulations such as those common in methodological statistics papers. The design principles of this package are described in greater depth in Bien, J. (2016) The simulator: An Engine to Streamline Simulations, which is available at < <a href="http://faculty.bscb.cornell.edu/~bien/simulator.pdf">http://faculty.bscb.cornell.edu/~bien/simulator.pdf</a> >. / GPL-3	noarch
<a href="#">r-simule</a>	1.3.0	This is an R implementation of a constrained l1 minimization approach for estimating multiple Sparse Gaussian or Nonparanormal Graphical Models (SIMULE). The SIMULE algorithm can be used to estimate multiple related precision matrices. For instance, it can identify context-specific gene networks from multi-context gene expression datasets. By performing data-driven network inference from high-dimensional and heterogenous data sets, this tool can help users effectively translate aggregated data into knowledge that take the form of graphs among entities. Please run <code>demo(simuleDemo)</code> to learn the basic functions provided by this package. For further details, please read the original paper: Beilun Wang, Ritambhara Singh, Yanjun Qi (2017) <DOI:10.1007/s10994-017-5635-7>. / GPL-2	noarch
<a href="#">r-sin</a>	0.6	This package provides routines to perform SIN model selection as described in Drton & Perlman (2004, 2008). The selected models are represented in the format of the ‘ggm’ package, which allows in particular parameter estimation in the selected model. / GPL-2	noarch
<a href="#">r-sinaplot</a>	1.1.0	The sinaplot is a data visualization chart suitable for plotting any single variable in a multiclass data set. It is an enhanced jitter strip chart, where the width of the jitter is controlled by the density distribution of the data within each class. / GPL-2	noarch
<a href="#">r-sinib</a>	1.0.0	Density, distribution function, quantile function and random generation for the sum of independent non-identical binomial distribution with parameters <code>code{size}</code> and <code>code{prob}</code> . / GPL-3	noarch
<a href="#">r-sirad</a>	2.3_3	Calculating daily global solar radiation at horizontal surface using several well-known models (i.e. Angstrom-Prescott, Supit-Van Kappel, Hargreaves, Bristow and Campbell, and Mahmood-Hubbard), and model calibration based on ground-truth data, and (3) model auto-calibration. The FAO Penmann-Monteith equation to calculate evapotranspiration is also included. / GPL-2	noarch
<a href="#">r-sisvive</a>	1.4	Selects invalid instruments amongst a candidate of potentially bad instruments. The algorithm selects potentially invalid instruments and provides an estimate of the causal effect between exposure and outcome. / GPL-2	noarch
<a href="#">r-sitmo</a>	2.0.1	Provided within are two high quality and fast PPRNGs that may be used in an ‘OpenMP’ parallel environment. In addition, there is a generator for one dimensional low-discrepancy sequence. The objective of this library to consolidate the distribution of the ‘sitmo’ (C98 & C11), ‘threefry’ and ‘vandercomput’ (C11-only) engines on CRAN by enabling others to link to the header files inside of ‘sitmo’ instead of including a copy of each engine within their individual package. Lastly, the package contains example implementations using the ‘sitmo’ package and three accompanying vignette that provide additional information. / MIT	linux-64, osx-64, win-64
<a href="#">r-sitools</a>	1.4	Format a number (or a list of numbers) to a string (or a list of strings) with SI prefix. Use SI prefixes as constants like $(4 * \text{milli})^2$ / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-sitree	0.1_7	Forecasts plots at tree level. / GPL-2	noarch
r-sizer	0.1_5	Calculates and plots the SiZer map for scatterplot data. A SiZer map is a way of examining when the p-th derivative of a scatterplot-smoother is significantly negative, possibly zero or significantly positive across a range of smoothing bandwidths. / GPL-2	noarch
r-sjdbc	1.6.0	Provides a database-independent JDBC interface. / BSD_3_clause	noarch
r-skat	1.3.2	Functions for kernel-regression-based association tests including Burden test, SKAT and SKAT-O. These methods aggregate individual SNP score statistics in a SNP set and efficiently compute SNP-set level p-values. / GPL-2	linux-64, osx-64, win-64
r-skda	0.1	Sparse (Multicategory) Kernel Discriminant Analysis does variable selection for nonparametric classification / GPL-2	linux-64, osx-64, win-64
r-skeletor	1.0.4	A tool for bootstrapping new packages with useful defaults, including a test suite outline that passes checks and helpers for running tests, checking test coverage, building vignettes, and more. Package skeletons it creates are set up for pushing your package to 'GitHub' and using other hosted services for building and test automation. / MIT	noarch
r-skellam	0.2.0	Functions for the Skellam distribution, including: density (pmf), cdf, quantiles and regression. / GPL-2	noarch
r-skewt	0.1	Density, distribution function, quantile function and random generation for the skewed t distribution of Fernandez and Steel. / GPL-3	noarch
r-skmeans	0.2_1	Algorithms to compute spherical k-means partitions. Features several methods, including a genetic and a fixed-point algorithm and an interface to the CLUTO vcluster program. / GPL-2	noarch
r-skywatchr	0.8_2	Query and download satellite imagery and climate/atmospheric datasets using the SkyWatch API. Search datasets by wavelength (band), cloud cover, resolution, location, date, etc. Get the query results as data frame and as HTML. To learn more about the SkyWatch API, see < <a href="https://github.com/skywatchspaceapps/api">https://github.com/skywatchspaceapps/api</a> >. / GPL-2	noarch
r-slam	0.1_4	Data structures and algorithms for sparse arrays and matrices, based on index arrays and simple triplet representations, respectively. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
r-slc	0.3	Estimates the slope and level change present in data after removing phase A trend. Represents graphically the original and the detrended data. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-sldassay</a>	1.8	Calculates maximum likelihood estimate, exact and asymptotic confidence intervals, and exact and asymptotic goodness of fit p-values for concentration of infectious units from serial limiting dilution assays. This package uses the likelihood equation, exact goodness of fit p-values, and exact confidence intervals described in Meyers et al. (1994) < <a href="http://jcm.asm.org/content/32/3/732.full.pdf">http://jcm.asm.org/content/32/3/732.full.pdf</a> >. This software is also implemented as a web application through the Shiny R package < <a href="https://iupm.shinyapps.io/sldassay/">https://iupm.shinyapps.io/sldassay/</a> >. / GPL-3	noarch
<a href="#">r-sleekts</a>	1.0.2	Compute Time series Resistant Smooth 4253H, twice smoothing method. / GPL-3	noarch
<a href="#">r-sleepr</a>	0.3.0	Use behavioural variables to score activity and infer sleep from bouts of immobility. It is primarily designed to score sleep in fruit flies from Drosophila Activity Monitor (TriKinetics) and Ethoscope data. It implements sleep scoring using the five-minute rule (Hendricks et al. (2000) <DOI:10.1016/S0896-6273(00)80877-6>), activity classification for Ethoscopes (Geissmann et al. (2017) <DOI:10.1371/journal.pbio.2003026>) and a new algorithm to detect when animals are dead. / GPL-3	noarch
<a href="#">r-sleuth2</a>	2.0_5	Data sets from Ramsey, F.L. and Schafer, D.W. (2002), The Statistical Sleuth: A Course in Methods of Data Analysis (2nd ed), Duxbury. / GPL-2	noarch
<a href="#">r-sleuth3</a>	1.0_3	Data sets from Ramsey, F.L. and Schafer, D.W. (2013), The Statistical Sleuth: A Course in Methods of Data Analysis (3rd ed), Cengage Learning. / GPL-2	noarch
<a href="#">r-slfm</a>	1.0.0	Set of tools to find coherent patterns in microarray data using a Bayesian Sparse Latent Factor Model - SLFM; see Duarte and Mayrink (2015) <DOI:10.1007/978-3-319-12454-4_15>. Considerable effort has been put into making slfm fast and memory efficient, turning it an interesting alternative to simpler methods in terms of execution time. It implements versions of the SLFM based on two type of mixtures priors for the loadings: one relying on a degenerate component at zero and the other using a small variance normal distribution for the spike part of the mixture. It also implements additional functions to allow pre-processing procedures for the data and to fit the model for a large number of probesets or genes. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-slhd</a>	2.1_1	Generate the optimal Latin Hypercube Designs (LHDs) for computer experiments with quantitative factors and the optimal Sliced Latin Hypercube Designs (SLHDs) for computer experiments with both quantitative and qualitative factors. Details of the algorithm can be found in Ba, S., Brennenman, W. A. and Myers, W. R. (2015), Optimal Sliced Latin Hypercube Designs, Technometrics. Important function in this package is maximinSLHD. / LGPL-2.1	linux-64, osx-64, win-64
<a href="#">r-slickr</a>	0.2.4	Create and customize interactive carousels using the ‘Slick’ JavaScript library and the ‘htmlwidgets’ package. The carousels can contain plots produced in R, images, ‘iframes’, videos and other ‘htmlwidgets’. These carousels can be used directly from the R console, from ‘RStudio’, in Shiny apps and R Markdown documents. / MIT	noarch
<a href="#">r-slide</a>	1.0.0	This statistical method uses the nearest neighbor algorithm to estimate absolute distances between single cells based on a chosen constellation of surface proteins, with these distances being a measure of the similarity between the two cells being compared. Based on Sen, N., Mukherjee, G., and Arvin, A.M. (2015) <DOI:10.1016/j.ymeth.2015.07.008>. / GPL-3	noarch
<a href="#">r-slideview</a>	0.1.0	Create a side-by-side view of raster(image)s with an interactive slider to switch between regions of the images. This can be especially useful for image comparison of the same region at different time stamps. / MIT	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-slim</a>	0.1.1	Fits singular linear models to longitudinal data. Singular linear models are useful when the number, or timing, of longitudinal observations may be informative about the observations themselves. They are described in Farewell (2010) <doi:10.1093/biomet/asp068>, and are extensions of the linear increments model <doi:10.1111/j.1467-9876.2007.00590.x> to general longitudinal data. / GPL-3	noarch
<a href="#">r-slippymath</a>	0.3.1	Provides functions for performing common tasks when working with slippy map tile service APIs e.g. Google maps, Open Street Map, Mapbox, Stamen, among others. Functionality includes converting from latitude and longitude to tile numbers, determining tile bounding boxes, and compositing tiles to a georeferenced raster image. / MIT	noarch
<a href="#">r-slope</a>	0.1.3	Efficient procedures for Sorted L1 Penalized Estimation (SLOPE). The sorted L1 norm is useful for statistical estimation and testing, particularly for variable selection in the linear model. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-slouch</a>	2.1.2	An implementation of a phylogenetic comparative method. It can fit univariate among-species Ornstein-Uhlenbeck models of phenotypic trait evolution, where the trait evolves towards a primary optimum. The optimum can be modelled as a single parameter, as multiple discrete regimes on the phylogenetic tree, and/or with continuous covariates. See also Hansen (1997) doi:10.2307/2411186, Butler & King (2004) doi:10.1086/426002, Hansen et al. (2008) doi:10.1111/j.1558-5646.2008.00412.x. / GPL-2	noarch
<a href="#">r-slp</a>	1.0_5	Interface for creation of ‘slp’ class smoother objects for use in Generalized Additive Models (as implemented by packages ‘gam’ and ‘mgcv’). / GPL-2	linux-64, osx-64, win-64
<a href="#">r-sm</a>	2.2_5	This is software linked to the book ‘Applied Smoothing Techniques for Data Analysis - The Kernel Approach with S-Plus Illustrations’ Oxford University Press. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-smaa</a>	0.3_0	Implementation of the Stochastic Multi-Criteria Acceptability Analysis (SMAA) family of Multiple Criteria Decision Analysis (MCDA) methods. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-smac</a>	1.0	This package provides a solution path for L1-penalized angle-based classification. Three loss functions are implemented in smac, including the deviance loss in logistic regression, the exponential loss in boosting, and the proximal support vector machine loss. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-smallarea</a>	0.1	Inference techniques for Fay Herriot Model. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-smartsizer	1.0.1	A set of tools for determining the necessary sample size in order to identify the optimal dynamic treatment regime in a sequential, multiple assignment, randomized trial (SMART). Utilizes multiple comparisons with the best methodology to adjust for multiple comparisons. Designed for an arbitrary SMART design. Please see Artman (2018) <arXiv:1804.04587> for more details. / GPL-3	noarch
r-smatr	3.4_8	Methods for fitting bivariate lines in allometry using the major axis (MA) or standardised major axis (SMA), and for making inferences about such lines. The available methods of inference include confidence intervals and one-sample tests for slope and elevation, testing for a common slope or elevation amongst several allometric lines, constructing a confidence interval for a common slope or elevation, and testing for no shift along a common axis, amongst several samples. See Warton et al. 2012 <doi:10.1111/j.2041-210X.2011.00153.x> for methods description. / GPL-2	noarch
r-smc	1.1	particle filtering, auxiliary particle filtering and sequential Monte Carlo algorithms / GPL-2	linux-64, osx-64, win-64
r-smcfcs	1.4.0	Implements multiple imputation of missing covariates by Substantive Model Compatible Fully Conditional Specification. This is a modification of the popular FCS/chained equations multiple imputation approach, and allows imputation of missing covariate values from models which are compatible with the user specified substantive model. / GPL-3	noarch
r-smco	0.1	This package is for optimizing non-linear complex functions based on Monte Carlo random sampling. / GPL-2	noarch
r-smcrm	0.0_3	Data Sets for Kumar and Petersen (2012). Statistical Methods in Customer Relationship Management, Wiley: New York. / GPL-3	noarch
r-smcure	2.0	An R-package for Estimating Semiparametric PH and AFT Mixture Cure Models / GPL-2	noarch
r-smdata	1.2	Contains data files to accompany Smithson & Merkle (2013), Generalized Linear Models for Categorical and Continuous Limited Dependent Variables. / GPL-2	noarch
r-smds	1.0	Symbolic multidimensional scaling for interval-valued dissimilarities. The hypersphere model and the hyperbox model are available. / GPL-2	linux-64, osx-64, win-64
r-sme	1.0.2	Fit smoothing-splines mixed-effects models to replicated functional data sets and visualise the results. / GPL-3	linux-64, osx-64, win-64
r-smfilter	1.0.3	Provides the filtering algorithms for the state space models on the Stiefel manifold as well as the corresponding sampling algorithms for uniform, vector Langevin-Bingham and matrix Langevin-Bingham distributions on the Stiefel manifold. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-smfsb</a>	1.3	Code and data for modelling and simulation of stochastic kinetic biochemical network models. It contains the code and data associated with the second and third editions of the book Stochastic Modelling for Systems Biology, published by Chapman & Hall/CRC Press. / LGPL-3	linux-64, osx-64, win-64
<a href="#">r-smirnov</a>	1.0.1	This tiny package contains one function <code>smirnov()</code> which calculates two scaled taxonomic coefficients, <code>Txy</code> (coefficient of similarity) and <code>Txx</code> (coefficient of originality). These two characteristics may be used for the analysis of similarities between any number of taxonomic groups, and also for assessing uniqueness of giving taxon. It is possible to use <code>smirnov()</code> output as a distance measure: convert it to distance by <code>as.dist(1 - smirnov(x))</code> . / GPL-2	noarch
<a href="#">r-smisc</a>	0.3.9	A collection of functions for statistical computing and data manipulation in R. Includes routines for data ingestion, operating on dataframes and matrices, conversion to and from lists, converting factors, filename manipulation, programming utilities, parallelization, plotting, statistical and mathematical operations, and time series. / BSD_3_clause	linux-64, osx-64, win-64
<a href="#">r-smithwilsonyieldcurve</a>	1.0.1	Constructs a yield curve by the Smith-Wilson method from a table of LIBOR and SWAP rates / GPL-3	noarch
<a href="#">r-smitidvisu</a>	0.0.6	Visualisation tools for 'SMITIDstruct' package. Allow to visualize host timeline, transmission tree, index diversities and variant graph using HTMLwidgets. It mainly using D3JS javascript framework. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-smloutliers</a>	0.1	Local Correlation Integral (LOCI) method for outlier identification is implemented here. The LOCI method developed here is invented in Breunig, et al. (2000), see <doi:10.1145/342009.335388>. / GPL-2	noarch
<a href="#">r-smma</a>	1.0.2	Efficient design matrix free procedure for solving a soft maximin problem for large scale array-tensor structured models. Currently Lasso and SCAD penalized estimation is implemented. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-smoother</a>	1.1	A collection of methods for smoothing numerical data, commencing with a port of the Matlab gaussian window smoothing function. In addition, several functions typically used in smoothing of financial data are included. / GPL-2	noarch
<a href="#">r-smoothhazard</a>	1.4.1	Estimation of two-state (survival) models and irreversible illness-death models with possibly interval-censored, left-truncated and right-censored data. Proportional intensities regression models can be specified to allow for covariates effects separately for each transition. We use either a parametric approach with Weibull baseline intensities or a semi-parametric approach with M-splines approximation of baseline intensities in order to obtain smooth estimates of the hazard functions. Parameter estimates are obtained by maximum likelihood in the parametric approach and by penalized maximum likelihood in the semi-parametric approach. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-smoothhr</a>	1.0.2	Provides flexible hazard ratio curves allowing non-linear relationships between continuous predictors and survival. To better understand the effects that each continuous covariate has on the outcome, results are expressed in terms of hazard ratio curves, taking a specific covariate value as reference. Confidence bands for these curves are also derived. / GPL-2	noarch
<a href="#">r-smoothie</a>	1.0.1	Functions to smooth two-dimensional fields using FFT and the convolution theorem / GPL-2	noarch
<a href="#">r-smoothmest</a>	0.1.2	Some M-estimators for 1-dimensional location (Bisquare, ML for the Cauchy distribution, and the estimators from application of the smoothing principle introduced in Hampel, Hennig and Ronchetti (2011) to the above, the Huber M-estimator, and the median, main function is smoothm), and Pitman estimator. / GPL-3	noarch
<a href="#">r-smoothsurv</a>	2.0.1	Contains, as a main contribution, a function to fit a regression model with possibly right, left or interval censored observations and with the error distribution expressed as a mixture of G-splines. Core part of the computation is done in compiled C written using the Scythe Statistical Library Version 0.3. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-smpracticals</a>	1.4.3	Contains the datasets and a few functions for use with the practicals outlined in Appendix A of the book Statistical Models (Davison, 2003, Cambridge University Press). The practicals themselves can be found at <a href="http://statwww.epfl.ch/davison/SM/">http://statwww.epfl.ch/davison/SM/</a> . / GPL-2	noarch
<a href="#">r-smr</a>	2.0.1	Computes the studentized midrange distribution (pdf, cdf and quantile) and generates random numbers / GPL-2	noarch
<a href="#">r-sms</a>	2.3.1	Produce small area population estimates by fitting census data to survey data. / GPL-3	noarch
<a href="#">r-smss</a>	1.0.2	Datasets used in Statistical Methods for the Social Sciences (SMSS) by Alan Agresti and Barbara Finlay. / GPL-3	noarch
<a href="#">r-smvar</a>	1.3.3	Implements the structural model for variances in order to detect differentially expressed genes from gene expression data / GPL-3	noarch
<a href="#">r-sn</a>	1.5.4	Build and manipulate probability distributions of the skew-normal family and some related ones, notably the skew-t family, and provide related statistical methods for data fitting and model diagnostics, in the univariate and the multivariate case. / GPL-2   GPL-3	noarch
<a href="#">r-snakecase</a>	0.11.0	A consistent, flexible and easy to use tool to parse and convert strings into cases like snake or camel among others. / GPL-3	noarch
<a href="#">r-snakecharm</a>	1.0.7	Run 'Python' code, make function calls, assign and retrieve variables, etc. from R. A fork from 'rPython' which uses 'jsonlite', 'Rcpp' and has several fixes and improvements. / GPL-2	linux-64, osx-64
<a href="#">r-snakesandladdersanalysis</a>	2.1.0	Plays the game of Snakes and Ladders and has tools for analyses. The tools included allow you to find the average moves to win, frequency of each square, importance of the snakes and the ladders, the most common square and the plotting of the game played. / GPL-2	noarch
<a href="#">r-snappier</a>	0.1.0	Compression and decompression with 'Snappy'. / BSD_3_clause	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-snapshot</a>	0.1.2	Functions for reading and writing Gadget N-body snapshots. The Gadget code is popular in astronomy for running N-body / hydrodynamical cosmological and merger simulations. To find out more about Gadget see the main distribution page at <a href="http://www.mpa-garching.mpg.de/gadget/">www.mpa-garching.mpg.de/gadget/</a> / GPL-2	noarch
<a href="#">r-snem</a>	0.1.0	Efficient estimation of multivariate skew-normal distribution in closed form. / GPL-2	noarch
<a href="#">r-snipem</a>	1.0.1	Snipping methods optimally removing scattered cells for robust estimation and cluster analysis. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-snn</a>	1.1	Implement K-nearest neighbor classifier, weighted nearest neighbor classifier, bagged nearest neighbor classifier, optimal weighted nearest neighbor classifier and stabilized nearest neighbor classifier, and perform model selection via 5 fold cross-validation for them. This package also provides functions for computing the classification error and classification instability of a classification procedure. / GPL-3	noarch
<a href="#">r-snnr</a>	1.0	Solve the problem of over-parameterization in neural networks for genomic selection. Daniel Gianola, Hayrettin OkutEmail, Kent A Weigel and Guilherme JM Rosa (2011) <doi:10.1186/1471-2156-12-87>. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-snow</a>	0.4.3	Support for simple parallel computing in R. / GPL-3	noarch
<a href="#">r-snowballc</a>	0.6.0	An R interface to the C libstemmer library that implements Porter's word stemming algorithm for collapsing words to a common root to aid comparison of vocabulary. Currently supported languages are Danish, Dutch, English, Finnish, French, German, Hungarian, Italian, Norwegian, Portuguese, Romanian, Russian, Spanish, Swedish and Turkish. / BSD_3_clause file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-snowflakes</a>	1.0.0	The function generates and plots random snowflakes. Each snowflake is defined by a given diameter, width of the crystal, color, and random seed. Snowflakes are plotted in such way that they always remain round, no matter what the aspect ratio of the plot is. Snowflakes can be created using transparent colors, which creates a more interesting, somewhat realistic, image. Images of the snowflakes can be separately saved as svg files and used in websites as static or animated images. / GPL-2	noarch
<a href="#">r-snpar</a>	1.0	contains several supplementary non-parametric statistics methods including quantile test, Cox-Stuart trend test, runs test, normal score test, kernel PDF and CDF estimation, kernel regression estimation and kernel Kolmogorov-Smirnov test. / GPL-2	noarch
<a href="#">r-snpmaxsel</a>	1.0.3	This package implements asymptotic methods related to maximally selected statistics, with applications to SNP data. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-sns</a>	1.1.2	Stochastic Newton Sampler (SNS) is a Metropolis-Hastings-based, Markov Chain Monte Carlo sampler for twice differentiable, log-concave probability density functions (PDFs) where the proposal density function is a multivariate Gaussian resulting from a second-order Taylor-series expansion of log-density around the current point. The mean of the Gaussian proposal is the full Newton-Raphson step from the current point. A Boolean flag allows for switching from SNS to Newton-Raphson optimization (by choosing the mean of proposal function as next point). This can be used during burn-in to get close to the mode of the PDF (which is unique due to concavity). For high-dimensional densities, mixing can be improved via ‘state space partitioning’ strategy, in which SNS is applied to disjoint subsets of state space, wrapped in a Gibbs cycle. Numerical differentiation is available when analytical expressions for gradient and Hessian are not available. Facilities for validation and numerical differentiation of log-density are provided. / GPL-2	noarch
<a href="#">r-soar</a>	0.99	Allows objects to be stored on disc and automatically recalled into memory, as required, by delayed assignment. / GPL-2   GPL-3	noarch
<a href="#">r-sobolsequence</a>	1.0	R implementation of S. Joe and F. Y. Kuo(2008) <DOI:10.1137/070709359>. The implementation is based on the data file new-joe-kuo-6.21201 < <a href="http://web.maths.unsw.edu.au/~fkuo/sobol/">http://web.maths.unsw.edu.au/~fkuo/sobol/</a> >. / BSD_3_clause	linux-64, osx-64, win-64
<a href="#">r-soccer</a>	0.1.1	Functions for evaluating tournament predictions, simulating results from individual soccer matches and tournaments. See < <a href="http://sandsynligvis.dk/2018/08/03/world-cup-prediction-winners/">http://sandsynligvis.dk/2018/08/03/world-cup-prediction-winners/</a> > for more information. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-social</a>	1.0	A set of functions to quantify and visualise social autocorrelation. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-socialnetworks</a>	1.1	Generates social networks using either of two approaches: using either pairwise distances or territorial area intersections. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-socialposition</a>	1.0.1	Provides to sociologists (and related scientists) a toolbox to facilitate the construction of social position indicators from survey data. Social position indicators refer to what is commonly known as social class and social status. There exists in the sociological literature many theoretical conceptualisation and empirical operationalization of social class and social status. This first version of the package offers tools to construct the International Socio-Economic Index of Occupational Status (ISEI) and the Oesch social class schema. It also provides tools to convert several occupational classifications (PCS82, PCS03, and ISCO08) into a common one (ISCO88) to facilitate data harmonisation work, and tools to collapse (i.e. group) modalities of social position indicators. / GPL-2   GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-soda	1.0_6	Functions, examples and other software related to the book Software for Data Analysis: Programming with R. See package?SoDA for an overview. / GPL-2	linux-64, osx-64, win-64
r-sodavis	1.2	Variable and interaction selection are essential to classification in high-dimensional setting. In this package, we provide the implementation of SODA procedure, which is a forward-backward algorithm that selects both main and interaction effects under logistic regression and quadratic discriminant analysis. We also provide an extension, S-SODA, for dealing with the variable selection problem for semi-parametric models with continuous responses. / GPL-2	noarch
r-sofia	1.0	Software that leverages the capabilities of Circos by manipulating data, preparing configuration files, and running the Perl-native Circos directly from the R environment with minimal user intervention. Circos is a novel software that addresses the challenges in visualizing genetic data by creating circular ideograms composed of tracks of heatmaps, scatter plots, line plots, histograms, links between common markers, glyphs, text, and etc. Please see < <a href="http://www.circos.ca">http://www.circos.ca</a> >. / GPL-3	noarch
r-softclustering	1.19012	It contains soft clustering algorithms, in particular approaches derived from rough set theory: Lingras & West original rough k-means, Peters' refined rough k-means, and PI rough k-means. It also contains classic k-means and a corresponding illustrative demo. / GPL-2	noarch
r-softimpute	1.4	Iterative methods for matrix completion that use nuclear-norm regularization. There are two main approaches. The one approach uses iterative soft-thresholded svds to impute the missing values. The second approach uses alternating least squares. Both have an EM flavor, in that at each iteration the matrix is completed with the current estimate. For large matrices there is a special sparse-matrix class named Incomplete that efficiently handles all computations. The package includes procedures for centering and scaling rows, columns or both, and for computing low-rank SVDs on large sparse centered matrices (i.e. principal components) / GPL-2	linux-64, osx-64, win-64
r-softmaxreg	1.2	Implementation of 'softmax' regression and classification models with multiple layer neural network. It can be used for many tasks like word embedding based document classification, 'MNIST' dataset handwritten digit recognition and so on. Multiple optimization algorithm including 'SGD', 'Adagrad', 'RM-Sprop', 'Moment', 'NAG', etc are also provided. / GPL-2	noarch
r-softrandomforest	0.1.0	Performs random forests for soft decision trees for a classification problem. Current limitations are for a maximum depth of 5 resulting in 16 terminal nodes. Some data cleaning is required before input. Final graphic output requires currently requires exporting to 'Microsoft Excel' for visualization. Method based on Irsoy, Yildiz and Alpaydin (2012, ISBN: 978-4-9906441-1-6). / CC0	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-soilhyp	0.1.3	Provides functions for (1) soil water retention (SWC) and unsaturated hydraulic conductivity (Ku) (van Genuchten-Mualem (vGM or vG) [1, 2], Peters-Durner-Iden (PDI) [3, 4, 5], Brooks and Corey (bc) [8]), (2) fitting of parameter for SWC and/or Ku using Shuffled Complex Evolution (SCE) optimisation and (3) calculation of soil hydraulic properties (Ku and soil water contents) based on the simplified evaporation method (SEM) [6, 7]. Main references: [1] van Genuchten (1980) <doi:10.2136/sssaj1980.03615995004400050002x>, Mualem (1976) <doi:10.1029/WR012i003p00513>, [3] Peters (2013) <doi:10.1002/wrcr.20548>, Iden and Durner (2013) <doi:10.1002/2014WR015937>, [5] Peters (2014) <doi:10.1002/2014WR015937>, [6] Wind G. P. (1966), [7] Peters and Durner (2008) <doi:10.1016/j.jhydrol.2008.04.016> and [8] Brooks and Corey (1964). / GPL-2	noarch
r-soilphysics	3.1	Basic and model-based soil physical analyses. / GPL-2	noarch
r-soiltexture	1.5.1	The Soil Texture Wizard is a set of R functions designed to produce texture triangles (also called texture plots, texture diagrams, texture ternary plots), classify and transform soil textures data. These functions virtually allows to plot any soil texture triangle (classification) into any triangle geometry (isosceles, right-angled triangles, etc.). This set of function is expected to be useful to people using soil textures data from different soil texture classification or different particle size systems. Many (> 15) texture triangles from all around the world are predefined in the package. A simple text based graphical user interface is provided: soiltexture_gui(). / AGPL-3	noarch
r-soilwater	1.0.5	It implements parametric formulas of soil water retention or conductivity curve. At the moment, only Van Genuchten (for soil water retention curve) and Mualem (for hydraulic conductivity) were implemented. See reference (< <a href="http://en.wikipedia.org/wiki/Water_retention_curve">http://en.wikipedia.org/wiki/Water_retention_curve</a> >). / GPL-2	noarch
r-sokoban	0.1.0	Interactively play a game of sokoban ,which has nine game levels.Sokoban is a type of transport puzzle, in which the player pushes boxes or crates around in a warehouse, trying to get them to storage locations. / GPL-3	noarch
r-solar	0.44	Calculation methods of solar radiation and performance of photovoltaic systems from daily and intradaily irradiation data sources. / GPL-3	noarch
r-solarpos	1.0	Calculation of solar zenith and azimuth angles. / GPL-2	noarch
r-solartime	0.0.1	Provide utilities to work with solar time, i.e. where noon is exactly when sun culminates. Provides functions for computing sun position and times of sunrise and sunset. / GPL-3	noarch
r-solomon	1.0	Parentage analysis using Bayes' theorem / GPL-2	noarch
r-solrad	1.0.0	For surface energy models and estimation of solar positions and components with varying topography, time and locations. The functions calculate solar top-of-atmosphere, open, diffuse and direct components, atmospheric transmittance and diffuse factors, day length, sunrise and sunset, solar azimuth, zenith, altitude, incidence, and hour angles, earth declination angle, equation of time, and solar constant. Details about the methods and equations are explained in Seyednasrollah, Bijan, Mukesh Kumar, and Timothy E. Link. 'On the role of vegetation density on net snow cover radiation at the forest floor.' Journal of Geophysical Research: Atmospheres 118.15 (2013): 8359-8374, <doi:10.1002/jgrd.50575>. / AGPL-3	noarch
r-solverationalmatrixequation	0.1.0	Given a symmetric positive definite matrix Q and a non-singular matrix L, find symmetric positive definite solution X such that $X = Q L (X \text{ inv}) L^T$ . Reference: Benner, P., Faßbender, H. On the Solution of the Rational Matrix Equation. Benner, Faßbender (2007) <doi:10.1155/2007/21850>. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-som	0.3.5	Self-Organizing Map (with application in gene clustering). / GPL-3	linux-64, osx-64, win-64
r-somebm	0.1	some Brownian motions simulation functions / MIT	noarch
r-somekfw	1.2	This package collects some procedures controlling the Generalized Family-wise Error Rate. / GPL-2	noarch
r-somemtp	1.4.1	It's a collection of functions for Multiplicity Correction and Multiple Testing. / GPL-2	noarch
r-sommer	4.0.4	Structural multivariate-univariate linear mixed model solver for estimation of multiple random effects and unknown variance-covariance structures (i.e. heterogeneous and unstructured variance models) (Covarrubias-Pazarán, 2016 <doi:10.1371/journal.pone.0156744>; Maier et al., 2015 <doi:10.1016/j.ajhg.2014.12.006>). ML/REML estimates can be obtained using the Direct-Inversion Newton-Raphson and Direct-Inversion Average Information algorithms. Designed for genomic prediction and genome wide association studies (GWAS), particularly focused in the $p > n$ problem (more coefficients than observations) and dense known covariance structures for levels of random effects. Spatial models can also be fitted using i.e. the two-dimensional spline functionality available in sommer. / GPL-2	linux-64, osx-64, win-64
r-somplot	1.6.4	The package provides the plot function som.plot() to create high quality visualisations of hexagonal Kohonen maps (self-organising maps). / GPL-2	noarch
r-sonar	1.0.2	Formulas for calculating sound velocity, water pressure, depth, density, absorption and sonar equations. / GPL-3	noarch
r-soniclength	1.4.6	Estimate the abundance of cell clones from the distribution of lengths of DNA fragments (as created by sonication, whence 'sonicLength'). The algorithm in Estimating abundances of retroviral insertion sites from DNA fragment length data by Berry CC, Gillet NA, Melamed A, Gormley N, Bangham CR, Bushman FD. Bioinformatics; 2012 Mar 15;28(6):755-62 is implemented. The experimental setting and estimation details are described in detail there. Briefly, integration of new DNA in a host genome (due to retroviral infection or gene therapy) can be tracked using DNA sequencing, potentially allowing characterization of the abundance of individual cell clones bearing distinct integration sites. The locations of integration sites can be determined by fragmenting the host DNA (via sonication or fragmentase), breaking the newly integrated DNA at a known sequence, amplifying the fragments containing both host and integrated DNA, sequencing those amplicons, then mapping the host sequences to positions on the reference genome. The relative number of fragments containing a given position in the host genome estimates the relative abundance of cells hosting the corresponding integration site, but that number is not available and the count of amplicons per fragment varies widely. However, the expected number of distinct fragment lengths is a function of the abundance of cells hosting an integration site at a given position and a certain nuisance parameter. The algorithm implicitly estimates that function to estimate the relative abundance. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-soobench</a>	1.0_7	Collection of different single objective test functions useful for benchmarks and algorithm development. / BSD	linux-64, osx-64, win-64
<a href="#">r-sopie</a>	1.5	Provides functions to non-parametrically estimate the off-pulse interval of a source function originating from a pulsar. The technique is based on a sequential application of P-values obtained from goodness-of-fit tests for the uniform distribution, such as the Kolmogorov-Smirnov, Cramer-von Mises, Anderson-Darling and Rayleigh goodness-of-fit tests. / GPL-3	noarch
<a href="#">r-soql</a>	0.1.1	Used to construct the URLs and parameters of ‘Socrata Open Data API’ < <a href="https://dev.socrata.com">https://dev.socrata.com</a> > calls, using the API’s ‘SoQL’ parameter format. Has method-chained and sensical syntax. Plays well with pipes. / MIT	noarch
<a href="#">r-sor</a>	0.23.1	Estimation for longitudinal data following outcome dependent sampling using the sequential offsetted regression technique. Includes support for binary, count, and continuous data. The first regression is a logistic regression, which uses a known ratio (the probability of being sampled given that the subject/observation was referred divided by the probability of being sampled given that the subject/observation was no referred) as an offset to estimate the probability of being referred given outcome and covariates. The second regression uses this estimated probability to calculate the mean population response given covariates. / GPL-3	noarch
<a href="#">r-sorptionanalysis</a>	0.1.0	Provides tools to efficiently analyze and visualize laboratory data from aqueous static adsorption experiments. The package provides functions to plot Langmuir, Freundlich, and Temkin isotherms and functions to determine the statistical conformity of data points to the Langmuir, Freundlich, and Temkin adsorption models through statistical characterization of the isothermic least squares regressions lines. Scientific Reference: Dada, A.O, Olalekan, A., Olatunya, A. (2012) <doi:10.9790/5736-0313845>. / GPL-2	noarch
<a href="#">r-sortablehtmltables</a>	0.1_3	SortableHTMLTables writes a data frame to an HTML file that contains a sortable table. The sorting is done using the jQuery plugin Tablesorter. The appearance is controlled through a CSS file and several GIF’s. / MIT	noarch
<a href="#">r-sotkanet</a>	0.9.48	Access data from the sotkanet open data portal < <a href="https://www.sotkanet.fi/sotkanet/fi/index">https://www.sotkanet.fi/sotkanet/fi/index</a> >. / BSD_2_clause	noarch
<a href="#">r-sotu</a>	1.0.2	The President of the United States is constitutionally obligated to provide a report known as the ‘State of the Union’. The report summarizes the current challenges facing the country and the president’s upcoming legislative agenda. While historically the State of the Union was often a written document, in recent decades it has always taken the form of an oral address to a joint session of the United States Congress. This package provides the raw text from every such address with the intention of being used for meaningful examples of text analysis in R. The corpus is well suited to the task as it is historically important, includes material intended to be read and material intended to be spoken, and it falls in the public domain. As the corpus spans over two centuries it is also a good test of how well various methods hold up to the idiosyncrasies of historical texts. Associated data about each address, such as the year, president, party, and format, are also included. / GPL-2	noarch
<a href="#">r-sound</a>	1.4.5	Basic functions for dealing with wav files and sound samples. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-soundexbr</a>	1.2	The SoundexBR package provides an algorithm for decoding names into phonetic codes, as pronounced in Portuguese. The goal is for homophones to be encoded to the same representation so that they can be matched despite minor differences in spelling. The algorithm mainly encodes consonants; a vowel will not be encoded unless it is the first letter. The soundex code resultant consists of a four digits long string composed by one letter followed by three numerical digits: the letter is the first letter of the name, and the digits encode the remaining consonants. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-source.gist</a>	1.0.0	Analogous to source(), but works when given a Gist URL or ID. / MIT	noarch
<a href="#">r-sourcetools</a>	0.1.7	Tools for the reading and tokenization of R code. The ‘sourcetools’ package provides both an R and C interface for the tokenization of R code, and helpers for interacting with the tokenized representation of R code. / MIT file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-sp</a>	1.3_1	Classes and methods for spatial data; the classes document where the spatial location information resides, for 2D or 3D data. Utility functions are provided, e.g. for plotting data as maps, spatial selection, as well as methods for retrieving coordinates, for subsetting, print, summary, etc. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-sp23design</a>	0.9	Provides methods for generating, exploring and executing seamless Phase II-III designs of Lai, Lavori and Shih using generalized likelihood ratio statistics. Includes pdf and source files that describe the entire R implementation with the relevant mathematical details. / LGPL-3	noarch
<a href="#">r-spa3g</a>	1.0	The package implements the model-based kernel machine method for detecting gene-centric gene-gene interactions of Li and Cui (2012). / GPL-3	noarch
<a href="#">r-spaa</a>	0.2.2	Miscellaneous functions for analysing species association and niche overlap. / GPL-2	noarch
<a href="#">r-space</a>	0.1_1	Partial correlation estimation with joint sparse regression model / GPL-2	linux-64, osx-64, win-64
<a href="#">r-spacejam</a>	1.1	This package provides an extension of conditional independence (CIG) and directed acyclic graph (DAG) estimation to the case where conditional relationships are (non-linear) additive models. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-spacesrgb	1.2_2	Standard RGB spaces included are sRGB, ‘Adobe’ RGB, ‘ProPhoto’ RGB, BT.709, and others. User-defined RGB spaces are also possible. There is partial support for ACES Color workflows. / GPL-3	noarch
r-spacesxyz	1.0_4	Functions for converting among CIE XYZ, xyY, Lab, and Luv. The XYZs of some standard illuminants and some standard linear chromatic adaptation transforms (CATs) are included. Compute CCT and the Planckian and daylight loci. Three different standard color difference metrics are included. / GPL-3	noarch
r-spacyr	1.2	An R wrapper to the ‘Python’ ‘spaCy’ ‘NLP’ library, from <a href="http://spacy.io">http://spacy.io</a> . / GPL-3	noarch
r-spaddins	0.2.0	A set of RStudio addons that are designed to be used in combination with user-defined RStudio keyboard shortcuts. These addons either: 1) insert text at a cursor position (e.g. insert operators %>%, <<-, %\$%, etc.), 2) replace symbols in selected pieces of text (e.g., convert backslashes to forward slashes which results in stings like c:dataconverted into c:/data/) or 3) enclose text with special symbols (e.g., converts bold into <b>bold</b> ) which is convenient for editing R Markdown files. / MIT	noarch
r-spader	0.1.1	Estimation of various biodiversity indices and related (dis)similarity measures based on individual-based (abundance) data or sampling-unit-based (incidence) data taken from one or multiple communities/assemblages. / GPL-3	noarch
r-spaero	0.5.0	Implements methods for anticipating the emergence and eradication of infectious diseases from surveillance time series. Also provides support for computational experiments testing the performance of such methods. / GPL-2	noarch
r-spam	2.2_2	Set of functions for sparse matrix algebra. Differences with other sparse matrix packages are: (1) we only support (essentially) one sparse matrix format, (2) based on transparent and simple structure(s), (3) tailored for MCMC calculations within G(M)RF. (4) and it is fast and scalable (with the extension package spam64). / LGPL-2   BSD_3_clause	linux-64, osx-64, win-64
r-spam64	2.2_2	Provides the Fortran code of the R package ‘spam’ with 64-bit integers. Loading this package together with the R package spam enables the sparse matrix class spam to handle huge sparse matrices with more than 2 <sup>31</sup> -1 non-zero elements. / LGPL-2   BSD_3_clause	linux-64, osx-64, win-64
r-spanel	0.1	Fit the spatial panel data models: the fixed effects, random effects and between models. / GPL-3	noarch
r-spanish	0.4.2	Character vector to numerical translation in Euros from Spanish spelled monetary quantities. Reverse translation from integer to Spanish. Upper limit is up to the millions range. Geocoding via Cadastral web site. / GPL-3	noarch
r-spar	0.1	This package performs robust nonparametric tests for rare variants association analysis using summation of partition approaches that incorporate gene-gene and gene-environmental interactions / GPL-2	noarch
r-sparcl	1.0.4	Implements the sparse clustering methods of Witten and Tibshirani (2010): A framework for feature selection in clustering; published in Journal of the American Statistical Association 105(490): 713-726. / GPL-2	linux-64, osx-64, win-64
r-sparkline	2.0	Include interactive sparkline charts <a href="http://omnipotent.net/jquery.sparkline">http://omnipotent.net/jquery.sparkline</a> in all R contexts with the convenience of ‘htmlwidgets’. / MIT	noarch

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Table 51 – continued from previous page

Name	Version	Summary/License	Platforms
r-sparklyr	1.0.0	R interface to Apache Spark, a fast and general engine for big data processing, see < <a href="http://spark.apache.org">http://spark.apache.org</a> >. This package supports connecting to local and remote Apache Spark clusters, provides a ‘dplyr’ compatible back-end, and provides an interface to Spark’s built-in machine learning algorithms. / Apache License 2.0   file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-sparkr	2.4.4	Provides an R Front end for ‘Apache Spark’ < <a href="https://spark.apache.org">https://spark.apache.org</a> >. / Apache License (== 2.0)	noarch
r-sparktex	0.1	Generate syntax for use with the sparklines package for LaTeX. / GPL-2	noarch
r-sparql	1.16	Use SPARQL to pose SELECT or UPDATE queries to an end-point. / GPL-3	noarch
r-sparsebnutils	0.0.7	A set of tools for representing and estimating sparse Bayesian networks from continuous and discrete data, as described in Aragam, Gu, and Zhou (2017) <arXiv:1703.04025>. / GPL-2	noarch
r-sparsedc	0.1.17	Implements the algorithm described in Barron, M., Zhang, S. and Li, J. 2017, A sparse differential clustering algorithm for tracing cell type changes via single-cell RNA-sequencing data, Nucleic Acids Research, gkx1113, <doi:10.1093/nar/gkx1113>. This algorithm clusters samples from two different populations, links the clusters across the conditions and identifies marker genes for these changes. The package was designed for scRNA-Seq data but is also applicable to many other data types, just replace cells with samples and genes with variables. The package also contains functions for estimating the parameters for SparseDC as outlined in the paper. We recommend that users further select their marker genes using the magnitude of the cluster centers. / GPL-3	noarch
r-sparseeigen	0.1.0	Computation of sparse eigenvectors of a matrix (aka sparse PCA) with running time 2-3 orders of magnitude lower than existing methods and better final performance in terms of recovery of sparsity pattern and estimation of numerical values. Can handle covariance matrices as well as data matrices with real or complex-valued entries. Different levels of sparsity can be specified for each individual ordered eigenvector and the method is robust in parameter selection. See vignette for a detailed documentation and comparison, with several illustrative examples. The package is based on the paper: K. Benidis, Y. Sun, P. Babu, and D. P. Palomar (2016). Orthogonal Sparse PCA and Covariance Estimation via Procrustes Reformulation, IEEE Transactions on Signal Processing <doi:10.1109/TSP.2016.2605073>. / GPL-3	noarch
r-sparsegrid	0.8.2	SparseGrid is a package to create sparse grids for numerical integration, based on code from <a href="http://www.sparse-grids.de">www.sparse-grids.de</a> / GPL-3	noarch
r-sparsehessianfd	0.3.3	Estimates Hessian of a scalar-valued function, and returns it in a sparse Matrix format. The sparsity pattern must be known in advance. The algorithm is especially efficient for hierarchical models with a large number of heterogeneous units. See Braun, M. (2017) <doi:10.18637/jss.v082.i10>. / MPL (== 2.0)	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-sparseindextracking</a>	0.1.1	Computation of sparse portfolios for financial index tracking, i.e., joint selection of a subset of the assets that compose the index and computation of their relative weights (capital allocation). The level of sparsity of the portfolios, i.e., the number of selected assets, is controlled through a regularization parameter. Different tracking measures are available, namely, the empirical tracking error (ETE), downside risk (DR), Huber empirical tracking error (HETE), and Huber downside risk (HDR). See vignette for a detailed documentation and comparison, with several illustrative examples. The package is based on the paper: K. Benidis, Y. Feng, and D. P. Palomar, Sparse Portfolios for High-Dimensional Financial Index Tracking, IEEE Trans. on Signal Processing, vol. 66, no. 1, pp. 155-170, Jan. 2018. <doi:10.1109/TSP.2017.2762286>. / GPL-3	noarch
<a href="#">r-sparsem</a>	1.77	Some basic linear algebra functionality for sparse matrices is provided: including Cholesky decomposition and backsolving as well as standard R subsetting and Kronecker products. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-sparsemdc</a>	0.99.5	Implements the algorithm described in Barron, M., and Li, J. (Not yet published). This algorithm clusters samples from multiple ordered populations, links the clusters across the conditions and identifies marker genes for these changes. The package was designed for scRNA-Seq data but is also applicable to many other data types, just replace cells with samples and genes with variables. The package also contains functions for estimating the parameters for SparseMDC as outlined in the paper. We recommend that users further select their marker genes using the magnitude of the cluster centers. / GPL-3	noarch
<a href="#">r-sparsemse</a>	1.2.1	Implements the routines and algorithms developed and analysed in Multiple systems estimation for Sparse Capture Data: Inferential Challenges when there are Non-Overlapping Lists Chan, L, Silverman, B. W., Vincent, K (2019) <arXiv:1902.05156>. This package explicitly handles situations where there are pairs of lists which have no observed individuals in common. / GPL-2	noarch
<a href="#">r-sparsemvn</a>	0.2.1	Computes multivariate normal (MVN) densities, and samples from MVN distributions, when the covariance or precision matrix is sparse. / MPL (>= 2.0)	noarch
<a href="#">r-sparsepp</a>	1.22	Provides interface to 'sparsepp' - fast, memory efficient hash map. It is derived from Google's excellent 'sparsehash' implementation. We believe 'sparsepp' provides an unparalleled combination of performance and memory usage, and will outperform your compiler's unordered_map on both counts. Only Google's 'dense_hash_map' is consistently faster, at the cost of much greater memory usage (especially when the final size of the map is not known in advance). / BSD_3_clause	noarch
<a href="#">r-sparsesem</a>	2.5	Sparse-aware maximum likelihood for structural equation models in inferring gene regulatory networks / GPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-sparsestep	1.0.0	Implements the SparseStep model for solving regression problems with a sparsity constraint on the parameters. The SparseStep regression model was proposed in Van den Burg, Groenen, and Alfons (2017) < <a href="https://arxiv.org/abs/1701.06967">https://arxiv.org/abs/1701.06967</a> >. In the model, a regularization term is added to the regression problem which approximates the counting norm of the parameters. By iteratively improving the approximation a sparse solution to the regression problem can be obtained. In this package both the standard SparseStep algorithm is implemented as well as a path algorithm which uses golden section search to determine solutions with different values for the regularization parameter. / GPL-2	noarch
r-sparsesvd	0.2	Wrapper around the ‘SVDLIBC’ library for (truncated) singular value decomposition of a sparse matrix. Currently, only sparse real matrices in Matrix package format are supported. / BSD_3_clause	linux-64, osx-64, win-64
r-sparsesvm	1.1_6	Fast algorithm for fitting solution paths of sparse SVM models with lasso or elastic-net regularization. / GPL-3	linux-64, osx-64, win-64
r-sparsio	1.0.0	Fast ‘SVMlight’ reader and writer. ‘SVMlight’ is most commonly used format for storing sparse matrices (possibly with some target variable) on disk. For additional information about ‘SVMlight’ format see < <a href="http://svmlight.joachims.org/">http://svmlight.joachims.org/</a> >. / GPL-2	linux-64, osx-64, win-64
r-spatest	3.0.0	Performs score test using saddlepoint approximation to estimate the null distribution. Also prepares summary statistics for meta-analysis and performs meta-analysis to combine multiple association results. For the latest version, please check < <a href="https://github.com/leeshawn/SPAtest">https://github.com/leeshawn/SPAtest</a> >. / GPL-2	noarch
r-spatgraphs	3.2_1	Graphs (or networks) and graph component calculations for spatial locations in 1D, 2D, 3D etc. / GPL-2	linux-64, osx-64, win-64
r-spatial	7.3_1	Functions for kriging and point pattern analysis. / GPL-2   GPL-3	linux-32, linux-64, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-spatialacc</a>	0.1_3	Provides a set of spatial accessibility measures from a set of locations (demand) to another set of locations (supply). It aims, among others, to support research on spatial accessibility to health care facilities. Includes the locations and some characteristics of major public hospitals in Greece. / GPL-2	noarch
<a href="#">r-spatialcovariance</a>	0.6_9	Functions that compute the spatial covariance matrix for the matern and power classes of spatial models, for data that arise on rectangular units. This code can also be used for the change of support problem and for spatial data that arise on irregularly shaped regions like counties or zipcodes by laying a fine grid of rectangles and aggregating the integrals in a form of Riemann integration. / GPL-3	noarch
<a href="#">r-spatialml</a>	0.1.3	Implements a spatial extension of the random forest algorithm (Georganos et al. (2019) <doi:10.1080/10106049.2019.1595177>). Future updates include more local machine learning methods as well as a geographically weighted random forest. / GPL-2	noarch
<a href="#">r-spatialnp</a>	1.1_3	Test and estimates of location, tests of independence, tests of sphericity and several estimates of shape all based on spatial signs, symmetrized signs, ranks and signed ranks. For details, see Oja and Randles (2004) <doi:10.1214/088342304000000558> and Oja (2010) <doi:10.1007/978-1-4419-0468-3>. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-spatialpack</a>	0.3_8	Tools to assess the association between two spatial processes. Currently, several methodologies are implemented: A modified t-test to perform hypothesis testing about the independence between the processes, a suitable nonparametric correlation coefficient, the codispersion coefficient, and an F test for assessing the multiple correlation between one spatial process and several others. Functions for image processing and computing the spatial association between images are also provided. SpatialPack gives methods to complement methodologies that are available in geoR for one spatial process. / GPL (>= 2.0)	linux-64, osx-64, win-64
<a href="#">r-spatimeclus</a>	1.0	Mixture model is used to achieve the clustering goal. Each component is itself a mixture model of polynomial autoregressive regressions whose the logistic weights consider the spatial and temporal information. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-spatiotemporal</a>	1.1.9	Utilities that estimate, predict and cross-validate the spatio-temporal model developed for MESA Air. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-spatstat.utils</a>	1.13	Contains utility functions for the ‘spatstat’ package which may also be useful for other purposes. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-spbayes</a>	0.4.2	Fits univariate and multivariate spatio-temporal random effects models for point-referenced data using Markov chain Monte Carlo (MCMC). Details are given in Finley, Banerjee, and Gelfand (2015) <doi:10.18637/jss.v063.i13> and Finley, Banerjee, and Cook (2014) <doi:10.1111/2041-210X.12189>. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-spbsampling</a>	1.3.0	Selection of spatially balanced samples. In particular, the implemented sampling designs allow to select probability samples well spread over the population of interest, in any dimension and using any distance function (e.g. Euclidean distance, Manhattan distance). For more details, Benedetti R and Piersimoni F (2017) <doi:10.1002/bimj.201600194> and Benedetti R and Piersimoni F (2017) <arXiv:1710.09116>. The implementation has been done in C through the use of ‘Rcpp’ and ‘RcppArmadillo’. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-spcadjust</a>	1.1	Calibration of thresholds of control charts such as CUSUM charts based on past data, taking estimation error into account. / GPL-2	noarch
<a href="#">r-spcalda</a>	1.0	A new reduced-rank LDA method which works for high dimensional multi-class data. / GPL-2	noarch
<a href="#">r-spcavrp</a>	0.4	Implements the SPCAvRP algorithm, developed and analysed in Sparse principal component analysis via random projections Gataric, M., Wang, T. and Samworth, R. J. (2018) <arXiv:1712.05630>. The algorithm is based on the aggregation of eigenvector information from carefully-selected random projections of the sample covariance matrix. / GPL-3	noarch
<a href="#">r-spcdanalyze</a>	0.1.0	Programs to find the sample size or power of studies using the Sequential Parallel Comparison Design (SPCD) and programs to analyze such studies. This is a clinical trial design where patients initially on placebo who did not respond are re-randomized between placebo and active drug in a second phase and the results of the two phases are pooled. The method of analyzing binary data with this design is described in Fava, Evins, Dorer and Schoenfeld (2003) <doi:10.1159/000069738>, and the method of analyzing continuous data is described in Chen, Yang, Hung and Wang (2011) <doi:10.1016/j.cct.2011.04.006>. / Unlimited	noarch
<a href="#">r-spcov</a>	1.01	Provides a covariance estimator for multivariate normal data that is sparse and positive definite. Implements the majorize-minimize algorithm described in Bien, J., and Tibshirani, R. (2011), Sparse Estimation of a Covariance Matrix, Biometrika. 98(4). 807–820. / GPL-2	noarch
<a href="#">r-spd</a>	2.0.1	The Semi Parametric Piecewise Distribution blends the Generalized Pareto Distribution for the tails with a kernel based interior. / GPL-3	noarch
<a href="#">r-spdata</a>	0.3.0	Diverse spatial datasets for demonstrating, benchmarking and teaching spatial data analysis. It includes R data of class sf (defined by the package ‘sf’), Spatial (‘sp’), and nb (‘spdep’). Unlike other spatial data packages such as ‘rnatuarearth’ and ‘maps’, it also contains data stored in a range of file formats including GeoJSON, ESRI Shapefile and GeoPackage. Some of the datasets are designed to illustrate specific analysis techniques. cycle_hire() and cycle_hire_osm(), for example, is designed to illustrate point pattern analysis techniques. / CC0	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-spdownscale</a>	0.1.0	Spatial downscaling of climate data (Global Circulation Models/Regional Climate Models) using quantile-quantile bias correction technique. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-spearman	1.0	Functions for conducting jackknife Euclidean / empirical likelihood inference for Spearman's rho (de Carvalho and Marques (2012) <10.1080/10920277.2012.10597644>). / GPL-3	noarch
r-spec	0.1.7	Creates a data specification that describes the columns of a table (data.frame). Provides methods to read, write, and update the specification. Checks whether a table matches its specification. See specification.data.frame(), read.spec(), write.spec(), as.csv.spec(), respecify.character(), and %matches%.data.frame(). / GPL-3	noarch
r-speccalt	0.1.1	Alternative to the kernlab::specc function. Includes a spectral clustering implementation, a locally adapted kernel function akin to what is already proposed in kernlab, and an optional procedure that automatically estimates the optimal number of clusters. Several sample data sets are also included. / LGPL-3	noarch
r-specdetec	1.0.0	Calculate change point based on spectral clustering with the option to automatically calculate the number of clusters if this information is not available. / GPL-3	noarch
r-spectralgp	1.3.3	Routines for creating, manipulating, and performing Bayesian inference about Gaussian processes in one and two dimensions using the Fourier basis approximation: simulation and plotting of processes, calculation of coefficient variances, calculation of process density, coefficient proposals (for use in MCMC). It uses R environments to store GP objects as references/pointers. / GPL-2	noarch
r-spedinstabr	1.8	From output files obtained from the software 'ModestR', the relative contribution of factors to explain species distribution is depicted using several plots. A global geographic raster file for each environmental variable may be also obtained with the mean relative contribution, considering all species present in each raster cell, of the factor to explain species distribution. Finally, for each variable it is also possible to compare the frequencies of any variable obtained in the cells where the species is present with the frequencies of the same variable in the cells of the extent. / GPL-2	noarch
r-speedglm	0.3_2	Fitting linear models and generalized linear models to large data sets by updating algorithms. / GPL-3	noarch
r-speff2trial	1.0.4	The package performs estimation and testing of the treatment effect in a 2-group randomized clinical trial with a quantitative, dichotomous, or right-censored time-to-event endpoint. The method improves efficiency by leveraging baseline predictors of the endpoint. The inverse probability weighting technique of Robins, Rotnitzky, and Zhao (JASA, 1994) is used to provide unbiased estimation when the endpoint is missing at random. / GPL-2	noarch
r-spelling	2.1	Spell checking common document formats including latex, markdown, manual pages, and description files. Includes utilities to automate checking of documentation and vignettes as a unit test during 'R CMD check'. Both British and American English are supported out of the box and other languages can be added. In addition, packages may define a 'wordlist' to allow custom terminology without having to abuse punctuation. / MIT	noarch
r-sprgrass6	0.8_9	Interpreted interface between GRASS 6 geographical information system and R, based on starting R from within the GRASS environment, or running free-standing R in a temporary GRASS location; the package provides facilities for using all GRASS commands from the R command line. This package may not be used for GRASS 7, for which rgrass7 should be used. / GPL-2	noarch
r-spherick	1.2	Spherical K-function for point-pattern analysis on the sphere. / GPL-2	noarch
r-spi	1.1	Compute the SPI index using R / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-spiassay	1.1.0	The SNP Panel Identification Assay (SPIA) is a package that enables an accurate determination of cell line identity from the genotype of single nucleotide polymorphisms (SNPs). The SPIA test allows to discern when two cell lines are close enough to be called similar and when they are not. Details about the method are available at Demichelis et al. (2008) SNP panel identification assay (SPIA): a genetic-based assay for the identification of cell lines. Nucleic Acids Res., 3, 2446-2456. / GPL-2	noarch
r-spiders	1.2	Fits and simulates data from our predator preferences model, <DOI:10.1007/s10651-016-0341-3>. / GPL (>= 2.0)	noarch
r-spikes	1.1	Applies re-sampled kernel density method to detect vote fraud. It estimates the proportion of coarse vote-shares in the observed data relative to the null hypothesis of no fraud. / GPL-2	noarch
r-spin	1.1	An optimal weighting strategy to compute simulation-efficient shortest probability intervals (spins). / GPL-2	noarch
r-spina	4.1.0	Calculates constant structure parameters of endocrine homeostatic systems from equilibrium hormone concentrations. Methods and equations have been described in Dietrich et al. (2012) <doi:10.1155/2012/351864> and Dietrich et al. (2016) <doi:10.3389/fendo.2016.00057>. / BSD_3_clause	noarch
r-spinyreg	0.1_0	Implements a generative model that uses a spike-and-slab like prior distribution obtained by multiplying a deterministic binary vector. Such a model allows an EM algorithm, optimizing a type-II log-likelihood. / GPL-2	noarch
r-spirit	0.1.1	Contains an R Markdown template for a clinical trial protocol adhering to the SPIRIT statement. The SPIRIT (Standard Protocol Items for Interventional Trials) statement outlines recommendations for a minimum set of elements to be addressed in a clinical trial protocol. Also contains functions to create a xml document from the template and upload it to clinicaltrials.gov< <a href="https://www.clinicaltrials.gov/">https://www.clinicaltrials.gov/</a> > for trial registration. / MIT	noarch
r-splines2	0.2.8	Constructs B-splines and its integral, monotone splines (M-splines) and its integral (I-splines), convex splines (C-splines), and their derivatives of given order. Piecewise constant basis is allowed for B-splines and M-splines. See De Boor (1978) <doi:10.1002/zamm.19800600129>, Ramsay (1988) <doi:10.1214/ss/1177012761>, and Meyer (2008) <doi:10.1214/08-AOAS167> for more information. / GPL-3	noarch
r-splitfeas	0.1.0	An implementation of the majorization-minimization (MM) algorithm introduced by Xu, Chi, Yang, and Lange (2017) <arXiv:1612.05614> for solving multi-set split feasibility problems. In the multi-set split feasibility problem, we seek to find a point x in the intersection of multiple closed sets and whose image under a mapping also must fall in the intersection of several closed sets. / MIT	noarch
r-splitstackshape	1.4.8	Online data collection tools like Google Forms often export multiple-response questions with data concatenated in cells. The concat.split (cSplit) family of functions splits such data into separate cells. The package also includes functions to stack groups of columns and to reshape wide data, even when the data are unbalanced—something which reshape (from base R) does not handle, and which melt and dcast from reshape2 do not easily handle. / GPL-3	noarch
r-plot	0.5.0	Automates common plotting tasks to ease data exploration. Makes density plots (potentially overlaid on histograms), scatter plots with prediction lines, or bar or line plots with error bars. For each type, y, or x and y variables can be plotted at levels of other variables, all with minimal specification. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-spls	2.2_3	Provides functions for fitting a sparse partial least squares (SPLS) regression and classification (Chun and Keles (2010) <doi:10.1111/j.1467-9868.2009.00723.x>). / GPL-2	noarch
r-spongebob	0.4.0	Convert text (and text in R objects) to Mocking SpongeBob case < <a href="https://knowyourmeme.com/memes/mocking-spongebob">https://knowyourmeme.com/memes/mocking-spongebob</a> > and show them off in fun ways. CoNVERt TeXt (AnD TeXt In r ObJeCtS) To MOCKINg SpoNge-bOb CAsE < <a href="https://knowyourmeme.com/memes/mocking-spongebob">https://knowyourmeme.com/memes/mocking-spongebob</a> > aND shOw tHeM Off IN Fun WayS. / BSD_3_clause	noarch
r-sporm	1.1	R implementation of the methods described in A rank-based empirical likelihood approach to two-sample proportional odds model and its goodness-of-fit by Zhong Guan and Cheng Peng, Journal of Nonparametric Statistics, to appear. / GPL-2	noarch
r-sportsanalytics	0.2	The aim of this package is to provide infrastructure for sports analysis. Anyway, currently it is a selection of data sets, functions to fetch sports data, examples, and demos – with the ambition to develop bit by bit a set of classes to represent general concepts of sports analysis. / GPL-2	noarch
r-spreda	1.1	The Statistical Package for REliability Data Analysis (SPREDA) implements recently-developed statistical methods for the analysis of reliability data. Modern technological developments, such as sensors and smart chips, allow us to dynamically track product/system usage as well as other environmental variables, such as temperature and humidity. We refer to these variables as dynamic covariates. The package contains functions for the analysis of time-to-event data with dynamic covariates and degradation data with dynamic covariates. The package also contains functions that can be used for analyzing time-to-event data with right censoring, and with left truncation and right censoring. Financial support from NSF and DuPont are acknowledged. / GPL-2	noarch
r-sprsmld	0.1_0	R functions to mine sparse models from data. / GPL-2	noarch
r-sprt	1.0	Perform Wald's Sequential Probability Ratio Test on variables with a Normal, Bernoulli, Exponential and Poisson distribution. Plot acceptance and continuation regions, or create your own with the help of closures. / BSD_2_clause	noarch
r-spsl	0.1_9	Provides basic functionality for labeling iso- & anisotropic percolation clusters on 2D & 3D square lattices with various lattice sizes, occupation probabilities, von Neumann & Moore (1,d)-neighborhoods, and random variables weighting the percolation lattice sites. / GPL-3	noarch
r-spurs	2.0.2	Provides functions and datasets from Jones, O.D., R. Maillardet, and A.P. Robinson. 2014. An Introduction to Scientific Programming and Simulation, Using R. 2nd Ed. Chapman And Hall/CRC. / GPL-3	noarch
r-spyvsspy	0.1.1	Data on the Spy vs. Spy comic strip of Mad magazine, created and written by Antonio Prohias. / LGPL-3	noarch
r-sqlrender	1.6.2	A rendering tool for parameterized SQL that also translates into different SQL dialects. These dialects include 'Microsoft Sql Server', 'Oracle', 'PostgreSql', 'Amazon RedShift', 'Apache Impala', 'IBM Netezza', 'Google BigQuery', 'Microsoft PDW', and 'SQLite'. / Apache License 2.0	noarch
r-sqlutils	1.2	This package provides utilities for working with a library of SQL files. / GPL-3	noarch
r-sqrl	0.6.3	Facilitates interaction with ODBC data sources by managing communications on behalf of the user. Supports multi-statement SQL scripts, with or without embedded R. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-squarem</a>	2017.10	Algorithms for accelerating the convergence of slow, monotone sequences from smooth, contraction mapping such as the EM algorithm. It can be used to accelerate any smooth, linearly convergent acceleration scheme. A tutorial style introduction to this package is available in a vignette on the CRAN download page or, when the package is loaded in an R session, with vignette(SQUAREM). / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-squash</a>	1.0.8	Functions for color-based visualization of multivariate data, i.e. colorgrams or heatmaps. Lower-level functions map numeric values to colors, display a matrix as an array of colors, and draw color keys. Higher-level plotting functions generate a bivariate histogram, a dendrogram aligned with a color-coded matrix, a triangular distance matrix, and more. / Artistic-2.0	noarch
<a href="#">r-sra</a>	0.1.1	This package (sra) provides a set of tools to analyse artificial-selection response datasets. The data typically feature for several generations the average value of a trait in a population, the variance of the trait, the population size and the average value of the parents that were chosen to breed. Sra implements two families of models aiming at describing the dynamics of the genetic architecture of the trait during the selection response. The first family relies on purely descriptive (phenomenological) models, based on an autoregressive framework. The second family provides different mechanistic models, accounting e.g. for inbreeding, mutations, genetic and environmental canalization, or epistasis. The parameters underlying the dynamics of the time series are estimated by maximum likelihood. The sra package thus provides (i) a wrapper for the R functions mle() and optim() aiming at fitting in a convenient way a predetermined set of models, and (ii) some functions to plot and analyze the output of the models. / GPL-2	noarch
<a href="#">r-srccs</a>	1.1	Implementation of the SRCS method for a color-based visualization of the results of multiple pairwise tests on a large number of problem configurations, proposed in: I.G. del Amo, D.A. Pelta. SRCS: a technique for comparing multiple algorithms under several factors in dynamic optimization problems. In: E. Alba, A. Nakib, P. Siarry (Eds.), Metaheuristics for Dynamic Optimization. Series: Studies in Computational Intelligence 433, Springer, Berlin/Heidelberg, 2012. / LGPL-3	noarch
<a href="#">r-srda</a>	1.0.0	Sparse redundancy analysis for high dimensional (biomedical) data. Directional multivariate analysis to express the maximum variance in the predicted data set by a linear combination of variables of the predictive data set. Implemented in a partial least squares framework, for more details see Csala et al. (2017) <doi:10.1093/bioinformatics/btx374>. / MIT	noarch
<a href="#">r-srttools</a>	1.2.0	Srt file is a common subtitle format for videos, it contains subtitle and when the subtitle showed. This package is for align time of srt file, and also change color, style and position of subtitle in videos, the srt file will be read as a vector into R, and can be write into srt file after modified using this package. / GPL-2	noarch
<a href="#">r-ssanv</a>	1.1	A set of functions to calculate sample size for two-sample difference in means tests. Does adjustments for either nonadherence or variability that comes from using data to estimate parameters. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-ssbtools</a>	0.4.0	Functions used by other packages from Statistics Norway are gathered. General data manipulation functions, and functions for hierarchical computations are included. The hierarchy specification functions are useful within statistical disclosure control. / Apache License 2.0   file LICENSE	noarch
<a href="#">r-sscor</a>	0.2	Provides the spatial sign correlation and the two-stage spatial sign correlation as well as a one-sample test for the correlation coefficient. / GPL-2   GPL-3	noarch
<a href="#">r-ssd</a>	0.3	ssd calculates the sample size needed to detect the differences between two sets of unordered categorical data. / GPL-2	noarch
<a href="#">r-ssdr</a>	1.2.0	Performs structured OLS (sOLS) and structured SIR (sSIR). / GPL-2	noarch
<a href="#">r-sse</a>	0.7_1	Provides functions to evaluate user-defined power functions for a parameter range, and draws a sensitivity plot. It also provides a resampling procedure for semi-parametric sample size estimation and methods for adding information to a Sweave report. / GPL-3	noarch
<a href="#">r-ssh.utils</a>	1.0	This package provides utility functions for system command execution, both locally and remotely using ssh/scp. The command output is captured and provided to the caller. This functionality is intended to streamline calling shell commands from R, retrieving and using their output, while instrumenting the calls with appropriate error handling. NOTE: this first version is limited to unix with local and remote systems running bash as the default shell. / Apache License (== 2.0)	linux-64
<a href="#">r-ssize.fdr</a>	1.2	This package contains a set of functions that calculates appropriate sample sizes for one-sample t-tests, two-sample t-tests, and F-tests for microarray experiments based on desired power while controlling for false discovery rates. For all tests, the standard deviations (variances) among genes can be assumed fixed or random. This is also true for effect sizes among genes in one-sample and two sample experiments. Functions also output a chart of power versus sample size, a table of power at different sample sizes, and a table of critical test values at different sample sizes. / GPL-3	noarch
<a href="#">r-ssm</a>	1.0.1	Creates an S4 class SSM and defines functions for fitting smooth supersaturated models, a polynomial model with spline-like behaviour. Functions are defined for the computation of Sobol indices for sensitivity analysis and plotting the main effects using FANOVA methods. It also implements the estimation of the SSM metamodel error using a GP model with a variety of defined correlation functions. / GPL-3	noarch
<a href="#">r-sss</a>	0.1_0	Tools to import survey files in the .sss (triple-s) format. The package provides the function read.sss() that reads the .asc (or .csv) and .sss files of a triple-s survey data file. / GPL-2   GPL-3	noarch
<a href="#">r-sssimple</a>	0.6.4	Simulate, solve state space models / GPL-2	noarch
<a href="#">r-ssvd</a>	1.0	Fast iterative thresholding sparse SVD, together with an initialization algorithm / GPL-2	noarch
<a href="#">r-stabledist</a>	0.7_1	Density, Probability and Quantile functions, and random number generation for (skew) stable distributions, using the parametrizations of Nolan. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-stableestim</a>	2.1	Estimate the four parameters of stable laws using maximum likelihood method, generalised method of moments with finite and continuum number of points, iterative Koutrouvelis regression and Kogon-McCulloch method. The asymptotic properties of the estimators (covariance matrix, confidence intervals) are also provided. / GPL-2	noarch
<a href="#">r-stabm</a>	1.1.0	An implementation of many measures for the assessment of the stability of feature selection. Both simple measures and measures which take into account the similarities between features are available, see Bommert et al. (2017) <doi:10.1155/2017/7907163>. / LGPL-3	noarch
<a href="#">r-stabs</a>	0.6.3	Resampling procedures to assess the stability of selected variables with additional finite sample error control for high-dimensional variable selection procedures such as Lasso or boosting. Both, standard stability selection (Meinshausen & Bühlmann, 2010, <doi:10.1111/j.1467-9868.2010.00740.x>) and complementary pairs stability selection with improved error bounds (Shah & Samworth, 2013, <doi:10.1111/j.1467-9868.2011.01034.x>) are implemented. The package can be combined with arbitrary user specified variable selection approaches. / GPL-2	noarch
<a href="#">r-stackoverflow</a>	0.3.0	Helper functions collected from StackOverflow.com, a question and answer site for professional and enthusiast programmers. / CC BY-SA 4.0	noarch
<a href="#">r-stacomirtools</a>	0.5.3	S4 class wrappers for the ‘ODBC’ connection, also provides some utilities to paste small datasets to clipboard, rename columns. It is used by the package ‘stacomir’ for connections to the database. Development versions of ‘stacomir’ are available in R-forge. / GPL-2	noarch
<a href="#">r-stagedchoicesplinemix</a>	1.0.0	Analyzing a mixture of two-stage logistic regressions with fixed candidate knots. See Bruch, E., F. Feinberg, K. Lee (in press)<DOI:10.1073/pnas.1522494113>. / GPL-2	noarch
<a href="#">r-stakeholderanalysis</a>	1.2	Proposes an original instrument for measuring stakeholder influence on the development of an infrastructure project that is carried through by a municipality, drawing on stakeholder classifications (Mitchell, Agle, & Wood, 1997) and input-output modelling (Hester & Adams, 2013). Mitchell R., Agle B.R., & Wood D.J. <doi:10.2307/259247> Hester, P.T., & Adams, K.M. (2013) <doi:10.1016/j.procs.2013.09.282>. / GPL-2	noarch
<a href="#">r-stand</a>	2.0	Provides functions for the analysis of occupational and environmental data with non-detects. Maximum likelihood (ML) methods for censored log-normal data and non-parametric methods based on the product limit estimate (PLE) for left censored data are used to calculate all of the statistics recommended by the American Industrial Hygiene Association (AIHA) for the complete data case. Functions for the analysis of complete samples using exact methods are also provided for the lognormal model. Revised from 2007-11-05 ‘survfit~1’. / GPL-2	noarch
<a href="#">r-standardize</a>	0.2.1	Tools which allow regression variables to be placed on similar scales, offering computational benefits as well as easing interpretation of regression output. / GPL-3	noarch
<a href="#">r-standardizetext</a>	1.0	Standardizes text according to a template; particularly useful for country names. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-stanheaders	2.18.1	The C header files of the Stan project are provided by this package, but it contains no R code, vignettes, or function documentation. There is a shared object containing part of the 'CVODES' library, but it is not accessible from R. 'StanHeaders' is only useful for developers who want to utilize the 'LinkingTo' directive of their package's DESCRIPTION file to build on the Stan library without incurring unnecessary dependencies. The Stan project develops a probabilistic programming language that implements full or approximate Bayesian statistical inference via Markov Chain Monte Carlo or 'variational' methods and implements (optionally penalized) maximum likelihood estimation via optimization. The Stan library includes an advanced automatic differentiation scheme, 'templated' statistical and linear algebra functions that can handle the automatically 'differentiable' scalar types (and doubles, 'ints', etc.), and a parser for the Stan language. The 'rstan' package provides user-facing R functions to parse, compile, test, estimate, and analyze Stan models. / BSD_3_clause file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
r-staplr	2.9.0	Provides function to manipulate PDF files: fill out PDF forms; merge multiple PDF files into one; remove selected pages from a file; rename multiple files in a directory; rotate entire pdf document; rotate selected pages of a pdf file; Select pages from a file; splits single input PDF document into individual pages; splits single input PDF document into parts from given points. / GPL-3	noarch
r-stargazer	5.2.2	Produces LaTeX code, HTML/CSS code and ASCII text for well-formatted tables that hold regression analysis results from several models side-by-side, as well as summary statistics. / GPL-2	noarch
r-startup	0.12.0	Adds support for R startup configuration via '.Renviron.d' and '.Rprofile.d' directories in addition to '.Renviron' and '.Rprofile' files. This makes it possible to keep private / secret environment variables separate from other environment variables. It also makes it easier to share specific startup settings by simply copying a file to a directory. / LGPL-2.1	noarch
r-startupmsg	0.9.6	Provides utilities to create or suppress start-up messages. / LGPL-3	noarch
r-stat2data	2.0.0	Datasets for the textbook Stat2: Modeling with Regression and ANOVA (second edition). The package also includes data for the first edition, Stat2: Building Models for a World of Data and a few functions for plotting diagnostics. / GPL-3	noarch
r-statdataml	1.0_26	Support for reading and writing files in StatDataML—an XML-based data exchange format. / GPL-2	noarch
r-statgraph	0.2.0	Contains statistical methods to analyze graphs, such as graph parameter estimation, model selection based on the GIC (Graph Information Criterion), statistical tests to discriminate two or more populations of graphs (ANOGVA -Analysis of Graph Variability), correlation between graphs, and clustering of graphs. / GPL-3	noarch
r-statmeasures	1.0	Offers useful functions to perform day-to-day data manipulation operations, data quality checks and post modelling statistical checks. One can effortlessly change class of a number of variables to factor, remove duplicate observations from the data, create deciles of a variable, perform data quality checks for continuous (integer or numeric), categorical (factor) and date variables, and compute goodness of fit measures such as auc for statistical models. The functions are consistent for objects of class 'data.frame' and 'data.table', which is an enhanced 'data.frame' implemented in the package 'data.table'. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-statpermeco	0.1.0	Statistical performance measures used in the econometric literature to evaluate conditional covariance/correlation matrix estimates (MSE, MAE, Euclidean distance, Frobenius distance, Stein distance, asymmetric loss function, eigenvalue loss function and the loss function defined in Eq. (4.6) of Engle et al. (2016) <doi:10.2139/ssrn.2814555>). Additionally, compute Eq. (3.1) and (4.2) of Li et al. (2016) <doi:10.1080/07350015.2015.1092975> to compare the factor loading matrix. The statistical performance measures implemented have been previously used in, for instance, Laurent et al. (2012) <doi:10.1002/jae.1248>, Amendola et al. (2015) <doi:10.1002/for.2322> and Becker et al. (2015) <doi:10.1016/j.ijforecast.2013.11.007>. / GPL-2	noarch
r-statprograms	0.2.0	A small collection of data on graduate statistics programs from the United States. / MIT	noarch
r-stcov	0.1.0	Estimates a covariance matrix using Stein's isotonized covariance estimator, or a related estimator suggested by Haff. / GPL-2	noarch
r-stddiff	2.0	Contains three main functions including stddiff.numeric(), stddiff.binary() and stddiff.category(). These are used to calculate the standardized difference between two groups. It is especially used to evaluate the balance between two groups before and after propensity score matching. / GPL-3	noarch
r-steinernet	3.0.1	A set of functions for finding and analysing Steiner trees. It has applications in biological pathway network analysis. Sadeghi (2013) <doi:10.1186/1471-2105-14-144>. / GPL-3	noarch
r-steiniv	0.1.1	Routines for computing different types of linear estimators, based on instrumental variables (IVs), including the semi-parametric Stein-like (SPS) estimator, originally introduced by Judge and Mittelhammer (2004) <DOI:10.1198/016214504000000430>. / GPL-2	noarch
r-stellar	0.3.3	A package to manage and display stellar tracks and isochrones from Pisa low-mass database. Includes tools for isochrones construction and tracks interpolation. / GPL-2	noarch
r-stem	1.0	Estimation of the parameters of a spatio-temporal model using the EM algorithm, estimation of the parameter standard errors using a spatio-temporal parametric bootstrap, spatial mapping. / GPL-2	noarch
r-stemmatology	0.3.2	Explore and analyse the genealogy of textual or musical traditions, from their variants, with various stemmatological methods, mainly the disagreement-based algorithms suggested by Camps and Cafiero (2015) <doi:10.1484/M.LECTIO-EB.5.102565>. / GPL-3	noarch
r-stevedore	0.9.1	Work with containers over the Docker API. Rather than using system calls to interact with a docker client, using the API directly means that we can receive richer information from docker. The interface in the package is automatically generated using the 'OpenAPI' (a.k.a., 'swagger') specification, and all return values are checked in order to make them type stable. / MIT	noarch
r-theoreme	1.2	Functions implementing the procedure of entropy comparison between two data samples after the renormalization of respective probability distributions with the algorithm designed by Klimontovich (Zeitschrift fur Physik B Condensed Matter. 1987, Volume 66, Issue 1, pp 125-127) and extended by Anishchenko (Proc. SPIE 2098, Computer Simulation in Nonlinear Optics. 1994, pp.130-136). The package also includes data preparation tools which can also be used separately for various applications. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-sticky</a>	0.5.2	In base R, object attributes are lost when objects are modified by common data operations such as subset, filter, slice, append, extract etc. This packages allows objects to be marked as ‘sticky’ and have attributes persisted during these operations or when inserted into or extracted from recursive (i.e. list- or table-like) objects. / GPL-2	noarch
<a href="#">r-stinepack</a>	1.4	A consistently well behaved method of interpolation based on piecewise rational functions using Stineman’s algorithm. / GPL-2	noarch
<a href="#">r-stmgp</a>	1.0.1	Rapidly build accurate genetic prediction models for genome-wide association or whole-genome sequencing study data by smooth-threshold multivariate genetic prediction (STMGP) method. Variable selection is performed using marginal association test p-values with an optimal p-value cut-off selected by Cp-type criterion. Quantitative and binary traits are modeled respectively via linear and logistic regression models. A function that works through PLINK software (Purcell et al. 2007 <DOI:10.1086/519795>, Chang et al. 2015 <DOI:10.1186/s13742-015-0047-8>) < <a href="https://www.cog-genomics.org/plink2">https://www.cog-genomics.org/plink2</a> > is provided. Covariates can be included in regression model. / GPL-2	noarch
<a href="#">r-stochprofml</a>	1.2	This is an R package accompanying the paper Parameterizing cell-to-cell regulatory heterogeneities via stochastic transcriptional profiles by Sameer S Bajikar, Christiane Fuchs, Andreas Roller, Fabian J Theis and Kevin A Janes (PNAS 2014, 111(5), E626-635). In this paper, we measure expression profiles from small heterogeneous populations of cells, where each cell is assumed to be from a mixture of lognormal distributions. We perform maximum likelihood estimation in order to infer the mixture ratio and the parameters of these lognormal distributions from the cumulated expression measurements. / GPL-2	noarch
<a href="#">r-stockchina</a>	0.3.1	With this package, users can obtain the real-time price and volume information of stocks in China market, as well as the information of the stock index. This package adopted the API from Sina Finance ( <a href="http://finance.sina.com.cn/">http://finance.sina.com.cn/</a> ). / GPL-2	noarch
<a href="#">r-stoichcalc</a>	1.1_3	Given a list of substance compositions, a list of substances involved in a process, and a list of constraints in addition to mass conservation of elementary constituents, the package contains functions to build the substance composition matrix, to analyze the uniqueness of process stoichiometry, and to calculate stoichiometric coefficients if process stoichiometry is unique. (See Reichert, P. and Schuwirth, N., A generic framework for deriving process stoichiometry in enviromental models, Environmental Modelling and Software 25, 1241-1251, 2010 for more details.) / GPL-2	noarch
<a href="#">r-stopos</a>	0.1	A variable selection procedure for low to moderate size linear regressions models. This method repeatedly splits the data into two sets, one for estimation and one for validation, to obtain an empirically optimized threshold which is then used to screen for variables to include in the final model. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<code>r-stopwords</code>	0.9.0	Provides multiple sources of stopwords, for use in text analysis and natural language processing. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<code>r-storr</code>	1.2.1	Creates and manages simple key-value stores. These can use a variety of approaches for storing the data. This package implements the base methods and support for file system, in-memory and DBI-based database stores. / MIT	noarch
<code>r-strategy</code>	1.0.1	Users can build and test customized quantitative trading strategies. Some quantitative trading strategies are already implemented, e.g. various moving-average filters with trend following approaches. The implemented class called Strategy allows users to access several methods to analyze performance figures, plots and backtest the strategies. Furthermore, custom strategies can be added, a generic template is available. The custom strategies require a certain input and output so they can be called from the Strategy-constructor. / GPL-3	noarch
<code>r-stratifiedbalancing</code>	0.3.0	Performs Stratified Covariate Balancing with Markov blanket feature selection and use of synthetic cases. See Alemi et al. (2016) <DOI:10.1111/1475-6773.12628>. / GPL-2	noarch
<code>r-streammetabolism</code>	1.1.2	I provide functions to calculate Gross Primary Productivity, Net Ecosystem Production, and Ecosystem Respiration from single station diurnal Oxygen curves. / GPL-3	noarch
<code>r-stressr</code>	1.0.0	Forms queries to submit to the Cleveland Federal Reserve Bank web site's financial stress index data site. Provides query functions for both the composite stress index and the components data. By default the download includes daily time series data starting September 25, 1991. The functions return a class of either type easing or cfsi which contain a list of items related to the query and its graphical presentation. The list includes the time series data as an xts object. The package provides four lattice time series plots to render the time series data in a manner similar to the bank's own presentation. / MIT	noarch
<code>r-stressstrength</code>	1.0.2	Reliability of (normal) stress-strength models and for building two-sided or one-sided confidence intervals according to different approximate procedures. / GPL-3	noarch
<code>r-string2adjmatrix</code>	0.1.0	Takes a list of character strings and forms an adjacency matrix for the times the specified characters appear together in the strings provided. For use in social network analysis and data wrangling. Simple package, comprised of three functions. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-stringb	0.1.13	Base R already ships with string handling capabilities ‘out- of-the-box’ but lacks streamlined function names and workflow. The ‘stringi’ (‘stringr’) package on the other hand has well named functions, extensive Unicode support and allows for a streamlined workflow. On the other hand it adds dependencies and regular expression interpretation between base R functions and ‘stringi’ functions might differ. This packages aims at providing a solution to the use case of unwanted dependencies on the one hand but the need for streamlined text processing on the other. The packages’ functions are solely based on wrapping base R functions into ‘stringr’/‘stringi’ like function names. Along the way it adds one or two extra functions and last but not least provides all functions as generics, therefore allowing for adding methods for other text structures besides plain character vectors. / MIT	noarch
r-stringdist	0.9.5	Implements an approximate string matching version of R’s native ‘match’ function. Can calculate various string distances based on edits (Damerau-Levenshtein, Hamming, Levenshtein, optimal sting alignment), qgrams (q-gram, cosine, jaccard distance) or heuristic metrics (Jaro, Jaro-Winkler). An implementation of soundex is provided as well. Distances can be computed between character vectors while taking proper care of encoding or between integer vectors representing generic sequences. / GPL-3	linux-32, linux-64, osx-64, win-32, win-64
r-stringformatt	0.1.2	Pass named and unnamed character vectors into specified positions in strings. This represents an attempt to replicate some of python’s string formatting. / MIT	noarch
r-stringi	1.4.3	Allows for fast, correct, consistent, portable, as well as convenient character string/text processing in every locale and any native encoding. Owing to the use of the ICU library, the package provides R users with platform-independent functions known to Java, Perl, Python, PHP, and Ruby programmers. Available features include: pattern searching (e.g., with ICU Java-like regular expressions or the Unicode Collation Algorithm), random string generation, case mapping, string transliteration, concatenation, Unicode normalization, date-time formatting and parsing, etc. / file LICENSE (FOSS)	linux-32, linux-64, osx-64, win-32, win-64
r-stringr	1.4.0	A consistent, simple and easy to use set of wrappers around the fantastic ‘stringi’ package. All function and argument names (and positions) are consistent, all functions deal with NA’s and zero length vectors in the same way, and the output from one function is easy to feed into the input of another. / GPL-2   file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-strip	1.0.0	The strip function deletes components of R model outputs that are useless for specific purposes, such as predict[ing], print[ing], summary[izing], etc. / MIT	noarch

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Name	Version	Summary/License	Platforms
r-stripless	1.0.3	For making Trellis-type conditioning plots without strip labels. This is useful for displaying the structure of results from factorial designs and other studies when many conditioning variables would clutter the display with layers of redundant strip labels. Settings of the variables are encoded by layout and spacing in the trellis array and decoded by a separate legend. The functionality is implemented by a single S3 generic strucplot() function that is a wrapper for the Lattice package's xyplot() function. This allows access to all Lattice graphics capabilities in the usual way. / GPL-2   GPL-3	noarch
r-strucchange	1.5.1	Testing, monitoring and dating structural changes in (linear) regression models. strucchange features tests/methods from the generalized fluctuation test framework as well as from the F test (Chow test) framework. This includes methods to fit, plot and test fluctuation processes (e.g., CUSUM, MOSUM, recursive/moving estimates) and F statistics, respectively. It is possible to monitor incoming data online using fluctuation processes. Finally, the breakpoints in regression models with structural changes can be estimated together with confidence intervals. Emphasis is always given to methods for visualizing the data. / GPL-2   GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-structfdr	1.3	Perform more powerful false discovery control (FDR) for microbiome data, taking into account the prior phylogenetic relationship among bacteria species. As a general methodology, it is applicable to any type of (genomic) data with prior structure information. / GPL-2	noarch
r-stsm.class	1.3	This package defines an S4 class for structural time series models and provides some basic methods to work with it. / GPL-2	noarch
r-stuart	0.8.0	Construct subtests from a pool of items by using ant-colony-optimization, genetic algorithms, brute force, or random sampling. Schultze (2017) <doi:10.17169/refubium-622>. / GPL-3	noarch
r-stubthat	1.2.1	Create stubs of functions for use while testing. / MIT	noarch
r-stv	1.0.1	Implementations of the Single Transferable Vote counting system. By default, it uses the Cambridge method for surplus allocation and Droop method for quota calculation. Fractional surplus allocation and the Hare quota are available as options. / LGPL-3	noarch
r-stylest	0.1.0	Estimates distinctiveness in speakers' (authors') style. Fits models that can be used for predicting speakers of new texts. Methods developed in Spirling et al (2018) <doi:10.2139/ssrn.3235506> (working paper). / GPL-3	noarch
r-subcopem2d	1.3	Calculate empirical subcopula and dependence measures from a given bivariate sample, and Bernstein copula approximations. / GPL-3	noarch
r-subcultcon	1.0	The three functions in the package compute the maximum likelihood estimates of the informants' competence scores, tests for two answer keys with known groups, and finds best split of the informants into sub-culture groups. / GPL-2   GPL-3	noarch
r-subdetect	1.1	A test for the existence of a subgroup with enhanced treatment effect. And, a sample size calculation procedure for the subgroup detection test. / GPL-3	noarch
r-subgroup	1.1	Produces various measures of expected treatment effect heterogeneity under an assumption of homogeneity across subgroups. Graphical presentations are created to compare these expected differences with the observed differences. / GPL-2   GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-subgroup.discovery</a>	0.2.1	Developed to assist in discovering interesting subgroups in high-dimensional data. The PRIM implementation is based on the 1998 paper Bump hunting in high-dimensional data by Jerome H. Friedman and Nicholas I. Fisher. <doi:10.1023/A:1008894516817> PRIM involves finding a set of rules which combined imply unusually large (or small) values of some other target variable. Specifically one tries to find a set of sub regions in which the target variable is substantially larger than overall mean. The objective of bump hunting in general is to find regions in the input (attribute/feature) space with relatively high (low) values for the target variable. The regions are described by simple rules of the type if: condition-1 and ... and condition-n then: estimated target value. Given the data (or a subset of the data), the goal is to produce a box B within which the target mean is as large as possible. There are many problems where finding such regions is of considerable practical interest. Often these are problems where a decision maker can in a sense choose or select the values of the input variables so as to optimize the value of the target variable. In bump hunting it is customary to follow a so-called covering strategy. This means that the same box construction (rule induction) algorithm is applied sequentially to subsets of the data. / GPL-3	noarch
<a href="#">r-subgxe</a>	0.9.0	Classical methods for combining summary data from genome-wide association studies (GWAS) only use marginal genetic effects and power can be compromised in the presence of heterogeneity. ‘subgxe’ is a R package that implements p-value assisted subset testing for association (pASTA), a method developed by Yu et al. (2019) <doi:10.1159/000496867>. pASTA generalizes association analysis based on subsets by incorporating gene-environment interactions into the testing procedure. / GPL-3	noarch
<a href="#">r-subniche</a>	0.9.7	Complementary indexes calculation to the Outlying Mean Index analysis to explore niche shift of a community and biological constraint within an Euclidean space, with graphical displays. / GPL-2	noarch
<a href="#">r-subpathwaygmir</a>	1.0	Routines for identifying metabolic subpathways mediated by microRNAs (miRNAs) through topologically locating miRNAs and genes within reconstructed Kyoto Encyclopedia of Genes and Genomes (KEGG) metabolic pathway graphs embedded by miRNAs. (1) This package can obtain the reconstructed KEGG metabolic pathway graphs with genes and miRNAs as nodes, through converting KEGG metabolic pathways to graphs with genes as nodes and compounds as edges, and then integrating miRNA-target interactions verified by low-throughput experiments from four databases (TarBase, miRecords, mirTarBase and miR2Disease) into converted pathway graphs. (2) This package can locate metabolic subpathways mediated by miRNAs by topologically analyzing the lenient distance of miRNAs and genes within reconstructed KEGG metabolic pathway graphs.(3) This package can identify significantly enriched miRNA-mediated metabolic subpathways based on located subpathways by hypergenomic test. (4) This package can support six species for metabolic subpathway identification, such as caenorhabditis elegans, drosophila melanogaster, danio rerio, homo sapiens, mus musculus and rattus norvegicus, and user only need to update interested organism-specific environment variables. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-subsamp	0.1.0	This subsample winner algorithm (SWA) for regression with a large-p data (X, Y) selects the important variables (or features) among the p features X in explaining the response Y. The SWA first uses a base procedure, here a linear regression, on each of subsamples randomly drawn from the p variables, and then computes the scores of all features, i.e., the p variables, according to the performance of these features collected in each of the subsample analyses. It then obtains the ‘semifinalist’ of the features based on the resulting scores and determines the ‘finalists’, i.e., the important features, from the ‘semifinalist’. Fan, Sun and Qiao (2017) < <a href="http://sr2c.case.edu/swa-reg/">http://sr2c.case.edu/swa-reg/</a> >. / GPL-2   GPL-3	noarch
r-sudoku	2.6	Generates, plays, and solves Sudoku puzzles. The GUI playSudoku() needs package tkrplot if you are not on Windows. / GPL-3	noarch
r-sudokualt	0.2.0	Tools for making, retrieving, displaying and solving sudoku games. This package is an alternative to the earlier sudoku-solver package, ‘sudoku’. The present package uses a slightly different algorithm, has a simpler coding and presents a few more sugar tools, such as plot and print methods. Solved sudoku games are of some interest in Experimental Design as examples of Latin Square designs with additional balance constraints. / GPL-2	noarch
r-sue	1.0	This is a package for the subsampling method of robust estimation of linear regression models / GPL-2	noarch
r-suncalc	0.5.0	Get sun position, sunlight phases (times for sunrise, sunset, dusk, etc.), moon position and lunar phase for the given location and time. Most calculations are based on the formulas given in Astronomy Answers articles about position of the sun and the planets : < <a href="https://www.aa.quae.nl/en/reken/zonpositie.html">https://www.aa.quae.nl/en/reken/zonpositie.html</a> >. / GPL-2	noarch
r-sunclarco	1.0.0	Survival analysis for unbalanced clusters using Archimedean copulas (Prenen et al. (2016) <DOI:10.1111/rssb.12174>). / GPL-3	noarch
r-suntersampling	1.0.1	Functions for drawing samples according to Sunter’s sampling design, and for computing first and second order inclusion probabilities / GPL-3	noarch
r-supcluster	1.0	Clusters features under the assumption that each cluster has a random effect and there is an outcome variable that is related to the random effects by a linear regression. In this way the cluster analysis is “supervised” by the outcome variable. An alternate specification is that features in each cluster have the same compound symmetric normal distribution, and the conditional distribution of the outcome given the features has the same coefficient for each feature in a cluster. / GPL-2	noarch
r-superdiag	1.1	A Comprehensive Test Suite for Markov Chain Nonconvergence. / GPL-3	noarch
r-supermds	1.0.2	Witten and Tibshirani (2011) Supervised multidimensional scaling for visualization, classification, and bipartite ranking. Computational Statistics and Data Analysis 55(1): 789-801. / GPL-2	noarch
r-supernova	2.0.0	Produces ANOVA tables in the format used by Judd, McClelland, and Ryan (2017, ISBN:978-1138819832) in their introductory textbook, Data Analysis. This includes proportional reduction in error and formatting to improve ease the transition between the book and R. / GPL-3	noarch
r-superpc	1.09	Supervised principal components for regression and survival analysis. Especially useful for high-dimensional data, including microarray data. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-suppdist</a>	1.1_9.4	Ten distributions supplementing those built into R. Inverse Gauss, Kruskal-Wallis, Kendall's Tau, Friedman's chi squared, Spearman's rho, maximum F ratio, the Pearson product moment correlation coefficient, Johnson distributions, normal scores and generalized hypergeometric distributions. In addition two random number generators of George Marsaglia are included. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-support.bws</a>	0.2_0	Provides three basic functions that support an implementation of object case (Case 1) best-worst scaling: one for converting a two-level orthogonal main-effect design/balanced incomplete block design into questions; one for creating a data set suitable for analysis; and one for calculating count-based scores. / GPL-2	noarch
<a href="#">r-support.bws2</a>	0.2_2	Provides three basic functions that support an implementation of Case 2 (profile case) best-worst scaling. The first is to convert an orthogonal main-effect design into questions, the second is to create a dataset suitable for analysis, and the third is to calculate count-based scores. / GPL-2	noarch
<a href="#">r-surrogateoutcome</a>	1.0	Provides functions to estimate the proportion of treatment effect on a censored primary outcome that is explained by the treatment effect on a censored surrogate outcome/event. All methods are described in detail in Assessing the Value of a Censored Surrogate Outcome by Parast L, Tian L, and Cai T which is currently in press at Lifetime Data Analysis. The main functions are (1) R.q.event() which calculates the proportion of the treatment effect (the difference in restricted mean survival time at time t) explained by surrogate outcome information observed up to a selected landmark time, (2) R.t.estimate() which calculates the proportion of the treatment effect explained by primary outcome information only observed up to a selected landmark time, and (3) IV.event() which calculates the incremental value of the surrogate outcome information. / GPL-3	noarch
<a href="#">r-surrogatetest</a>	1.1	Provides functions to test for a treatment effect in terms of the difference in survival between a treatment group and a control group using surrogate marker information obtained at some early time point in a time-to-event outcome setting. Nonparametric kernel estimation is used to estimate the test statistic and perturbation resampling is used for variance estimation. More details will be available in the future in: Parast L, Cai T, Tian L (2019). Using a Surrogate Marker for Early Testing of a Treatment Effect. Biometrics, In press. / GPL-3	noarch
<a href="#">r-surrosurvroc</a>	0.1.0	Nonparametric and semiparametric estimations of the time-dependent ROC curve for an incomplete failure time data with surrogate failure time endpoints. / GPL-2	noarch
<a href="#">r-surtex</a>	0.9	suRtex was designed for easy descriptive statistic reporting of categorical survey data (e.g., Likert scales) in LaTeX. suRtex takes a matrix or data frame and produces the LaTeX code necessary for a sideways table creation. Mean, median, standard deviation, and sample size are optional. / GPL-3	noarch
<a href="#">r-survawkmt2</a>	1.0.0	Tests for equality of two survival functions based on integrated weighted differences of two Kaplan-Meier curves. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-survbootoutliers</a>	1.0	Three new methods to perform outlier detection in a survival context. In total there are six methods provided, the first three methods are traditional residual-based outlier detection methods, the second three are the concordance-based. Package developed during the work on the two following publications: Pinto J., Carvalho A. and Vinga S. (2015) <doi:10.5220/0005225300750082>; Pinto J.D., Carvalho A.M., Vinga S. (2015) <doi:10.1007/978-3-319-27926-8_22>. / GPL-2	noarch
<a href="#">r-survexp.fr</a>	1.0	Relative survival, AER and SMR based on French death rates / GPL-2	noarch
<a href="#">r-surveyeditor</a>	1.0	Help generate slides for surveys or experiments. The resulted slides allow the subject to respond with the use of the mouse (usual keyboard input is replaced with clicking on a virtual keyboard on the slide). Subjects' responses are saved to the user- specified location in the form of R-readable text file. To allow flexibility, each function in this package generates a particular type of slides thus general R function writing skills are required to compile these edited slides. / GPL-2	noarch
<a href="#">r-surveyoutliers</a>	0.1	At present, the only functionality is the calculation of optimal one-sided winsorizing cutoffs. The main function is <code>optimal.onesided.cutoff.bygroup</code> . It calculates the optimal tuning parameter for one-sided winsorisation, and so calculates winsorised values for a variable of interest. See the help file for this function for more details and an example. / GPL-2   GPL-3	noarch
<a href="#">r-survgini</a>	1.0	The Gini concentration test for survival data is a nonparametric test based on the Gini index for testing the equality of two survival distributions from the point of view of concentration. The package compares different nonparametric tests (asymptotic Gini test, permutation Gini test, log-rank test, Gray-Tsiatis test and Wilcoxon test) and computes their p-values. / GPL-2	noarch
<a href="#">r-survival</a>	2.44	Contains the core survival analysis routines, including definition of Surv objects, Kaplan-Meier and Aalen-Johansen (multi-state) curves, Cox models, and parametric accelerated failure time models. / LGPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-survjamda.data</a>	1.0.2	Three breast cancer gene expression data sets that can be used for package 'survJamda'. This package contains the gene expression and phenotype data of GSE1992, GSE3143 and GSE4335. / GPL-2	noarch
<a href="#">r-survlong</a>	1.0	Kernel weighting methods for estimation of proportional hazards models with intermittently observed longitudinal covariates. / GPL-2	noarch
<a href="#">r-survregcenscov</a>	1.4	The main function of this package allows estimation of a Weibull Regression for a right-censored endpoint, one interval-censored covariate, and an arbitrary number of non-censored covariates. Additional functions allow to switch between different parametrizations of Weibull regression used by different R functions, inference for the mean difference of two arbitrarily censored Normal samples, and estimation of canonical parameters from censored samples for several distributional assumptions. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-survrm2</a>	1.0.2	Performs two-sample comparisons using the restricted mean survival time (RMST) as a summary measure of the survival time distribution. Three kinds of between-group contrast metrics (i.e., the difference in RMST, the ratio of RMST and the ratio of the restricted mean time lost (RMTL)) are computed. It performs an ANCOVA-type covariate adjustment as well as unadjusted analyses for those measures. / GPL-2	noarch
<a href="#">r-survrm2adapt</a>	1.0.1	Performs the procedure proposed by Horiguchi et al. (2018) <doi:10.1002/sim.7661>. The method specifies a set of truncation time points tau's for calculating restricted mean survival times (RMST), performs testing for equality, and estimates the difference in RMST between two groups at the specified tau's. Multiplicity by specifying several tau's is taken into account in this procedure. / GPL-2	noarch
<a href="#">r-survtrunc</a>	0.1.0	Package performs Cox regression and survival distribution function estimation when the survival times are subject to double truncation. The estimation procedure for each method involves inverse probability weighting, where the weights correspond to the inverse of the selection probabilities and are estimated using the survival times and truncation times only. Both methods require that the survival and truncation times are quasi-independent. A test for checking this independence assumption is also included in this package. The functions available in this package for Cox regression, survival distribution function estimation, and testing independence under double truncation are based on the following methods, respectively: Rennert and Xie (2017) <doi:10.1111/biom.12809>, Shen (2010) <doi:10.1007/s10463-008-0192-2>, Martin and Betensky (2005) <doi:10.1198/016214504000001538>. / GPL-2	noarch
<a href="#">r-svapls</a>	1.4	Accurate identification of genes that are truly differentially expressed over two sample varieties, after adjusting for hidden subject-specific effects of residual heterogeneity. / GPL-3	noarch
<a href="#">r-svdvisual</a>	1.1	Some visualization tools based on Singular Value Decomposition / GPL-2	noarch
<a href="#">r-svenssonm</a>	0.1.0	Obtain parameters of Svensson's Method, including percentage agreement, systematic change and individual change. Also, the contingency table can be generated. Svensson's Method is a rank-invariant nonparametric method for the analysis of ordered scales which measures the level of change both from systematic and individual aspects. For the details, please refer to Svensson E. Analysis of systematic and random differences between paired ordinal categorical data [dissertation]. Stockholm: Almqvist & Wiksell International; 1993. / GPL-3	noarch
<a href="#">r-svgpanzoom</a>	0.3.3	This 'htmlwidget' provides pan and zoom interactivity to R graphics, including 'base', 'lattice', and 'ggplot2'. The interactivity is provided through the 'svg-pan-zoom.js' library. Various options to the widget can tailor the pan and zoom experience to nearly any user desire. / MIT	noarch
<a href="#">r-svgui</a>	1.0.0	The SciViews svGUI package eases the management of Graphical User Interfaces (GUI) in R. It is independent from any particular GUI widgets (Tk, Gtk2, native, ...). It centralizes info about GUI elements currently used, and it dispatches GUI calls to the particular toolkits in use in function of the context (is R run at the terminal, within a Tk application, a HTML page?). / GPL-2	noarch
<a href="#">r-svmisc</a>	1.1.0	Miscellaneous functions for SciViews or general use: manage a temporary environment attached to the search path for temporary variables you do not want to save() or load(), test if Aqua, Mac, Win, ... Show progress bar, etc. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-svmplus</a>	1.0.1	Implementation of Support Vector Machines Plus (SVM) for classification problems. See (Vladimir et. al, 2009, <doi:10.1016/j.neunet.2009.06.042>) for theoretical details and see (Li et. al, 2016, < <a href="https://github.com/okbalefthanded/svmplus_matlab">https://github.com/okbalefthanded/svmplus_matlab</a> >) for implementation details in ‘MATLAB’. / GPL-3	noarch
<a href="#">r-svn</a>	1.0	Determines networks of significant synchronization between the discrete states of nodes; see Tumminello et al <doi:10.1371/journal.pone.0017994>. / GPL (>= 2.0)	noarch
<a href="#">r-svs</a>	1.1.0	Various tools for semantic vector spaces, such as correspondence analysis (simple, multiple and discriminant), latent semantic analysis, probabilistic latent semantic analysis, non-negative matrix factorization, latent class analysis and EM clustering. Furthermore, there are specialized distance measures, plotting functions and some helper functions. / GPL-3	noarch
<a href="#">r-svsweave</a>	0.9.8	Supporting functions for the GUI API (Sweave functions) / GPL-2	noarch
<a href="#">r-svunit</a>	0.7.1	A complete unit test system and functions to implement its GUI part / GPL-2	noarch
<a href="#">r-swagger</a>	3.9.2	A collection of ‘HTML’, ‘JavaScript’, and ‘CSS’ assets that dynamically generate beautiful documentation from a ‘Swagger’ compliant API: < <a href="https://swagger.io/specification/">https://swagger.io/specification/</a> >. / Apache License 2.0   file LICENSE	noarch
<a href="#">r-swapclass</a>	1.0.1	A null model randomizing semi-quantitative multi-classes (or ordinal) data by swapping sub-matrices while both the row and the column marginal sums are held constant. / GPL-3	noarch
<a href="#">r-swcrtdesign</a>	3.0	A set of tools for examining the design and analysis aspects of stepped wedge cluster randomized trials (SW CRT) based on a repeated cross-sectional sampling scheme (Hussey MA and Hughes JP (2007) Contemporary Clinical Trials 28:182-191. <doi:10.1016/j.cct.2006.05.007>). / GPL-2	noarch
<a href="#">r-swdft</a>	1.0.0	Implements the Sliding Window Discrete Fourier Transform (SWDFT). Also provides statistical methods based on the SWDFT, and graphical tools to display the outputs. / MIT	noarch
<a href="#">r-sweidnumbr</a>	1.4.1	Structural handling of identity numbers used in the Swedish administration such as personal identity numbers (‘personnummer’) and organizational identity numbers (‘organisationsnummer’). / BSD_2_clause	noarch
<a href="#">r-swirl</a>	2.4.4	Use the R console as an interactive learning environment. Users receive immediate feedback as they are guided through self-paced lessons in data science and R programming. / MIT	noarch
<a href="#">r-swissair</a>	1.1.5	Ozone, NOx (= Sum of nitrogen monoxide and nitrogen dioxide), nitrogen monoxide, ambient temperature, dew point, wind speed and wind direction at 3 sites around lake of Lucerne in Central Switzerland in 30 min time resolution for year 2004. / GPL-3	noarch
<a href="#">r-swissmrp</a>	0.62	Provides a number of useful functions to employ MrP for small area prediction in Switzerland. Based on a hierarchical model and survey data one can derive cantonal preference measures. The package allows to automatize the prediction and post-stratification steps. It further provides adequate print, summary, map, and plot functions for objects of its class. / GPL-2	noarch
<a href="#">r-switchr</a>	0.13.5	Provides an abstraction for managing, installing, and switching between sets of installed R packages. This allows users to maintain multiple package libraries simultaneously, e.g. to maintain strict, package-version-specific reproducibility of many analyses, or work within a development/production release paradigm. Introduces a generalized package installation process which supports multiple repository and non-repository sources and tracks package provenance. / Artistic-2.0	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-sybil</a>	2.1.5	This Systems Biology Package (Gelius-Dietrich et. al. (2012) <doi:10.1186/1752-0509-7-125>) implements algorithms for constraint based analyses of metabolic networks, e.g. flux-balance analysis (FBA), minimization of metabolic adjustment (MOMA), regulatory on/off minimization (ROOM), robustness analysis and flux variability analysis. The package is easily extendable for additional algorithms. Most of the current LP/MILP solvers are supported via additional packages. / GPL-3	noarch
<a href="#">r-sylly</a>	0.1_5	Provides the hyphenation algorithm used for ‘TeX’/‘LaTeX’ and similar software, as proposed by Liang (1983, < <a href="https://tug.org/docs/liang/">https://tug.org/docs/liang/</a> >). Mainly contains the function hyphen() to be used for hyphenation/syllable counting of text objects. It was originally developed for and part of the ‘koRpus’ package, but later released as a separate package so it’s lighter to have this particular functionality available for other packages. Support for various languages needs be added on-the-fly or by plugin packages (< <a href="https://undocumeantit.github.io/repos/">https://undocumeantit.github.io/repos/</a> >); this package does not include any language specific data. Due to some restrictions on CRAN, the full package sources are only available from the project homepage. To ask for help, report bugs, request features, or discuss the development of the package, please subscribe to the koRpus-dev mailing list (< <a href="http://korporusml.reaktanz.de">http://korporusml.reaktanz.de</a> >). / GPL-3	noarch
<a href="#">r-sym.arma</a>	1.0	Functions for fitting the Autoregressive and Moving Average Symmetric Model for univariate time series introduced by Maior and Cysneiros (2018), <doi:10.1007/s00362-016-0753-z>. Fitting method: conditional maximum likelihood estimation. For details see: Wei (2006), Time Series Analysis: Univariate and Multivariate Methods, Section 7.2. / GPL-2	noarch
<a href="#">r-synbreeddata</a>	1.5	Data sets for the ‘synbreed’ package with three data sets from cattle, maize and mice to illustrate the functions in the ‘synbreed’ R package. All data sets are stored in the gpData format introduced in the ‘synbreed’ package. This research was funded by the German Federal Ministry of Education and Research (BMBF) within the AgroClustEr Synbreed - Synergistic plant and animal breeding (FKZ 0315528A). / GPL-2	noarch
<a href="#">r-synchrony</a>	0.3.7	Methods for computing spatial, temporal, and spatiotemporal statistics including: empirical univariate, bivariate and multivariate variograms; fitting variogram models; phase locking and synchrony analysis; generating autocorrelated and cross-correlated matrices. / GPL-2	noarch
<a href="#">r-syncmove</a>	0.1_0	The function ‘syncSubsample’ subsamples temporal data of different entities so that the result only contains synchronal events. The function ‘mci’ calculates the Movement Coordination Index (MCI, see reference on help page for function ‘mci’) of a data set created with the function ‘syncSubsample’. / GPL-2	noarch
<a href="#">r-synet</a>	2.0	Infers sympatry matrices from distributional data and analyzes them in order to identify groups of species cohesively connected. / GPL-3	noarch
<a href="#">r-syntaxr</a>	0.8.0	A set of functions for generating ‘SPSS’ syntax files from the R environment. / MIT	noarch
<a href="#">r-sys</a>	3.2	Drop-in replacements for the base system2() function with fine control and consistent behavior across platforms. Supports clean interruption, timeout, background tasks, and streaming STDIN / STDOUT / STDERR over binary or text connections. Arguments on Windows automatically get encoded and quoted to work on different locales. / MIT file LICENSE	linux-64, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
<code>r-t2eq</code>	1.1	Contains functions for applying the T <sup>2</sup> -test for equivalence. The T <sup>2</sup> -test for equivalence is a multivariate two-sample equivalence test. Distance measure of the test is the Mahalanobis distance. For multivariate normally distributed data the T <sup>2</sup> -test for equivalence is exact and UMPI. The function T2EQ() implements the T <sup>2</sup> -test for equivalence according to Wellek (2010) <DOI:10.1201/ebk1439808184>. The function T2EQ.dissolution.profiles.hoffelder() implements a variant of the T <sup>2</sup> -test for equivalence according to Hoffelder (2016) < <a href="http://www.ecv.de/suse_item.php?suseId=Zlpil8430">http://www.ecv.de/suse_item.php?suseId=Zlpil8430</a> > for the equivalence comparison of highly variable dissolution profiles. / GPL-3	noarch
<code>r-tablaxlsx</code>	1.2.2	Some functions are included in this package for writing tables in Excel format suitable for distribution. / GPL-3	noarch
<code>r-table1</code>	1.1	Create HTML tables of descriptive statistics, as one would expect to see as the first table (i.e. Table 1) in a medical/epidemiological journal article. / GPL-3	noarch
<code>r-table1heatmap</code>	1.1	Table 1 is the classical way to describe the patients in a clinical study. The amount of splits in the data in such a table is limited. Table1Heatmap draws a heatmap of all crosstables that can be generated with the data. Users can choose between showing the actual crosstables or direction of effect of associations, and highlight associations by number of patients or p-values. / LGPL-3	noarch
<code>r-tablehtml</code>	2.0.0	A tool to create and style HTML tables with CSS. These can be exported and used in any application that accepts HTML (e.g. 'shiny', 'rmarkdown', 'PowerPoint'). It also provides functions to create CSS files (which also work with shiny). / MIT	noarch
<code>r-tablematrix</code>	0.82.0	Provides two classes extending 'data.table' class. Simple 'tableList' class wraps 'data.table' and any additional structures together. More complex 'tableMatrix' class combines 'data.table' and 'matrix'. See < <a href="http://github.com/InferenceTechnologies/tableMatrix">http://github.com/InferenceTechnologies/tableMatrix</a> > for more information and examples. / GPL-2	noarch
<code>r-tablemonster</code>	1.7	Provides a user friendly interface to generation of booktab style tables using 'xtable'. / GPL-2	noarch
<code>r-tableplot</code>	0.3.5	Description: / GPL-3	noarch
<code>r-tablerdash</code>	0.1.0	'R' interface to the 'Tabler' HTML template. See more here < <a href="https://tabler.io">https://tabler.io</a> >. 'tablerDash' is a light 'Bootstrap 4' dashboard template. There are different layouts available such as a one page dashboard or a multi page template, where the navigation menu is contained in the navigation bar. A fancy example is available at < <a href="https://dgranjon.shinyapps.io/shinyMons/">https://dgranjon.shinyapps.io/shinyMons/</a> >. / GPL-2	noarch
<code>r-tabletolongform</code>	1.3.2	A wrapper to a set of algorithms designed to recognise positional cues present in hierarchical for-human Tables (which would normally be interpreted visually by the human brain) to decompose, then reconstruct the data into machine-readable LongForm Dataframes. / GPL-3	noarch
<code>r-tabulizerjars</code>	1.0.1	'Java' .jar files for the 'Tabula' < <a href="http://tabula.technology/">http://tabula.technology/</a> > 'Java' library, which are required by the 'tabulizer' R package. The version numbering of this package corresponds to versions of 'tabula-java' library releases < <a href="https://github.com/tabulapdf/tabula-java/releases/">https://github.com/tabulapdf/tabula-java/releases/</a> >. / MIT	noarch
<code>r-tabulog</code>	0.1.1	Convert semi-structured log files (such as 'Apache' access.log files) into a tabular format (data.frame) using a standard template system. / MIT	noarch
<code>r-tabusearch</code>	1.1.1	Tabu search algorithm for binary configurations. A basic version of the algorithm as described by Fouskakis and Draper (2007) <doi:10.1111/j.1751-5823.2002.tb00174.x>. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-tactile</a>	0.2.0	Extensions to ‘lattice’, providing new high-level functions, methods for existing functions, panel functions, and a theme. / GPL-3	noarch
<a href="#">r-tailloss</a>	1.0	Set of tools to estimate the probability in the upper tail of the aggregate loss distribution using different methods: Panjer recursion, Monte Carlo simulations, Markov bound, Cantelli bound, Moment bound, and Chernoff bound. / GPL-2   GPL-3	noarch
<a href="#">r-taipan</a>	0.1.2	A tool to help create shiny apps for selecting and annotating elements of images. Users must supply images, questions, and answer choices. The user interface is a dynamic shiny app, that displays the images and questions and answer choices. The data generated can be saved to a file that can be used for subsequent analysis. The original purpose was to annotate still images from tennis video for face recognition and emotion detection purposes. / GPL-3	noarch
<a href="#">r-tandem</a>	1.0.2	A two-stage regression method that can be used when various input data types are correlated, for example gene expression and methylation in drug response prediction. In the first stage it uses the upstream features (such as methylation) to predict the response variable (such as drug response), and in the second stage it uses the downstream features (such as gene expression) to predict the residuals of the first stage. In our manuscript (Aben et al., 2016, <doi:10.1093/bioinformatics/btw449>), we show that using TANDEM prevents the model from being dominated by gene expression and that the features selected by TANDEM are more interpretable. / GPL-2	noarch
<a href="#">r-tangram</a>	0.4	Provides an extensible formula system to quickly and easily create production quality tables. The steps of the process are formula parser, statistical content generation from data, to rendering. Each step of the process is separate and user definable thus creating a set of building blocks for highly extensible table generation. A user is not limited by any of the choices of the package creator other than the formula grammar. For example, one could chose to add a different S3 rendering function and output a format not provided in the default package. Or possibly one would rather have Gini coefficients for their statistical content. Routines to achieve New England Journal of Medicine style, Lancet style and Hmisc::summaryM() statistics are provided. The package contains rendering for HTML5, Rmarkdown and an indexing format for use in tracing and tracking are provided. / GPL-3	noarch
<a href="#">r-taoteprogramming</a>	1.0	Art-like behavior based on randomness / Unlimited	noarch
<a href="#">r-tapkee</a>	1.0	Wrapper for using ‘tapkee’ command line utility, it allows to run it from inside R and catch the results for further analysis and plotting. ‘Tapkee’ is a program for fast dimension reduction (see < <a href="http://tapkee.lisitsyn.me/">http://tapkee.lisitsyn.me/</a> > for more details). / GPL-2	noarch
<a href="#">r-tar</a>	1.0	Identification and estimation of the autoregressive threshold models with Gaussian noise, as well as positive-valued time series. The package provides the identification of the number of regimes, the thresholds and the autoregressive orders, as well as the estimation of remain parameters. The package implements the methodology from the 2005 paper: Modeling Bivariate Threshold Autoregressive Processes in the Presence of Missing Data <DOI:10.1081/STA-200054435>. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-tariff	1.0.5	Implement the Tariff algorithm for coding cause-of-death from verbal autopsies. The Tariff method was originally proposed in James et al (2011) <DOI:10.1186/1478-7954-9-31> and later refined as Tariff 2.0 in Serina, et al. (2015) <DOI:10.1186/s12916-015-0527-9>. Note that this package was not developed by authors affiliated with the Institute for Health Metrics and Evaluation and thus unintentional discrepancies may exist between the this implementation and the implementation available from IHME. / GPL-2	noarch
r-tariffx	1.0.6	A collection of various utility and convenience functions. / GPL-2	noarch
r-tatest	1.0	The ta-test is a modified two-sample or two-group t-test of Gosset (1908). In small samples with less than 15 replicates, the ta-test significantly reduces type I error rate but has almost the same power with the t-test and hence can greatly enhance reliability or reproducibility of discoveries in biology and medicine. The ta-test can test single null hypothesis or multiple null hypotheses without needing to correct p-values. / GPL-3	noarch
r-tatoo	1.1.1	Functions to combine data.frames in ways that require additional effort in base R, and to add metadata (id, title, ...) that can be used for printing and xlsx export. The 'Tatoo_report' class is provided as a convenient helper to write several such tables to a workbook, one table per worksheet. Tatoo is built on top of 'openxlsx', but intimate knowledge of that package is not required to use tatoo. / MIT	noarch
r-taup.r	1.5	Evaluates traveltimes and ray paths using predefined Earth (or other planet) models. Includes phase plotting routines. The IASP91 (Kennett and Engdahl, 1991 <doi:10.1111/j.1365-246X.1991.tb06724.x>) and AK135 (Kennett et al., 1995 <doi:10.1111/j.1365-246X.1995.tb03540.x>) Earth models are included, and most important arrival phases can be evaluated. / GPL-3	noarch
r-taxicabca	0.1.0	Computation and visualization of Taxicab Correspondence Analysis, Choulakian (2006) <doi:10.1007/s11336-004-1231-4>. Classical correspondence analysis (CA) is a statistical method to analyse 2-dimensional tables of positive numbers and is typically applied to contingency tables (Benzecri, J.-P. (1973). L'Analyse des Donnees. Volume II. L'Analyse des Correspondances. Paris, France: Dunod). Classical CA is based on the Euclidean distance. Taxicab CA is like classical CA but is based on the Taxicab or Manhattan distance. For some tables, Taxicab CA gives more informative results than classical CA. / GPL-2	noarch
r-tbd	0.1.0	Estimation of the survivor average causal effect under outcomes truncated by death, which requires the existence of a substitution variable. It can be applied to both experimental and observational data. / GPL-2	noarch
r-tbdiag	0.1	This package provides functions to assist researchers working in the field of tuberculosis diagnostics. Functions for the interpretation of two popular interferon-gamma release assays are provided, and additional functionality is planned. / MIT	noarch
r-tcgaretriever	1.3	The Cancer Genome Atlas (TCGA) is a program aimed at improving our understanding of Cancer Biology. Several TCGA Datasets are available online. 'TCGAretriever' helps accessing and downloading TCGA data hosted on 'cBioPortal' via its Web Interface (see < <a href="http://www.cbioportal.org/web_api.jsp">http://www.cbioportal.org/web_api.jsp</a> > for more information). Features of 'TCGAretriever' include: 1) it is very simple to use (get all the TCGA data you need with a few lines of code); 2) performance (smooth and reliable data download via 'http'); 3) it is tailored for downloading large volumes of data. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-tciapathfinder</a>	1.0.5	A wrapper for The Cancer Imaging Archive’s REST API. The Cancer Imaging Archive (TCIA) hosts de-identified medical images of cancer available for public download, as well as rich metadata for each image series. TCIA provides a REST API for programmatic access to the data. This package provides simple functions to access each API endpoint. For more information, see < <a href="https://github.com/pamelarussell/TCIApathfinder">https://github.com/pamelarussell/TCIApathfinder</a> > and TCIA’s website. / MIT	noarch
<a href="#">r-tcltk2</a>	1.2.1	A series of additional Tcl commands and Tk widgets with style and various functions (under Windows: DDE exchange, access to the registry and icon manipulation) to supplement the tcltk package / LGPL-3	noarch
<a href="#">r-tdamapper</a>	1.0	Topological Data Analysis using Mapper (discrete Morse theory). Generate a 1-dimensional simplicial complex from a filter function defined on the data: 1. Define a filter function (lens) on the data. 2. Perform clustering within within each level set and generate one node (vertex) for each cluster. 3. For each pair of clusters in adjacent level sets with a nonempty intersection, generate one edge between vertices. The function mapper1D uses a filter function with codomain R, while the the function mapper2D uses a filter function with codomain $R^2$ . / GPL-3	noarch
<a href="#">r-tdcor</a>	0.1.2	The Time-Delay Correlation algorithm (TDCor) reconstructs the topology of a gene regulatory network (GRN) from time-series transcriptomic data. The algorithm is described in details in Lavenus et al., Plant Cell, 2015. It was initially developed to infer the topology of the GRN controlling lateral root formation in Arabidopsis thaliana. The time-series transcriptomic dataset which was used in this study is included in the package to illustrate how to use it. / GPL-2	noarch
<a href="#">r-tdpanalysis</a>	0.99	Set of functions designed to help in the analysis of TDP sensors. Features includes dates and time conversion, weather data interpolation, daily maximum of tension analysis and calculations required to convert sap flow density data to sap flow rates at the tree and plot scale (For more information see : Granier (1985) <DOI:10.1051/forest:19850204> & Granier (1987) <DOI:10.1093/treephys/3.4.309>). / GPL-2	noarch
<a href="#">r-tdroc</a>	1.0	Compute time-dependent ROC curve from censored survival data using non-parametric weight adjustments. / GPL-2	noarch
<a href="#">r-tdsc</a>	1.0.0	Functions for performing time domain signal coding as used in Chesmore (2001) <doi:10.1016/S0003-682X(01)00009-3>, and related tasks. This package creates the standard S-matrix and A-matrix (with variable lag), has tools to convert coding matrices into distributed matrices, provides published code-books and allows for extraction of code sequences. / GPL-3	noarch
<a href="#">r-teachingdemos</a>	2.10	Demonstration functions that can be used in a classroom to demonstrate statistical concepts, or on your own to better understand the concepts or the programming. / Artistic-2.0	noarch
<a href="#">r-teachingsampling</a>	3.4.2	Allows the user to draw probabilistic samples and make inferences from a finite population based on several sampling designs. / GPL-2	noarch
<a href="#">r-teachnet</a>	0.7.1	Can fit neural networks with up to two hidden layer and two different error functions. Also able to handle a weight decay. But just able to compute one output neuron and very slow. / GPL-2	noarch
<a href="#">r-teamr</a>	0.0.1	Package of wrapper functions using R6 class to send requests to Microsoft ‘Teams’ < <a href="https://products.office.com/en-us/microsoft-teams/group-chat-software">https://products.office.com/en-us/microsoft-teams/group-chat-software</a> > through webhooks. When you need to share information or data from R to ‘Teams’, rather than copying/pasting, you can use this package to send well-formatted output from multiple R objects. / MIT	noarch

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Name	Version	Summary/License	Platforms
r-teda	0.1.1	The typicality and eccentricity data analysis (TEDA) framework was put forward by Angelov (2013) <DOI:10.14313/JAMRIS_2-2014/16>. It has been further developed into multiple different techniques since, and provides a non-parametric way of determining how similar an observation, from a process that is not purely random, is to other observations generated by the process. This package provides code to use the batch and recursive TEDA methods that have been published. / GPL-3	noarch
r-teereg	1.1	For fitting multiple linear regressions, the ordinary least squares approach is sensitive to outliers and/or violations of model assumptions. The trimmed elemental estimators are more robust to such situations. This package contains functions for computing the trimmed elemental estimates, as well as for creating the bias-corrected and accelerated bootstrap confidence intervals based on elemental regressions. / GPL-2	noarch
r-tejapi	1.0.1	Functions for interacting directly with the Taiwan Economic Journal API to offer data in R. For more information go to < <a href="https://api.tej.com.tw">https://api.tej.com.tw</a> >. / MIT	noarch
r-telegram	0.6.0	R wrapper around the Telegram Bot API ( <a href="http://core.telegram.org/bots/api">http://core.telegram.org/bots/api</a> ) to access Telegram's messaging facilities with ease (e.g. you send messages, images, files from R to your smartphone). / GPL-3	noarch
r-telegram.bot	2.3.1	Provides a pure interface for the 'Telegram Bot API' < <a href="http://core.telegram.org/bots/api">http://core.telegram.org/bots/api</a> >. In addition to the pure API implementation, it features a number of tools to make the development of 'Telegram' bots with R easy and straightforward, providing an easy-to-use interface that takes some work off the programmer. / GPL-3	noarch
r-tempcont	0.1.0	Method to estimate the effect of the trend in predictor variables on the observed trend of the response variable using mixed models with temporal autocorrelation. See Fernández-Martínez et al. (2017 and 2019) <doi:10.1038/s41598-017-08755-8> <doi:10.1038/s41558-018-0367-7>. / GPL-2	noarch
r-tempcyclesdata	1.0.1	This is the data companion package to the package tempcycles. This package includes the metadata, linear, and cycling parameters from Recent geographic convergence in diurnal and annual temperature cycling flattens global thermal profiles, Wang & Dillon, Nature Climate Change, 4, 988-992 (2014). doi:10.1038/nclimate2378. / GPL-2	noarch
r-tempdisagg	0.25.0	Temporal disaggregation methods are used to disaggregate and interpolate a low frequency time series to a higher frequency series, where either the sum, the average, the first or the last value of the resulting high frequency series is consistent with the low frequency series. Temporal disaggregation can be performed with or without one or more high frequency indicator series. Contains the methods of Chow-Lin, Santos-Silva-Cardoso, Fernandez, Litterman, Denton and Denton-Cholette. / GPL-3	noarch
r-tempor	1.0.4	TEMPO (TEmporal Modeling of Pathway Outliers) is a pathway-based outlier detection approach for finding pathways showing significant changes in temporal expression patterns across conditions. Given a gene expression data set where each sample is characterized by an age or time point as well as a phenotype (e.g. control or disease), and a collection of gene sets or pathways, TEMPO ranks each pathway by a score that characterizes how well a partial least squares regression (PLSR) model can predict age as a function of gene expression in the controls and how poorly that same model performs in the disease. TEMPO v1.0.3 is described in Pietras (2018) <doi:10.1145/3233547.3233559>. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<code>r-temptr</code>	0.9.9	Analysis and visualization of data from temporal sensory methods, including for temporal check-all-that-apply (TCATA) and temporal dominance of sensations (TDS). / GPL-2	noarch
<code>r-tenispolar</code>	0.1.4	Implementation of ZENIT-POLAR substitution cipher method of encryption using by default the TENIS-POLAR cipher. This last cipher of encryption became famous through the collection of Brazilian books Os Karas by the author Pedro Bandeira. For more details, see A Cryptographic Dictionary (GC&CS, 1944). / GPL-3	noarch
<code>r-tensor</code>	1.5	The tensor product of two arrays is notionally an outer product of the arrays collapsed in specific extents by summing along the appropriate diagonals. / GPL-2	noarch
<code>r-tensorflow</code>	1.13	Interface to ‘TensorFlow’ < <a href="https://www.tensorflow.org/">https://www.tensorflow.org/</a> >, an open source software library for numerical computation using data flow graphs. Nodes in the graph represent mathematical operations, while the graph edges represent the multidimensional data arrays (tensors) communicated between them. The flexible architecture allows you to deploy computation to one or more ‘CPUs’ or ‘GPUs’ in a desktop, server, or mobile device with a single ‘API’. ‘TensorFlow’ was originally developed by researchers and engineers working on the Google Brain Team within Google’s Machine Intelligence research organization for the purposes of conducting machine learning and deep neural networks research, but the system is general enough to be applicable in a wide variety of other domains as well. / Apache License 2.0	linux-32, linux-64, noarch, osx-64, win-32, win-64
<code>r-tensorr</code>	0.1.1	Provides methods to manipulate and store sparse tensors. Tensors are multidimensional generalizations of matrices (two dimensional) and vectors (one dimensional). / GPL-3	noarch
<code>r-tenstr</code>	1.0.1	A collection of functions for Kronecker structured covariance estimation and testing under the array normal model. For estimation, maximum likelihood and Bayesian equivariant estimation procedures are implemented. For testing, a likelihood ratio testing procedure is available. This package also contains additional functions for manipulating and decomposing tensor data sets. This work was partially supported by NSF grant DMS-1505136. Details of the methods are described in Gerard and Hoff (2015) < <a href="https://doi.org/10.1016/j.jmva.2015.01.020">doi:10.1016/j.jmva.2015.01.020</a> > and Gerard and Hoff (2016) < <a href="https://doi.org/10.1016/j.laa.2016.04.033">doi:10.1016/j.laa.2016.04.033</a> >. / GPL-3	noarch
<code>r-teqr</code>	6.0_0	The TEQR package contains software to calculate the operating characteristics for the TEQR and the ACT designs. The TEQR (toxicity equivalence range) design is a toxicity based cumulative cohort design with added safety rules. The ACT (Activity constrained for toxicity) design is also a cumulative cohort design with additional safety rules. The unique feature of this design is that dose is escalated based on lack of activity rather than on lack of toxicity and is de-escalated only if an unacceptable level of toxicity is experienced. / GPL-2	noarch
<code>r-terapplusb</code>	1.0	This package is for the comparison of various types of AB escalation rules for dose finding trials. / LGPL-2.1	noarch
<code>r-ternary</code>	1.1.1	Plots ternary diagrams using the standard graphics functions. An alternative to ‘ggtern’, which uses the ‘ggplot2’ family of plotting functions. / GPL-2	noarch
<code>r-ternvis</code>	1.2	A suite of functions for visualising ternary probabilistic forecasts, as discussed in the paper by Jupp (2012) < <a href="https://doi.org/10.1098/rsta.2011.0350">doi:10.1098/rsta.2011.0350</a> >. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-testassay</a>	0.1.0	A common way of validating a biological assay for is through a procedure, where $m$ levels of an analyte are measured with $n$ replicates at each level, and if all $m$ estimates of the coefficient of variation (CV) are less than some pre-specified level, then the assay is declared validated for precision within the range of the $m$ analyte levels. Two limitations of this procedure are: there is no clear statistical statement of precision upon passing, and it is unclear how to modify the procedure for assays with constant standard deviation. We provide tools to convert such a procedure into a set of $m$ hypothesis tests. This reframing motivates the $m:n:q$ procedure, which upon completion delivers a 100q% upper confidence limit on the CV. Additionally, for a post-validation assay output of $y$ , the method gives an “effective standard deviation interval” of $\log(y)$ plus or minus $r$ , which is a 68% confidence interval on $\log(\mu)$ , where $\mu$ is the expected value of the assay output for that sample. Further, the $m:n:q$ procedure can be straightforwardly applied to constant standard deviation assays. We illustrate these tools by applying them to a growth inhibition assay. / MIT	noarch
<a href="#">r-testdriver</a>	0.5.1	Provides data sets for teaching statistics and data science courses. It includes a sample of data from John Edmund Kerrich’s famous coinflip experiment. These are data that I use for teaching SOC 4015 / SOC 5050 at Saint Louis University (SLU). The package also contains an R Markdown template with the required formatting for assignments in my courses SOC 4015, SOC 4650, SOC 5050, and SOC 5650 at SLU. / GPL-3	noarch
<a href="#">r-testequavar</a>	0.1.2	Tests the hypothesis that variances are homogeneous or not using bootstrap. The procedure uses a variance-based statistic, and is derived from a normal-theory test. The test equivalently expressed the hypothesis as a function of the log contrasts of the population variances. A box-type acceptance region is constructed to test the hypothesis. See Cahoy (2010) <doi:10.1016/j.csda.2010.04.012>. / GPL-3	noarch
<a href="#">r-tester</a>	0.1.7	tester allows you to test characteristics of common R objects. / GPL-3	noarch
<a href="#">r-testfunctions</a>	0.2.0	Test functions are often used to test computer code. They are used in optimization to test algorithms and in metamodeling to evaluate model predictions. This package provides test functions that can be used for any purpose. Some functions are taken from < <a href="https://www.sfu.ca/~ssurjano">https://www.sfu.ca/~ssurjano</a> >, but their R code is not used. / GPL-3	noarch
<a href="#">r-testingsimilarity</a>	1.1	Provides a bootstrap test which decides whether two dose response curves can be assumed as equal concerning their maximum absolute deviation. A plenty of choices for the model types are available, which can be found in the ‘DoseFinding’ package, which is used for the fitting of the models. See <doi:10.1080/01621459.2017.1281813> for details. / GPL-3	noarch
<a href="#">r-testit</a>	0.9	Provides two convenience functions <code>assert()</code> and <code>test_pkg()</code> to facilitate testing R packages. / GPL	linux-32, linux-64, noarch, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-testscorer</a>	1.7.2	GUI for entering test items and obtaining raw and transformed scores. The results are shown on the console and can be saved to a tabular text file for further statistical analysis. The user can define his own tests and scoring procedures through a GUI. / GPL-2	noarch
<a href="#">r-testthat</a>	2.1.1	Software testing is important, but, in part because it is frustrating and boring, many of us avoid it. ‘testthat’ is a testing framework for R that is easy learn and use, and integrates with your existing ‘workflow’. / MIT file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-texreg</a>	1.36.2	Converts coefficients, standard errors, significance stars, and goodness-of-fit statistics of statistical models into LaTeX tables or HTML tables/MS Word documents or to nicely formatted screen output for the R console for easy model comparison. A list of several models can be combined in a single table. The output is highly customizable. New model types can be easily implemented. / GPL-2   GPL-3	noarch
<a href="#">r-textgrid</a>	1.0.1	The software application Praat can be used to annotate waveform data (e.g., to mark intervals of interest or to label events). (See <a href="http://www.fon.hum.uva.nl/praat/">http://www.fon.hum.uva.nl/praat/</a> for more information about Praat.) These annotations are stored in a Praat TextGrid object, which consists of a number of interval tiers and point tiers. An interval tier consists of sequential (i.e., not overlapping) labeled intervals. A point tier consists of labeled events that have no duration. The ‘textgRid’ package provides S4 classes, generics, and methods for accessing information that is stored in Praat TextGrid objects. / GPL-3	noarch
<a href="#">r-textile</a>	0.1.2	Contains real images of the same textile material with/without local defects, which were used in Bui and Apley (2017) <doi:10.1080/00401706.2017.1302362>. / GPL-2	noarch
<a href="#">r-textometry</a>	0.1.4	Statistical exploration of textual corpora using several methods from French ‘Textometrie’ (new name of ‘Lexicometrie’) and French ‘Data Analysis’ schools. It includes methods for exploring irregularity of distribution of lexicon features across text sets or parts of texts (Specificity analysis); multi-dimensional exploration (Factorial analysis), etc. Those methods are used in the TXM software. / GPL-3	noarch
<a href="#">r-textrank</a>	0.3.0	The ‘textrank’ algorithm is an extension of the ‘Pagerank’ algorithm for text. The algorithm allows to summarize text by calculating how sentences are related to one another. This is done by looking at overlapping terminology used in sentences in order to set up links between sentences. The resulting sentence network is next plugged into the ‘Pagerank’ algorithm which identifies the most important sentences in your text and ranks them. In a similar way ‘textrank’ can also be used to extract keywords. A word network is constructed by looking if words are following one another. On top of that network the ‘Pagerank’ algorithm is applied to extract relevant words after which relevant words which are following one another are combined to get keywords. More information can be found in the paper from Mihalcea, Rada & Tarau, Paul (2004) < <a href="http://www.aclweb.org/anthology/W04-3252">http://www.aclweb.org/anthology/W04-3252</a> >. / MPL-2.0	noarch

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Name	Version	Summary/License	Platforms
r-textreg	0.1.5	Function for sparse regression on raw text, regressing a labeling vector onto a feature space consisting of all possible phrases. / MIT	linux-64, osx-64, win-64
r-textshape	1.6.0	Tools that can be used to reshape and restructure text data. / GPL-2	noarch
r-texttinyr	1.1.3	It offers functions for splitting, parsing, tokenizing and creating a vocabulary for big text data files. Moreover, it includes functions for building a document-term matrix and extracting information from those (term-associations, most frequent terms). It also embodies functions for calculating token statistics (collocations, look-up tables, string dissimilarities) and functions to work with sparse matrices. Lastly, it includes functions for Word Vector Representations (i.e. ‘GloVe’, ‘fasttext’) and incorporates functions for the calculation of (pairwise) text document dissimilarities. The source code is based on ‘C11’ and exported in R through the ‘Rcpp’, ‘RcppArmadillo’ and ‘BH’ packages. / GPL-3	linux-64, osx-64, win-64
r-textutils	0.1_1	Utilities for handling character vectors that store human-readable text (either plain or with markup, such as HTML or LaTeX). The package provides, in particular, functions that help with the preparation of plain-text reports (e.g. for expanding and aligning strings that form the lines of such reports); the package also provides generic functions for transforming R objects to HTML and to plain text. / GPL-3	noarch
r-tfcox	0.1.0	In Cox’s proportional hazard model, covariates are modeled as linear function and may not be flexible. This package implements additive trend filtering Cox proportional hazards model as proposed in Jiacheng Wu & Daniela Witten (2019) Flexible and Interpretable Models for Survival Data, Journal of Computational and Graphical Statistics, <DOI:10.1080/10618600.2019.1592758>. The fitted functions are piecewise polynomial with adaptively chosen knots. / GPL-2	linux-64, osx-64, win-64
r-tfdatasets	1.13.1	Interface to ‘TensorFlow’ Datasets, a high-level library for building complex input pipelines from simple, re-usable pieces. See < <a href="https://www.tensorflow.org/programmers_guide/datasets">https://www.tensorflow.org/programmers_guide/datasets</a> > for additional details. / Apache License 2.0	noarch
r-tfer	1.1	Statistical interpretation of forensic glass transfer (Simulation of the probability distribution of recovered glass fragments). / GPL-2	noarch
r-tfmpvalue	0.0.8	In putative Transcription Factor Binding Sites (TFBSs) identification from sequence/alignments, we are interested in the significance of certain match score. TFMPvalue provides the accurate calculation of P-value with score threshold for Position Weight Matrices, or the score with given P-value. It is an interface to code originally made available by Helene Touzet and Jean-Stephane Varre, 2007, Algorithms Mol Biol:2, 15. Touzet and Varre (2007) <DOI:10.1186/1748-7188-2-15>. / GPL-2	linux-64, osx-64, win-64
r-tframe	2015.12.1	A kernel of functions for programming time series methods in a way that is relatively independently of the representation of time. Also provides plotting, time windowing, and some other utility functions which are specifically intended for time series. See the Guide distributed as a vignette, or ?tframe.Intro for more details. (User utilities are in package tfplot.) / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<code>r-tfruns</code>	1.4	Create and manage unique directories for each ‘TensorFlow’ training run. Provides a unique, time stamped directory for each run along with functions to retrieve the directory of the latest run or latest several runs. / Apache License 2.0	linux-32, linux-64, noarch, osx-64, win-32, win-64
<code>r-tfse</code>	0.5.0	A collection of useful tools for programming and writing-scripts. Several functions are simple wrappers around base R functions that extend their functionality while also providing some convenient properties—regular expression functions that automatically detect look-ahead and look-behind statements, a read-line function that suppresses incomplete-final-line warnings and automatically opens and closes connections, a version of substrings that starts from the end of strings, etc. Other functions are useful for checking whether packages are installed, omitting missing data, and showing in-use connections. / MIT	noarch
<code>r-tfx</code>	0.1.0	Connects R to TrueFX(tm) for free streaming real-time and historical tick-by-tick market data for dealable interbank foreign exchange rates with millisecond detail. / GPL-3	noarch
<code>r-tgcd</code>	2.1	Deconvolving thermoluminescence glow curves according to various kinetic models (first-order, second-order, general-order, and mixed-order) using a modified Levenberg-Marquardt algorithm. It provides the possibility of setting constraints or fixing any of parameters. It offers an interactive way to initialize parameters by clicking with a mouse on a plot at positions where peak maxima should be located. The optimal estimate is obtained by trial-and-error. It also provides routines for simulating first-order, second-order, and general-order glow peaks. / GPL-2   GPL-3	linux-64, osx-64, win-64
<code>r-tggd</code>	0.1.1	Density, distribution function, quantile function and random generation for the Truncated Generalised Gamma Distribution (also in log10(x) and ln(x) space). / GPL-3	noarch
<code>r-tgram</code>	0.2_3	Functions to compute and plot tracheidograms, as in De Soto et al. (2011) <doi:10.1139/x11-045>. / GPL-2	noarch
<code>r-th.data</code>	1.0_1	Contains data sets used in other packages Torsten Hothorn maintains. / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
<code>r-thankr</code>	1.0.0	Find out who maintains the packages you use in your current session or in your package library and maybe say ‘thank you’. / MIT	noarch
<code>r-thankyoustars</code>	0.2.0	A tool for starring GitHub repositories. / MIT	noarch

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Name	Version	Summary/License	Platforms
r-thermindex	0.2.0	Calculates several thermal comfort indexes using temperature, wind speed and relative humidity values, calculating indexes such as Humidex, windchill, Discomfort Index and others. / GPL-2	noarch
r-thermocouple	1.0.2	Temperature measurement data, equations and methods for thermocouples, wire RTD, thermistors, IC thermometers, bimetallic strips and the ITS-90. / GPL-3	noarch
r-thgenetics	0.4.2	A step-up test for genetic rare variants in a gene or in a pathway. The method determines an optimal grouping of rare variants analytically. The method has been described in Hoffmann TJ, Marini NJ, and Witte JS (2010) <doi:10.1371/journal.pone.0013584>. / GPL-3	linux-64, osx-64, win-64
r-thinknum	1.3.0	This package interacts directly with the Thinknum API to offer data in a number of formats usable in R / GPL-2	noarch
r-threearmedtrials	1.0.3	Design and analyze three-arm non-inferiority or superiority trials which follow a gold-standard design, i.e. trials with an experimental treatment, an active, and a placebo control. Method for the following distributions are implemented: Poisson (Mielke and Munk (2009) <arXiv:0912.4169>), negative binomial (Muetze et al. (2016) <doi:10.1002/sim.6738>), normal (Pigeot et al. (2003) <doi:10.1002/sim.1450>; Hasler et al. (2009) <doi:10.1002/sim.3052>), binary (Friede and Kieser (2007) <doi:10.1002/sim.2543>), nonparametric (Muetze et al. (2017) <doi:10.1002/sim.7176>), exponential (Mielke and Munk (2009) <arXiv:0912.4169>). / GPL-2	linux-64, osx-64, win-64
r-threeboost	1.1	This package implements a thresholded version of the EEBoost algorithm described in [Wolfson (2011, JASA)]. EEBoost is a general-purpose method for variable selection which can be applied whenever inference would be based on an estimating equation. The package currently implements variable selection based on the Generalized Estimating Equations, but can also accommodate user-provided estimating functions. Thresholded EEBoost is a generalization which allows multiple variables to enter the model at each boosting step. / GPL-3	noarch
r-threegroups	0.21	Implements the Maximum Likelihood estimator for baseline, placebo, and treatment groups (three-group) experiments with non-compliance proposed by Gerber, Green, Kaplan, and Kern (2010). / GPL-2	noarch
r-threejs	0.3.1	Create interactive 3D scatter plots, network plots, and globes using the ‘three.js’ visualization library (< <a href="https://threejs.org">https://threejs.org</a> >). / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-threeway	1.1.3	Component analysis for three-way data arrays by means of Candecomp/Parafac, Tucker3, Tucker2 and Tucker1 models. / GPL-2	noarch
r-threewords	0.1.0	A connector to the ‘What3Words’ ( <a href="http://what3words.com/">http://what3words.com/</a> ) service, which represents each 3m by 3m square on earth with a unique trio of English-language words. / MIT	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-threg</a>	1.0.3	Fit a threshold regression model based on the first-hitting-time of a boundary by the sample path of a Wiener diffusion process. The threshold regression methodology is well suited to applications involving survival and time-to-event data. / GPL-2	noarch
<a href="#">r-thregi</a>	1.0.4	Fit a threshold regression model for Interval Censored Data based on the first-hitting-time of a boundary by the sample path of a Wiener diffusion process. The threshold regression methodology is well suited to applications involving survival and time-to-event data. / GPL-2	noarch
<a href="#">r-thresholdroc</a>	2.7	Functions that provide point and interval estimations of optimum thresholds for continuous diagnostic tests. The methodology used is based on minimizing an overall cost function in the two- and three-state settings. The package also provides functions for sample size determination and estimation of diagnostic accuracy measures. It also includes graphical tools. / GPL-2	noarch
<a href="#">r-thsls</a>	0.1	Fit the Simultaneous Systems of Linear Equations using Three-stage Least Squares. / GPL-3	noarch
<a href="#">r-tibble</a>	2.1.1	Provides a ‘tbl_df’ class (the ‘tibble’) that provides stricter checking and better formatting than the traditional data frame. / MIT file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-tibbrconnector</a>	1.5.1	Post messages to tibbr from within R. / BSD_3_clause	noarch
<a href="#">r-tickexec</a>	1.1	Functions to execute orders in backtesting using tick data. A testing platform was established by the four major execution functions, namely ‘LimitBuy’, ‘LimitSell’, ‘MarketBuy’ and ‘MarketSell’, which enclosed all tedious aspects (such as queueing for order executions and calculate actual executed volumes) for order execution using tick data. Such that one can focus on the logic of strategies, rather than its execution. / GPL-3	noarch
<a href="#">r-tictoc</a>	1.0	This package provides the timing functions ‘tic’ and ‘toc’ that can be nested. One can record all timings while a complex script is running, and examine the values later. It is also possible to instrument the timing calls with custom callbacks. In addition, this package provides class ‘Stack’, implemented as a vector, and class ‘List’, implemented as a list, both of which support operations ‘push’, ‘pop’, ‘first’, ‘last’ and ‘clear’. / Apache License (== 2.0)   file LICENSE	noarch
<a href="#">r-tiddlywikir</a>	1.0.1	Utilities to generate wiki reports in TiddlyWiki format. / GPL-2	noarch
<a href="#">r-tideharmonics</a>	0.1_1	Implements harmonic analysis of tidal and sea-level data. Over 400 harmonic tidal constituents can be estimated, all with daily nodal corrections. Time-varying mean sea-levels can also be used. / BSD_3_clause	noarch
<a href="#">r-tides</a>	2.1	Calculate Characteristics of Quasi-Periodic Time Series, e.g. Estuarine Water Levels. / GPL-3	noarch
<a href="#">r-tidetables</a>	0.0.2	Tide analysis and prediction of predominantly semi-diurnal tides with two high waters and two low waters during one lunar day (~24.842 hours, ~1.035 days). The analysis should preferably cover an observation period of at least 19 years. For shorter periods, for example, the nodal cycle can not be taken into account, which particularly affects the height calculation. The main objective of this package is to produce tide tables. / GPL-3	noarch

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Name	Version	Summary/License	Platform
r-tidyr	0.8.3	An evolution of 'reshape2'. It's designed specifically for data tidying (not general reshaping or aggregating) and works well with 'dplyr' data pipelines. / MIT file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
r-tidysselect	0.2.5	A backend for the selecting functions of the 'tidyverse'. It makes it easy to implement select-like functions in your own packages in a way that is consistent with other 'tidyverse' interfaces for selection. / GPL-3	linux-32, linux-64, osx-64, win-32, win-64
r-tidytext	0.2.0	Text mining for word processing and sentiment analysis using 'dplyr', 'ggplot2', and other tidy tools. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-tidyverse	1.2.1	The 'tidyverse' is a set of packages that work in harmony because they share common data representations and 'API' design. This package is designed to make it easy to install and load multiple 'tidyverse' packages in a single step. Learn more about the 'tidyverse' at < <a href="https://tidyverse.org">https://tidyverse.org</a> >. / GPL-3   file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-tiff	0.1.5	This package provides an easy and simple way to read, write and display bitmap images stored in the TIFF format. It can read and write both files and in-memory raw vectors. / GPL-2   GPL-3	linux-64, osx-64, win-64
r-tightclust	1.1	The functions needed to perform tight clustering Algorithm. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-tilegramsr	0.2.0	R spatial objects for Tilegrams. Tilegrams are tiled maps where the region size is proportional to the certain characteristics of the dataset. / MIT file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
r-tilting	1.1.1	Implements an algorithm for variable selection in high-dimensional linear regression using the tilted correlation, a new way of measuring the contribution of each variable to the response which takes into account high correlations among the variables in a data-driven way. / GPL-2	noarch
r-timechange	0.0.1	Efficient routines for manipulation of date-time objects while accounting for time-zones and daylight saving times. The package includes utilities for updating of date-time components (year, month, day etc.), modification of time-zones, rounding of date-times, period addition and subtraction etc. Parts of the ‘CCTZ’ source code, released under the Apache 2.0 License, are included in this package. See < <a href="https://github.com/google/cctz">https://github.com/google/cctz</a> > for more details. / GPL-3	linux-64, osx-64, win-64
r-timedate	3043.102	The ‘timeDate’ class fulfils the conventions of the ISO 8601 standard as well as of the ANSI C and POSIX standards. Beyond these standards it provides the Financial Center concept which allows to handle data records collected in different time zones and mix them up to have always the proper time stamps with respect to your personal financial center, or alternatively to the GMT reference time. It can thus also handle time stamps from historical data records from the same time zone, even if the financial centers changed day light saving times at different calendar dates. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-timedelay	1.0.8	We provide a toolbox to estimate the time delay between the brightness time series of gravitationally lensed quasar images via Bayesian and profile likelihood approaches. The model is based on a state-space representation for irregularly observed time series data generated from a latent continuous-time Ornstein-Uhlenbeck process. Our Bayesian method adopts scientifically motivated hyper-prior distributions and a Metropolis-Hastings within Gibbs sampler, producing posterior samples of the model parameters that include the time delay. A profile likelihood of the time delay is a simple approximation to the marginal posterior distribution of the time delay. Both Bayesian and profile likelihood approaches complement each other, producing almost identical results; the Bayesian way is more principled but the profile likelihood is easier to implement. / GPL-2	noarch
r-timeordered	0.9.9	Approaches for incorporating time into network analysis. Methods include: construction of time-ordered networks (temporal graphs); shortest-time and shortest-path-length analyses; resource spread calculations; data resampling and rarefaction for null model construction; reduction to time-aggregated networks with variable window sizes; application of common descriptive statistics to these networks; vector clock latencies; and plotting functionalities. The package supports <doi:10.1371/journal.pone.0020298>. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-timeprojection</a>	0.2.0	Extract useful time components of a date object, such as day of week, week-end, holiday, day of month, etc, and put it in a data frame. This can be used to create many predictor variables out of a single time variable, which can then be used in a regression or decision tree. Also includes function plotCalendarHeatmap which draws a calendar and overlays a heatmap based on values. / GPL-3	noarch
<a href="#">r-timer</a>	1.1.0	Provides a 'timeR' class that makes timing codes easier. One can create 'timeR' objects and use them to record all timings, and extract recordings as data frame for later use. / Apache License (== 2.0)   file LICENSE	noarch
<a href="#">r-timereg</a>	1.9.4	Programs for Martinussen and Scheike (2006), 'Dynamic Regression Models for Survival Data', Springer Verlag. Plus more recent developments. Additive survival model, semiparametric proportional odds model, fast cumulative residuals, excess risk models and more. Flexible competing risks regression including GOF-tests. Two-stage frailty modelling. PLS for the additive risk model. Lasso in the 'ahaz' package. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-timesboot</a>	1.0	Computes bootstrap CI for the sample ACF and periodogram / GPL-2	noarch
<a href="#">r-timeseries</a>	3042.002	Provides a class and various tools for financial time series. This includes basic functions such as scaling and sorting, subsetting, mathematical operations and statistical functions. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-timetools</a>	1.14	Objects to manipulate sequential and seasonal time series. Sequential time series based on time instants and time durations are handled. Both can be regularly or unevenly spaced (overlapping durations are allowed). Only POSIX* format are used for dates and times. The following classes are provided : 'POSIXcti', 'POSIXctp', 'TimeIntervalDataFrame', 'TimeInstantDataFrame', 'SubtimeDataFrame' ; methods to switch from a class to another and to modify the time support of series (hourly time series to daily time series for instance) are also defined. Tools provided can be used for instance to handle environmental monitoring data (not always produced on a regular time base). / GPL-3	linux-64, osx-64, win-64
<a href="#">r-timevis</a>	0.5	Create rich and fully interactive timeline visualizations. Timelines can be included in Shiny apps and R markdown documents, or viewed from the R console and 'RStudio' Viewer. 'timevis' includes an extensive API to manipulate a timeline after creation, and supports getting data out of the visualization into R. Based on the 'vis.js' Timeline module and the 'htmlwidgets' R package. / MIT	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-timevtree</a>	0.3.1	Estimates time varying regression effects under Cox type models in survival data using classification and regression tree. The codes in this package were originally written in S-Plus for the paper Survival Analysis with Time-Varying Regression Effects Using a Tree-Based Approach, by Xu, R. and Adak, S. (2002) <doi:10.1111/j.0006-341X.2002.00305.x>, Biometrics, 58: 305-315. Development of this package was supported by NIH grants AG053983 and AG057707, and by the UCSD Altman Translational Research Institute, NIH grant UL1TR001442. The content is solely the responsibility of the authors and does not necessarily represent the official views of the NIH. The example data are from the Honolulu Heart Program/Honolulu Asia Aging Study (HHP/HAAS). / GPL-2	noarch
<a href="#">r-timewarp</a>	1.0.15	Date sequence, relative date calculations, and date manipulation with business days and holidays. Works with Date and POSIXt classes. / GPL-3	noarch
<a href="#">r-timsac</a>	1.3.6	Functions for statistical analysis, prediction and control of time series based mainly on Akaike and Nakagawa (1988) <ISBN 978-90-277-2786-2>. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-tinflex</a>	1.5	A universal non-uniform random number generator for quite arbitrary distributions with piecewise twice differentiable densities. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-tinsel</a>	0.0.1	Instead of nesting function calls, annotate and transform functions using #. comments. / MIT	noarch
<a href="#">r-tint</a>	0.1.2	A ‘tufte’-alike style for ‘rmarkdown’. A modern take on the ‘Tufte’ design for pdf and html vignettes, building on the ‘tufte’ package with additional contributions from the ‘knitr’ and ‘ggtufte’ package, and also acknowledging the key influence of ‘envisioned css’. / GPL-3	noarch
<a href="#">r-tinyproject</a>	0.6.1	Creates useful files and folders for data analysis projects and provides functions to manage data, scripts and output files. Also provides a project template for ‘Rstudio’. / GPL-2	noarch
<a href="#">r-tinytest</a>	1.0.0	Provides a lightweight (zero-dependency) and easy to use unit testing framework. Main features: install tests with the package. Test results are treated as data that can be stored and manipulated. Test files are R scripts interspersed with test commands, that can be programmed over. Fully automated build-install-test sequence for packages. Skip tests when not run locally (e.g. on CRAN). Flexible and configurable output printing. Compare computed output with output stored with the package. Run tests in parallel. Extensible by other packages. Report side effects. / GPL-3	noarch
<a href="#">r-tinytex</a>	0.12	Helper functions to install and maintain the ‘LaTeX’ distribution named ‘TinyTeX’ (< <a href="https://yihui.name/tinytex/">https://yihui.name/tinytex/</a> >), a lightweight, cross-platform, portable, and easy-to-maintain version of ‘TeX Live’. This package also contains helper functions to compile ‘LaTeX’ documents, and install missing ‘LaTeX’ packages automatically. / MIT file LICENSE	linux-64, noarch, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
r-tiobeindexr	0.1.1	Get latest ‘TIOBE’ Programming Index Tables. The ‘TIOBE’ Programming Community index is an indicator of the popularity of programming languages from < <a href="https://www.tiobe.com/tiobe-index/">https://www.tiobe.com/tiobe-index/</a> >. / AGPL-3	noarch
r-tipom	1.0.2	TIPOM is based on a methodology that was developed in the 1960s by Bernardino Bagolini. The basic idea is to use the three simple dimensions of length, width and thickness of each lithic artefact to classify them in discrete groups and infer their function. / GPL-3	noarch
r-tippy	0.0.1	‘Htmlwidget’ of ‘Tippyjs’ to add tooltips to ‘Shiny’ apps and ‘R markdown’ documents. / MIT	noarch
r-tis	1.37	IFunctions and S3 classes for time indexes and time indexed series, which are compatible with FAME frequencies. / Unlimited	linux-64, osx-64, win-64
r-titan	1.0_1	GUI to analyze mass spectrometric data on the relative abundance of two substances from a titration series. / GPL-2	noarch
r-titanic	0.1.0	This data set provides information on the fate of passengers on the fatal maiden voyage of the ocean liner Titanic, summarized according to economic status (class), sex, age and survival. Whereas the base R Titanic data found by calling data(Titanic) is an array resulting from cross-tabulating 2201 observations, these data sets are the individual non-aggregated observations and formatted in a machine learning context with a training sample, a testing sample, and two additional data sets that can be used for deeper machine learning analysis. These data sets are also the data sets downloaded from the Kaggle competition and thus lowers the barrier to entry for users new to R or machine learning. / CC0	noarch
r-titrationcurves	0.1.0	A collection of functions to plot acid/base titration curves (pH vs. volume of titrant), complexation titration curves (pMetal vs. volume of EDTA), redox titration curves (potential vs. volume of titrant), and precipitation titration curves (either pAnalyte or pTitrant vs. volume of titrant). Options include the titration of mixtures, the ability to overlay two or more titration curves, and the ability to show equivalence points. / GPL-2	noarch
r-tkrgl	0.8	Provides ‘TK’ widget tools for the ‘rgl’ package. / GPL	linux-32, linux-64, noarch, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
r- <a href="#">tkrplot</a>	0.0_24	Simple mechanism for placing R graphics in a Tk widget / GPL	linux-32, linux-64, osx-64, win-32, win-64
r- <a href="#">tkrplotr</a>	0.1.1	Display a plot in a Tk canvas. / GPL-2	noarch
r- <a href="#">tlemix</a>	0.1.3	TLE implements a general framework for robust fitting of finite mixture models. Parameter estimation is performed using the EM algorithm. / GPL-3	noarch
r- <a href="#">tlim</a>	0.1.5	Computation of effects under linear, logistic and Poisson regression models with transformed variables. Logarithm and power transformations are allowed. Effects can be displayed both numerically and graphically in both the original and the transformed space of the variables. / GPL-2	noarch
r- <a href="#">tlmec</a>	0.0_2	Fit a linear mixed effects model for censored data with Student-t or normal distributions. The errors are assumed independent and identically distributed. / GPL (>= 3.0)	noarch
r- <a href="#">tls</a>	0.1.0	Functions for point and interval estimation in error-in-variables models via total least squares or generalized total least squares method. See Golub and Van Loan (1980) <doi:10.1137/0717073>, Gleser (1981) < <a href="https://www.jstor.org/stable/2240867">https://www.jstor.org/stable/2240867</a> >, Ivan Markovsky and Huffel (2007) <doi:10.1016/j.sigpro.2007.04.004> for more information. / GPL-3	noarch
r- <a href="#">tm</a>	0.7_6	A framework for text mining applications within R. / GPL-3	linux-32, linux-64, osx-64, win-32, win-64
r- <a href="#">tm.plugin.alceste</a>	1.1	This package provides a tm Source to create corpora from a corpus prepared in the format used by the Alceste application (i.e. a single text file with inline meta-data). It is able to import both text contents and meta-data (starred) variables. / GPL-2	noarch
r- <a href="#">tm.plugin.dc</a>	0.2_8	A plug-in for the text mining framework tm to support text mining in a distributed way. The package provides a convenient interface for handling distributed corpus objects based on distributed list objects. / GPL-2	noarch
r- <a href="#">tm.plugin.europresse</a>	1.4	Provides a 'tm' Source to create corpora from articles exported from the 'Europresse' content provider as HTML files. It is able to read both text content and meta-data information (including source, date, title, author and pages). / GPL-2	noarch
r- <a href="#">tm.plugin.factiva</a>	1.7	Provides a 'tm' Source to create corpora from articles exported from the Dow Jones 'Factiva' content provider as XML or HTML files. It is able to read both text content and meta-data information (including source, date, title, author, subject, geographical coverage, company, industry, and various provider-specific fields). / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<code>r-tm.plugin.lexisnexis</code>	1.4.0	Provides a 'tm' Source to create corpora from articles exported from the 'LexisNexis' content provider as HTML files. It is able to read both text content and meta-data information (including source, date, title, author and pages). Note that the file format is highly unstable: there is no warranty that this package will work for your corpus, and you may have to adjust the code to adapt it to your particular format. / GPL-2	noarch
<code>r-tm.plugin.mail</code>	0.2.1	A plug-in for the tm text mining framework providing mail handling functionality. / GPL-3	noarch
<code>r-tm.plugin.webmining</code>	1.3	Facilitate text retrieval from feed formats like XML (RSS, ATOM) and JSON. Also direct retrieval from HTML is supported. As most (news) feeds only incorporate small fractions of the original text tm.plugin.webmining even retrieves and extracts the text of the original text source. / GPL-3	noarch
<code>r-tmlr</code>	1.1.2	Useful functions to connect to 'TM1' < <a href="https://www.ibm.com/uk-en/marketplace/planning-and-analytics">https://www.ibm.com/uk-en/marketplace/planning-and-analytics</a> > instance from R via REST API. With the functions in the package, data can be imported from 'TM1' via mdx view or native view, data can be sent to 'TM1', processes and chores can be executed, and cube and dimension metadata information can be taken. / GPL-2	noarch
<code>r-tmb</code>	1.7.15	With this tool, a user should be able to quickly implement complex random effect models through simple C templates. The package combines 'CppAD' (C automatic differentiation), 'Eigen' (templated matrix-vector library) and 'CHOLMOD' (sparse matrix routines available from R) to obtain an efficient implementation of the applied Laplace approximation with exact derivatives. Key features are: Automatic sparseness detection, parallelism through 'BLAS' and parallel user templates. / GPL-2	linux-64, osx-64, win-64
<code>r-tmcalculator</code>	1.0.0	The melting temperature of nucleic acid sequences can be calculated in three method, the Wallace rule (Thein & Wallace (1986) <doi:10.1016/S0140-6736(86)90739-7>), empirical formulas based on G and C content (Marmur J. (1962) <doi:10.1016/S0022-2836(62)80066-7>, Schildkraut C. (2010) <doi:10.1002/bip.360030207>, Wetmur J G (1991) <10.3109/10409239109114069>, Untergasser,A. (2012) <doi:10.1093/nar/gks596>, von Ahsen N (2001) <PMID:11673362>) and nearest neighbor thermodynamics (Breslauer K J (1986) <doi:10.1073/pnas.83.11.3746>, Sugimoto N (1996) <doi:10.1093/nar/24.22.4501>, Allawi H (1998) <doi:10.1093/nar/26.11.2694>, SantaLucia J (2004) <doi:10.1146/annurev.biophys.32.110601.141800>, Freier S (1986) <doi:10.1073/pnas.83.24.9373>, Xia T (1998) <doi:10.1021/bi9809425>, Chen JL (2012) <doi:10.1021/bi3002709>, Bommarito S (2000) <doi:10.1093/nar/28.9.1929>, Turner D H (2010) <doi:10.1093/nar/gkp892>, Sugimoto N (1995) <doi:10.1016/S0048-9697(98)00088-6>, Allawi H T (1997) <doi:10.1021/bi962590c>, Santalucia N (2005) <doi:10.1093/nar/gki918>), and it can also be corrected with salt ions and chemical compound (SantaLucia J (1996) <doi:10.1021/bi951907q>, SantaLucia J(1998) <doi:10.1073/pnas.95.4.1460>, Owczarzy R (2004) <doi:10.1021/bi034621r>, Owczarzy R (2008) <doi:10.1021/bi702363u>). / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-tmcn</a>	0.2.13	A Text mining toolkit for Chinese, which includes facilities for Chinese string processing, Chinese NLP supporting, encoding detecting and converting. Moreover, it provides some functions to support ‘tm’ package in Chinese. / LGPL-3	linux-64, osx-64, win-64
<a href="#">r-tmdb</a>	1.0	Provides an R-interface to the TMDb API (see TMDb API on <a href="http://docs.themoviedb.apiary.io/#&gt;">http://docs.themoviedb.apiary.io/#&gt;</a> ). The Movie Database (TMDb) is a popular user editable database for movies and TV shows (see <a href="https://www.themoviedb.org/">https://www.themoviedb.org/</a> ). / Artistic-2.0	noarch
<a href="#">r-tmg</a>	0.3	Random number generation of truncated multivariate Gaussian distributions using Hamiltonian Monte Carlo. The truncation is defined using linear and/or quadratic polynomials. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-tmpm</a>	1.0.3	Trauma Mortality prediction for ICD-9, ICD-10, and AIS lexicons in long or wide format based on Dr. Alan Cook’s tmpm mortality model. / GPL-2	noarch
<a href="#">r-tmvmixnorm</a>	1.0.2	Efficient sampling of truncated multivariate (scale) mixtures of normals under linear inequality constraints is nontrivial due to the analytically intractable normalizing constant. Meanwhile, traditional methods may subject to numerical issues, especially when the dimension is high and dependence is strong. Algorithms proposed by Li and Ghosh (2015) <doi: 10.1080/15598608.2014.996690> are adopted for overcoming difficulties in simulating truncated distributions. Efficient rejection sampling for simulating truncated univariate normal distribution is included in the package, which shows superiority in terms of acceptance rate and numerical stability compared to existing methods and R packages. An efficient function for sampling from truncated multivariate normal distribution subject to convex polytope restriction regions based on Gibbs sampler for conditional truncated univariate distribution is provided. By extending the sampling method, a function for sampling truncated multivariate Student’s t distribution is also developed. Moreover, the proposed method and computation remain valid for high dimensional and strong dependence scenarios. Empirical results in Li and Ghosh (2015) <doi: 10.1080/15598608.2014.996690> illustrated the superior performance in terms of various criteria (e.g. mixing and integrated auto-correlation time). / GPL-2	noarch
<a href="#">r-tmvnsim</a>	1.0.2	Importance sampling from the truncated multivariate normal using the GHK (Geweke-Hajivassiliou-Keane) simulator. Unlike Gibbs sampling which can get stuck in one truncation sub-region depending on initial values, this package allows truncation based on disjoint regions that are created by truncation of absolute values. The GHK algorithm uses simple Cholesky transformation followed by recursive simulation of univariate truncated normals hence there are also no convergence issues. Importance sample is returned along with sampling weights, based on which, one can calculate integrals over truncated regions for multivariate normals. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-tnc	0.1.0	Node centrality measures for temporal networks. Available measures are temporal degree centrality, temporal closeness centrality and temporal betweenness centrality defined by Kim and Anderson (2012) <doi:10.1103/PhysRevE.85.026107>. Applying the REN algorithm by Hanke and Foraita (2017) <doi:10.1186/s12859-017-1677-x> when calculating the centrality measures keeps the computational running time linear in the number of graph snapshots. Further, all methods can run in parallel up to the number of nodes in the network. / GPL-3	noarch
r-tnet	3.0.14	R package for analyzing weighted, two-mode, and longitudinal networks. / GPL-3	noarch
r-todor	0.0.5	This is a simple addin to 'RStudio' that finds all 'TODO', 'FIX ME', 'CHANGED' etc. comments in your project and shows them as a markers list. / MIT	noarch
r-tokenbrowser	0.1.0	Create browsers for reading full texts from a token list format. Information obtained from text analyses (e.g., topic modeling, word scaling) can be used to annotate the texts. / GPL-3	linux-64, osx-64, win-64
r-tokenizers	0.2.1	Convert natural language text into tokens. Includes tokenizers for shingled n-grams, skip n-grams, words, word stems, sentences, paragraphs, characters, shingled characters, lines, tweets, Penn Treebank, regular expressions, as well as functions for counting characters, words, and sentences, and a function for splitting longer texts into separate documents, each with the same number of words. The tokenizers have a consistent interface, and the package is built on the 'stringi' and 'Rcpp' packages for fast yet correct tokenization in 'UTF-8'. / MIT file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
r-tokenizers.bpe	0.1.0	Unsupervised text tokenizer focused on computational efficiency. Wraps the 'YouTokenToMe' library < <a href="https://github.com/VKCOM/YouTokenToMe">https://github.com/VKCOM/YouTokenToMe</a> > which is an implementation of fast Byte Pair Encoding (BPE) < <a href="https://www.aclweb.org/anthology/P16-1162">https://www.aclweb.org/anthology/P16-1162</a> >. / MPL-2.0	linux-64, osx-64, win-64
r-toordinal	1.1_0	Language specific cardinal to ordinal number conversion. / GPL-3	noarch
r-topicmodels	0.2_9	Provides an interface to the C code for Latent Dirichlet Allocation (LDA) models and Correlated Topics Models (CTM) by David M. Blei and co-authors and the C code for fitting LDA models using Gibbs sampling by Xuan-Hieu Phan and co-authors. / GPL-2	linux-64, osx-64, win-64
r-topmodel	0.7.3	Set of hydrological functions including an R implementation of the hydrological model TOPMODEL, which is based on the 1995 FORTRAN version by Keith Beven. From version 0.7.0, the package is put into maintenance mode. / GPL-2	linux-64, osx-64, win-64
r-topsis	1.0	Evaluation of alternatives based on multiple criteria using TOPSIS method. / GPL-2	noarch
r-tosls	1.0	Fit an Instrumental Variables Two Stage Least Squares model / Artistic-2.0	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-totalcensus</a>	0.6.1	Download summary files from Census Bureau < <a href="https://www2.census.gov/">https://www2.census.gov/</a> > and extract data, in particular high resolution data at block, block group, and tract level, from decennial census and American Community Survey 1-year and 5-year estimates. / MIT	noarch
<a href="#">r-totalcopheneticindex</a>	1.0.1	For a given phylogenetic tree, calculates the Total Cophenetic Index. Reference: A. Mir, F. Rossello, L. A. Rotger (2013). A new balance index for phylogenetic trees. Math. Biosci. 241, 125-136 <doi:10.1016/j.mbs.2012.10.005>. / Unlimited	noarch
<a href="#">r-touch</a>	0.1_4	R implementation of the software tools developed in the H-CUP (Healthcare Cost and Utilization Project) < <a href="https://www.hcup-us.ahrq.gov">https://www.hcup-us.ahrq.gov</a> > and AHRQ (Agency for Healthcare Research and Quality) < <a href="https://www.ahrq.gov">https://www.ahrq.gov</a> >. It currently contains functions for mapping ICD-9 codes to the AHRQ comorbidity measures and translating ICD-9 (resp. ICD-10) codes to ICD-10 (resp. ICD-9) codes based on GEM (General Equivalence Mappings) from CMS (Centers for Medicare and Medicaid Services). / GPL-3	linux-64, osx-64, win-64
<a href="#">r-tourr</a>	0.5.6	Implements geodesic interpolation and basis generation functions that allow you to create new tour methods from R. / MIT	noarch
<a href="#">r-toxtestd</a>	2.0	Calculates sample size and dose allocation for binary toxicity tests, using the Fish Embryo Toxicity Test as example. An optimal test design is obtained by running (i) spoD (calculate the number of individuals to test under control conditions), (ii) setD (estimate the minimal sample size per treatment given the users precision requirements) and (iii) doseD (construct an individual dose scheme). / GPL-2	noarch
<a href="#">r-tp.idm</a>	1.5	Estimation of transition probabilities for the illness-death model. Both the Aalen-Johansen estimator for a Markov model and a novel non-Markovian estimator by de Una-Alvarez and Meira-Machado (2015) <doi:10.1111/biom.12288>, see also Balboa and de Una-Alvarez (2018) <doi:10.18637/jss.v083.i10>, are included. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-tpauc</a>	2.1.1	Tools for estimating and inferring two-way partial area under receiver operating characteristic curves (two-way pAUC), partial area under receiver operating characteristic curves (pAUC), and partial area under ordinal dominance curves (pODC). Methods includes Mann-Whitney statistic and Jackknife, etc. / GPL-2	noarch
<a href="#">r-tpe</a>	1.0.1	This package implements the greedy approximation for tree preserving embedding. / MIT	noarch
<a href="#">r-tpes</a>	1.0.0	A bioinformatics tool for the estimation of the tumor purity from sequencing data. It uses the set of putative clonal somatic single nucleotide variants within copy number neutral segments to call tumor cellularity. / MIT	noarch
<a href="#">r-tpmsm</a>	1.2.2	Estimation of transition probabilities for the illness-death model and or the three-state progressive model. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-tracerer	2.0.1	‘BEAST2’ (< <a href="http://www.beast2.org">http://www.beast2.org</a> >) is a widely used Bayesian phylogenetic tool, that uses DNA/RNA/protein data and many model priors to create a posterior of jointly estimated phylogenies and parameters. ‘Tracer’ (< <a href="http://tree.bio.ed.ac.uk/software/tracer/">http://tree.bio.ed.ac.uk/software/tracer/</a> >) is a GUI tool to parse and analyze the files generated by ‘BEAST2’. This package provides a way to parse and analyze ‘BEAST2’ input files without active user input, but using R function calls instead. / GPL-3	linux-64, osx-64, win-64
r-track	1.1.9	Automatically stores objects in files on disk so that files are rewritten when objects are changed, and so that objects are accessible but do not occupy memory until they are accessed. Keeps track of times when objects are created and modified, and caches some basic characteristics of objects to allow for fast summaries of objects. Also provides a command history mechanism that saves the last command to a history file after each command completes. / GPL-3	noarch
r-trading	1.2	Contains trades from the five major assets classes and also functionality to use pricing curves, rating tables, CSAs and add-on tables. The implementation follows an object oriented logic whereby each trade inherits from more abstract classes while also the curves/tables are objects. There is a lot of functionality focusing on the counterparty credit risk calculations however the package can be used for trading applications in general. / GPL-3	noarch
r-trampr	1.0.8	Matching terminal restriction fragment length polymorphism (‘TRFLP’) profiles between unknown samples and a database of known samples. TRAMPR facilitates analysis of many unknown profiles at once, and provides tools for working directly with electrophoresis output through to generating summaries suitable for community analyses with R’s rich set of statistical functions. TRAMPR also resolves the issues of multiple ‘TRFLP’ profiles within a species, and shared ‘TRFLP’ profiles across species. / GPL-2	noarch
r-transcriber	0.0.0	Transcribes audio to text with the HP IDOL API. Includes functions to upload files, retrieve transcriptions, and monitor jobs. / GPL-3	noarch
r-translation.ko	0.0.1	R2version 2.1.0 and later support Korean translations of program messages. The continuous efforts have been made by < <a href="http://developer.r-project.org/TranslationTeams.html">http://developer.r-project.org/TranslationTeams.html</a> > The R Documentation files are licensed under the General Public License, version 2 or 3. This means that the pilot project to translate them into Korean has permission to reproduce them and translate them. This work is done with GNU ‘gettext’ utilities. The portable object template is updated a weekly basis or whenever changes are necessary. Comments and corrections via email to the maintainer is of course most welcome. In order to voluntarily participate in or offer your help with this translation, please contact the maintainer. To check the change and progress of Korean translation, please visit < <a href="http://www.openstatistics.net">http://www.openstatistics.net</a> >. / GPL-2	noarch
r-transmodel	2.1	A unified estimation procedure for the analysis of right censored data using linear transformation models. / GPL-2	noarch
r-transp	0.1	Implementation of two transportation problem algorithms. 1. North West Corner Method 2. Minimum Cost Method or Least cost method. For more technical details about the algorithms please refer below URLs. < <a href="http://www.universalteacherpublications.com/univ/ebooks/or/Ch5/nw.htm">http://www.universalteacherpublications.com/univ/ebooks/or/Ch5/nw.htm</a> >. < <a href="http://personal.maths.surrey.ac.uk/st/J.F/chapter7.pdf">http://personal.maths.surrey.ac.uk/st/J.F/chapter7.pdf</a> >. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-transport	0.12_0	Solve optimal transport problems. Compute Wasserstein distances (a.k.a. Kantorovitch, Fortet–Mourier, Mallows, Earth Mover’s, or minimal L <sub>p</sub> distances), return the corresponding transference plans, and display them graphically. Objects that can be compared include grey-scale images, (weighted) point patterns, and mass vectors. / GPL-2	linux-64, osx-64, win-64
r-transurv	1.2.0	A structural transformation model for a latent, quasi-independent truncation time as a function of the observed dependent truncation time and the event time, and an unknown dependence parameter. The dependence parameter is chosen to minimize the conditional Kendall’s tau (Martin and Betensky, 2005) <doi:10.1198/016214504000001538>. The marginal distribution for the truncation time and the event time are completely left unspecified. / GPL-3	linux-64, osx-64, win-64
r-trapezoid	2.0_0	The trapezoid package provides dtrapezoid, ptrapezoid, qtrapezoid, and rtrapezoid functions for the trapezoidal distribution. / GPL-3	linux-64, osx-64, win-64
r-tree	1.0_4	Classification and regression trees. / GPL-2   GPL-3	linux-64, osx-64, win-64
r-treebase	0.1.4	Interface to the API for ‘TreeBASE’ < <a href="http://treebase.org">http://treebase.org</a> > from ‘R.’ ‘TreeBASE’ is a repository of user-submitted phylogenetic trees (of species, population, or genes) and the data used to create them. / CC0	noarch
r-treeclust	1.1_7	Create a measure of inter-point dissimilarity useful for clustering mixed data, and, optionally, perform the clustering. / GPL-2	noarch
r-treecm	1.2.2	The centre of mass is a crucial data for arborists in order to consolidate a tree using steel or dynamic cables. Given field-recorded data on branchiness of a tree, the package: (i) computes and plots the centre of mass of the tree itself, (ii) computes branches slenderness coefficient in order to aid the arborist identify potentially dangerous branches, and (iii) computes the force acting on a ground plinth and its best position relating to the tree centre of mass, should the tree need to be stabilized by a steel cable. / GPL-2	noarch
r-treelet	1.1	Treelets provides a novel construction of multi-scale bases that extends wavelets to non-smooth signals. It returns a multi-scale orthonormal basis, where the final computed basis functions are supported on nested clusters in a hierarchical tree. Both the tree and the basis, which are constructed simultaneously, reflect the internal structure of the data. / GPL-2	noarch
r-treeman	1.1.3	S4 class and methods for intuitive and efficient phylogenetic tree manipulation. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-treeperm</a>	1.6	An implementation of permutation tests in R, supporting both exact and asymptotic K sample test of data locations. The p value of exact tests is found using tree algorithms. Tree algorithms treat permutations of input data as tree nodes and perform constraint depth-first searches for permutations that fall into the critical region of a test systematically. Pruning of tree search and optimisations at C level enable exact tests for certain large data sets. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-trekfont</a>	0.9.3	Provides a collection of true type and open type Star Trek-themed fonts. / GPL-3	noarch
<a href="#">r-trendchange</a>	0.1.0	Innovative Trend Analysis is a graphical method to examine the trends in time series data. Sequential Mann-Kendall test uses the intersection of prograde and retrograde series to indicate the possible change point in time series data. Distribution free cumulative sum charts indicate location and significance of the change point in time series. Zekai, S. (2011). <doi:10.1061/(ASCE)HE.1943-5584.0000556>. Grayson, R. B. et al. (1996). Hydrological Recipes: Estimation Techniques in Australian Hydrology. Cooperative Research Centre for Catchment Hydrology, Australia, p. 125. Sneyers, S. (1990). On the statistical analysis of series of observations. Technical note no 5 143, WMO No 725 415. Secretariat of the World Meteorological Organization, Geneva, 192 pp. / GPL-3	noarch
<a href="#">r-trendsegmentr</a>	1.0.0	Performs the detection of point anomalies and linear trend changes for univariate time series by implementing the bottom-up unbalanced wavelet transformation proposed by H. Maeng and P. Fryzlewicz (2019) < <a href="http://personal.lse.ac.uk/maeng/">http://personal.lse.ac.uk/maeng/</a> >. The estimated number and locations of the change-points are returned with the piecewise-linear estimator for signal. / GPL-3	noarch
<a href="#">r-trialsize</a>	1.3	functions and examples in Sample Size Calculation in Clinical Research. / GPL (>= 2.15.1)	linux-64, osx-64, win-64
<a href="#">r-triangle</a>	0.12	Provides the r, q, p, and d distribution functions for the triangle distribution. / GPL-2	noarch
<a href="#">r-triangulation</a>	0.5.0	Measuring angles between points in a landscape is much easier than measuring distances. When the location of three points is known the position of the observer can be determined based solely on the angles between these points as seen by the observer. This task (known as triangulation) however requires onerous calculations - these calculations are automated by this package. / LGPL-3	noarch
<a href="#">r-triebeard</a>	0.3.0	‘Radix trees’, or ‘tries’, are key-value data structures optimised for efficient lookups, similar in purpose to hash tables. ‘triebeard’ provides an implementation of ‘radix trees’ for use in R programming and in developing packages with ‘Rcpp’. / MIT	linux-64, osx-64, win-64
<a href="#">r-trimcluster</a>	0.1_2	Trimmed k-means clustering. / GPL-3	noarch
<a href="#">r-trimr</a>	1.0.1	Provides various commonly-used response time trimming methods, including the recursive / moving-criterion methods reported by Van Selst and Jolicoeur (1994). By passing trimming functions raw data files, the package will return trimmed data ready for inferential testing. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-triosgl</a>	1.1.0	Fit a trio model via penalized maximum likelihood. The model is fit for a path of values of the penalty parameter. This package is based on Noah Simon, et al. (2011) <doi:10.1080/10618600.2012.681250>. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-tripack</a>	1.3_8	A constrained two-dimensional Delaunay triangulation package providing both triangulation and generation of voronoi mosaics of irregular spaced data. / ACM   file LICENSE (Restricts use)	linux-64, osx-64, win-64
<a href="#">r-tripsanddipr</a>	0.1.0	Uses read counts for biallelic single nucleotide polymorphisms (SNPs) to compare the likelihoods for the observed read counts given that a sample is either diploid or triploid. It allows parameters to be specified to account for sequencing error rates and allelic bias. For details of the algorithm, please see Delomas (2019) <doi:10.1111/1755-0998.13073>. / MIT	noarch
<a href="#">r-tropalgebra</a>	0.1.1	It includes functions like tropical addition, tropical multiplication for vectors and matrices. In tropical algebra, the tropical sum of two numbers is their minimum and the tropical product of two numbers is their ordinary sum. For more information see also I. Simon (1988) Recognizable sets with multiplicities in the tropical semi ring: Volume 324 Lecture Notes I Computer Science, pages 107-120 <doi: 10.1007/BFb0017135>. / GPL-3	noarch
<a href="#">r-tropicalsparse</a>	0.1.0	Some of the basic tropical algebra functionality is provided for sparse matrices by applying sparse matrix storage techniques. Some of these are addition and multiplication of vectors and matrices, dot product of the vectors in tropical form and some general equations are also solved using tropical algebra. / GPL-3	noarch
<a href="#">r-trotter</a>	0.6	Class definitions and constructors for pseudo-vectors containing all permutations, combinations and subsets of objects taken from a vector. Simplifies working with structures commonly encountered in combinatorics. / GPL-3	noarch
<a href="#">r-trueskill</a>	0.1	An implementation of the TrueSkill algorithm (Herbrich, R., Minka, T. and Grapel, T) in R; a Bayesian skill rating system with inference by approximate message passing on a factor graph. Used by Xbox to rank gamers and identify appropriate matches. <a href="http://research.microsoft.com/en-us/projects/trueskill/default.aspx">http://research.microsoft.com/en-us/projects/trueskill/default.aspx</a> Current version allows for one player per team. Will update as time permits. Requires R version 3.0 as it is written with Reference Classes. URL: <a href="https://github.com/bhoung/trueskill-in-r">https://github.com/bhoung/trueskill-in-r</a> Acknowledgements to Doug Zongker and Heungsub Lee for their python implementations of the algorithm and for the liberal reuse of Doug's code comments (@dougz and @sublee on github). / GPL-3	noarch
<a href="#">r-truncgof</a>	0.6_0	Goodness-of-fit tests and some adjusted exploratory tools allowing for left truncated data / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-truncnorm	1.0_8	Density, probability, quantile and random number generation functions for the truncated normal distribution. / GPL-2	linux-64, osx-64, win-64
r-truncreg	0.2_5	Estimation of models for truncated Gaussian variables by maximum likelihood. / GPL-2	noarch
r-trust	0.1_7	Does local optimization using two derivatives and trust regions. Guaranteed to converge to local minimum of objective function. / MIT	noarch
r-trustedtimestamping	0.2.6	Trusted Timestamps (tts) are created by incorporating a hash of a file or dataset into a transaction on the decentralized blockchain (Stellar network). The package makes use of a free service provided by < <a href="https://stellarapi.io">https://stellarapi.io</a> >. / AGPL-3	noarch
r-trustoptim	0.8.6.2	Trust region algorithm for nonlinear optimization. Efficient when the Hessian of the objective function is sparse (i.e., relatively few nonzero cross-partial derivatives). See Braun, M. (2014) <doi:10.18637/jss.v060.i04>. / MPL (>= 2.0)	linux-64, osx-64, win-64
r-trycatchlog	1.1.4	Advanced tryCatch() and try() functions for better error handling (logging, stack trace with source code references and support for post-mortem analysis via dump files). / GPL-3	noarch
r-tsallisqexp	0.9_3	Tsallis distribution also known as the q-exponential family distribution. Provide distribution d, p, q, r functions, fitting and testing functions. Project initiated by Paul Higbie and based on Cosma Shalizi's code. / GPL-2	noarch
r-tsbox	0.2.0	Time series toolkit with identical behavior for all time series classes: 'ts', 'xts', 'data.frame', 'data.table', 'tibble', 'zoo', 'timeSeries', 'tsibble', 'tis' or 'irts'. Also converts reliably between these classes. / GPL-3	noarch
r-tsc	1.0_3	Performs the two-sample comparisons using the following exact test procedures: the exact likelihood-ratio test (LRT) for equality of two normal populations proposed in Zhang et al. (2012); the combined test based on the LRT and Shapiro-Wilk test for normality via the Bonferroni correction technique; the newly proposed density-based empirical likelihood (DBEL) ratio test. To calculate p-values of the DBEL procedures, three procedures are used: (a) the traditional Monte Carlo (MC) method implemented in C, (b) a new interpolation method based on regression techniques to operate with tabulated critical values of the test statistic; (c) a Bayesian type method that uses the tabulated critical values as the prior information and MC generated DBEL-test-statistic's values as data. / GPL-2	linux-64, osx-64, win-64
r-tsdata	2016.8.11	Illustrates the various 'TSdbi' packages with a vignette using time series data from several sources. The vignette also illustrates some simple time series manipulation and plotting using packages 'tframe' and 'tfplot'. / GPL-2	noarch
r-tsdecomp	0.2	ARIMA-model-based decomposition of quarterly and monthly time series data. The methodology is developed and described, among others, in Burman (1980) <DOI:10.2307/2982132> and Hillmer and Tiao (1982) <DOI:10.2307/2287770>. / GPL-2	noarch
r-tsdf	1.1_7	Calculate optimal Zhong's two-/three-stage Phase II designs (see Zhong (2012) <doi:10.1016/j.cct.2012.07.006>). Generate Target Toxicity decision table for Phase I dose-finding (two-/three-stage). This package also allows users to run dose-finding simulations based on customized decision table. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-tsdfgs</a>	1.0	Determining training set for genomic selection using a genetic algorithm (Holland J.H. (1975) <DOI:10.1145/1216504.1216510>) or simple exchange algorithm (change an individual every iteration). Three different criteria are used in both algorithms, which are r-score (Ou J.H., Liao C.T. (2018) <DOI:10.6342/NTU201802290>), PEV-score (Akdemir D. et al. (2015) <DOI:10.1186/s12711-015-0116-6>) and CD-score (Laloe D. (1993) <DOI:10.1186/1297-9686-25-6-557>). Phenotypic data for candidate set is not necessary for all these methods. By using it, one may readily determine a training set that can be expected to provide a better training set comparing to random sampling. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-tsdisagg2</a>	0.1.0	Disaggregates low frequency time series data to higher frequency series. Implements the following methods for temporal disaggregation: Boot, Feibes and Lisman (1967) <DOI:10.2307/2985238>, Chow and Lin (1971) <DOI:10.2307/1928739>, Fernandez (1981) <DOI:10.2307/1924371> and Litterman (1983) <DOI:10.2307/1391858>. / GPL-2	noarch
<a href="#">r-tse</a>	0.1.0	Calculates total survey error (TSE) for one or more surveys, using common scale-dependent and/or scale-independent metrics. On TSE, see: Weisberg, Herbert (2005, ISBN:0-226-89128-3); Biemer, Paul (2010) <doi:10.1093/poq/nfq058>. / GPL-2	noarch
<a href="#">r-tseind</a>	0.1.0	Calculates total survey error (TSE) for one or more surveys, using both scale-dependent and scale-independent metrics. Package works directly from the data set, with no hand calculations required: just upload a properly structured data set (see TESTIND and its documentation), properly input column names (see functions documentation), and run your functions. For more on TSE, see: Weisberg, Herbert (2005, ISBN:0-226-89128-3); Biemer, Paul (2010) <doi:10.1093/poq/nfq058>; Biemer, Paul et.al. (2017, ISBN:9781119041672); etc. / GPL-2	noarch
<a href="#">r-tsentropies</a>	0.9	Computes various entropies of given time series. This is the initial version that includes ApEn() and SampEn() functions for calculating approximate entropy and sample entropy. Approximate entropy was proposed by S.M. Pincus in Approximate entropy as a measure of system complexity, Proceedings of the National Academy of Sciences of the United States of America, 88, 2297-2301 (March 1991). Sample entropy was proposed by J. S. Richman and J. R. Moorman in Physiological time-series analysis using approximate entropy and sample entropy, American Journal of Physiology, Heart and Circulatory Physiology, 278, 2039-2049 (June 2000). This package also contains FastApEn() and FastSampEn() functions for calculating fast approximate entropy and fast sample entropy. These are newly designed very fast algorithms, resulting from the modification of the original algorithms. The calculated values of these entropies are not the same as the original ones, but the entropy trend of the analyzed time series determines equally reliably. Their main advantage is their speed, which is up to a thousand times higher. A scientific article describing their properties has been submitted to The Journal of Supercomputing and in present time it is waiting for the acceptance. / GPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-tseries	0.10_46	Time series analysis and computational finance. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
r-tserieschaos	0.1_13	Routines for the analysis of nonlinear time series. This work is largely inspired by the TISEAN project, by Rainer Hegger, Holger Kantz and Thomas Schreiber: < <a href="http://www.mpipks-dresden.mpg.de/~tisean/">http://www.mpipks-dresden.mpg.de/~tisean/</a> >. / GPL-2	linux-64, osx-64, win-64
r-tseriesmma	0.1.1	Multiscale multifractal analysis (MMA) (Gierałtowski et al., 2012)<DOI:10.1103/PhysRevE.85.021915> is a time series analysis method, designed to describe scaling properties of fluctuations within the signal analyzed. The main result of this procedure is the so called Hurst surface $h(q,s)$ , which is a dependence of the local Hurst exponent $h$ (fluctuation scaling exponent) on the multifractal parameter $q$ and the scale of observation $s$ (data window width). / GPL-2	noarch
r-tsetools	0.1.3	Tools for downloading and organizing data from Tehran Stock Exchange (TSE) < <a href="http://new.tse.ir/en/">http://new.tse.ir/en/</a> >. It also performs some descriptive data analysis for assets. / BSD_2_clause	noarch
r-tsewgt	0.1.0	Calculates total survey error (TSE) for a survey under multiple, different weighting schemes, using both scale-dependent and scale-independent metrics. Package works directly from the data set, with no hand calculations required: just upload a properly structured data set (see TESTWGT and its documentation), properly input column names (see functions documentation), and run your functions. For more on TSE, see: Weisberg, Herbert (2005, ISBN:0-226-89128-3); Biemer, Paul (2010) <doi:10.1093/poq/nfq058>; Biemer, Paul et.al. (2017, ISBN:9781119041672); etc. / GPL-2	noarch
r-tsgsis	0.1	To provide a high dimensional grouped variable selection approach for detection of whole-genome SNP effects and SNP-SNP interactions, as described in Fang et al. (2017, under review). / GPL-2	noarch
r-tshrc	0.1_6	Two-stage procedure compares hazard rate functions, which may or may not cross each other. / MIT	linux-64, osx-64, win-64
r-tsmn	1.0.0	Return the first four moments of the SMN distributions (Normal, Student-t, Pearson VII, Slash or Contaminated Normal). / GPL (>= 3.0)	noarch
r-tsmode	0.6	Tools for specifying time series regression models / GPL-2	noarch
r-tsne	0.1_3	A pure R implementation of the t-SNE algorithm. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-tsp</a>	1.1.7	Basic infrastructure and some algorithms for the traveling salesperson problem (also traveling salesman problem; TSP). The package provides some simple algorithms and an interface to the Concorde TSP solver and its implementation of the Chained-Lin-Kernighan heuristic. The code for Concorde itself is not included in the package and has to be obtained separately. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-tsqn</a>	1.0.0	Time Series Qn is a package with applications of the Qn estimator of Rousseeuw and Croux (1993) <doi:10.1080/01621459.1993.10476408> to univariate and multivariate Time Series in time and frequency domains. More specifically, the robust estimation of autocorrelation or autocovariance matrix functions from Ma and Genton (2000, 2001) <doi:10.1111/1467-9892.00203>, <doi:10.1006/jmva.2000.1942> and Cotta (2017) <doi:10.13140/RG.2.2.14092.10883> are provided. The robust pseudo-periodogram of Molinares et. al. (2009) <doi:10.1016/j.jspi.2008.12.014> is also given. This packages also provides the M-estimator of the long-memory parameter d based on the robustification of the GPH estimator proposed by Reisen et al. (2017) <doi:10.1016/j.jspi.2017.02.008>. / GPL-2	noarch
<a href="#">r-tsss</a>	1.2.4	Functions for statistical analysis, modeling and simulation of time series with state space model, based on the methodology in Kitagawa (1993, ISBN: 4-00-007703-1 and 2005, ISBN: 4-00-005455-4). / GPL-2	linux-64, osx-64, win-64
<a href="#">r-tstools</a>	0.3.8	Plot official statistics' time series conveniently: automatic legends, highlight windows, stacked bar charts with positive and negative contributions, sum-as-line option, two y-axes with automatic horizontal grids that fit both axes and other popular chart types. 'tstools' comes with a plethora of defaults to let you plot without setting an abundance of parameters first, but gives you the flexibility to tweak the defaults. In addition to charts, 'tstools' provides a super fast, 'data.table' backed time series I/O that allows the user to export / import long format, wide format and transposed wide format data to various file types. / GPL-2	noarch
<a href="#">r-tstr</a>	1.2	A ternary search tree is a type of prefix tree with up to three children and the ability for incremental string search. The package uses this ability for word auto-completion and spell checking. Includes a dataset with the 10001 most frequent English words. / GPL-2	noarch
<a href="#">r-tstutorial</a>	1.2.3	Interactive laboratory of Time Series based in Box-Jenkins methodology. / GPL (>= 2.0)	noarch
<a href="#">r-tsvr</a>	1.0.0	Tools for timescale decomposition of the classic variance ratio of community ecology. Tools are as described in Zhao et al (in prep), extending commonly used methods introduced by Peterson et al (1975) <doi: 10.2307/1936306>. / GPL-3	noarch
<a href="#">r-ttbbeer</a>	1.1.0	U.S. Department of the Treasury, Alcohol and Tobacco Tax and Trade Bureau (TTB) collects data and reports on monthly beer industry production and operations. This data package includes a collection of 10 years (2006 - 2015) worth of data on materials used at U.S. breweries in pounds reported by the Brewer's Report of Operations and the Quarterly Brewer's Report of Operations forms, ready for data analysis. This package also includes historical tax rates on distilled spirits, wine, beer, champagne, and tobacco products as individual data sets. / CC0	noarch

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Name	Version	Summary/License	Platforms
r-tth	4.3.2	C source code and R wrappers for the tth/ttm TeX to HTML/MathML translators. / GPL-2	linux-64, osx-64, win-64
r-ttmoment	1.0	Computing the first two moments of the truncated multivariate t (TMVT) distribution under the double truncation. Applying the slice sampling algorithm to generate random variates from the TMVT distribution. / GPL-2	noarch
r-ttr	0.23.4	Functions and data to construct technical trading rules with R. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
r-tts	1.0	Time-Temperature Superposition analysis is often applied to frequency modulated data obtained by Dynamic Mechanic Analysis (DMA) and Rheometry in the analytical chemistry and physics areas. These techniques provide estimates of material mechanical properties (such as moduli) at different temperatures in a wider range of time. This package provides the Time-Temperature superposition Master Curve at a referred temperature by the three methods: the two wider used methods, Arrhenius based methods and WLF, and the newer methodology based on derivatives procedure. The Master Curve is smoothed by B-splines basis. The package output is composed of plots of experimental data, horizontal and vertical shifts, TTS data, and TTS data fitted using B-splines with bootstrap confidence intervals. / GPL-2	noarch
r-ttplot	1.1.1	Implementation of Time to Target plot based on the work of Ribeiro and Rosseti (2015) <DOI:10.1007/s11590-014-0760-8>, that describe a numerical method that gives the probability of an algorithm A finds a solution at least as good as a given target value in smaller computation time than algorithm B. / GPL-2	noarch
r-ttutils	1.0.1	Contains some auxiliary functions. / GPL-2	noarch
r-ttwa	0.8.5	This package makes Travel To Work Area from a commuting flow data frame. / GPL (>= 2.0)	noarch
r-tubern	0.1.0	Get statistics and reports from YouTube. To learn more about the YouTube Analytics and Reporting API, see < <a href="https://developers.google.com/youtube/reporting/">https://developers.google.com/youtube/reporting/</a> >. / MIT	noarch
r-tuckerr.mmgg	1.5.1	Performs Three-Mode Principal Components Analysis, which carries out Tucker Models. / GPL-3	noarch
r-tufte	0.5	Provides R Markdown output formats to use Tufte styles for PDF and HTML output. / GPL-3	noarch
r-tufterhandout	1.2.1	Custom template and output formats for use with rmarkdown. Produce Edward Tufte-style handouts in html formats with full support for rmarkdown features / MIT	noarch
r-tukeytrend	0.6	Provides wrapper functions to the multiple marginal model function mmm() of package ‘multcomp’ to implement the trend test of Tukey, Ciminera and Heyse (1985) <DOI:10.2307/2530666> for general parametric models. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-tumblr</a>	1.1	Provides an R-interface to the Tumblr web API (see Tumblr v2 API on <a href="https://www.tumblr.com/docs/en/api/v2">https://www.tumblr.com/docs/en/api/v2</a> ). Tumblr is a microblogging platform and social networking website ( <a href="https://www.tumblr.com">https://www.tumblr.com</a> ). / Artistic-2.0	noarch
<a href="#">r-tunepareto</a>	2.5	Generic methods for parameter tuning of classification algorithms using multiple scoring functions. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-tuple</a>	0.4_0	Functions to find all matches or non-matches, orphans, and duplicate or other replicated elements. / LGPL-3	noarch
<a href="#">r-turboem</a>	2018.	Algorithms for accelerating the convergence of slow, monotone sequences from smooth, contraction mapping such as the EM and MM algorithms. It can be used to accelerate any smooth, linearly convergent acceleration scheme. A tutorial style introduction to this package is available in a vignette on the CRAN download page or, when the package is loaded in an R session, with <code>vignette(turboEM)</code> . / GPL-2	noarch
<a href="#">r-turtlegraphics</a>	1.0_8	An implementation of turtle graphics < <a href="http://en.wikipedia.org/wiki/Turtle_graphics">http://en.wikipedia.org/wiki/Turtle_graphics</a> >. Turtle graphics comes from Papert's language Logo and has been used to teach concepts of computer programming. / GPL-3	noarch
<a href="#">r-tutorial</a>	0.4.3	DataCamp Light (< <a href="https://github.com/datacamp/datacamp-light">https://github.com/datacamp/datacamp-light</a> >) is a light-weight implementation of the DataCamp UI, that allows you to embed interactive exercises inside HTML documents. The tutorial package makes it easy to create these HTML files from R Markdown files. An extension to knitr, tutorial detects appropriately formatted code chunks and replaces them with DataCamp Light readable chunks in the resulting HTML file. / MIT	noarch
<a href="#">r-tuwmodel</a>	1.0_2	The model, developed at the Vienna University of Technology, is a lumped conceptual rainfall-runoff model, following the structure of the HBV model. The model can also be run in a semi-distributed fashion. The model runs on a daily or shorter time step and consists of a snow routine, a soil moisture routine and a flow routing routine. See Parajka, J., R. Merz, G. Bloeschl (2007) <DOI:10.1002/hyp.6253> Uncertainty and multiple objective calibration in regional water balance modelling: case study in 320 Austrian catchments, Hydrological Processes, 21, 435-446. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-tvd</a>	0.1.0	Total Variation Denoising is a regularized denoising method which effectively removes noise from piecewise constant signals whilst preserving edges. This package contains a C implementation of Condat's very fast 1D squared error loss TVD algorithm. Additional methods and loss functions may be added in future versions. / EPL (>= 1.0)	linux-64, osx-64, win-64
<a href="#">r-tvsmiss</a>	0.1.1	Use a regularization likelihood method to achieve variable selection purpose. Likelihood can be worked with penalty lasso, smoothly clipped absolute deviations (SCAD), and minimax concave penalty (MCP). Tuning parameter selection techniques include cross validation (CV), Bayesian information criterion (BIC) (low and high), stability of variable selection (sVS), stability of BIC (sBIC), and stability of estimation (sEST). More details see Jiwei Zhao, Yang Yang, and Yang Ning (2018) <arXiv:1703.06379> Penalized pairwise pseudo likelihood for variable selection with nonignorable missing data. Statistica Sinica. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-tweedie</a>	2.3.2	Maximum likelihood computations for Tweedie families, including the series expansion (Dunn and Smyth, 2005; <doi:10.1007/s11222-005-4070-y>) and the Fourier inversion (Dunn and Smyth, 2008; <doi:10.1007/s11222-007-9039-6>), and related methods. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-twfy</a>	0.1.0	An R wrapper around the API of TheyWorkForYou, a parliamentary monitoring site that scrapes and repackages Hansard (the UK's parliamentary record) and augments it with information from the Register of Members' Interests, election results, and voting records to provide a unified source of information about UK legislators and their activities. See < <a href="http://www.theyworkforyou.com">http://www.theyworkforyou.com</a> > for details. / GPL-3	noarch
<a href="#">r-twiddler</a>	0.5_0	Twiddler is an interactive tool that automatically creates a Tcl/Tk GUI for manipulating variables in any R expression. See the documentation of the function twiddle to get started. / GPL-2	noarch
<a href="#">r-twilio</a>	0.1.0	The Twilio web service provides an API for computer programs to interact with telephony. The included functions wrap the SMS and MMS portions of Twilio's API, allowing users to send and receive text messages from R. See < <a href="https://www.twilio.com/docs/">https://www.twilio.com/docs/</a> > for more information. / MIT	noarch
<a href="#">r-twitter</a>	1.1.9	Provides an interface to the Twitter web API. / Artistic-2.0	noarch
<a href="#">r-twitterwidget</a>	0.1.1	Include the Twitter status widgets in HTML pages created using R markdown. The package uses the Twitter javascript APIs to embed in your document Twitter cards associated to specific statuses. The main targets are regular HTML pages or dashboards. / MIT	noarch
<a href="#">r-twocop</a>	1.0	This package implements the nonparametric test of equality between two copulas proposed by Remillard and Scaillet in their 2009 JMVA paper. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-twophaseind</a>	1.1.1	Estimation of gene-treatment interactions in randomized clinical trials exploiting gene-treatment independence. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-twosamples</a>	1.0.0	Fast randomization based two sample tests. Testing the hypothesis that two samples come from the same distribution using randomization to create p-values. Included tests are: Kolmogorov-Smirnov, Kuiper, Cramer-von Mises, and Anderson-Darling. There is also a very efficient test based on the Wasserstein Distance. The default test 'two_sample' builds on the Wasserstein distance by using a weighting scheme like that of Anderson-Darling. We also include the permutation scheme to make test building simple for others. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-twosampletest.hd	1.0	For high-dimensional data whose main feature is a large number, $p$ , of variables but a small sample size, the null hypothesis that the marginal distributions of $p$ variables are the same for two groups is tested. We propose a test statistic motivated by the simple idea of comparing, for each of the $p$ variables, the empirical characteristic functions computed from the two samples. If one rejects this global null hypothesis of no differences in distributions between the two groups, a set of permutation $p$ -values is reported to identify which variables are not equally distributed in both groups. / GPL-2	noarch
r-twostepclogit	1.2.5	Conditional logistic regression with longitudinal follow up and individual-level random coefficients: A stable and efficient two-step estimation method. / GPL-2	noarch
r-twoway	0.6.2	Carries out analyses of two-way tables with one observation per cell, together with graphical displays for an additive fit and a diagnostic plot for removable ‘non-additivity’ via a power transformation of the response. It implements Tukey’s Exploratory Data Analysis methods, including a 1-degree-of-freedom test for row*column ‘non-additivity’, linear in the row and column effects. / GPL-3	noarch
r-txtplot	1.0_3	Provides functions to produce rudimentary ascii graphics directly in the terminal window. Provides a basic plotting function (and equivalents of curve, density, acf and barplot) as well as a boxplot function. / LGPL-3	noarch
r-types	1.0.0	Provides a simple type annotation for R that is usable in scripts, in the R console and in packages. It is intended as a convention to allow other packages to use the type information to provide error checking, automatic documentation or optimizations. / MIT	noarch
r-ubcrm	1.0.1	Two Phase I designs are implemented in the package: the classical 33 and the Continual Reassessment Method. Simulations tools are also available to estimate the operating characteristics of the methods with several user-dependent options. / GPL-2	noarch
r-ucbthesis	1.0	This package contains latex, knitr and R Markdown templates that adhere to the UC Berkeley Graduate Division’s thesis guidelines. The templates are located in the inst/ directory. / GPL-2	noarch
r-ucminf	1.1_4	An algorithm for general-purpose unconstrained non-linear optimization. The algorithm is of quasi-Newton type with BFGS updating of the inverse Hessian and soft line search with a trust region type monitoring of the input to the line search algorithm. The interface of ‘ucminf’ is designed for easy interchange with ‘optim’. / GPL-2	linux-64, osx-64, win-64
r-ucr.columnnames	0.1.0	Changes the column names of the inputted dataset to the correct names from the Uniform Crime Report codebook for the Offenses Known and Clearance by Arrest datasets from 1998-2014. / GPL-3	noarch
r-udapi	0.1.3	A client for the Urban Dictionary < <a href="http://www.urbandictionary.com/">http://www.urbandictionary.com/</a> > API. / MIT	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-udderquarterinfectiondata</a>	1.0.0	The udder quarter infection data set contains infection times of individual cow udder quarters with <i>Corynebacterium bovis</i> (Laevens et al. 1997 <DOI:10.3168/jds.S0022-0302(97)76295-7>). Obviously, the four udder quarters are clustered within a cow, and udder quarters are sampled only approximately monthly, generating interval-censored data. The data set contains both covariates that change within a cow (e.g., front and rear udder quarters) and covariates that change between cows (e.g., parity [the number of previous calvings]). The correlation between udder infection times within a cow also is of interest, because this is a measure of the infectivity of the agent causing the disease. Various models have been applied to address the problem of interdependence for right-censored event times. These models, as applied to this data set, can be found back in the publications found in the reference list. / GPL-3	noarch
<a href="#">r-udpipe</a>	0.8.3	This natural language processing toolkit provides language-agnostic ‘tokenization’, ‘parts of speech tagging’, ‘lemmatization’ and ‘dependency parsing’ of raw text. Next to text parsing, the package also allows you to train annotation models based on data of ‘treebanks’ in ‘CoNLL-U’ format as provided at < <a href="http://universaldependencies.org/format.html">http://universaldependencies.org/format.html</a> >. The techniques are explained in detail in the paper: ‘Tokenizing, POS Tagging, Lemmatizing and Parsing UD 2.0 with UDPipe’, available at <doi:10.18653/v1/K17-3009>. / MPL-2.0	linux-64, osx-64, win-64
<a href="#">r-udunits2</a>	0.13	Provides simple bindings to Unidata’s udunits library. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-ui</a>	0.1.0	Implements functions to derive uncertainty intervals for (i) regression (linear and probit) parameters when outcome is missing not at random (non-ignorable missingness) introduced in Genbaeck, M., Stanghellini, E., de Luna, X. (2015) <doi:10.1007/s00362-014-0610-x> and Genbaeck, M., Ng, N., Stanghellini, E., de Luna, X. (2018) <doi:10.1007/s10433-017-0448-x>; and (ii) double robust and outcome regression estimators of average causal effects (on the treated) with possibly unobserved confounding introduced in Genbaeck, M., de Luna, X. (2018) <doi:10.1111/biom.13001>. / GPL-2	noarch
<a href="#">r-uiuc themes</a>	0.2.1	A set of custom ‘R’ ‘Markdown’ templates for documents and presentations with the University of Illinois at Urbana-Champaign (UIUC) color scheme and identity standards. / MIT	noarch
<a href="#">r-ukbabynames</a>	0.1.1	Full listing of UK baby names occurring more than three times per year between 1996 and 2015, and rankings of baby name popularity by decade from 1904 to 1994. / CC0	noarch
<a href="#">r-ukgasapi</a>	0.16	Allows users to access live UK gas market information via National Grid’s API. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-ulid</a>	0.3.0	Universally unique identifiers ('UUIDs') can be suboptimal for many use-cases because they aren't the most character efficient way of encoding 128 bits of randomness; v1/v2 versions are impractical in many environments, as they require access to a unique, stable MAC address; v3/v5 versions require a unique seed and produce randomly distributed IDs, which can cause fragmentation in many data structures; v4 provides no other information than randomness which can cause fragmentation in many data structures. 'ULIDs' (< <a href="https://github.com/ulid/spec">https://github.com/ulid/spec</a> >) have 128-bit compatibility with 'UUID', 1.21e24 unique 'ULIDs' per millisecond, are lexicographically sortable, canonically encoded as a 26 character string, as opposed to the 36 character 'UUID', use Crockford's 'base32' for better efficiency and readability (5 bits per character), are case insensitive, have no special characters (i.e. are 'URL' safe) and have a monotonic sort order (correctly detects and handles the same millisecond). / MIT	linux-64, osx-64, win-64
<a href="#">r-ultimixt</a>	2.1	A generic reference Bayesian analysis of unidimensional mixture distributions obtained by a location-scale parameterisation of the model is implemented. The including functions simulate and summarize posterior samples for location-scale mixture models using a weakly informative prior. There is no need to define priors for scale-location parameters except two hyperparameters in which are associated with a Dirichlet prior for weights and a simplex. / GPL (>= 2.0)	noarch
<a href="#">r-umoments</a>	0.1.0	Calculates one-sample unbiased central moment estimates and two-sample pooled estimates up to 6th order, including unbiased estimates of powers and products of central moments. Provides the machinery for obtaining unbiased central moment estimators beyond 6th order. / GPL-2	noarch
<a href="#">r-ump</a>	0.5.8	Does uniformly most powerful (UMP) and uniformly most powerful unbiased (UMPU) tests. At present only distribution implemented is binomial distribution. Also does fuzzy tests and confidence intervals (following Geyer and Meeden, 2005, <doi:10.1214/088342305000000340>) for the binomial distribution (one-tailed procedures based on UMP test and two-tailed procedures based on UMPU test). / MIT	linux-64, osx-64, win-64
<a href="#">r-umpire</a>	1.3.7	The Ultimate Microrray Prediction, Reality and Inference Engine (UMPIRE) is a package to facilitate the simulation of realistic microarray data sets with link to associate outcomes. See Zhang and Coombes (2012) <doi:10.1186/1471-2105-13-S13-S1>. / Apache License (== 2.0)	noarch
<a href="#">r-unbalhaar</a>	2.0	The package implements top-down and bottom-up algorithms for nonparametric function estimation in Gaussian noise using Unbalanced Haar wavelets. / GPL-2	noarch
<a href="#">r-uncdecomp</a>	0.0.4	If a procedure consists of several stages and there are several scenarios that can be selected for each stage, uncertainty of the procedure can be decomposed by stages or scenarios. cum_uncertainty() is used to decompose uncertainty based on the cumulative uncertainty. stage_uncertainty() and scenario_uncertainty() is used to decompose uncertainty based on the second order interaction ANOVA model. In stage_uncertainty() and scenario_uncertainty(), the uncertainty from interaction effect from two stages is distributed equally to each stage. / GPL-2	noarch
<a href="#">r-unf</a>	2.0.6	Computes a universal numeric fingerprint (UNF) for an R data object. UNF is a cryptographic hash or signature that can be used to uniquely identify (a version of) a rectangular dataset, or a subset thereof. UNF can be used, in tandem with a DOI, to form a persistent citation to a versioned dataset. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-unfoldr</a>	0.7	Stereological unfolding of the joint size-shape-orientation distribution of spheroidal shaped particles. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-unicode</a>	12.0.0	Data from Unicode 12.0.0 and related utilities. / GPL-2	noarch
<a href="#">r-unidoe</a>	1.0.2	Efficient procedures for constructing uniform design of experiments under various space-filling criteria. It is based on a stochastic and adaptive threshold accepting algorithm with flexible initialization, adaptive threshold, and stochastic evolution. The package may also construct the augmented uniform designs in a sequential manner. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-unifed</a>	1.1.1	Probability functions and family for glm() of the unified distribution (Quijano Xacur, 2018; <arXiv:1812.00251>). / GPL-3	linux-64, osx-64, win-64
<a href="#">r-unisoregression</a>	0.0_0	Perform L1 or L2 isotonic and unimodal regression on 1D weighted or unweighted input vector and isotonic regression on 2D weighted or unweighted input vector. It also performs L infinity isotonic and unimodal regression on 1D unweighted input vector. Reference: Quentin F. Stout (2008) <doi:10.1016/j.csda.2008.08.005>. Spouge, J., Wan, H. & Wilbur, W.(2003) <doi:10.1023/A:1023901806339>. Q.F. Stout (2013) <doi:10.1007/s00453-012-9628-4>. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-unikn</a>	0.1.0	Define and use graphical elements of corporate design manuals in R. The ‘unikn’ package provides color functions (by defining dedicated colors and color palettes, and commands for changing, viewing, and using them) and styled text elements (e.g., for marking, underlining, or plotting colored titles). The pre-defined range of colors and text functions is based on the corporate design of the University of Konstanz < <a href="https://www.uni-konstanz.de/">https://www.uni-konstanz.de/</a> >, but can be adapted and extended for other institutions and purposes. / CC BY-SA 4.0	noarch
<a href="#">r-unine</a>	0.2.0	Implementation of light stemmers for French, German, Italian, Spanish, Portuguese, Finnish, Swedish. They are based on the same work as the light stemmers found in ‘SolR’ < <a href="https://lucene.apache.org/solr/">https://lucene.apache.org/solr/</a> > or ‘ElasticSearch’ < <a href="https://www.elastic.co/fr/products/elasticsearch">https://www.elastic.co/fr/products/elasticsearch</a> >. A light stemmer consists in removing inflections only for noun and adjectives. Indexing verbs for these languages is not of primary importance compared to nouns and adjectives. The stemming procedure for French is described in (Savoy, 1999) <doi:10.1002/(SICI)1097-4571(1999)50:10%3C944::AID-ASI9%3E3.3.CO;2-H>. / MIT	linux-64, osx-64, win-64
<a href="#">r-uniqtag</a>	1.0	For each string in a set of strings, determine a unique tag that is a substring of fixed size k unique to that string, if it has one. If no such unique substring exists, the least frequent substring is used. If multiple unique substrings exist, the lexicographically smallest substring is used. This lexicographically smallest substring of size k is called the UniqTag of that string. / MIT	noarch
<a href="#">r-unitcircle</a>	0.1.3	The uc.check() function checks whether the roots of a given polynomial lie outside the Unit circle. You can also easily draw an unit circle. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-unitedr</a>	0.3.1	United is a software tool which can be downloaded at the following web-site < <a href="http://www.schroepl.net/pbm/software/united/">http://www.schroepl.net/pbm/software/united/</a> >. In general, it is a virtual manager game for football teams. This package contains helpful functions for determining an optimal formation for a virtual match in United. E.g. knowing that the opponent has a strong defensive it is advisable to beat him in the mid-field. Furthermore, this package contains functions for computing the optimal usage of hardness in a game. / GPL-2	noarch
<a href="#">r-unitizer</a>	1.4.8	Simplifies regression tests by comparing objects produced by test code with earlier versions of those same objects. If objects are unchanged the tests pass, otherwise execution stops with error details. If in interactive mode, tests can be reviewed through the provided interactive environment. / GPL-2	noarch
<a href="#">r-units</a>	0.6_2	Support for measurement units in R vectors, matrices and arrays: automatic propagation, conversion, derivation and simplification of units; raising errors in case of unit incompatibility. Compatible with the POSIXct, Date and diff-time classes. Uses the UNIDATA udunits library and unit database for unit compatibility checking and conversion. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-unittest</a>	1.3_0	Concise TAP < <a href="http://testanything.org/">http://testanything.org/</a> > compliant unit testing package. Authored tests can be run using CMD check with minimal implementation overhead. / GPL-3	noarch
<a href="#">r-univrng</a>	1.2	Pseudo-random number generation of 17 univariate distributions. / GPL-2   GPL-3	noarch
<a href="#">r-unix</a>	1.5	Bindings to system utilities found in most Unix systems such as POSIX functions which are not part of the Standard C Library. / MIT	linux-64, osx-64
<a href="#">r-unmarked</a>	0.12	Fits hierarchical models of animal abundance and occurrence to data collected using survey methods such as point counts, site occupancy sampling, distance sampling, removal sampling, and double observer sampling. Parameters governing the state and observation processes can be modeled as functions of covariates. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-unrepx</a>	1.0	Provides half-normal plots, reference plots, and Pareto plots of effects from an unreplicated experiment, along with various pseudo-standard-error measures, simulated reference distributions, and other tools. Many of these methods are described in Daniel C. (1959) <doi:10.1080/00401706.1959.10489866> and/or Lenth R.V. (1989) <doi:10.1080/00401706.1989.10488595>, but some new approaches are added and integrated in one package. / GPL-2	noarch
<a href="#">r-unsystation</a>	0.2.0	Performs a test for second-order stationarity of time series based on unsystematic sub-samples. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-unvotes</a>	0.2.0	Historical voting data of the United Nations General Assembly. This includes votes for each country in each roll call, as well as descriptions and topic classifications for each vote. / MIT	noarch

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Name	Version	Summary/License	Platforms
r-upsvarapprox	0.1.1	Variance approximations for the Horvitz-Thompson total estimator in Unequal Probability Sampling using only first-order inclusion probabilities. See Matei and Tillä© (2005) and Haziza, Mecatti and Rao (2008) for details. / GPL-3	noarch
r-uptimerobot	1.0.0	Provide a set of wrappers to call all the endpoints of UptimeRobot API which includes various kind of ping, keep-alive and speed tests. See < <a href="https://uptimerobot.com/">https://uptimerobot.com/</a> > for more information. / MIT	noarch
r-urbin	0.1_8	Calculate unified measures that quantify the effect of a covariate on a binary dependent variable (e.g., for meta-analyses). This can be particularly important if the estimation results are obtained with different models/estimators (e.g., linear probability model, logit, probit, ...) and/or with different transformations of the explanatory variable of interest (e.g., linear, quadratic, interval-coded, ...). The calculated unified measures are: (a) semi-elasticities of linear, quadratic, or interval-coded covariates and (b) effects of linear, quadratic, interval-coded, or categorical covariates when a linear or quadratic covariate changes between distinct intervals, the reference category of a categorical variable or the reference interval of an interval-coded variable needs to be changed, or some categories of a categorical covariate or some intervals of an interval-coded covariate need to be grouped together. Approximate standard errors of the unified measures are also calculated. All methods that are implemented in this package are described in the 'vignette' Extracting and Unifying Semi-Elasticities and Effect Sizes from Studies with Binary Dependent Variables that is included in this package. / GPL-2	noarch
r-urca	1.3_0	Unit root and cointegration tests encountered in applied econometric analysis are implemented. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
r-uroot	2.0_9	Seasonal unit roots and seasonal stability tests. P-values based on response surface regressions are available for both tests. P-values based on bootstrap are available for seasonal unit root tests. A parallel implementation of the bootstrap method requires a CUDA capable GPU with compute capability >= 3.0, otherwise a debugging version fully coded in R is used. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
r-usaboundaries	0.3.1	The boundaries for geographical units in the United States of America contained in this package include state, county, congressional district, and zip code tabulation area. Contemporary boundaries are provided by the U.S. Census Bureau (public domain). Historical boundaries for the years from 1629 to 2000 are provided form the Newberry Library's 'Atlas of Historical County Boundaries' (licensed CC BY-NC-SA). Additional data is provided in the 'US-AboundariesData' package; this package provides an interface to access that data. / MIT	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-uscensus2000cdp</a>	0.03	US Census 2000 Designated Places shapefiles and additional demographic data from the SF1 100 percent files. This data set contains polygon files in lat/lon coordinates and the corresponding demographic data for a number of different variables. / GPL-2	noarch
<a href="#">r-uscensus2000tract</a>	0.03	US 2000 Census Tract shapefiles and additional demographic data from the SF1 100 percent files. This data set contains polygon files in lat/lon coordinates and the corresponding demographic data for a number of different variables. / GPL-2	noarch
<a href="#">r-uscensus2010</a>	0.11	US Census 2010 shape files and additional demographic data from the SF1 100 percent files. This package contains a number of helper functions for the US-census2010blk, UScensus2010blkgrp, UScensus2010tract, UScensus2010cdp packages. / GPL-2	noarch
<a href="#">r-usdm</a>	1.1_18	This is a framework that aims to provide methods and tools for assessing the impact of different sources of uncertainties (e.g. positional uncertainty) on performance of species distribution models (SDMs.) / GPL-3	noarch
<a href="#">r-usedist</a>	0.1.0	Functions to re-arrange, extract, and work with distances. / GPL-3	noarch
<a href="#">r-usethis</a>	1.5.0	Automate package and project setup tasks that are otherwise performed manually. This includes setting up unit testing, test coverage, continuous integration, Git, 'GitHub', licenses, 'Rcpp', 'RStudio' projects, and more. / GPL-3	noarch
<a href="#">r-usgsstates2k</a>	1.0.1	A map of the USA from the United States Geological Survey (USGS). Irucka worked with this data set while a Cherokee Nation Technology Solutions (CNTS) USGS Contractor and/or USGS employee. It is replaced by 'states2k'. / CC0	noarch
<a href="#">r-usmap</a>	0.4.0	Obtain United States map data frames of varying region types (e.g. county, state). The map data frames include Alaska and Hawaii conveniently placed to the bottom left, as they appear in most maps of the US. Convenience functions for plotting choropleths and working with FIPS codes are also provided. / GPL-3	noarch
<a href="#">r-ustatbookabsc</a>	1.0.0	A set of functions leading to multivariate response L1 regression. This includes functions on computing Euclidean inner products and norms, weighted least squares estimates on multivariate responses, function to compute fitted values and residuals. This package is a companion to the book U-Statistics, M-estimation and Resampling, by Arup Bose and Snigdhanu Chatterjee, to appear in 2017 as part of the Texts and Readings in Mathematics (TRIM) series of Hindustan Book Agency and Springer-Verlag. / GPL-3	noarch
<a href="#">r-ustyc</a>	1.0.0	Forms a query to submit for US Treasury yield curve data, posting this query to the US Treasury web site's data feed service. By default the download includes data yield data for 12 products from January 1, 1990, some of which are NA during this span. The caller can pass parameters to limit the query to a certain year or year and month, but the full download is not especially large. The download data from the service is in XML format. The package's main function transforms that XML data into a numeric data frame with treasury product items (constant maturity yields for 12 kinds of bills, notes, and bonds) as columns and dates as row names. The function returns a list which includes an item for this data frame as well as query-related values for reference and the update date from the service. / MIT	noarch
<a href="#">r-utc</a>	0.1.5	Three functions are provided: first function changes time from local to UTC, other changes from UTC to local and third returns difference between local and UTC. %h% operator is also provided it adds hours to a time. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-utf8</a>	1.1.4	Process and print ‘UTF-8’ encoded international text (Unicode). Input, validate, normalize, encode, format, and display. / Apache License (== 2.0)   file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-utility</a>	1.4.3	Construct and plot objective hierarchies and associated value and utility functions. Evaluate the values and utilities and visualize the results as colored objective hierarchies or tables. Visualize uncertainty by plotting median and quantile intervals within the nodes of objective hierarchies. Get numerical results of the evaluations in standard R data types for further processing. / GPL-3	noarch
<a href="#">r-uuid</a>	0.1_2	Tools for generating and handling of UUIDs (Universally Unique Identifiers). / MIT file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-v8</a>	2.3	An R interface to Google’s open source JavaScript engine. This package can now be compiled either with V8 version 6 or 7 (LTS) from nodejs or with the legacy 3.14/3.15 branch of V8. / MIT	win-64
<a href="#">r-vaersndvax</a>	1.0.4	Non-Domestic VAERS vaccine data for 01/01/2016 - 06/14/2016. If you want to explore the full VAERS data for 1990 - Present (data, symptoms, and vaccines), then check out the ‘vaersND’ package from the URL below. The URL and BugReports below correspond to the ‘vaersND’ package, of which ‘vaersNDvax’ is a small subset (2016 only). ‘vaersND’ is not hosted on CRAN due to the large size of the data set. To install the Suggested ‘vaers’ and ‘vaersND’ packages, use the following R code: ‘devtools::install_git( <a href="https://gitlab.com/iembry/vaers.git">https://gitlab.com/iembry/vaers.git</a> , build_vignettes = TRUE)’ and ‘devtools::install_git( <a href="https://gitlab.com/iembry/vaersND.git">https://gitlab.com/iembry/vaersND.git</a> , build_vignettes = TRUE)’. VAERS is a national vaccine safety surveillance program co-sponsored by the US Centers for Disease Control and Prevention (CDC) and the US Food and Drug Administration (FDA). VAERS is a post-marketing safety surveillance program, collecting information about adverse events (possible side effects) that occur after the administration of vaccines licensed for use in the United States. For more information about the data, visit < <a href="https://vaers.hhs.gov/index">https://vaers.hhs.gov/index</a> >. For information about vaccination/immunization hazards, visit < <a href="http://www.questionuniverse.com/rethink.html/#vaccine">http://www.questionuniverse.com/rethink.html/#vaccine</a> >. / CC0	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-vaersvax</a>	1.0.5	US VAERS vaccine data for 01/01/2018 - 06/14/2018. If you want to explore the full VAERS data for 1990 - Present (data, symptoms, and vaccines), then check out the 'vaers' package from the URL below. The URL and BugReports below correspond to the 'vaers' package, of which 'vaersvax' is a small subset (2018 only). 'vaers' is not hosted on CRAN due to the large size of the data set. To install the Suggested 'vaers' and 'vaersND' packages, use the following R code: 'devtools::install_git(< <a href="https://gitlab.com/iembry/vaers.git">https://gitlab.com/iembry/vaers.git</a> >, build_vignettes = TRUE)' and 'devtools::install_git(< <a href="https://gitlab.com/iembry/vaersND.git">https://gitlab.com/iembry/vaersND.git</a> >, build_vignettes = TRUE)'. The Vaccine Adverse Event Reporting System (VAERS) is a national early warning system to detect possible safety problems in U.S.-licensed vaccines. VAERS is co-managed by the Centers for Disease Control and Prevention (CDC) and the U.S. Food and Drug Administration (FDA). For more information about the data, visit < <a href="https://vaers.hhs.gov/">https://vaers.hhs.gov/</a> >. For information about vaccination/immunization hazards, visit < <a href="http://www.questionuniverse.com/rethink.html#vaccine">http://www.questionuniverse.com/rethink.html#vaccine</a> >. / CC0	noarch
<a href="#">r-valaddin</a>	1.0.0	A set of basic tools to transform functions into functions with input validation checks, in a manner suitable for both programmatic and interactive use. / MIT	noarch
<a href="#">r-valection</a>	1.0.0	A binding for the 'valection' program which offers various ways to sample the outputs of competing algorithms or parameterizations, and fairly assess their performance against each other. The 'valection' C library is required to use this package and can be downloaded from: < <a href="http://labs.oicr.on.ca/boutros-lab/software/valection">http://labs.oicr.on.ca/boutros-lab/software/valection</a> >. Cooper CI, et al; Valection: Design Optimization for Validation and Verification Studies; Biorxiv 2018; <doi:10.1101/254839>. / GPL-3	noarch
<a href="#">r-valetr</a>	0.1.0	Interface to Bank of Canada's 'Valet' API (< <a href="https://www.bankofcanada.ca/valet/docs">https://www.bankofcanada.ca/valet/docs</a> >). Please read the API terms and conditions: < <a href="https://www.bankofcanada.ca/terms/">https://www.bankofcanada.ca/terms/</a> >. / GPL-3	noarch
<a href="#">r-validatejsonr</a>	1.0.4	The current implementation uses the C library 'RapidJSON' to supply the schema functionality, it supports JSON Schema Draft v4. As of 2016-09-09, 'RapidJSON' passed 262 out of 263 tests in JSON Schema Test Suite (JSON Schema draft 4). / BSD_2_clause	linux-64, osx-64, win-64
<a href="#">r-valorate</a>	1.0.1	The algorithm implemented in this package was designed to quickly estimate the distribution of the log-rank especially for heavy unbalanced groups. VALORATE estimates the null distribution and the p-value of the log-rank test based on a recent formulation. For a given number of alterations that define the size of survival groups, the estimation involves a weighted sum of distributions that are conditional on a co-occurrence term where mutations and events are both present. The estimation of conditional distributions is quite fast allowing the analysis of large datasets in few minutes < <a href="http://bioinformatica.mty.itesm.mx/valorate">http://bioinformatica.mty.itesm.mx/valorate</a> >. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-valottery</a>	0.0.1	Historical results for the state of Virginia lottery draw games. Data were downloaded from <a href="https://www.valottery.com/">https://www.valottery.com/</a> . / CC0	noarch
<a href="#">r-var.etp</a>	0.7	Estimation, Hypothesis Testing, Prediction for Stationary Vector Autoregressive Models / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-varband	0.9.0	Implementation of the variable banding procedure for modeling local dependence and estimating precision matrices that is introduced in Yu & Bien (2016) and is available at < <a href="https://arxiv.org/abs/1604.07451">https://arxiv.org/abs/1604.07451</a> >. / GPL-3	linux-64, osx-64, win-64
r-varbin	0.2.1	Tool for easy and efficient discretization of continuous and categorical data. The package calculates the most optimal binning of a given explanatory variable with respect to a user-specified target variable. The purpose is to assign a unique Weight-of-Evidence value to each of the calculated binpoints in order to recode the original variable. The package allows users to impose certain restrictions on the functional form on the resulting binning while maximizing the overall information value in the original data. The package is well suited for logistic scoring models where input variables may be subject to restrictions such as linearity by e.g. regulatory authorities. An excellent source describing in detail the development of scorecards, and the role of Weight-of-Evidence coding in credit scoring is (Siddiqi 2006, ISBN: 978-0-471-75451-0). The package utilizes the discrete nature of decision trees and Isotonic Regression to accommodate the trade-off between flexible functional forms and maximum information value. / GPL-2	noarch
r-variag	0.2_1	Interactive variogram diagnostics. / GPL-2	noarch
r-vared	1.0.0	Generating functions for both optimal and ordinary difference sequences, and the difference-based estimation functions. / GPL-2	noarch
r-vares	1.0	Computes Value at risk and expected shortfall, two most popular measures of financial risk, for over one hundred parametric distributions, including all commonly known distributions. Also computed are the corresponding probability density function and cumulative distribution function. / GPL-2	noarch
r-varhandle	2.0.3	Variables are the fundamental parts of each programming language but handling them might be frustrating for programmers from time to time. This package contains some functions to help user (especially data explorers) to make more sense of their variables and take the most out of variables and hardware resources. These functions are written, collected and crafted over 5 years of experience in statistical data analysis on high-dimensional data and for each of them there was a need. Functions in this package are suppose to be efficient and easy to use, hence they will be frequently updated to make them more convenient. / GPL-2	noarch
r-variables	1.0_2	Abstract descriptions of (yet) unobserved variables. / GPL-2	noarch
r-vars	1.5_3	Estimation, lag selection, diagnostic testing, forecasting, causality analysis, forecast error variance decomposition and impulse response functions of VAR models and estimation of SVAR and SVEC models. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
r-varsedig	1.9	An algorithm which identifies the morphometric features that significantly discriminate two taxa and validates the morphological distinctness between them via a Monte-Carlo test, polar coordinates and overlap of the area under the density curve. / GPL-2	noarch
r-varsel	0.1	Feature selection using Sequential Forward Floating feature Selection and Jeffries-Matusita distance. It returns a suboptimal set of features to use for image classification. Reference: Dalponte, M., Oerka, H.O., Gobakken, T., Gianelle, D. & Naeset, E. (2013). Tree Species Classification in Boreal Forests With Hyperspectral Data. IEEE Transactions on Geoscience and Remote Sensing, 51, 2632-2645, <DOI:10.1109/TGRS.2012.2216272>. / GPL-3	noarch
r-varselrf	0.7_8	Variable selection from random forests using both backwards variable elimination (for the selection of small sets of non-redundant variables) and selection based on the importance spectrum (somewhat similar to scree plots; for the selection of large, potentially highly-correlated variables). Main applications in high-dimensional data (e.g., microarray data, and other genomics and proteomics applications). / GPL-2	noarch
r-varswapprice	1.0	Computes a portfolio of European options that replicates the cost of capturing the realised variance of an equity index. / GPL-3	noarch
r-vbdm	0.0.4	Efficient algorithm for solving discrete mixture regression model for rare variant association analysis. Uses variational Bayes algorithm to efficiently search over model space. Outputs an approximate likelihood ratio test as well as variant level posterior probabilities of association. / GPL-2	linux-64, osx-64, win-64
r-vbsr	0.0.5	Efficient algorithm for solving ultra-sparse regularized regression models using a variational Bayes algorithm with a spike (l0) prior. Algorithm is solved on a path, with coordinate updates, and is capable of generating very sparse models. There are very general model diagnostics for controlling type-1 error included in this package. / GPL-2	linux-64, osx-64, win-64
r-vca	1.4.0	ANOVA and REML estimation of linear mixed models is implemented, once following Searle et al. (1991, ANOVA for unbalanced data), once making use of the 'lme4' package. The primary objective of this package is to perform a variance component analysis (VCA) according to CLSI EP05-A3 guideline Evaluation of Precision of Quantitative Measurement Procedures (2014). There are plotting methods for visualization of an experimental design, plotting random effects and residuals. For ANOVA type estimation two methods for computing ANOVA mean squares are implemented (SWEEP and quadratic forms). The covariance matrix of variance components can be derived, which is used in estimating confidence intervals. Linear hypotheses of fixed effects and LS means can be computed. LS means can be computed at specific values of covariables and with custom weighting schemes for factor variables. See ?VCA for a more comprehensive description of the features. / GPL-3	linux-64, osx-64, win-64
r-vcd	1.4_4	Visualization techniques, data sets, summary and inference procedures aimed particularly at categorical data. Special emphasis is given to highly extensible grid graphics. The package was package was originally inspired by the book Visualizing Categorical Data by Michael Friendly and is now the main support package for a new book, Discrete Data Analysis with R by Michael Friendly and David Meyer (2015). / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-vcov	0.0.1	Methods for faster extraction (about 5x faster in a few test cases) of variance-covariance matrices and standard errors from models. Methods in the ‘stats’ package tend to rely on the summary method, which may waste time computing other summary statistics which are summarily ignored. / GPL-2	noarch
r-vcvcomp	1.0.1	Comparison of variance - covariance patterns using relative principal component analysis (relative eigenanalysis). Also provides functions to compute group covariance matrices, distance matrices, and perform proportionality tests. A working sample on the body shape of cichlid fishes is included. / GPL-3	noarch
r-vdgraph	2.2_2	Uses a modification of the published FORTRAN code in A Computer Program for Generating Variance Dispersion Graphs by G. Vining, Journal of Quality Technology, Vol. 25 No. 1 January 1993, to produce variance dispersion graphs. Also produces fraction of design space plots, and contains data frames for several minimal run response surface designs. / GPL-2	linux-64, osx-64, win-64
r-vdgermlines	0.1	Contains variable, diversity, and joining sequences and accompanying functions that enable both the extraction of and comparison between immune V-D-J genomic segments from a variety of species. Sources include IMGT from MP Lefranc (2009) <doi:10.1093/nar/gkn838> and Vgenerepertoire from publication DN Olivieri (2014) <doi:10.1007/s00251-014-0784-3>. / GPL-2	noarch
r-vdspcalibration	1.0	Provides statistical methods for the design and analysis of a calibration study, which aims for calibrating measurements using two different methods. The package includes sample size calculation, sample selection, regression analysis with error-in measurements and change-point regression. The method is described in Tian, Durazo-Arvizu, Myers, et al. (2014) <DOI:10.1002/sim.6235>. / GPL-3	noarch
r-vec2dtransf	1.1	A package for applying affine and similarity transformations on vector spatial data (sp objects). Transformations can be defined from control points or directly from parameters. If redundant control points are provided Least Squares is applied allowing to obtain residuals and RMSE. / GPL-2	noarch
r-vecsets	1.2.1	The base ‘sets’ tools follow the algebraic definition that each element of a set must be unique. Since it’s often helpful to compare all elements of two vectors, this toolset treats every element as unique for counting purposes. For ease of use, all functions in vecsets have an argument ‘multiple’ which, when set to FALSE, reverts them to the base::set tools functionality. / LGPL-3	noarch
r-vecstatgraphs2d	1.8	A 2D statistical analysis is performed, both numerical and graphical, of a set of vectors. Since a vector has two components (module and azimuth) vector analysis is performed in three stages: modules are analyzed by means of linear statistics, azimuths are analyzed by circular statistics, and the joint analysis of modules and azimuths is done using density maps that allow detecting another distribution properties (i.e. anisotropy) and outliers. Tests and circular statistic parameters have associated a full range of graphing: histograms, maps of distributions, point maps, vector maps, density maps, distribution modules and azimuths. / GPL-3	noarch
r-vegalite	0.6.1	The ‘Vega-Lite’ ‘JavaScript’ framework provides a higher-level grammar for visual analysis, akin to ‘ggplot’ or ‘Tableau’, that generates complete ‘Vega’ specifications. Functions exist which enable building a valid ‘spec’ from scratch or importing a previously created ‘spec’ file. Functions also exist to export ‘spec’ files and to generate code which will enable plots to be embedded in properly configured web pages. The default behavior is to generate an ‘htmlwidget’. / AGPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-vegawidget</a>	0.2.1	‘Vega’ and ‘Vega-Lite’ parse text in ‘JSON’ notation to render chart-specifications into ‘HTML’. This package is used to facilitate the rendering. It also provides a means to interact with signals, events, and datasets in a ‘Vega’ chart using ‘JavaScript’ or ‘Shiny’. / MIT	noarch
<a href="#">r-vegdata</a>	0.9.5	Handling of vegetation data from different sources ( Turboveg < <a href="http://www.synbiosys.alterra.nl/turboveg/">http://www.synbiosys.alterra.nl/turboveg/</a> >; the German national repository < <a href="http://www.vegetweb.de">http://www.vegetweb.de</a> > and others. Taxonomic harmonization (given appropriate taxonomic lists, e.g. the German taxonomic standard list GermanSL, < <a href="http://germansl.infinitemature.org">http://germansl.infinitemature.org</a> >). / GPL-2	noarch
<a href="#">r-vegetarian</a>	1.2	This package computes diversity for community data sets using the methods outlined by Jost (2006, 2007). While there are differing opinions on the ideal way to calculate diversity (e.g. Magurran 2004), this method offers the advantage of providing diversity numbers equivalents, independent alpha and beta diversities, and the ability to incorporate ‘order’ (q) as a continuous measure of the importance of rare species in the metrics. The functions provided in this package largely correspond with the equations offered by Jost in the cited papers. The package computes alpha diversities, beta diversities, gamma diversities, and similarity indices. Confidence intervals for diversity measures are calculated using a bootstrap method described by Chao et al. (2008). For datasets with many samples (sites, plots), sim.table creates tables of all pairwise comparisons possible, and for grouped samples sim.groups calculates pairwise combinations of within- and between-group comparisons. / GPL-2	noarch
<a href="#">r-vegperiod</a>	0.2.6	Collection of common methods to determine growing season length in a simple manner. Start and end dates of the vegetation periods are calculated solely based on daily mean temperatures and the day of the year. / GPL-3	noarch
<a href="#">r-vembedr</a>	0.1.3	A set of functions for generating HTML to embed hosted video in your R Markdown documents or Shiny applications. / MIT	noarch
<a href="#">r-venn</a>	1.7	Draws and displays Venn diagrams up to 7 sets, and any Boolean union of set intersections. / GPL-2	noarch
<a href="#">r-venneuler</a>	1.1_0	Calculates and displays Venn and Euler Diagrams / MPL-1.1	noarch
<a href="#">r-versions</a>	0.3	Installs specified versions of R packages hosted on CRAN and provides functions to list available versions and the versions of currently installed packages. These tools can be used to help make R projects and packages more reproducible. ‘versions’ fits in the narrow gap between the ‘devtools’ install_version() function and the ‘checkpoint’ package. devtools::install_version() installs a stated package version from source files stored on the CRAN archives. However CRAN does not store binary versions of packages so Windows users need to have RTools installed and Windows and OSX users get longer installation times. ‘checkpoint’ uses the Revolution Analytics MRAN server to install packages (from source or binary) as they were available on a given date. It also provides a helpful interface to detect the packages in use in a directory and install all of those packages for a given date. ‘checkpoint’ doesn’t provide install.packages-like functionality however, and that’s what ‘versions’ aims to do, by querying MRAN. As MRAN only goes back to 2014-09-17, ‘versions’ can’t install packages archived before this date. / BSD_3_clause	noarch
<a href="#">r-vertexsimilarity</a>	0.1	Creates Vertex Similarity matrix of an undirected graph based on the method stated by E. A. Leicht, Petter Holme, AND M. E. J. Newman in their paper <DOI:10.1103/PhysRevE.73.026120>. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-verylargeintegers</a>	0.1.6	Multi-precision library that allows to store and operate with arbitrarily big integers without loss of precision. It includes a large list of tools to work with them, like: - Arithmetic and logic operators - Modular-arithmetic operators - Computer Number Theory utilities - Probabilistic primality tests - Factorization algorithms - Random generators of different types of integers. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-vetr</a>	0.2.7	Declarative template-based framework for verifying that objects meet structural requirements, and auto-composing error messages when they do not. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-vfprogression</a>	0.7.1	Realization of published methods to analyze visual field (VF) progression. Introduction to the plotting methods (designed by author TE) for VF output visualization. A sample dataset for two eyes, each with 10 follow-ups is included. The VF analysis methods could be found in – Musch et al. (1999) <doi:10.1016/S0161-6420(99)90147-1>, Nouri-Mahdavi et al. (2012) <doi:10.1167/iovs.11-9021>, Schell et al. (2014) <doi:10.1016/j.ophtha.2014.02.021>, Aptel et al. (2015) <doi:10.1111/aos.12788>. / GPL-2	noarch
<a href="#">r-vgam</a>	1.1_1	An implementation of about 6 major classes of statistical regression models. At the heart of it are the vector generalized linear and additive model (VGLM/VGAM) classes, and the book Vector Generalized Linear and Additive Models: With an Implementation in R (Yee, 2015) <DOI:10.1007/978-1-4939-2818-7> gives details of the statistical framework and VGAM package. Currently only fixed-effects models are implemented, i.e., no random-effects models. Many (150) models and distributions are estimated by maximum likelihood estimation (MLE) or penalized MLE, using Fisher scoring. VGLMs can be loosely thought of as multivariate GLMs. VGAMs are data-driven VGLMs (i.e., with smoothing). The other classes are RR-VGLMs (reduced-rank VGLMs), quadratic RR-VGLMs, reduced-rank VGAMs, RCIMs (row-column interaction models)—these classes perform constrained and unconstrained quadratic ordination (CQO/UQO) models in ecology, as well as constrained additive ordination (CAO). Note that these functions are subject to change; see the NEWS and ChangeLog files for latest changes. / GPL-3	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-vgamdata</a>	1.0_3	Data sets to accompany the VGAM package and the book Vector Generalized Linear and Additive Models: With an Implementation in R (Yee, 2015) <DOI:10.1007/978-1-4939-2818-7>. These are used to illustrate vector generalized linear and additive models (VGLMs/VGAMs), and associated models (Reduced-Rank VGLMs, Quadratic RR-VGLMs, Row-Column Interaction Models, and constrained and unconstrained ordination models in ecology). / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-vgamextra</a>	0.0.1	Extending the functionalities of the ‘VGAM’ package with additional functions and datasets. At present, ‘VGAMextra’ comprises new family functions (ffs) to estimate several time series models by maximum likelihood using Fisher scoring, unlike popular packages in CRAN relying on optim(), including ARMA-GARCH-like models, the Order-(p, d, q) ARIMAX model (non-seasonal), the Order-(p) VAR model, error correction models for cointegrated time series, and ARMA-structures with Student-t errors. For independent data, new ffs to estimate the inverse- Weibull, the inverse-gamma, the generalized beta of the second kind and the general multivariate normal distributions are available. In addition, ‘VGAMextra’ incorporates new VGLM-links for the mean-function, and the quantile-function (as an alternative to ordinary quantile modelling) of several 1-parameter distributions, that are compatible with the class of VGLM/VGAM family functions. Currently, only fixed-effects models are implemented. All functions are subject to change; see the NEWS for further details on the latest changes. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-vhdclassification</a>	0.3	This package provides an implementation of Linear discriminant analysis and quadratic discriminant analysis that works fine in very high dimension (when there are many more variables than observations). / GPL-2	noarch
<a href="#">r-vhica</a>	0.2.4	The Vertical and Horizontal Inheritance Consistence Analysis method is described in the following publication: VHICA: a new method to discriminate between vertical and horizontal transposon transfer: application to the mariner family within Drosophila by G. Wallau. et al. (2016) <DOI:10.1093/molbev/msv341>. The purpose of the method is to detect horizontal transfers of transposable elements, by contrasting the divergence of transposable element sequences with that of regular genes. / GPL-2	noarch
<a href="#">r-vicmodel</a>	0.1.2	The Variable Infiltration Capacity (VIC) model is a macroscale hydrologic model that solves full water and energy balances, originally developed by Xu Liang at the University of Washington (UW). The version of VIC source code used is of 5.0.1 on < <a href="https://github.com/UW-Hydro/VIC/">https://github.com/UW-Hydro/VIC/</a> >, see Hamman et al. (2018). Development and maintenance of the current official version of the VIC model at present is led by the UW Hydro (Computational Hydrology group) in the Department of Civil and Environmental Engineering at UW. VIC is a research model and in its various forms it has been applied to most of the major river basins around the world, as well as globally. If you make use of this model, please acknowledge the appropriate references listed in the help page of this package or on the references page < <a href="http://vic.readthedocs.io/en/master/Documentation/References/">http://vic.readthedocs.io/en/master/Documentation/References/</a> > of the VIC official documentation website. These should include Liang et al. (1994) plus any references relevant to the features you are using Reference: Liang, X., D. P. Lettenmaier, E. F. Wood, and S. J. Burges (1994), A simple hydrologically based model of land surface water and energy fluxes for general circulation models, J. Geophys. Res., 99(D7), 14415-14428, <doi:10.1029/94JD00483>. Hamman et al. (2018) about VIC 5.0.1 also can be considered: Hamman, J. J., Nijssen, B., Bohn, T. J., Gergel, D. R., and Mao, Y. (2018), The Variable Infiltration Capacity model version 5 (VIC-5): infrastructure improvements for new applications and reproducibility, Geosci. Model Dev., 11, 3481-3496, <doi:10.5194/gmd-11-3481-2018>. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-vietnamcode</a>	0.1.1	Converts Vietnam’s provinces’ names and ID across different formats. Handles diacritics and different spellings. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-vif	1.0	This package implements a fast regression algorithm for building linear model for large data as defined in the paper VIF-Regression: A Fast Regression Algorithm for Large Data (2011), Journal of the American Statistical Association, Vol. 106, No. 493: 232-247 by Dongyu Lin, Dean P. Foster, and Lyle H. Ungar. / GPL-2	noarch
r-vifcp	1.2	Contains a function to support the following paper: Xiaoping Shi, Xiang-Sheng Wang, Dongwei Wei, Yuehua Wu (2016), <DOI:10.1007/s00180-015-0587-5>, A sequential multiple change-point detection procedure via VIF regression, Computational Statistics, 31(2): 671-691. / LGPL-3	linux-64, osx-64, win-64
r-vigor	1.0	Conducts linear regression using variational Bayesian inference, particularly optimized for genome-wide association mapping and whole-genome prediction which use a number of DNA markers as the explanatory variables. Provides seven regression models which select the important variables (i.e., the variables related to response variables) among the given explanatory variables in different ways (i.e., model structures). / MIT	linux-64, osx-64, win-64
r-violinmplot	0.2.1	A lattice violin-plot is overlaid with the arithmetic mean and standard deviation. / GPL-2	noarch
r-viopoints	0.2.1	viopoints draws one dimensional scatter plots with jitter using kernel density estimates in a similar way to violin plots. / GPL-2	noarch
r-vipor	0.4.5	Generate a violin point plot, a combination of a violin/histogram plot and a scatter plot by offsetting points within a category based on their density using quasirandom noise. / GPL-2	noarch
r- viridis	0.5.1	Implementation of the 'viridis' - the default -, 'magma', 'plasma', 'inferno', and 'cividis' color maps for 'R'. 'viridis', 'magma', 'plasma', and 'inferno' are ported from 'matplotlib' < <a href="http://matplotlib.org/">http://matplotlib.org/</a> >, a popular plotting library for 'python'. 'cividis', was developed by Jamie R. Nuñez and Sean M. Colby. These color maps are designed in such a way that they will analytically be perfectly perceptually-uniform, both in regular form and also when converted to black-and-white. They are also designed to be perceived by readers with the most common form of color blindness (all color maps in this package) and color vision deficiency ('cividis' only). / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-viridislite	0.3.0	Implementation of the 'viridis' - the default -, 'magma', 'plasma', 'inferno', and 'cividis' color maps for 'R'. 'viridis', 'magma', 'plasma', and 'inferno' are ported from 'matplotlib' < <a href="http://matplotlib.org/">http://matplotlib.org/</a> >, a popular plotting library for 'python'. 'cividis', was developed by Jamie R. Nuñez and Sean M. Colby. These color maps are designed in such a way that they will analytically be perfectly perceptually-uniform, both in regular form and also when converted to black-and-white. They are also designed to be perceived by readers with the most common form of color blindness (all color maps in this package) and color vision deficiency ('cividis' only). This is the 'lite' version of the more complete 'viridis' package that can be found at < <a href="https://cran.r-project.org/package=viridis">https://cran.r-project.org/package=viridis</a> >. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-virustotal	0.2.1	Use VirusTotal, a Google service that analyzes files and URLs for viruses, worms, trojans etc., provides category of the content hosted by a domain from a variety of prominent services, provides passive DNS information, among other things. See < <a href="http://www.virustotal.com">http://www.virustotal.com</a> > for more information. / MIT	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-visielse</a>	1.2.1	A graphical tool designed to visualize and to give an overview of behavioral observations realized on individuals or groups. Visualization of raw data during experimental observations of the realization of a procedure. It graphically presents an overview of individuals and group actions usually acquired from timestamps during video recorded sessions. Options of the package allow adding graphical information as statistical indicators (mean, standard deviation, quantile or statistical test) but also for each action green or black zones providing visual information about the accuracy of the realized actions. / AGPL-3	noarch
<a href="#">r-visnetwork</a>	2.0.6	Provides an R interface to the 'vis.js' JavaScript charting library. It allows an interactive visualization of networks. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-visreg</a>	2.5.1	Provides a convenient interface for constructing plots to visualize the fit of regression models arising from a wide variety of models in R ('lm', 'glm', 'coxph', 'rlm', 'gam', 'locfit', 'lmer', 'randomForest', etc.) / GPL-3	noarch
<a href="#">r-visualize</a>	4.3.0	Graphs the pdf or pmf and highlights what area or probability is present in user defined locations. Visualize is able to provide lower tail, bounded, upper tail, and two tail calculations. Supports strict and equal to inequalities. Also provided on the graph is the mean and variance of the distribution. / MIT	noarch
<a href="#">r-vita</a>	1.0.0	Implements the novel testing approach by Janitza et al.(2015) < <a href="http://nbn-resolving.de/urn/resolver.pl?urn=nbn:de:bvb:19-epub-25587-4">http://nbn-resolving.de/urn/resolver.pl?urn=nbn:de:bvb:19-epub-25587-4</a> > for the permutation variable importance measure in a random forest and the PIMP-algorithm by Altmann et al.(2010) <doi:10.1093/bioinformatics/btq134>. Janitza et al.(2015) < <a href="http://nbn-resolving.de/urn/resolver.pl?urn=nbn:de:bvb:19-epub-25587-4">http://nbn-resolving.de/urn/resolver.pl?urn=nbn:de:bvb:19-epub-25587-4</a> > do not use the standard permutation variable importance but the cross-validated permutation variable importance for the novel test approach. The cross-validated permutation variable importance is not based on the out-of-bag observations but uses a similar strategy which is inspired by the cross-validation procedure. The novel test approach can be applied for classification trees as well as for regression trees. However, the use of the novel testing approach has not been tested for regression trees so far, so this routine is meant for the expert user only and its current state is rather experimental. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-vitality</a>	1.3	Provides fitting routines for four versions of the Vitality family of mortality models. / GPL-2	noarch
<a href="#">r-vkr</a>	0.1	Provides an interface to the VK API < <a href="https://vk.com/dev/methods">https://vk.com/dev/methods</a> >. VK < <a href="https://vk.com/">https://vk.com/</a> > is the largest European online social networking service, based in Russia. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-vlad	0.2.0	Contains functions to set up risk-adjusted quality control charts in health care. For the variable life adjusted display (VLAD) proposed by Lovegrove et al. (1997) <doi:10.1016/S0140-6736(97)06507-0> signaling rules derived in Wittenberg et al. (2018) <doi: 10.1002/sim.7647> are implemented. Additionally, for the risk-adjusted cumulative sum chart based on log-likelihood ratio statistic introduced by Steiner et al. (2000) <doi:10.1093/biostatistics/1.4.441> average run length and control limits can be computed. / GPL-2	linux-64, osx-64, win-64
r-vlf	1.0	Using frequency matrices, very low frequency variants (VLFs) are assessed for amino acid and nucleotide sequences. The VLFs are then compared to see if they occur in only one member of a species, singleton VLFs, or if they occur in multiple members of a species, shared VLFs. The amino acid and nucleotide VLFs are then compared to see if they are concordant with one another. Amino acid VLFs are also assessed to determine if they lead to a change in amino acid residue type, and potential changes to protein structures. / GPL-3	noarch
r-vlmc	1.4.3	Functions, Classes & Methods for estimation, prediction, and simulation (bootstrap) of Variable Length Markov Chain ('VLMC') Models. / GPL-2	linux-64, osx-64, win-64
r-vmask	1.0	The cumulative sum (CUSUM) control chart is considered to be an alternative or complementary to Shewhart control charts in statistical process control (SPC) applications, owing to its higher sensitivity to small shifts in the process mean. It utilizes all the available data rather than the last few ones used in Shewhart control charts for quick decision making. V-mask is a traditional technique for separating meaningful data from unusual circumstances in a Cumulative Sum (CUSUM) control chart; for see details about v-mask see Montgomery (1985, ISBN:978-0471656319). The mask is a V-shaped overlay placed on the CUSUM chart so that one arm of the V lines up with the slope of data points, making it easy to see data points that lie outside the slope and to determine whether these points should be discarded as random events, or treated as a performance trend that should be addressed. But, complex computations is one disadvantage V-mask method for detect small changes in mean using CUSUM control chart. Package 'vMask' can help to the applied users to overcome this challenge by considering six different methods which each of them are based on different information. / LGPL-3	noarch
r-vnm	7.1	Provide tools for finding multiple-objective optimal designs for estimating the shape of dose-response, the ED50 (the dose producing an effect midway between the expected responses at the extreme doses) and the MED (the minimum effective dose level) for the 2,3,4-parameter logistic models and for evaluating its efficiencies for the three objectives. The acronym VNM stands for V-algorithm using Newton Raphson method to search multiple-objective optimal design. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-vocaldia	0.8.2	Create adjacency matrices of vocalisation graphs from dataframes containing sequences of speech and silence intervals, transforming these matrices into Markov diagrams, and generating datasets for classification of these diagrams by ‘flattening’ them and adding global properties (functionals) etc. Vocalisation diagrams date back to early work in psychiatry (Jaffe and Feldstein, 1970) and social psychology (Dabbs and Ruback, 1987) but have only recently been employed as a data representation method for machine learning tasks including meeting segmentation (Luz, 2012) <doi:10.1145/2328967.2328970> and classification (Luz, 2013) <doi:10.1145/2522848.2533788>. / GPL-3	noarch
r-volesti	1.0.3	Provides an R interface for ‘volesti’ C package. ‘volesti’ computes estimations of volume of polytopes given by a set of points or linear inequalities or Minkowski sum of segments (zonotopes). There are two algorithms for volume estimation (I.Z. Emiris and V. Fisikopoulos (2014) <arXiv:1312.2873> and B. Cousins, S. Vempala (2016) <arXiv:1409.6011>) as well as algorithms for sampling, rounding and rotating polytopes. Moreover, ‘volesti’ provides algorithms for estimating copulas (L. Cales, A. Chalkis, I.Z. Emiris, V. Fisikopoulos (2018) <arXiv:1803.05861>). / LGPL-3	linux-64, osx-64, win-64
r-volleystat	0.2.0	Volleyball match statistics of the German volleyball first division league (seasons 2013/2014 to 2018/2019). The data has been collected from the official volleyball first division homepage (<www.volleyball-bundesliga.de>) and contains information on teams, staff, sets, matches, and player-in-match statistics (extracted automatically from the official match reports). / CC0	noarch
r-vortexrdata	1.0.5	Contains selected data from two publications, Campbell ‘et’ ‘al’. (2016) <DOI:10.1080/14486563.2015.1028486> and ‘Pacioni’ ‘et’ ‘al’. (2017) <DOI:10.1071/PC17002>. The data is provided both as raw outputs from the population viability analysis software ‘Vortex’ and packaged as R objects. The R package ‘vortexR’ uses the raw data provided here to illustrate its functionality of parsing raw ‘Vortex’ output into R objects. / GPL-3	noarch
r-vote	1.1_0	Counting election votes and determining election results by different methods, including the single transferable vote, approval, score and plurality methods. / GPL-2	noarch
r-votesys	0.1.1	Various methods to count ballots in voting systems are provided. Functions to check validity of ballots are also provided to ensure flexibility. / GPL-3	noarch
r-votrans	1.0	Calculates voter transitions comparing two elections, using the function solve.QP() in package ‘quadprog’. / GPL-3	noarch
r-vowels	1.2_2	Procedures for the manipulation, normalization, and plotting of phonetic and sociophonetic vowel formant data. vowels is the backend for the NORM website. / GPL-3	noarch
r-voxr	0.5.1	Tools for tree crown structure description based on T-LiDAR data voxelisation / GPL (>= 2.0)	noarch
r-vrmlgen	1.4.9	vrmlgen creates 3D scatter and bar plots, visualizations of 3D meshes, parametric functions and height maps in web-formats like the Virtual Reality Markup Language (VRML, filetype .wrl) and the LiveGraphics3D format. / GPL-2	noarch
r-vrtest	0.97	A collection of statistical tests for martingale difference hypothesis / GPL-2	noarch
r-vstsr	1.0.0	Implementation of Visual Studio Team Services < <a href="https://www.visualstudio.com/team-services/">https://www.visualstudio.com/team-services/</a> > API calls. It enables the extraction of information about repositories, build and release definitions and individual releases. It also helps create repositories and work items within a project without logging into Visual Studio. There is the ability to use any API service with a shell for any non-predefined call. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-vudc</a>	1.1	Contains functions for visualization univariate data: ccdplot and qddplot. / GPL-2	noarch
<a href="#">r-vwr</a>	0.3.0	Functions and data for use in visual word recognition research: Computation of neighbors (Hamming and Levenshtein distances), average distances to neighbors (e.g., OLD20), and Coltheart's N. Also includes the LD1NN algorithm to detect bias in the composition of a lexical decision task. Most of the functions support parallel execution. Supplies wordlists for several languages. Uses the string distance functions from the stringdist package by Mark van der Loo. / GPL-3	noarch
<a href="#">r-w3markupvalidator</a>	0.1_6	R interface to a W3C Markup Validation service. See < <a href="http://validator.w3.org/">http://validator.w3.org/</a> > for more information. / GPL-2	noarch
<a href="#">r-waffect</a>	1.2	waffect (pronounced 'double-u affect' for 'weighted affectation') is a package to simulate phenotypic (case or control) datasets under a disease model H1 such that the total number of cases is constant across all the simulations (the constrain in the title). The package also makes it possible to generate phenotypes in the case of more than two classes, so that the number of phenotypes belonging to each class is constant across all the simulations. waffect is used to assess empirically the statistical power of Genome Wide Association studies. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-wahc</a>	1.0	Fit the fixed effect panel data model with heteroskedasticity and autocorrelation correction. / GPL-3	noarch
<a href="#">r-waiter</a>	0.0.1	Full screen splash loading screens for 'Shiny'. / MIT	noarch
<a href="#">r-walkscoreapi</a>	1.2	A collection of functions to perform the Application Programming Interface (API) calls associated with the Walk Score website ( <a href="http://www.walkscore.com">www.walkscore.com</a> ) within the R environment. These functions can be used to query the Walk Score and Transit Score database for a wide variety of information using R scripts. This package includes the simple Walk Score and Transit Score API calls, which return the scores associated with an input location, as well as calls which return some data used to calculate the scores. These functions are especially useful for mass data collection and gathering Walk Score and Transit Score values for large lists of locations. / GPL-2	noarch
<a href="#">r-wamasim</a>	1.0.0	The outcome of various rehabilitation strategies for water distribution systems can be modeled with the Water Management Simulator (WaMaSim). Pipe breaks and the corresponding damage and rehabilitation costs are simulated. It is mainly intended to be used as educational tool for the Water Infrastructure Experimental and Computer Laboratory at ETH Zurich, Switzerland. / GPL-3	noarch
<a href="#">r-wand</a>	0.5.0	'MIME' types are shorthand descriptors for file contents and can be determined from magic bytes in file headers, file contents or intuited from file extensions. Tools are provided to perform curated magic tests as well as mapping 'MIME' types from a database of over 1,500 extension mappings. / MIT	noarch
<a href="#">r-warn</a>	1.2_3	This estimates precise weaning ages for a given skeletal population by analyzing the stable nitrogen isotope ratios of them. Bone collagen turnover rates estimated anew and the approximate Bayesian computation (ABC) were adopted in this package. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-washdata</a>	0.1.2	Urban water and sanitation survey dataset collected by Water and Sanitation for the Urban Poor (WSUP) with technical support from Valid International. These citywide surveys have been collecting data allowing water and sanitation service levels across the entire city to be characterised, while also allowing more detailed data to be collected in areas of the city of particular interest. These surveys are intended to generate useful information for others working in the water and sanitation sector. Current release version includes datasets collected from a survey conducted in Dhaka, Bangladesh in March 2017. This survey in Dhaka is one of a series of surveys to be conducted by WSUP in various cities in which they operate including Accra, Ghana; Nakuru, Kenya; Antananarivo, Madagascar; Maputo, Mozambique; and, Lusaka, Zambia. This package will be updated once the surveys in other cities are completed and datasets have been made available. / CC0	noarch
<a href="#">r-washer</a>	0.1.2	Time series outlier detection by mean of non parametric test. Outlier detection regarding two methodologies: single time series variability (a vector) and grouped similar time series (a data frame). Andrea Venturini(2011) Statistica-Universita' Bologna, Vol.71, pp.329-344. / GPL-2	noarch
<a href="#">r-waterfall</a>	1.0.2	Provides support for creating waterfall charts in R using both traditional base and lattice graphics. / BSD_2_clause	noarch
<a href="#">r-wateryear</a>	1.0.1	Provides Water Year Hydrologic Classification Indices based on measured unimpaired runoff (in million acre-feet). Data is provided by California Department of Water Resources and subject to revision. / MIT	noarch
<a href="#">r-waved</a>	1.2	Makes available code necessary to reproduce figures and tables in papers on the WaveD method for wavelet deconvolution of noisy signals as presented in The WaveD Transform in R, Journal of Statistical Software Volume 21, No. 3, 2007. / GPL-3	noarch
<a href="#">r-wavefunction</a>	1.0.0	Real probability distributions can be represented as the square of an orthogonal sum in the Hermite basis. This representation is formally similar to the representation of quantum mechanical states as wave functions, whose squared modulus is a probability density. This is described in more detail in Wave function representation of probability distributions, by Madeleine B. Thompson <arXiv:1712.07764>. This package provides a reference implementation of the technique. / Apache License (== 2.0)	noarch
<a href="#">r-waveletcomp</a>	1.1	Wavelet analysis and reconstruction of time series, cross-wavelets and phase-difference (with filtering options), significance with simulation algorithms. / GPL-2	noarch
<a href="#">r-wavelets</a>	0.3_0	Contains functions for computing and plotting discrete wavelet transforms (DWT) and maximal overlap discrete wavelet transforms (MODWT), as well as their inverses. Additionally, it contains functionality for computing and plotting wavelet transform filters that are used in the above decompositions as well as multiresolution analyses. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-waveslim</a>	1.7.5	Basic wavelet routines for time series (1D), image (2D) and array (3D) analysis. The code provided here is based on wavelet methodology developed in Percival and Walden (2000); Gencay, Selcuk and Whitcher (2001); the dual-tree complex wavelet transform (DTCWT) from Kingsbury (1999, 2001) as implemented by Selesnick; and Hilbert wavelet pairs (Selesnick 2001, 2002). All figures in chapters 4-7 of GSW (2001) are reproducible using this package and R code available at the book website(s) below. / BSD_3_clause	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-wavethresh</a>	4.6.8	Performs 1, 2 and 3D real and complex-valued wavelet transforms, nondecimated transforms, wavelet packet transforms, nondecimated wavelet packet transforms, multiple wavelet transforms, complex-valued wavelet transforms, wavelet shrinkage for various kinds of data, locally stationary wavelet time series, nonstationary multiscale transfer function modeling, density estimation. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-wbs</a>	1.4	Provides efficient implementation of the Wild Binary Segmentation and Binary Segmentation algorithms for estimation of the number and locations of multiple change-points in the piecewise constant function plus Gaussian noise model. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-wce</a>	1.0.2	A flexible method for modeling cumulative effects of time-varying exposures, weighted according to their relative proximity in time, and represented by time-dependent covariates. The current implementation estimates the weight function in the Cox proportional hazards model. The function that assigns weights to doses taken in the past is estimated using cubic regression splines. / GPL-2	noarch
<a href="#">r-wcorr</a>	1.9.1	Calculates Pearson, Spearman, polychoric, and polyserial correlation coefficients, in weighted or unweighted form. The package implements tetrachoric correlation as a special case of the polychoric and biserial correlation as a specific case of the polyserial. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-wcq</a>	0.2	The package contains the WCQ method for detection of QTL effects in a small mapping population. It also contains implementation of the Chen-Qin two-sample and one-sample test of means. / GPL-3	noarch
<a href="#">r-wdi</a>	2.6.0	Search, extract and format data from the World Bank's World Development Indicators. / GPL-3	noarch
<a href="#">r-wdm</a>	0.2.1	Provides efficient implementations of weighted dependence measures and related asymptotic tests for independence. Implemented measures are the Pearson correlation, Spearman's rho, Kendall's tau, Blomqvist's beta, and Hoeffding's D; see, e.g., Nelsen (2006) <doi:10.1007/0-387-28678-0> and Hollander et al. (2015, ISBN:9780470387375). / MIT	linux-64, osx-64, win-64
<a href="#">r-weatherdata</a>	0.5.0	Functions that help in fetching weather data from websites. Given a location and a date range, these functions help fetch weather data (temperature, pressure etc.) for any weather related analysis. / GPL	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-weathermetrics</a>	1.2.2	Functions to convert between weather metrics, including conversions for metrics of temperature, air moisture, wind speed, and precipitation. This package also includes functions to calculate the heat index from air temperature and air moisture. / GPL-2	noarch
<a href="#">r-webchem</a>	0.4.0	Chemical information from around the web. This package interacts with a suite of web APIs for chemical information. / MIT	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-webddx</a>	0.1.0	Freely available online differential-diagnosis generating tools are changing clinical medicine and biomedical research. With webddx, useRs can generate differential diagnosis lists given a set of symptoms. The web tools would likely be directly used in clinical practice, but programmatic interaction and data manipulation can sharply increase efficiency and reproducibility of research in clinical informatics. Relevant visualizations can also be created with webddx. / GPL-3	noarch
<a href="#">r-webex</a>	0.9.1	Functions for easily creating interactive web pages using ‘R Markdown’ that students can use in self-guided learning. / CC BY-SA 4.0	noarch
<a href="#">r-webp</a>	1.0	Lossless webp images are 26% smaller in size compared to PNG. Lossy webp images are 25-34% smaller in size compared to JPEG. This package reads and writes webp images into a 3 (rgb) or 4 (rgba) channel bitmap array using conventions from the ‘jpeg’ and ‘png’ packages. / MIT	linux-64, osx-64, win-64
<a href="#">r-websearchr</a>	0.0.3	Functions that allow for accessing domains and a number of search engines. / MIT	noarch
<a href="#">r-webshot</a>	0.5.1	Takes screenshots of web pages, including Shiny applications and R Markdown documents. / GPL-2	linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-websocket</a>	1.1.0	Provides a ‘WebSocket’ client interface for R. ‘WebSocket’ is a protocol for low-overhead real-time communication: <a href="https://en.wikipedia.org/wiki/WebSocket">https://en.wikipedia.org/wiki/WebSocket</a> . / GPL-2	linux-64, osx-64, win-64
<a href="#">r-webutils</a>	1.0	Parses http request data in application/json, multipart/form-data, or application/x-www-form-urlencoded format. Includes example of hosting and parsing html form data in R using either ‘httpuv’ or ‘Rhttpd’. / MIT	linux-64, osx-64, win-64
<a href="#">r-weco</a>	1.2	Western Electric Company Rules (WECO) have been widely used for Shewhart control charts in order to increase the sensitivity of detecting assignable causes of process change. This package implements eight commonly used WECO rules and allow to apply the combination of these individual rules for detecting the deviation from a stable process. The package also provides a web-based graphical user interface to help users conduct the analysis. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-wee</a>	1.0	Secondary analysis of case-control studies using a weighted estimating equation (WEE) approach: logistic regression for binary secondary outcomes, linear regression and quantile regression for continuous secondary outcomes. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-weibullness	1.19.8	Performs a goodness-of-fit test of Weibull distribution (weibullness test) and provides the maximum likelihood estimates of the three-parameter Weibull distribution. Note that the threshold parameter is estimated based on the correlation from the Weibull plot. For more details, see Park (2018) <doi:10.1155/2018/6056975>. This work was supported by the National Research Foundation of Korea (NRF) grant funded by the Korea government (No. NRF-2017R1A2B4004169). / GPL-2   GPL-3	noarch
r-weibullr	1.0.10	Life data analysis in the graphical tradition of Waloddi Weibull. Methods derived from Robert B. Abernethy (2008, ISBN 0-965306-3-2), Wayne Nelson (1982, ISBN: 9780471094586) <DOI:10.1002/0471725234>, William Q. Meeker and Lois A. Escobar (1998, ISBN: 1-471-14328-6), John I. McCool, (2012, ISBN: 9781118217986) <DOI:10.1002/9781118351994>. / GPL-3	linux-64, osx-64, win-64
r-weighted.desc.stat	1.0	Weighted descriptive statistics is the discipline of quantitatively describing the main features of real-valued fuzzy data which usually given from a fuzzy population. One can summarize this special kind of fuzzy data numerically or graphically using this package. To interpret some of the properties of one or several sets of real-valued fuzzy data, numerically summarize is possible by some weighted statistics which are designed in this package such as mean, variance, covariance and correlation coefficient. Also, graphically interpretation can be given by weighted histogram and weighted scatter plot using this package to describe properties of real-valued fuzzy data set. / LGPL-3	noarch
r-weightedporttest	1.0	This packages contains the Weighted Portmanteau Tests as described in New Weighted Portmanteau Statistics for Time Series Goodness-of-Fit Testing' accepted for publication by the Journal of the American Statistical Association. / GPL-3	noarch
r-weightedroc	2018.1	Fast computation of Receiver Operating Characteristic (ROC) curves and Area Under the Curve (AUC) for weighted binary classification problems (weights are example-specific cost values). / GPL-3	noarch
r-weightquant	1.0	Estimation of observation-specific weights for incomplete longitudinal data and bootstrap procedure for weighted quantile regressions. / GPL (>= 2.0)	noarch
r-weirs	0.25	Provides computational support for flow over weirs, such as sharp-crested, broad-crested, and embankments. Initially, the package supports broad- and sharp-crested weirs. / GPL-2	noarch
r-welchadf	0.3.2	Implementation of Johansen's general formulation of Welch-James's statistic with Approximate Degrees of Freedom, which makes it suitable for testing any linear hypothesis concerning cell means in univariate and multivariate mixed model designs when the data pose non-normality and non-homogeneous variance. Some improvements, namely trimmed means and Winsorized variances, and bootstrapping for calculating an empirical critical value, have been added to the classical formulation. The code departs from a previous SAS implementation by L.M. Lix and H.J. Keselman, available at < <a href="http://supp.apa.org/psycarticles/supplemental/met_13_2_110/SAS_Program.pdf">http://supp.apa.org/psycarticles/supplemental/met_13_2_110/SAS_Program.pdf</a> > and published in Keselman, H.J., Wilcox, R.R., and Lix, L.M. (2003) <DOI:10.1111/1469-8986.00060>. / LGPL-3	noarch
r-wesanderson	0.3.6	Palettes generated mostly from 'Wes Anderson' movies. / MIT	noarch

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Name	Version	Summary/License	Platforms
r-wfe	1.9.1	Provides a computationally efficient way of fitting weighted linear fixed effects estimators for causal inference with various weighting schemes. Weighted linear fixed effects estimators can be used to estimate the average treatment effects under different identification strategies. This includes stratified randomized experiments, matching and stratification for observational studies, first differencing, and difference-in-differences. The package implements methods described in Imai and Kim (2017) When should We Use Linear Fixed Effects Regression Models for Causal Inference with Longitudinal Data?, available at < <a href="https://imai.fas.harvard.edu/research/FEmatch.html">https://imai.fas.harvard.edu/research/FEmatch.html</a> >. / GPL-2	linux-64, osx-64, win-64
r-wfg	0.1	Implementation of Weighted Fast Greedy algorithm for community detection in networks with mixed types of attributes. / GPL-2	noarch
r-wgteff	0.1.2	Functions for determining the effect of data weights on the variance of survey data: users will load a data set which has a weights column, and the package will calculate the design effect (DEFF), weighting loss, root design effect (DEFT), effective sample size (ESS), and/or weighted margin of error. / GPL-2	noarch
r-wheatmap	0.1.0	Builds complex plots, heatmaps in particular, using natural semantics. Bigger plots can be assembled using directives such as ‘LeftOf’, ‘RightOf’, ‘TopOf’, and ‘Beneath’ and more. Other features include clustering, dendrograms and integration with ‘ggplot2’ generated grid objects. This package is particularly designed for bioinformaticians to assemble complex plots for publication. / GPL-3	noarch
r-whereami	0.1.8	Robust and reliable functions to return informative outputs to console with the run or source location of a command. This can be from the ‘RScript’/R terminal commands or ‘RStudio’ console, source editor, ‘Rmarkdown’ document and a Shiny application. / MIT	noarch
r-whiboclustering	0.1.2	White Box Cluster Algorithm Design allows you to create Representative based cluster algorithm by using reusable components. This way one can recreate already available cluster algorithms (i.e. K-Means, K-Means, PAM) but also create new cluster algorithms not available in the literature or any other software. For more information see papers <doi:10.1007/s10462-009-9133-6> and <doi:10.1016/j.datak.2012.03.005>. / GPL-3	noarch
r-whisker	0.3.2	logicless templating, reuse templates in many programming languages including R / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
r-whitechapelr	0.3.0	Provides a set of functions to make tracking the hidden movements of the ‘Jack’ player easier. By tracking every possible path Jack might have traveled from the point of the initial murder including special movement such as through alleyways and via carriages, the police can more accurately narrow the field of their search. Additionally, by tracking all possible hideouts from round to round, rounds 3 and 4 should have a vastly reduced field of search. / MIT	noarch

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Name	Version	Summary/License	Platforms
r-whitening	1.1.1	Implements the whitening methods (ZCA, PCA, Cholesky, ZCA-cor, and PCA-cor) discussed in Kessy, Lewin, and Strimmer (2018) Optimal whitening and decorrelation, <doi:10.1080/00031305.2016.1277159>, as well as the whitening approach to canonical correlation analysis allowing negative canonical correlations described in Jendoubi and Strimmer (2019) A whitening approach to probabilistic canonical correlation analysis for omics data integration, <doi:10.1186/s12859-018-2572-9>. / GPL-3	noarch
r-whoami	1.3.0	Look up the username and full name of the current user, the current user's email address and 'GitHub' username, using various sources of system and configuration information. / MIT	noarch
r-whoapi	0.1.2	Retrieve data from the 'Whoapi' ( <a href="https://whoapi.com">https://whoapi.com</a> ) store of domain information, including a domain's geographic location, registration status and search prominence. / MIT	noarch
r-whopgenome	0.9.7	Provides very fast access to whole genome, population scale variation data from VCF files and sequence data from FASTA-formatted files. It also reads in alignments from FASTA, Phylip, MAF and other file formats. Provides easy-to-use interfaces to genome annotation from UCSC and Bioconductor and gene ontology data from AmiGO and is capable to read, modify and write PLINK .PED-format pedigree files. / GPL-2	linux-64, osx-64, win-64
r-wicket	0.4.0	Utilities to generate bounding boxes from 'WKT' (Well-Known Text) objects and R data types, validate 'WKT' objects and convert object types from the 'sp' package into 'WKT' representations. / MIT	linux-64, osx-64, win-64
r-widgetframe	0.3.1	Provides two functions 'frameableWidget()', and 'frameWidget()'. The 'frameableWidget()' is used to add extra code to a 'htmlwidget' which allows is to be rendered correctly inside a responsive 'iframe'. The 'frameWidget()' is a 'htmlwidget' which displays content of another 'htmlwidget' inside a responsive 'iframe'. These functions allow for easier embedding of 'htmlwidgets' in content management systems such as 'wordpress', 'blogger' etc. They also allow for separation of widget content from main HTML content where CSS of the main HTML could interfere with the widget. / MIT	noarch
r-wikibooks	0.2	The german Wikibook GNU R introduces R to new users. This package is a collection of functions and datas used in the german WikiBook GNU R / GPL-2	noarch
r-wikifacts	0.1.0	Creates messages containing random facts from the Wikipedia homepage. Intended to keep users interested during long waiting periods. / CC0	noarch
r-wikipediarr	1.1	Provides an interface to the Wikipedia web application programming interface (API), using internet connexion. Three functions provide details for a specific Wikipedia page : all links that are present, all pages that link to, all the contributions (revisions for main pages, and discussions for talk pages). Two functions provide details for a specific user : all contributions, and general information (as name, gender, rights or groups). It provides additional information compared to others packages, as WikipediR. It does not need login. The multiplex network that can be constructed from the results of the functions of Wikipediarr can be modeled as Stochastic Block Model as in Barbillon P., Donnet, S., Lazega E., and Bar-Hen A. : Stochastic Block Models for Multiplex networks: an application to networks of researchers, ArXiv 1501.06444, <a href="http://arxiv.org/abs/1501.06444">http://arxiv.org/abs/1501.06444</a> . / GPL (> 2)	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-wikipedir</a>	1.5.0	A wrapper for the MediaWiki API, aimed particularly at the Wikimedia ‘production’ wikis, such as Wikipedia. It can be used to retrieve page text, information about users or the history of pages, and elements of the category tree. / MIT	noarch
<a href="#">r-wilcoxcv</a>	1.0_2	This package provides functions to perform fast variable selection based on the Wilcoxon rank sum test in the cross-validation or Monte-Carlo cross-validation settings, for use in microarray-based binary classification. / GPL-2	noarch
<a href="#">r-wildcard</a>	1.1.0	Generate data frames from templates. / GPL-3	noarch
<a href="#">r-wildpoker</a>	1.1	Provides insight into how the best hand for a poker game changes based on the game dealt, players who stay in until the showdown and wildcards added to the base game. At this time the package does not support player tactics, so draw poker variants are not included. / GPL-3	noarch
<a href="#">r-wingui</a>	0.2	Helps for interfacing with the operating system particularly for Windows. / GPL-2   GPL-3   MIT	linux-64, osx-64, win-64
<a href="#">r-wisam</a>	0.2.8	In the course of a genome-wide association study, the situation often arises that some phenotypes are known with greater precision than others. It could be that some individuals are known to harbor more micro-environmental variance than others. In the case of inbred strains of model organisms, it could be the case that more organisms were observed from some strains than others, so the strains with more organisms have better-estimated means. Package ‘wISAM’ handles this situation by allowing for weighting of each observation according to residual variance. Specifically, the ‘weight’ parameter to the function <code>conduct_scan()</code> takes the precision of each observation (one over the variance). / GPL-3	noarch
<a href="#">r-withr</a>	2.1.2	A set of functions to run code ‘with’ safely and temporarily modified global state. Many of these functions were originally a part of the ‘devtools’ package, this provides a simple package with limited dependencies to provide access to these functions. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-wkb</a>	0.3_0	Utility functions to convert between the ‘Spatial’ classes specified by the package ‘sp’, and the well-known binary ‘(WKB)’ representation for geometry specified by the Open Geospatial Consortium. Supports ‘Spatial’ objects of class ‘SpatialPoints’, ‘SpatialPointsDataFrame’, ‘SpatialLines’, ‘SpatialLinesDataFrame’, ‘SpatialPolygons’, and ‘SpatialPolygonsDataFrame’. Supports ‘WKB’ geometry types ‘Point’, ‘LineString’, ‘Polygon’, ‘MultiPoint’, ‘MultiLineString’, and ‘MultiPolygon’. Includes extensions to enable creation of maps with ‘TIBCO Spotfire’. / BSD_3_clause	noarch
<a href="#">r-wktmo</a>	1.0.5	Converts weekly data to monthly data. Users can use three types of week formats: ISO week, epidemiology week (epi week) and calendar date. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-wlreg	1.0.0	Use various regression models for the analysis of win loss endpoints adjusting for non-binary and multivariate covariates. / GPL-2	linux-64, osx-64, win-64
r-wmdb	1.0	Distance discriminant analysis method is one of classification methods according to multiindex performance parameters. However, the traditional Mahalanobis distance discriminant method treats with the importance of all parameters equally, and exaggerates the role of parameters which changes a little. The weighted Mahalanobis distance is used in discriminant analysis method to distinguish the importance of each parameter. In the concrete application, firstly based on the principal component analysis scheme, a new group of parameters and their corresponding percent contributions of the parameters are calculated, and the weighted matrix is regarded as the diagonal matrix of the contributions rates. Setting data to standardization, then the weighted Mahalanobis distance can be calculated. Besides the methods mentioned above, bayes method is also given. / GPL-2	noarch
r-wmwssp	0.4.0	Calculates the minimal sample size for the Wilcoxon-Mann-Whitney test that is needed for a given power and two sided type I error rate. The method works for metric data with and without ties, count data, ordered categorical data, and even dichotomous data. But data is needed for the reference group to generate synthetic data for the treatment group based on a relevant effect. For details, see Brunner, E., Bathke A. C. and Konietzschke, F: Rank- and Pseudo-Rank Procedures in Factorial Designs - Using R and SAS, Springer Verlag, to appear. / GPL-3	noarch
r-wnl	0.5.1	This is a set of minimization tools (maximum likelihood estimation and least square fitting) to solve examples in the Johan Gabrielsson and Dan Weiner's book Pharmacokinetic and Pharmacodynamic Data Analysis - Concepts and Applications 5th ed. (ISBN:9198299107). Examples include linear and non-linear compartmental model, turn-over model, single or multiple dosing bolus/infusion/oral models, allometry, toxicokinetics, reversible metabolism, in-vitro/in-vivo extrapolation, enterohepatic circulation, metabolite modeling, Emax model, inhibitory model, tolerance model, oscillating response model, enantiomer interaction model, effect compartment model, drug-drug interaction model, receptor occupancy model, and rebound phenomena model. / GPL-3	noarch
r-wnnsel	0.1	New tools for the imputation of missing values in high-dimensional data are introduced using the non-parametric nearest neighbor methods. It includes weighted nearest neighbor imputation methods that use specific distances for selected variables. It includes an automatic procedure of cross validation and does not require prespecified values of the tuning parameters. It can be used to impute missing values in high-dimensional data when the sample size is smaller than the number of predictors. For more information see Faisal and Tutz (2017) <doi:10.1515/sagmb-2015-0098>. / GPL-2	noarch
r-woe	0.2	Shows the relationship between an independent and dependent variable through Weight of Evidence and Information Value. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<code>r-woebinning</code>	0.1.6	Implements an automated binning of numeric variables and factors with respect to a dichotomous target variable. Two approaches are provided: An implementation of fine and coarse classing that merges granular classes and levels step by step. And a tree-like approach that iteratively segments the initial bins via binary splits. Both procedures merge, respectively split, bins based on similar weight of evidence (WOE) values and stop via an information value (IV) based criteria. The package can be used with single variables or an entire data frame. It provides flexible tools for exploring different binning solutions and for deploying them to (new) data. / GPL-2	noarch
<code>r-wooldridge</code>	1.3.1	Students learning both econometrics and R may find the introduction to both challenging. However, if the text is Introductory Econometrics: A Modern Approach by Jeffrey M. Wooldridge, they are in luck! The wooldridge data package aims to lighten the task by efficiently loading any data set found in the text with a single command. Data sets have all been compressed to a fraction of their original size and are well documented. Documentation files contain the page numbers of the text where each set is used, the original source, time of publication, and notes suggesting ideas for further exploratory data analysis and research. If one need's to brush-up on model syntax, a vignette contains R solutions to examples from each chapter of the text. Data sets are from the 6th edition (Wooldridge 2016, ISBN-13: 978-1-305-27010-7), and are backwards compatible with all versions of the text. / GPL-3	noarch
<code>r-word.alignment</code>	1.1	For a given Sentence-Aligned Parallel Corpus, it aligns words for each sentence pair. It considers one-to-many and symmetrization alignments. Moreover, it evaluates the quality of word alignment based on this package and some other software. It also builds an automatic dictionary of two languages based on given parallel corpus. / GPL-2	noarch
<code>r-wordcloud</code>	2.6	Functionality to create pretty word clouds, visualize differences and similarity between documents, and avoid over-plotting in scatter plots with text. / LGPL-2.1	linux-64, osx-64, win-64
<code>r-wordcloud2</code>	0.2.1	A fast visualization tool for creating wordcloud by using 'wordcloud2.js'. 'wordcloud2.js' is a JavaScript library to create wordle presentation on 2D canvas or HTML < <a href="https://timdream.org/wordcloud2.js/">https://timdream.org/wordcloud2.js/</a> >. / GPL-2	noarch
<code>r-wordmatch</code>	1.0	Matches words in one file with words in another file and shows index(row number) for the matches / GPL-2	noarch
<code>r-wordnet</code>	0.1_1	An interface to WordNet using the Jawbone Java API to WordNet. WordNet (< <a href="http://wordnet.princeton.edu/">http://wordnet.princeton.edu/</a> >) is a large lexical database of English. Nouns, verbs, adjectives and adverbs are grouped into sets of cognitive synonyms (synsets), each expressing a distinct concept. Synsets are interlinked by means of conceptual-semantic and lexical relations. Please note that WordNet(R) is a registered tradename. Princeton University makes WordNet available to research and commercial users free of charge provided the terms of their license (< <a href="http://wordnet.princeton.edu/wordnet/license/">http://wordnet.princeton.edu/wordnet/license/</a> >) are followed, and proper reference is made to the project using an appropriate citation (< <a href="http://wordnet.princeton.edu/wordnet/citing-wordnet/">http://wordnet.princeton.edu/wordnet/citing-wordnet/</a> >). / MIT	noarch
<code>r-wordpools</code>	1.1_1	Collects several classical word pools used most often to provide lists of words in psychological studies of learning and memory. It provides a simple function, 'pickList' for selecting random samples of words within given ranges. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-worms	0.2.2	Retrieves taxonomic information from < <a href="http://www.marinespecies.org">http://www.marinespecies.org</a> > using WoRMS' RESTful Webservice. Utility functions aim at taxonomic consistency. / AGPL-3	noarch
r-wperm	1.0.1	Supplies permutation-test alternatives to traditional hypothesis-test procedures such as two-sample tests for means, medians, and standard deviations; correlation tests; tests for homogeneity and independence; and more. Suitable for general audiences, including individual and group users, introductory statistics courses, and more advanced statistics courses that desire an introduction to permutation tests. / GPL-2	noarch
r-wpkde	0.1	Weighted Piecewise Kernel Density Estimation for large data. / GPL-3	linux-64, osx-64, win-64
r-wpp2008	1.0_1	Data from the United Nation's World Population Prospects 2008 / GPL-2	noarch
r-wpp2010	1.2_0	Data from the United Nation's World Population Prospects 2010 / GPL-2	noarch
r-wpp2012	2.2_1	Data from the United Nation's World Population Prospects 2012 / GPL-2	noarch
r-wpp2015	1.1_2	Provides data from the United Nation's World Population Prospects 2015. / GPL-2	noarch
r-wpp2017	1.2_1	Provides data from the United Nation's World Population Prospects 2017. / GPL-2	noarch
r-wpp2019	1.0_0	Provides data from the United Nation's World Population Prospects 2019. / file LICENSE	noarch
r-wrapr	1.8.9	Tools for writing and debugging R code. Provides: '%.>%' dot-pipe (an 'S3' configurable pipe), 'let()' (converts non-standard evaluation interfaces to parametric standard evaluation interfaces, inspired by 'gtools:strmacro()' and 'base::bquote()'), 'build_frame()'/draw_frame()' ('data.frame' example tools), 'qc()' (quoting concatenate), ':= ' (named map builder), and more. / GPL-2   GPL-3	noarch
r-wrassp	0.1.8	A wrapper around Michel Scheffers's 'libassp' (< <a href="http://libassp.sourceforge.net/">http://libassp.sourceforge.net/</a> >). The 'libassp' (Advanced Speech Signal Processor) library aims at providing functionality for handling speech signal files in most common audio formats and for performing analyses common in phonetic science/speech science. This includes the calculation of formants, fundamental frequency, root mean square, auto correlation, a variety of spectral analyses, zero crossing rate, filtering etc. This wrapper provides R with a large subset of 'libassp's signal processing functions and provides them to the user in a (hopefully) user-friendly manner. / GPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-wrightmap</a>	1.2.1	A powerful yet simple graphical tool available in the field of psychometrics is the Wright Map (also known as item maps or item-person maps), which presents the location of both respondents and items on the same scale. Wright Maps are commonly used to present the results of dichotomous or polytomous item response models. The ‘WrightMap’ package provides functions to create these plots from item parameters and person estimates stored as R objects. Although the package can be used in conjunction with any software used to estimate the IRT model (e.g. ‘TAM’, ‘mirt’, ‘eRm’ or ‘IRTtoys’ in ‘R’, or ‘Stata’, ‘Mplus’, etc.), ‘WrightMap’ features special integration with ‘ConQuest’ to facilitate reading and plotting its output directly. The ‘wrightMap’ function creates Wright Maps based on person estimates and item parameters produced by an item response analysis. The ‘CQmodel’ function reads output files created using ‘ConQuest’ software and creates a set of data frames for easy data manipulation, bundled in a ‘CQmodel’ object. The ‘wrightMap’ function can take a ‘CQmodel’ object as input or it can be used to create Wright Maps directly from data frames of person and item parameters. / BSD_2_clause	noarch
<a href="#">r-write.snns</a>	0.0_4	Function for writing a SNNS pattern file from a data.frame or matrix. / GPL-2	noarch
<a href="#">r-writexl</a>	1.1	Zero-dependency data frame to xlsx exporter based on ‘libxlsxwriter’. Fast and no Java or Excel required. / BSD_2_clause	linux-64, osx-64, win-64
<a href="#">r-writexls</a>	5.0.0	Cross-platform Perl based R function to create Excel 2003 (XLS) and Excel 2007 (XLSX) files from one or more data frames. Each data frame will be written to a separate named worksheet in the Excel spreadsheet. The worksheet name will be the name of the data frame it contains or can be specified by the user. / GPL-2	noarch
<a href="#">r-wrswor</a>	1.1	A collection of implementations of classical and novel algorithms for weighted sampling without replacement. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-wrswor.benchmark</a>	0.2	Includes performance measurements and results of repeated experiment runs (for correctness checks) for code in the ‘wrswor’ package. / GPL-3	noarch
<a href="#">r-wskm</a>	1.4.28	Entropy weighted k-means (ewkm) is a weighted subspace clustering algorithm that is well suited to very high dimensional data. Weights are calculated as the importance of a variable with regard to cluster membership. The two-level variable weighting clustering algorithm tw-k-means (twkm) introduces two types of weights, the weights on individual variables and the weights on variable groups, and they are calculated during the clustering process. The feature group weighted k-means (fgkm) extends this concept by grouping features and weighting the group in addition to weighting individual features. / GPL-3	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-wsrf	1.7.1	A parallel implementation of Weighted Subspace Random Forest. The Weighted Subspace Random Forest algorithm was proposed in the International Journal of Data Warehousing and Mining by Baoxun Xu, Joshua Zhexue Huang, Graham Williams, Qiang Wang, and Yunming Ye (2012) <DOI:10.4018/jdwm.2012040103>. The algorithm can classify very high-dimensional data with random forests built using small subspaces. A novel variable weighting method is used for variable subspace selection in place of the traditional random variable sampling. This new approach is particularly useful in building models from high-dimensional data. / GPL-2	linux-64, osx-64, win-64
r-wsvm	0.1.7	We propose weighted SVM methods with penalization form. By adding weights to loss term, we can build up weighted SVM easily and examine classification algorithm properties under weighted SVM. Through comparing each of test error rates, we conclude that our Weighted SVM with boosting has predominant properties than the standard SVM have, as a whole. / GPL-2	noarch
r-wtest	3.2	Perform the calculation of W-test, diagnostic checking, calculate minor allele frequency (MAF) and odds ratio. / GPL-2	linux-64, osx-64, win-64
r-wtss	1.1.0	An R client that provides remote access to satellite image time series. The client allows Earth observation users to obtain time series from data sets available in a Web Time Series Server. The functions include: (a) listing the data sets available in the server; (b) describing the contents of a data set; (c) retrieving a time series based on spatial location and temporal filters. / GPL-3	noarch
r-wvtool	1.0	This tool, wood vision tool, is intended to facilitate preprocessing and analyzing 2-dimensional wood images toward automated recognition. The former includes some basics such as functions to RGB to grayscale, gray to binary, cropping, rotation(bilinear), median/mean/Gaussian filter, and Canny/Sobel edge detection. The latter includes gray level co-occurrence matrix (GLCM), Haralick parameters, local binary pattern (LBP), higher order local autocorrelation (HLAC), Fourier transform (radial and azimuthal integration), and Gabor filtering. The functions are intended to read data using 'readTIFF(x,info=T)' from 'tiff' package. The functions in this packages basically assumes the grayscale images as input data, thus the color images should be subjected to the function rgb2gray() before used for some other functions. / GPL-2	noarch
r-wwgbook	1.0.1	Book is Linear Mixed Models: A Practical Guide Using Statistical Software published in 2006 by Chapman Hall / CRC Press / GPL-2	noarch
r-wwr	1.2.2	Calculate the (weighted) win loss statistics including the win ratio, win difference and win product and their variances, with which the p-values are also calculated. The variance estimation is based on Luo et al. (2015) <doi:10.1111/biom.12225> and Luo et al. (2017) <doi:10.1002/sim.7284>. This package also calculates general win loss statistics with user-specified win loss function with variance estimation based on Bebu and Lachin (2016) <doi:10.1093/biostatistics/kxv032>. This version corrected an error when outputting confidence interval for win difference. / GPL-2	linux-64, osx-64, win-64
r-x12	1.9.0	The 'X13-ARIMA-SEATS' < <a href="https://www.census.gov/srd/www/x13as/">https://www.census.gov/srd/www/x13as/</a> > methodology and software is a widely used software and developed by the US Census Bureau. It can be accessed from 'R' with this package and 'X13-ARIMA-SEATS' binaries are provided by the 'R' package 'x13binary'. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<code>r-x13binary</code>	1.1.39	The US Census Bureau provides a seasonal adjustment program now called ‘X-13ARIMA-SEATS’ building on both earlier programs called X-11 and X-12 as well as the SEATS program by the Bank of Spain. The US Census Bureau offers both source and binary versions – which this package integrates for use by other R packages. / file LICENSE	linux-64, noarch, osx-64, win-32, win-64
<code>r-xbrl</code>	0.99.1	Functions to extract business financial information from an Extensible Business Reporting Language (‘XBRL’) instance file and the associated collection of files that defines its ‘Discoverable’ Taxonomy Set (‘DTS’). / GPL-2	linux-64, osx-64, win-64
<code>r-xfun</code>	0.6	Miscellaneous functions commonly used in other packages maintained by ‘Yihui Xie’. / MIT file LICENSE	linux-64, noarch, osx-64, win-32, win-64
<code>r-xgboost</code>	0.90.0	Extreme Gradient Boosting, which is an efficient implementation of the gradient boosting framework from Chen & Guestrin (2016) <doi:10.1145/2939672.2939785>. This package is its R interface. The package includes efficient linear model solver and tree learning algorithms. The package can automatically do parallel computation on a single machine which could be more than 10 times faster than existing gradient boosting packages. It supports various objective functions, including regression, classification and ranking. The package is made to be extensible, so that users are also allowed to define their own objectives easily. / Apache License (== 2.0)   file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<code>r-xgboost-cpu</code>	0.90	None / None	linux-64, osx-64, win-64
<code>r-xgboost-gpu</code>	0.80	None / None	linux-64
<code>r-xgobi</code>	1.2_1	Interface to the XGobi and XGvis programs for graphical data analysis. / file LICENSE	noarch
<code>r-xhwe</code>	1.0	Conduct the likelihood ratio tests for Hardy-Weinberg equilibrium at marker loci on the X chromosome. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-ximble</a>	0.10.1	Provides a simple XML tree parser/generator. It includes functions to read XML files into R objects, get information out of and into nodes, and write R objects back to XML code. It's not as powerful as the 'XML' package and doesn't aim to be, but for simple XML handling it could be useful. It was originally developed for the R GUI and IDE 'RKWard' < <a href="https://rkward.kde.org">https://rkward.kde.org</a> >, to make plugin development easier. / GPL-3	noarch
<a href="#">r-xlconnectjars</a>	0.2.1	Provides external JAR dependencies for the XLConnect package. / GPL-3	noarch
<a href="#">r-xlink</a>	1.0.1	The expression of X-chromosome undergoes three possible biological processes: X-chromosome inactivation (XCI), escape of the X-chromosome inactivation (XCI-E), and skewed X-chromosome inactivation (XCI-S). To analyze the X-linked genetic association for phenotype such as continuous, binary, and time-to-event outcomes with the actual process unknown, we propose a unified approach of maximizing the likelihood or partial likelihood over all of the potential biological processes. The methods are described in Wei Xu, Meiling Hao (2017) <doi:10.1002/gepi.22097>. And also see Dongxiao Han, Meiling Hao, Lianqiang Qu, Wei Xu (2019) <doi:10.1177/0962280219859037>. / GPL-2	noarch
<a href="#">r-xllim</a>	2.1	Provides a tool for non linear mapping (non linear regression) using a mixture of regression model and an inverse regression strategy. The methods include the GLLiM model (see Deleforge et al (2015) <DOI:10.1007/s11222-014-9461-5>) based on Gaussian mixtures and a robust version of GLLiM, named SLLiM (see Perthame et al (2016) < <a href="https://hal.archives-ouvertes.fr/hal-01347455">https://hal.archives-ouvertes.fr/hal-01347455</a> >) based on a mixture of Generalized Student distributions. The methods also include BLLiM (see Devijver et al (2017) < <a href="https://arxiv.org/abs/1701.07899">https://arxiv.org/abs/1701.07899</a> >) which is an extension of GLLiM with a sparse block diagonal structure for large covariance matrices (particularly interesting for transcriptomic data). / GPL-2	noarch
<a href="#">r-xlsimple</a>	0.0.1	Provides a simple wrapper for some 'XLConnect' functions. 'XLConnect' is a package that allows for reading, writing, and manipulating Microsoft Excel files. This package, 'xlsimple', adds some documentation and pre-defined formatting to the outputted Excel file. Individual sheets can include a description on the first row to remind user what is in the data set. Auto filters and freeze rows are turned on. A brief readme file is created that provides a summary listing of the created sheets and, where provided, the description. / GPL-3	noarch
<a href="#">r-xlsx</a>	0.6.1	Provide R functions to read/write/format Excel 2007 and Excel 97/2000/XP/2003 file formats. / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
<a href="#">r-xlsxjars</a>	0.6.1	The xlsxjars package collects all the external jars required for the xlsx package. This release corresponds to POI 3.10.1. / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-xltabr</a>	0.1.2	Writes beautifully formatted cross tabulations to Excel using ‘openxlsx’. It has been developed to help automate the process of publishing Official Statistics. The user provides a dataframe, which is outputted to Excel with various types of rich formatting which are automatically detected from the structure of the cross tabulation. Documentation can be found at the following url < <a href="https://github.com/moj-analytical-services/xltabr">https://github.com/moj-analytical-services/xltabr</a> >. / GPL-3	noarch
<a href="#">r-xmisc</a>	0.2.1	This is Xiaobei’s miscellaneous classes and functions useful when developing R packages, particularly for OOP using R Reference Class. / GPL-2	noarch
<a href="#">r-xml</a>	3.98	Many approaches for both reading and creating XML (and HTML) documents (including DTDs), both local and accessible via HTTP or FTP. Also offers access to an ‘XPath’ interpreter. / BSD_2_clause file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-xml2</a>	1.2.0	Work with XML files using a simple, consistent interface. Built on top of the ‘libxml2’ C library. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-xml2r</a>	0.0.6	XML2R is a framework that reduces the effort required to transform XML content into number of tables while preserving parent to child relationships. / GPL-2	noarch
<a href="#">r-xmlparsedata</a>	1.0.2	Convert the output of ‘utils::getParseData()’ to an ‘XML’ tree, that one can search via ‘XPath’, and easier to manipulate in general. / MIT	noarch
<a href="#">r-xmlrpc2</a>	1.1	The ‘XML-RPC’ is a remote procedure call protocol based on ‘XML’. The ‘xmlrpc2’ package is inspired by the ‘XMLRPC’ package but uses the ‘curl’ and ‘xml2’ packages instead ‘RCurl’ and ‘XML’. / GPL-3	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-xnomial</a>	1.0.4	Tests whether a set of counts fit a given expected ratio. For example, a genetic cross might be expected to produce four types in the relative frequencies of 9:3:3:1. To see whether a set of observed counts fits this expectation, one can examine all possible outcomes with <code>xmulti()</code> or a random sample of them with <code>xmonte()</code> and find the probability of an observation deviating from the expectation by at least as much as the observed. As a measure of deviation from the expected, one can use the log-likelihood ratio, the multinomial probability, or the classic chi-square statistic. A histogram of the test statistic can also be plotted and compared with the asymptotic curve. / GPL-3	linux-64, osx-64, win-64
<a href="#">r-xopen</a>	1.0.0	Cross platform solution to open files, directories or ‘URLs’ with their associated programs. / MIT file LICENSE	noarch
<a href="#">r-xplorerr</a>	0.1.1	Tools for interactive data exploration built using ‘shiny’. Includes apps for descriptive statistics, visualizing probability distributions, inferential statistics, linear regression, logistic regression and RFM analysis. / MIT	noarch
<a href="#">r-xptr</a>	1.1.1	There is limited native support for external pointers in the R interface. This package provides some basic tools to verify, create and modify ‘externalptr’ objects. / MIT	linux-64, osx-64, win-64
<a href="#">r-xr</a>	0.7.2	Support for interfaces from R to other languages, built around a class for evaluators and a combination of functions, classes and methods for communication. Will be used through a specific language interface package. Described in the book Extending R. / GPL-2	noarch
<a href="#">r-xrscc</a>	0.1	This is a set of statistical quality control functions, that allows plotting control charts and its iterations, process capability for variable and attribute control, highlighting the <code>xrs_gr()</code> function, like a first iteration for variable chart, meanwhile the <code>we_rules()</code> function detects non random patterns in sample. / GPL-2	noarch
<a href="#">r-xslt</a>	1.3	An extension for the ‘xml2’ package to transform XML documents by applying an ‘xslt’ style-sheet. / GPL-2	linux-64, osx-64, win-64
<a href="#">r-xtable</a>	1.8_4	Coerce data to LaTeX and HTML tables. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">r-xtal</a>	1.15	This is the tool set for crystallographer to design and analyze crystallization experiments, especially for ribosome from Mycobacterium tuberculosis. / GPL-2   GPL-3	noarch

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Name	Version	Summary/License	Platforms
r-xtensor	0.11.1	The 'xtensor' C library for numerical analysis with multi-dimensional array expressions is provided as a header-only C14 library. It offers an extensible expression system enabling lazy broadcasting; an API following the idioms of the C standard library; and tools to manipulate array expressions and build upon 'xtensor'. / BSD_3_clause	linux-64, osx-64, win-64
r-xtermstyle	3.0.5	Can be used for coloring output in terminals. It was developed for the standard Ubuntu terminal but should be compatible with any terminal using xterm or ANSI escape sequences. If run in windows, RStudio, or any other platform not supporting such escape sequences it gracefully passes on any output without modifying it. / GPL-2	noarch
r-xts	0.11.2	Provide for uniform handling of R's different time-based data classes by extending zoo, maximizing native format information preservation and allowing for user level customization and extension, while simplifying cross-class interoperability. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
r-xwf	0.2.2	Extrema-weighted feature extraction for varying length functional data. Functional data analysis method that performs dimensionality reduction based on predefined features and allows for quantile weighting. Method implemented as presented in Van den Boom et al. (2018) <doi:10.1093/bioinformatics/bty120>. / MIT	noarch
r-xyloplot	1.6	A method for creating vertical histograms sharing a y-axis using base graphics. / GPL-2	noarch
r-xyz	0.2	High dimensional interaction search by brute force requires a quadratic computational cost in the number of variables. The xyz algorithm provably finds strong interactions in almost linear time. For details of the algorithm see: G. Thanei, N. Meinshausen and R. Shah (2016). The xyz algorithm for fast interaction search in high-dimensional data < <a href="https://arxiv.org/pdf/1610.05108v1.pdf">https://arxiv.org/pdf/1610.05108v1.pdf</a> >. / GPL-3	linux-64, osx-64, win-64
r-yacca	1.1.1	Provides an alternative canonical correlation/redundancy analysis function, with associated print, plot, and summary methods. A method for generating helio plots is also included. / GPL-3	noarch
r-yaimpute	1.0.3	Performs nearest neighbor-based imputation using one or more alternative approaches to processing multivariate data. These include methods based on canonical correlation analysis, canonical correspondence analysis, and a multivariate adaptation of the random forest classification and regression techniques of Leo Breiman and Adele Cutler. Additional methods are also offered. The package includes functions for comparing the results from running alternative techniques, detecting imputation targets that are notably distant from reference observations, detecting and correcting for bias, bootstrapping and building ensemble imputations, and mapping results. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
r-yakmor	0.1.1	This is a simple wrapper for the yakmo K-Means library (developed by Naoki Yoshinaga, see <a href="http://www.tkl.iis.u-tokyo.ac.jp/~ynaga/yakmo/">http://www.tkl.iis.u-tokyo.ac.jp/~ynaga/yakmo/</a> ). It performs fast and robust (orthogonal) K-Means. / GPL-2	linux-64, osx-64, win-64
r-yaletoolkit	4.2.2	This collection of data exploration tools was developed at Yale University for the graphical exploration of complex multivariate data; barcode and gpairs now have their own packages. The new big.read.table() provided here may be useful for large files when only a subset is needed. / LGPL-3	noarch
r-yaml	2.2.0	Implements the ‘libyaml’ ‘YAML’ 1.1 parser and emitter (< <a href="http://pyyaml.org/wiki/LibYAML">http://pyyaml.org/wiki/LibYAML</a> >) for R. / BSD_3_clause file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
r-yarr	0.1.2	A parser and a writer for ‘WEKA’ Attribute-Relation File Format < <a href="https://waikato.github.io/weka-wiki/arff_stable/">https://waikato.github.io/weka-wiki/arff_stable/</a> > in pure R, with no dependencies. As opposed to other R implementations, this package can read standard (dense) as well as sparse files, i.e. those where each row does only contain nonzero components. Unlike ‘RWeka’, ‘yarr’ does not require any ‘Java’ installation nor is dependent on external software. This implementation is generalized from those in packages ‘mldr’ and ‘mldr.datasets’. / GPL-3	noarch
r-yasp	0.2.0	A collection of string functions designed for writing compact and expressive R code. ‘yasp’ (Yet Another String Package) is simple, fast, dependency-free, and written in pure R. The package provides: a coherent set of abbreviations for paste() from package ‘base’ with a variety of defaults, such as p() for paste and pcc() for paste and collapse with commas; wrap(), bracket(), and others for wrapping a string in flanking characters; unwrap() for removing pairs of characters (at any position in a string); and sentence() for cleaning whitespace around punctuation and capitalization appropriate for prose sentences. / MIT	noarch
r-yatah	0.0.1	Provides functions to manage taxonomy when lineages are described with strings and ranks separated with special patterns like  *__ or ;*__. / GPL-3	noarch
r-yesno	0.1.0	Asks Yes-No questions with variable or custom responses. / GPL-2	noarch
r-yhatr	0.15.1	Deploy, maintain, and invoke models via the Yhat REST API. / FreeBSD	noarch
r-yieldcurve	4.1	Modelling the yield curve with some parametric models. The models implemented are: Nelson-Siegel, Diebold-Li and Svensson. The package also includes the data of the term structure of interest rate of Federal Reserve Bank and European Central Bank. / GPL-2	noarch
r-ykmeans	1.0	The clustering by k-means of using the target variable. To determine the number of clusters with the variance of the target variable in the cluster. / GPL-3	noarch
r-yll	1.0.0	Compute the standard expected years of life lost (YLL), as developed by the Global Burden of Disease Study (Murray, C.J., Lopez, A.D. and World Health Organization, 1996). The YLL is based on comparing the age of death to an external standard life expectancy curve. It also computes the average YLL, which highlights premature causes of death and brings attention to preventable deaths (Aragon et al., 2008). / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-yonder</a>	0.1.1	Build ‘shiny’ applications with the latest Bootstrap components and design utilities. Includes refreshed reactive inputs and outputs. Use responsive layouts to design and construct applications for devices of all sizes. / GPL-3	noarch
<a href="#">r-ypinterimtesting</a>	1.0.3	For any spending function specified by the user, this package provides corresponding boundaries for interim testing using the adaptively weighted log-rank test developed by Yang and Prentice (2010 <doi:10.1111/j.1541-0420.2009.01243.x>). The package uses a re-sampling method to obtain stopping boundaries at the interim looks. The output consists of stopping boundaries and observed values of the test statistics at the interim looks, along with nominal p-values defined as the probability of the test exceeding the specific observed test statistic value or critical value, regardless of the test behavior at other looks. The asymptotic validity of the stopping boundaries is established in Yang (2018 <doi:10.1002/sim.7958>). / GPL-3	linux-64, osx-64, win-64
<a href="#">r-ypmodel</a>	1.3	Inference procedures accommodate a flexible range of hazard ratio patterns with a two-sample semi-parametric model. This model contains the proportional hazards model and the proportional odds model as sub-models, and accommodates non-proportional hazards situations to the extreme of having crossing hazards and crossing survivor functions. Overall, this package has four major functions: 1) the parameter estimation, namely short-term and long-term hazard ratio parameters; 2) 95 percent and 90 percent point-wise confidence intervals and simultaneous confidence bands for the hazard ratio function; 3) p-value of the adaptive weighted log-rank test; 4) p-values of two lack-of-fit tests for the model. See the included read_me_first.pdf for brief instructions. In this version (1.1), there is no need to sort the data before applying this package. / GPL-3	noarch
<a href="#">r-yum</a>	0.0.1	Provides a number of functions to facilitate extracting information in ‘YAML’ fragments from one or multiple files, optionally structuring the information in a ‘data.tree’. ‘YAML’ (recursive acronym for YAML ain’t Markup Language) is a convention for specifying structured data in a format that is both machine- and human-readable. ‘YAML’ therefore lends itself well for embedding (meta)data in plain text files, such as Markdown files. This principle is implemented in ‘yum’ with minimal dependencies (i.e. only the ‘yaml’ packages, and the ‘data.tree’ package can be used to enable additional functionality). / GPL-3	noarch
<a href="#">r-yummlyr</a>	0.1.1	Yummly.com is one of the world’s largest and most powerful recipe search sites and this package aims to provide R bindings for publicly available Yummly.com Recipe API ( <a href="https://developer.yummly.com/">https://developer.yummly.com/</a> ). / GPL-2	noarch
<a href="#">r-zeallot</a>	0.1.0	Provides a %<-% operator to perform multiple, unpacking, and destructuring assignment in R. The operator unpacks the right-hand side of an assignment into multiple values and assigns these values to variables on the left-hand side of the assignment. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-64
<a href="#">r-zen4r</a>	0.3	Provides an Interface to ‘Zenodo’ (< <a href="https://zenodo.org">https://zenodo.org</a> >) REST API, including management of depositions, attribution of DOIs by ‘Zenodo’ and upload of files. / MIT	noarch
<a href="#">r-zendesk</a>	0.4	This package provides an R wrapper for the Zendesk API / GPL-2	noarch

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Name	Version	Summary/License	Platforms
r-zic	0.9.1	Provides MCMC algorithms for the analysis of zero-inflated count models. The case of stochastic search variable selection (SVS) is also considered. All MCMC samplers are coded in C for improved efficiency. A data set considering the demand for health care is provided. / GPL-2	linux-64, osx-64, win-64
r-zillowr	0.1.0	Zillow, an online real estate company, provides real estate and mortgage data for the United States through a REST API. The ZillowR package provides an R function for each API service, making it easy to make API calls and process the response into convenient, R-friendly data structures. See < <a href="http://www.zillow.com/howto/api/APIOverview.htm">http://www.zillow.com/howto/api/APIOverview.htm</a> > for the Zillow API Documentation. / GPL-3	noarch
r-zim	1.1.0	Analyze count time series with excess zeros. Two types of statistical models are supported: Markov regression by Yang et al. (2013) <doi:10.1016/j.stamet.2013.02.001> and state-space models by Yang et al. (2015) <doi:10.1177/1471082X14535530>. They are also known as observation-driven and parameter-driven models respectively in the time series literature. The functions used for Markov regression or observation-driven models can also be used to fit ordinary regression models with independent data under the zero-inflated Poisson (ZIP) or zero-inflated negative binomial (ZINB) assumption. Besides, the package contains some miscellaneous functions to compute density, distribution, quantile, and generate random numbers from ZIP and ZINB distributions. / GPL-3	noarch
r-zip	2.0.1	Cross-Platform ‘zip’ Compression Library. A replacement for the ‘zip’ function, that does not require any additional external tools on any platform. / CC0	linux-64, osx-64, win-32, win-64
r-zipcode	1.0	This package contains a database of city, state, latitude, and longitude information for U.S. ZIP codes from the CivicSpace Database (August 2004) augmented by Daniel Coven’s federalgovernmentzipcodes.us web site (updated January 22, 2012). Previous versions of this package (before 1.0) were based solely on the CivicSpace data, so an original version of the CivicSpace database is also included. / CC BY-SA 2.0 file LICENSE	noarch
r-zipfr	0.6.1	Statistical models and utilities for the analysis of word frequency distributions. The utilities include functions for loading, manipulating and visualizing word frequency data and vocabulary growth curves. The package also implements several statistical models for the distribution of word frequencies in a population. (The name of this package derives from the most famous word frequency distribution, Zipf’s law.) / GPL-3	noarch
r-zipr	0.1.1	Implements Python-style zip for R. Is a more flexible version of cbind. / GPL-3	noarch
r-zoeppritz	1.0.7	Calculate and plot scattering matrix coefficients for plane waves at interface. / GPL-2	noarch

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Name	Version	Summary/License	Platforms
<a href="#">r-zoo</a>	1.8_6	An S3 class with methods for totally ordered indexed observations. It is particularly aimed at irregular time series of numeric vectors/matrices and factors. zoo's key design goals are independence of a particular index/date/time class and consistency with ts and base R by providing methods to extend standard generics. / GPL-2   GPL-3	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">r-zoocat</a>	0.2.0	Tools for manipulating multivariate time series data by extending 'zoo' class. / GPL-3	noarch
<a href="#">r-zoom</a>	2.0.4	zm(), called with any active plot allow to enter an interactive session to zoom/navigate any plot. The development version, as well as binary releases can be found at <a href="https://github.com/cbarbu/R-package-zoom">https://github.com/cbarbu/R-package-zoom</a> / GPL-3	noarch
<a href="#">r-zoomgrid</a>	1.0.0	Provides the grid search algorithm with a zoom. The grid search algorithm with a zoom aims to help solving difficult optimization problem where there are many local optima inside the domain of the target function. It offers suitable initial or starting value for the following optimization procedure, provided that the global optimum exists in the neighbourhood of the initial or starting value. The grid search algorithm with a zoom saves time tremendously in cases with high-dimensional arguments. / GPL-3	noarch
<a href="#">r-zseq</a>	0.2.0	Generates well-known integer sequences. 'gmp' package is adopted for computing with arbitrarily large numbers. Every function has hyperlink to its corresponding item in OEIS (The On-Line Encyclopedia of Integer Sequences) in the function help page. For interested readers, see Sloane and Plouffe (1995, ISBN:978-0125586306). / GPL-3	noarch
<a href="#">r-ztree</a>	1.0.6	Read '.xls' and '.sbj' files which are written by the Microsoft Windows program 'z-Tree'. The latter is a software for developing and carrying out economic experiments (see <a href="http://www.ztree.uzh.ch/">http://www.ztree.uzh.ch/</a> for more information). / GPL-3	noarch
<a href="#">r.methodss3</a>	1.7.1	Methods that simplify the setup of S3 generic functions and S3 methods. Major effort has been made in making definition of methods as simple as possible with a minimum of maintenance for package developers. For example, generic functions are created automatically, if missing, and naming conflict are automatically solved, if possible. The method setMethodS3() is a good start for those who in the future may want to migrate to S4. This is a cross-platform package implemented in pure R that generates standard S3 methods. / LGPL (>= 2.1)	linux-32, linux-64, noarch, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
<code>r.oo</code>	1.22.0	Methods and classes for object-oriented programming in R with or without references. Large effort has been made on making definition of methods as simple as possible with a minimum of maintenance for package developers. The package has been developed since 2001 and is now considered very stable. This is a cross-platform package implemented in pure R that defines standard S3 classes without any tricks. / LGPL (>= 2.1)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<code>r.utils</code>	2.8.0	Utility functions useful when programming and developing R packages. / LGPL (>= 2.1)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<code>r2d3</code>	0.2.3	Suite of tools for using 'D3', a library for producing dynamic, interactive data visualizations. Supports translating objects into 'D3' friendly data structures, rendering 'D3' scripts, publishing 'D3' visualizations, incorporating 'D3' in R Markdown, creating interactive 'D3' applications with Shiny, and distributing 'D3' based 'htmlwidgets' in R packages. / BSD_3_clause file LICENSE	noarch
<code>r6</code>	2.4.0	Creates classes with reference semantics, similar to R's built-in reference classes. Compared to reference classes, R6 classes are simpler and lighter-weight, and they are not built on S4 classes so they do not require the methods package. These classes allow public and private members, and they support inheritance, even when the classes are defined in different packages. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<code>randomforest</code>	4.6-14	Classification and regression based on a forest of trees using random inputs, based on Breiman (2001) <DOI:10.1023/A:1010933404324>. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
<a href="#">ranger</a>	0.11.2	A fast implementation of Random Forests, particularly suited for high dimensional data. Ensembles of classification, regression, survival and probability prediction trees are supported. Data from genome-wide association studies can be analyzed efficiently. In addition to data frames, datasets of class 'gwaa.data' (R package 'GenABEL') and 'dgCMatix' (R package 'Matrix') can be directly analyzed. / GPL-3	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">rappdirs</a>	0.3.1	An easy way to determine which directories on the users computer you should use to save data, caches and logs. A port of Python's 'Appdirs' ( <a href="https://github.com/ActiveState/appdirs">url{https://github.com/ActiveState/appdirs}</a> ) to R. / MIT file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">raster</a>	2.8.1	Reading, writing, manipulating, analyzing and modeling of gridded spatial data. The package implements basic and high-level functions. Processing of very large files is supported. / GPL (>= 3)	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">rbokeh</a>	0.6.3	A native R plotting library that provides a flexible declarative interface for creating interactive web-based graphics, backed by the Bokeh visualization library < <a href="http://bokeh.pydata.org/">http://bokeh.pydata.org/</a> >. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">rcmdcheck</a>	1.3.2	Run 'R CMD check' from 'R' programmatically, and capture the results of the individual checks. / MIT file LICENSE	noarch

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Name	Version	Summary/License	Platforms
<code>colorbrewer</code>	1.1_2	Provides color schemes for maps (and other graphics) designed by Cynthia Brewer as described at <a href="http://colorbrewer2.org">http://colorbrewer2.org</a> / Apache License 2.0	linux-32, linux-64, noarch, osx-64, win-32, win-64
<code>rcpp</code>	1.0.1	The ‘Rcpp’ package provides R functions as well as C classes which offer a seamless integration of R and C. Many R data types and objects can be mapped back and forth to C equivalents which facilitates both writing of new code as well as easier integration of third-party libraries. Documentation about ‘Rcpp’ is provided by several vignettes included in this package, via the ‘Rcpp Gallery’ site at <a href="http://gallery.rcpp.org">http://gallery.rcpp.org</a> , the paper by Eddelbuettel and Francois (2011, <doi:10.18637/jss.v040.i08>), the book by Eddelbuettel (2013, <doi:10.1007/978-1-4614-6868-4>) and the paper by Eddelbuettel and Balamuta (2018, <doi:10.1080/00031305.2017.1375990>); see ‘citation(Rcpp)’ for details. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<code>rcpparmadillo</code>	0.9.3002	‘RcppArmadillo’ is a templated C linear algebra library (by Conrad Sanderson) that aims towards a good balance between speed and ease of use. Integer, floating point and complex numbers are supported, as well as a subset of trigonometric and statistics functions. Various matrix decompositions are provided through optional integration with LAPACK and ATLAS libraries. The ‘RcppArmadillo’ package includes the header files from the templated ‘Armadillo’ library. Thus users do not need to install ‘Armadillo’ itself in order to use ‘RcppArmadillo’. From release 7.800.0 on, ‘Armadillo’ is licensed under Apache License 2; previous releases were under licensed as MPL 2.0 from version 3.800.0 onwards and LGPL-3 prior to that; ‘RcppArmadillo’ (the ‘Rcpp’ bindings/bridge to Armadillo) is licensed under the GNU GPL version 2 or later, as is the rest of ‘Rcpp’. Note that Armadillo requires a fairly recent compiler; for the g family at least version 4.6.* is required. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<code>rcppeigen</code>	0.3.3.100	‘RcppEigen’ and ‘Eigen’ integration using ‘Rcpp’. ‘Eigen’ is a C template library for linear algebra: matrices, vectors, numerical solvers and related algorithms. It supports dense and sparse matrices on integer, floating point and complex numbers, decompositions of such matrices, and solutions of linear systems. Its performance on many algorithms is comparable with some of the best implementations based on ‘Lapack’ and level-3 ‘BLAS’. The ‘RcppEigen’ package includes the header files from the ‘Eigen’ C template library (currently version 3.3.4). Thus users do not need to install ‘Eigen’ itself in order to use ‘RcppEigen’. Since version 3.1.1, ‘Eigen’ is licensed under the Mozilla Public License (version 2); earlier version were licensed under the GNU LGPL version 3 or later. ‘RcppEigen’ (the ‘Rcpp’ bindings/bridge to ‘Eigen’) is licensed under the GNU GPL version 2 or later, as is the rest of ‘Rcpp’. / GPL (>= 2)   file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<code>rcppprogress</code>	0.4.1	Allows to display a progress bar in the R console for long running computations taking place in c code, and support for interrupting those computations even in multithreaded code, typically using OpenMP. / GPL (>= 3)	noarch

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Name	Version	Summary/License	Platforms
<a href="#">rcpproll</a>	0.3.0	Provides fast and efficient routines for common rolling / windowed operations. Routines for the efficient computation of windowed mean, median, sum, product, minimum, maximum, standard deviation and variance are provided. / GPL ( $\geq 2$ )	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">rcurl</a>	1.95	Wrapper for 'libcurl' < <a href="http://curl.haxx.se/libcurl/">http://curl.haxx.se/libcurl/</a> > Provides functions to allow one to compose general HTTP requests and provides convenient functions to fetch URIs, get & post forms, etc. and process the results returned by the Web server. This provides a great deal of control over the HTTP/FTP... connection and the form of the request while providing a higher-level interface than is available just using R socket connections. Additionally, the underlying implementation is robust and extensive, supporting FTP/FTPS/TFTP (uploads and downloads), SSL/HTTPS, telnet, dict, ldap, and also supports cookies, redirects, authentication, etc. / BSD	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">readr</a>	1.3.1	The goal of 'readr' is to provide a fast and friendly way to read rectangular data (like 'csv', 'tsv', and 'fwf'). It is designed to flexibly parse many types of data found in the wild, while still cleanly failing when data unexpectedly changes. / GPL ( $\geq 2$ )   file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">readxl</a>	1.3.1	Import excel files into R. Supports '.xls' via the embedded 'libxls' C library < <a href="https://github.com/libxls/libxls">https://github.com/libxls/libxls</a> > and '.xlsx' via the embedded 'RapidXML' C library < <a href="http://rapidxml.sourceforge.net">http://rapidxml.sourceforge.net</a> >. Works on Windows, Mac and Linux without external dependencies. / GPL-3	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">recipes</a>	0.1.5	An extensible framework to create and preprocess design matrices. Recipes consist of one or more data manipulation and analysis steps. Statistical parameters for the steps can be estimated from an initial data set and then applied to other data sets. The resulting design matrices can then be used as inputs into statistical or machine learning models. / GPL-2	linux-32, linux-64, noarch, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
<a href="#">recommended</a>	3.6.0	R is a free software environment for statistical computing and graphics. / GPL-3.0	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">registry</a>	0.5.1	Provides a generic infrastructure for creating and using registries. / GPL-2	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">rematch</a>	1.0.1	A small wrapper on 'regexpr' to extract the matches and captured groups from the match of a regular expression to a character vector. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">remotes</a>	2.0.4	Download and install R packages stored in 'GitHub', 'BitBucket', or plain 'subversion' or 'git' repositories. This package provides the 'install_*' functions in 'devtools'. Indeed most of the code was copied over from 'devtools'. / GPL (>= 2)	noarch
<a href="#">repr</a>	0.19.2	String and binary representations of objects for several formats / mime types. / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64

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Table 51 – continued from previous page

Name	Version	Summary/License	Platforms
<a href="#">reprex</a>	0.2.1	Convenience wrapper that uses the ‘rmarkdown’ package to render small snippets of code to target formats that include both code and output. The goal is to encourage the sharing of small, reproducible, and runnable examples on code-oriented websites, such as < <a href="https://stackoverflow.com">https://stackoverflow.com</a> > and < <a href="https://github.com">https://github.com</a> >, or in email. The user’s clipboard is the default source of input code and the default target for rendered output. ‘reprex’ also extracts clean, runnable R code from various common formats, such as copy/paste from an R session. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">reshape</a>	0.8.8	Flexibly restructure and aggregate data using just two functions: melt and cast. / MIT file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">reshape2</a>	1.4.3	Flexibly restructure and aggregate data using just two functions: melt and ‘dcast’ (or ‘acast’). / MIT file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">reticulate</a>	1.12	Interface to ‘Python’ modules, classes, and functions. When calling into ‘Python’, R data types are automatically converted to their equivalent ‘Python’ types. When values are returned from ‘Python’ to R they are converted back to R types. Compatible with all versions of ‘Python’ >= 2.7. / Apache License 2.0	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">revoioq</a>	10.0.0	Test suite for Microsoft R Services. / GPL-2	linux-64, osx-64, win-64

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Name	Version	Summary/License	Platforms
revomods	11.0.0	Microsoft modifications and extensions to standard R functions / GPL-2	linux-64, osx-64, win-64
revoutils	11.0.0	Utility functions for Microsoft R / GPL-2	linux-64, osx-64, win-64
revoutilsmath	11.0.0	Utility functions for managing math threading. / file LICENSE	linux-64, win-64
rex	1.1.2	A friendly interface for the construction of regular expressions. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
rgexf	0.15.3	Create, read and write GEXF (Graph Exchange XML Format) graph files (used in Gephi and others). Using the XML package, it allows the user to easily build/read graph files including attributes, GEXF viz attributes (such as color, size, and position), network dynamics (for both edges and nodes) and edge weighting. Users can build/handle graphs element-by-element or massively through data-frames, visualize the graph on a web browser through sigma.js (a javascript library) and interact with the igraph package. / GPL (>= 3)	linux-32, linux-64, osx-64, win-32, win-64
rgl	0.100.10	Provides medium to high level functions for 3D interactive graphics, including functions modelled on base graphics (plot3d(), etc.) as well as functions for constructing representations of geometric objects (cube3d(), etc.). Output may be on screen using OpenGL, or to various standard 3D file formats including WebGL, PLY, OBJ, STL as well as 2D image formats, including PNG, Postscript, SVG, PGF. / GPL	linux-32, linux-64, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
<a href="#">rglwidget</a>	0.2.1	The contents of this package have been merged into rgl, so it is no longer needed. / GPL-2	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">rhive</a>	2.0_0	<del>R</del> Hive is an R extension facilitating distributed computing via HIVE query. It provides an easy to use HQL like SQL and R objects and functions in HQL. / Apache License (== 2.0)	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">rio</a>	0.5.1	Streamlined data import and export by making assumptions that the user is probably willing to make: 'import()' and 'export()' determine the data structure from the file extension, reasonable defaults are used for data import and export (e.g., 'stringsAsFactors=FALSE'), web-based import is natively supported (including from SSL/HTTPS), compressed files can be read directly without explicit decompression, and fast import packages are used where appropriate. An additional convenience function, 'convert()', provides a simple method for converting between file types. / GPL-2	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">rjava</a>	0.9_1	Low-level interface to Java VM very much like .C/.Call and friends. Allows creation of objects, calling methods and accessing fields. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
<a href="#">rjdbc</a>	0.2_7	The RJDBC package is an implementation of R's DBI interface using JDBC as a back-end. This allows R to connect to any DBMS that has a JDBC driver. / MIT file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">rjson</a>	0.2.20	Converts R object into JSON objects and vice-versa. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">rjsonio</a>	1.3_1	This is a package that allows conversion to and from data in Javascript object notation (JSON) format. This allows R objects to be inserted into Javascript/ECMAScript/ActionScript code and allows R programmers to read and convert JSON content to R objects. This is an alternative to rjson package. Originally, that was too slow for converting large R objects to JSON and was not extensible. rjson's performance is now similar to this package, and perhaps slightly faster in some cases. This package uses methods and is readily extensible by defining methods for different classes, vectorized operations, and C code and callbacks to R functions for deserializing JSON objects to R. The two packages intentionally share the same basic interface. This package (RJSONIO) has many additional options to allow customizing the generation and processing of JSON content. This package uses libjson rather than implementing yet another JSON parser. The aim is to support other general projects by building on their work, providing feedback and benefit from their ongoing development. / BSD_3_clause file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">rlang</a>	0.3.4	A toolbox for working with base types, core R features like the condition system, and core 'Tidyverse' features like tidy evaluation. / GPL-3	linux-32, linux-64, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
<code>rlist</code>	0.4.6	Provides a set of functions for data manipulation with list objects, including mapping, filtering, grouping, sorting, updating, searching, and other useful functions. Most functions are designed to be pipeline friendly so that data processing with lists can be chained. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<code>rmariadb</code>	1.0.6	Implements a 'DBI'-compliant interface to 'MariaDB' (< <a href="https://mariadb.org/">https://mariadb.org/</a> >) and 'MySQL' (< <a href="https://www.mysql.com/">https://www.mysql.com/</a> >) databases. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
<code>rmarkdown</code>	1.12	Convert R Markdown documents into a variety of formats. / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
<code>rmr2</code>	3.3.1	Supports the map reduce programming model on top of hadoop streaming / Apache 2.0	linux-32, linux-64, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
<a href="#">rms</a>	5.1_3	Regression modeling, testing, estimation, validation, graphics, prediction, and typesetting by storing enhanced model design attributes in the fit. ‘rms’ is a collection of functions that assist with and streamline modeling. It also contains functions for binary and ordinal logistic regression models, ordinal models for continuous Y with a variety of distribution families, and the Buckley-James multiple regression model for right-censored responses, and implements penalized maximum likelihood estimation for logistic and ordinary linear models. ‘rms’ works with almost any regression model, but it was especially written to work with binary or ordinal regression models, Cox regression, accelerated failure time models, ordinary linear models, the Buckley-James model, generalized least squares for serially or spatially correlated observations, generalized linear models, and quantile regression. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">rmysql</a>	0.10.1	Legacy ‘DBI’ interface to ‘MySQL’ / ‘MariaDB’ based on old code ported from S-PLUS. A modern ‘MySQL’ client based on ‘Rcpp’ is available from the ‘RMariaDB’ package. / GPL-2	linux-32, linux-64, osx-64, win-64
<a href="#">rngtools</a>	1.3.1	Provides a set of functions for working with Random Number Generators (RNGs). In particular, a generic S4 framework is defined for getting/setting the current RNG, or RNG data that are embedded into objects for reproducibility. Notably, convenient default methods greatly facilitate the way current RNG settings can be changed. / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">robustbase</a>	0.93_4	Essential Robust Statistics. Tools allowing to analyze data with robust methods. This includes regression methodology including model selections and multivariate statistics where we strive to cover the book Robust Statistics, Theory and Methods by ‘Maronna, Martin and Yohai’; Wiley 2006. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
<a href="#">rocr</a>	1.0_7	ROC graphs, sensitivity/specificity curves, lift charts, and precision/recall plots are popular examples of trade-off visualizations for specific pairs of performance measures. ROCR is a flexible tool for creating cutoff-parameterized 2D performance curves by freely combining two from over 25 performance measures (new performance measures can be added using a standard interface). Curves from different cross-validation or bootstrapping runs can be averaged by different methods, and standard deviations, standard errors or box plots can be used to visualize the variability across the runs. The parameterization can be visualized by printing cutoff values at the corresponding curve positions, or by coloring the curve according to cutoff. All components of a performance plot can be quickly adjusted using a flexible parameter dispatching mechanism. Despite its flexibility, ROCR is easy to use, with only three commands and reasonable default values for all optional parameters. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">rodbc</a>	1.3_15	An ODBC database interface. / GPL-2   GPL-3	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">rook</a>	1.1_1	This package contains the Rook specification and convenience software for building and running Rook applications. To get started, be sure and read the ‘Rook’ help file first. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">roxygen2</a>	6.1.1	Generate your Rd documentation, ‘NAMESPACE’ file, and collation field using specially formatted comments. Writing documentation in-line with code makes it easier to keep your documentation up-to-date as your requirements change. ‘Roxygen2’ is inspired by the ‘Doxygen’ system for C. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
<a href="#">rpanel</a>	1.1_4	A set of functions to build simple GUI controls for R functions. These are built on the ‘tcltk’ package. Uses could include changing a parameter on a graph by animating it with a slider or a doublebutton, up to more sophisticated control panels. Some functions for specific graphical tasks, referred to as ‘cartoons’, are provided. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">rpart</a>	4.1_1	Recursive partitioning for classification, regression and survival trees. An implementation of most of the functionality of the 1984 book by Breiman, Friedman, Olshen and Stone. / GPL-2   GPL-3	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">rprojroot</a>	1.3_2	Robust, reliable and flexible paths to files below a project root. The ‘root’ of a project is defined as a directory that matches a certain criterion, e.g., it contains a certain regular file. / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">rpy2</a>	2.9.4	Python interface to the R language (embedded R) / GPL2	linux-32, linux-64, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
<a href="#">rsconnect</a>	0.8.13	Programmatic deployment interface for ‘Rpubs’, ‘shinyapps.io’, and ‘RStudio Connect’. Supported content types include R Markdown documents, Shiny applications, Plumber APIs, plots, and static web content. / GPL-2	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">rserve</a>	1.7.3	Rserve acts as a socket server (TCP/IP or local sockets) which allows binary requests to be sent to R. Every connection has a separate workspace and working directory. Client-side implementations are available for popular languages such as C/C and Java, allowing any application to use facilities of R without the need of linking to R code. Rserve supports remote connection, user authentication and file transfer. A simple R client is included in this package as well. / GPL-2   file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">rsqlite</a>	2.1.1	Embeds the ‘SQLite’ database engine in R and provides an interface compliant with the ‘DBI’ package. The source for the ‘SQLite’ engine is included. / LGPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">rstan</a>	2.18.2	User-facing R functions are provided to parse, compile, test, estimate, and analyze Stan models by accessing the header-only Stan library provided by the ‘StanHeaders’ package. The Stan project develops a probabilistic programming language that implements full Bayesian statistical inference via Markov Chain Monte Carlo, rough Bayesian inference via ‘variational’ approximation, and (optionally penalized) maximum likelihood estimation via optimization. In all three cases, automatic differentiation is used to quickly and accurately evaluate gradients without burdening the user with the need to derive the partial derivatives. / GPL (>= 3)	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">rstudio</a>	1.1.456	A set of integrated tools designed to help you be more productive with R / Commercial or AGPLv3	linux-32, linux-64, osx-64, win-32, win-64

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Name	Version	Summary/License	Platforms
<code>rstudioapi</code>	0.10	Access the RStudio API (if available) and provide informative error messages when it's not. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<code>rtools</code>	3.4.0	None / None	win-64
<code>runit</code>	0.4.26	R functions implementing a standard Unit Testing framework, with additional code inspection and report generation tools / GPL-2	linux-64, osx-64, win-64
<code>rversions</code>	1.1.0	Query the main 'R' 'SVN' repository to find the versions 'r-release' and 'r-oldrel' refer to, and also all previous 'R' versions and their release dates. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<code>rvest</code>	0.3.3	Wrappers around the 'xml2' and 'httr' packages to make it easy to download, then manipulate, HTML and XML. / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
<code>rzmq</code>	0.9.6	Interface to the 'ZeroMQ' lightweight messaging kernel (see < <a href="http://www.zeromq.org/">http://www.zeromq.org/</a> > for more information). / GPL-3	linux-32, linux-64, osx-64, win-32, win-64

Table 52: S

Name	Version	Summary/License	Platforms
<a href="#">sandwich</a>	2.5_1	Model-robust standard error estimators for cross-sectional, time series, clustered, panel, and longitudinal data. / GPL-2   GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">scales</a>	1.0.0	Graphical scales map data to aesthetics, and provide methods for automatically determining breaks and labels for axes and legends. / MIT file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">seacarb</a>	3.2.12	Calculates parameters of the seawater carbonate system and assists the design of ocean acidification perturbation experiments. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">selectr</a>	0.4_1	Translates a CSS3 selector into an equivalent XPath expression. This allows us to use CSS selectors when working with the XML package as it can only evaluate XPath expressions. Also provided are convenience functions useful for using CSS selectors on XML nodes. This package is a port of the Python package 'cssselect' (< <a href="https://cssselect.readthedocs.io/">https://cssselect.readthedocs.io/</a> >). / BSD_3_clause file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">sessioninfo</a>	1.1.1	Query and print information about the current R session. It is similar to 'utils::sessionInfo()', but includes more information about packages, and where they were installed from. / GPL-2	noarch

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Table 52 – continued from previous page

Name	Version	Summary/License	Platforms
<a href="#">sf</a>	0.6_3	Support for simple features, a standardized way to encode spatial vector data. Binds to 'GDAL' for reading and writing data, to 'GEOS' for geometrical operations, and to 'PROJ' for projection conversions and datum transformations. / GPL-2   MIT file LICENSE	linux-32, linux-64, osx-64, win-64
<a href="#">sfsmisc</a>	1.1_3	Useful utilities ['goodies'] from Seminar fuer Statistik ETH Zurich, some of which were ported from S-plus in the 1990's. For graphics, have pretty (Log-scale) axes, an enhanced Tukey-Anscombe plot, combining histogram and boxplot, 2d-residual plots, a 'tachoPlot()', pretty arrows, etc. For robustness, have a robust F test and robust range(). For system support, notably on Linux, provides 'Sys.*()' functions with more access to system and CPU information. Finally, miscellaneous utilities such as simple efficient prime numbers, integer codes, Duplicated(), toLatex.numeric() and is.whole(). / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">shiny</a>	1.3.2	Makes it incredibly easy to build interactive web applications with R. Automatic reactive binding between inputs and outputs and extensive prebuilt widgets make it possible to build beautiful, responsive, and powerful applications with minimal effort. / GPL-3   file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">shinybs</a>	0.61	Adds additional Twitter Bootstrap components to Shiny. / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64

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Table 52 – continued from previous page

Name	Version	Summary/License	Platforms
<a href="#">shinycssloaders</a>	0.2.0	Create a lightweight Shiny wrapper for the css-loaders created by Luke Hass < <a href="https://github.com/lukehaas/css-loaders">https://github.com/lukehaas/css-loaders</a> >. Wrapping a Shiny output will automatically show a loader when the output is (re)calculating. / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">shinydashboard</a>	0.7.1	Create dashboards with ‘Shiny’. This package provides a theme on top of ‘Shiny’, making it easy to create attractive dashboards. / GPL (>= 2)   file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">shinyjs</a>	1.0	Perform common useful JavaScript operations in Shiny apps that will greatly improve your apps without having to know any JavaScript. Examples include: hiding an element, disabling an input, resetting an input back to its original value, delaying code execution by a few seconds, and many more useful functions for both the end user and the developer. ‘shinyjs’ can also be used to easily call your own custom JavaScript functions from R. / AGPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">shinysky</a>	2.0.0	A set of Shiny UI components includings alerts and styled buttons / MIT	linux-32, linux-64, osx-64, win-32, win-64

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Table 52 – continued from previous page

Name	Version	Summary/License	Platforms
<a href="#">shinythemes</a>	1.1.2	Themes for use with Shiny. Includes several Bootstrap themes from <a href="http://bootswatch.com/">http://bootswatch.com/</a> , which are packaged for use with Shiny applications. / GPL-3   file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">slam</a>	0.1_4	Data structures and algorithms for sparse arrays and matrices, based on index arrays and simple triplet representations, respectively. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">snowballc</a>	0.6.0	An R interface to the C ‘libstemmer’ library that implements Porter’s word stemming algorithm for collapsing words to a common root to aid comparison of vocabulary. Currently supported languages are Danish, Dutch, English, Finnish, French, German, Hungarian, Italian, Norwegian, Portuguese, Romanian, Russian, Spanish, Swedish and Turkish. / BSD_3_clause file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">sourcetools</a>	0.1.7	Tools for the reading and tokenization of R code. The ‘sourcetools’ package provides both an R and C interface for the tokenization of R code, and helpers for interacting with the tokenized representation of R code. / MIT file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">sp</a>	1.3_1	Classes and methods for spatial data; the classes document where the spatial location information resides, for 2D or 3D data. Utility functions are provided, e.g. for plotting data as maps, spatial selection, as well as methods for retrieving coordinates, for subsetting, print, summary, etc. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64

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Table 52 – continued from previous page

Name	Version	Summary/License	Platforms
<a href="#">sparklyr</a>	1.0.0	R interface to Apache Spark, a fast and general engine for big data processing, see < <a href="http://spark.apache.org">http://spark.apache.org</a> >. This package supports connecting to local and remote Apache Spark clusters, provides a ‘dplyr’ compatible back-end, and provides an interface to Spark’s built-in machine learning algorithms. / Apache License 2.0   file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">sparsem</a>	1.77	Some basic linear algebra functionality for sparse matrices is provided: including Cholesky decomposition and backsolving as well as standard R subsetting and Kronecker products. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">spatial</a>	7.3_1	Functions for kriging and point pattern analysis. / GPL-2   GPL-3	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">spdata</a>	0.3.0	Diverse spatial datasets for demonstrating, benchmarking and teaching spatial data analysis. It includes R data of class sf (defined by the package ‘sf’), Spatial (‘sp’), and nb (‘spdep’). Unlike other spatial data packages such as ‘rnat-uralearth’ and ‘maps’, it also contains data stored in a range of file formats including GeoJSON, ESRI Shapefile and GeoPackage. Some of the datasets are designed to illustrate specific analysis techniques. cycle_hire() and cycle_hire_osm(), for example, is designed to illustrate point pattern analysis techniques. / CC0	linux-32, linux-64, noarch, osx-64, win-32, win-64

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Table 52 – continued from previous page

Name	Version	Summary/License	Platforms
<a href="#">squarem</a>	2017.10.1	Algorithms for accelerating the convergence of slow, monotone sequences from smooth, contraction mapping such as the EM algorithm. It can be used to accelerate any smooth, linearly convergent acceleration scheme. A tutorial style introduction to this package is available in a vignette on the CRAN download page or, when the package is loaded in an R session, with vignette(SQUAREM). / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">stabledist</a>	0.7_1	Density, Probability and Quantile functions, and random number generation for (skew) stable distributions, using the parametrizations of Nolan. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">stanheaders</a>	2.18.1	The C header files of the Stan project are provided by this package, but it contains no R code or function documentation. There is a shared object containing part of the 'CVODES' library, but it is not accessible from R. 'StanHeaders' is only useful for developers who want to utilize the 'LinkingTo' directive of their package's DESCRIPTION file to build on the Stan library without incurring unnecessary dependencies. The Stan project develops a probabilistic programming language that implements full or approximate Bayesian statistical inference via Markov Chain Monte Carlo or 'variational' methods and implements (optionally penalized) maximum likelihood estimation via optimization. The Stan library includes an advanced automatic differentiation scheme, 'templated' statistical and linear algebra functions that can handle the automatically 'differentiable' scalar types (and doubles, 'ints', etc.), and a parser for the Stan language. The 'rstan' package provides user-facing R functions to parse, compile, test, estimate, and analyze Stan models. / BSD_3_clause file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">stopwords</a>	0.9.0	Provides multiple sources of stopwords, for use in text analysis and natural language processing. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64

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Table 52 – continued from previous page

Name	Version	Summary/License	Platforms
<code>stringdist</code>	0.9.5	Implements an approximate string matching version of R's native 'match' function. Can calculate various string distances based on edits (Damerau-Levenshtein, Hamming, Levenshtein, optimal sting alignment), qgrams (q-gram, cosine, jaccard distance) or heuristic metrics (Jaro, Jaro-Winkler). An implementation of soundex is provided as well. Distances can be computed between character vectors while taking proper care of encoding or between integer vectors representing generic sequences. This package is built for speed and runs in parallel by using 'openMP'. An API for C or C is exposed as well. / GPL-3	linux-32, linux-64, osx-64, win-32, win-64
<code>stringi</code>	1.4.3	Fast, correct, consistent, portable, as well as convenient character string/text processing in every locale and any native encoding. Owing to the use of the 'ICU' (International Components for Unicode) library, the package provides 'R' users with platform-independent functions known to 'Java', 'Perl', 'Python', 'PHP', and 'Ruby' programmers. Available features include: pattern searching (e.g., with 'Java'-like regular expressions or the 'Unicode' collation algorithm), random string generation, case mapping, string transliteration, concatenation, Unicode normalization, date-time formatting and parsing, and many more. / file LICENSE (FOSS)	linux-32, linux-64, osx-64, win-32, win-64
<code>stringr</code>	1.4.0	A consistent, simple and easy to use set of wrappers around the fantastic 'stringi' package. All function and argument names (and positions) are consistent, all functions deal with NA's and zero length vectors in the same way, and the output from one function is easy to feed into the input of another. / GPL-2   file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<code>strucchange</code>	1.5_1	Testing, monitoring and dating structural changes in (linear) regression models. strucchange features tests/methods from the generalized fluctuation test framework as well as from the F test (Chow test) framework. This includes methods to fit, plot and test fluctuation processes (e.g., CUSUM, MOSUM, recursive/moving estimates) and F statistics, respectively. It is possible to monitor incoming data online using fluctuation processes. Finally, the breakpoints in regression models with structural changes can be estimated together with confidence intervals. Emphasis is always given to methods for visualizing the data. / GPL-2   GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64

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Table 52 – continued from previous page

Name	Version	Summary/License	Platforms
<a href="#">suppdists</a>	1.1_9.4	Ten distributions supplementing those built into R. Inverse Gauss, Kruskal-Wallis, Kendall's Tau, Friedman's chi squared, Spearman's rho, maximum F ratio, the Pearson product moment correlation coefficient, Johnson distributions, normal scores and generalized hypergeometric distributions. In addition two random number generators of George Marsaglia are included. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">survival</a>	2.44_1	Contains the core survival analysis routines, including definition of Surv objects, Kaplan-Meier and Aalen-Johansen (multi-state) curves, Cox models, and parametric accelerated failure time models. / LGPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">sys</a>	3.2	Drop-in replacements for the base system2() function with fine control and consistent behavior across platforms. Supports clean interruption, timeout, background tasks, and streaming STDIN / STDOUT / STDERR over binary or text connections. Arguments on Windows automatically get encoded and quoted to work on different locales. / MIT file LICENSE	linux-64, osx-64, win-32, win-64

Table 53: T

Name	Version	Summary/License	Platforms
<a href="#">tensorflow</a>	1.13.1	Interface to ‘TensorFlow’ < <a href="https://www.tensorflow.org/">https://www.tensorflow.org/</a> >, an open source software library for numerical computation using data flow graphs. Nodes in the graph represent mathematical operations, while the graph edges represent the multidimensional data arrays (tensors) communicated between them. The flexible architecture allows you to deploy computation to one or more ‘CPUs’ or ‘GPUs’ in a desktop, server, or mobile device with a single ‘API’. ‘TensorFlow’ was originally developed by researchers and engineers working on the Google Brain Team within Google’s Machine Intelligence research organization for the purposes of conducting machine learning and deep neural networks research, but the system is general enough to be applicable in a wide variety of other domains as well. / Apache License 2.0	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">testit</a>	0.9	Provides two convenience functions <code>assert()</code> and <code>test_pkg()</code> to facilitate testing R packages. / GPL	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">testthat</a>	2.1.1	Software testing is important, but, in part because it is frustrating and boring, many of us avoid it. ‘testthat’ is a testing framework for R that is easy learn and use, and integrates with your existing ‘workflow’. / MIT file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">tfruns</a>	1.4	Create and manage unique directories for each ‘TensorFlow’ training run. Provides a unique, time stamped directory for each run along with functions to retrieve the directory of the latest run or latest several runs. / Apache License 2.0	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">th.data</a>	1.0_10	Contains data sets used in other packages Torsten Hothorn maintains. / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
<b>2392</b>		<b>Chapter 4. Anaconda Cloud</b>	
<a href="#">threejs</a>	0.3.1	Create interactive 3D scatter plots, network plots, and globes using the ‘three.js’ visualization library (< <a href="https://threejs.org/">https://threejs.org/</a> >). / MIT file LICENSE	linux-32, linux-



Table 54: U

Name	Version	Summary/License	Platforms
udunits2	0.13	Provides simple bindings to Unidata's udunits library. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
units	0.6_2	Support for measurement units in R vectors, matrices and arrays: automatic propagation, conversion, derivation and simplification of units; raising errors in case of unit incompatibility. Compatible with the POSIXct, Date and diff-time classes. Uses the UNIDATA udunits library and unit database for unit compatibility checking and conversion. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
urca	1.3_0	Unit root and cointegration tests encountered in applied econometric analysis are implemented. / GPL (>= 2)	linux-32, linux-64, osx-64, win-32, win-64
uroot	2.0_9	Seasonal unit roots and seasonal stability tests. P-values based on response surface regressions are available for both tests. P-values based on bootstrap are available for seasonal unit root tests. A parallel implementation of the bootstrap method requires a CUDA capable GPU with compute capability >= 3.0, otherwise a debugging version fully coded in R is used. / GPL-2	linux-32, linux-64, osx-64, win-32, win-64
usethis	1.5.0	Automate package and project setup tasks that are otherwise performed manually. This includes setting up unit testing, test coverage, continuous integration, Git, 'GitHub', licenses, 'Rcpp', 'RStudio' projects, and more. / GPL-3	noarch
utf8	1.1.4	Process and print 'UTF-8' encoded international text (Unicode). Input, validate, normalize, encode, format, and display. / Apache License (== 2.0)   file LICENSE	linux-32, linux-64, osx-64, win-32, win-64
uuid	0.1_2	Tools for generating and handling of UUIDs (Universally Unique Identifiers). / MIT file LICENSE	linux-32, linux-64,

Table 55: V

Name	Version	Summary/License	Platforms
<a href="#">vars</a>	1.5_3	Estimation, lag selection, diagnostic testing, forecasting, causality analysis, forecast error variance decomposition and impulse response functions of VAR models and estimation of SVAR and SVEC models. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">vgam</a>	1.1_1	An implementation of about 6 major classes of statistical regression models. The central algorithm is Fisher scoring and iterative reweighted least squares. At the heart of this package are the vector generalized linear and additive model (VGLM/VGAM) classes. VGLMs can be loosely thought of as multivariate GLMs. VGAMs are data-driven VGLMs that use smoothing. The book Vector Generalized Linear and Additive Models: With an Implementation in R (Yee, 2015) <DOI:10.1007/978-1-4939-2818-7> gives details of the statistical framework and the package. Currently only fixed-effects models are implemented. Many (150) models and distributions are estimated by maximum likelihood estimation (MLE) or penalized MLE. The other classes are RR-VGLMs (reduced-rank VGLMs), quadratic RR-VGLMs, reduced-rank VGAMs, RCIMs (row-column interaction models)—these classes perform constrained and unconstrained quadratic ordination (CQO/UQO) models in ecology, as well as constrained additive ordination (CAO). Note that these functions are subject to change; see the NEWS and ChangeLog files for latest changes. / GPL-3	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">viridis</a>	0.5.1	Implementation of the ‘viridis’ - the default -, ‘magma’, ‘plasma’, ‘inferno’, and ‘cividis’ color maps for ‘R’. ‘viridis’, ‘magma’, ‘plasma’, and ‘inferno’ are ported from ‘matplotlib’ < <a href="http://matplotlib.org/">http://matplotlib.org/</a> >, a popular plotting library for ‘python’. ‘cividis’, was developed by Jamie R. Nuñez and Sean M. Colby. These color maps are designed in such a way that they will analytically be perfectly perceptually-uniform, both in regular form and also when converted to black-and-white. They are also designed to be perceived by readers with the most common form of color blindness (all color maps in this package) and color vision deficiency (‘cividis’ only). / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">viridislite</a>	0.3.0	Implementation of the ‘viridis’ - the default -, ‘magma’, ‘plasma’, ‘inferno’, and ‘cividis’ color maps for ‘R’. ‘viridis’, ‘magma’, ‘plasma’, and ‘inferno’ are ported from ‘matplotlib’ < <a href="http://matplotlib.org/">http://matplotlib.org/</a> >, a popular plotting library for ‘python’. ‘cividis’, was developed by Jamie R. Nuñez and Sean M. Colby. These color maps are designed in such a way that they will analytically be perfectly perceptually-uniform, both in regular form and also when converted to black-and-white. They are also designed to be perceived by readers with the most common form of color blindness (all color maps in this package) and color vision deficiency (‘cividis’ only). This is the ‘lite’ version of the more complete ‘viridis’ package that can be found at < <a href="https://cran.r-project.org/package=viridis">https://cran.r-project.org/package=viridis</a> >. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">visnetwork</a>	2.0.6	Provides an R interface to the ‘vis.js’ JavaScript charting library. It allows an interactive visualization of networks. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-32, win-64
2394		Chapter 4. Anaconda Cloud	linux-32, linux-64, noarch, osx-64, win-32, win-64

Table 56: W

Name	Version	Summary/License	Platforms
<a href="#">weatherdata</a>	0.5.0	Functions that help in fetching weather data from websites. Given a location and a date range, these functions help fetch weather data (temperature, pressure etc.) for any weather related analysis. / GPL	linux-32, linux-64, osx-64, win-32, win-64
<a href="#">webshot</a>	0.5.1	Takes screenshots of web pages, including Shiny applications and R Markdown documents. / GPL-2	linux-64, noarch, osx-64, win-32, win-64
<a href="#">whisker</a>	0.3.2	logicless templating, reuse templates in many programming languages including R / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
<a href="#">withr</a>	2.1.2	A set of functions to run code ‘with’ safely and temporarily modified global state. Many of these functions were originally a part of the ‘devtools’ package, this provides a simple package with limited dependencies to provide access to these functions. / GPL (>= 2)	linux-32, linux-64, noarch, osx-64, win-32, win-64

Table 57: X

Name	Version	Summary/License	Platforms
x13binary	1.1.39	The US Census Bureau provides a seasonal adjustment program now called ‘X-13ARIMA-SEATS’ building on both earlier programs called X-11 and X-12 as well as the SEATS program by the Bank of Spain. The US Census Bureau offers both source and binary versions – which this package integrates for use by other R packages. / file LICENSE	linux-64, noarch, osx-64, win-32, win-64
xfun	0.6	Miscellaneous functions commonly used in other packages maintained by ‘Yihui Xie’. / MIT file LICENSE	linux-64, noarch, osx-64, win-32, win-64
xgboost	0.80	eXtreme Gradient Boosting / Apache-2	linux-32, linux-64, osx-64, win-32, win-64
xgboost-cpu	0.80	None / None	linux-64, osx-64, win-64
xgboost-gpu	0.80	None / None	linux-64
xlsx	0.6.1	Provide R functions to read/write/format Excel 2007 and Excel 97/2000/XP/2003 file formats. / GPL-3	linux-32, linux-64, noarch, osx-64, win-32, win-64
xlsxjars	0.6.1	The xlsxjars package collects all the external jars required for the xlsx package. This release corresponds to POI 3.10.1. / GPL-3	linux-32, linux-64, osx-64, win-32, win-64
2396			linux-32, linux-64, noarch, osx-64, win-32, win-64

Table 58: Y

Name	Version	Summary/License	Platforms
yaml	2.2.0	Implements the ‘libyaml’ ‘YAML’ 1.1 parser and emitter (< <a href="http://pyyaml.org/wiki/LibYAML">http://pyyaml.org/wiki/LibYAML</a> >) for R. / BSD_3_clause file LICENSE	linux-32, linux-64, osx-64, win-32, win-64

Table 59: Z

Name	Version	Summary/License	Platforms
zeallot	0.1.0	Provides a %<-% operator to perform multiple, unpacking, and destructuring assignment in R. The operator unpacks the right-hand side of an assignment into multiple values and assigns these values to variables on the left-hand side of the assignment. / MIT file LICENSE	linux-32, linux-64, noarch, osx-64, win-64
zip	2.0.1	Cross-Platform ‘zip’ Compression Library. A replacement for the ‘zip’ function, that does not require any additional external tools on any platform. / CC0	linux-64, osx-64, win-32, win-64
zoo	1.8_5	An S3 class with methods for totally ordered indexed observations. It is particularly aimed at irregular time series of numeric vectors/matrices and factors. zoo’s key design goals are independence of a particular index/date/time class and consistency with ts and base R by providing methods to extend standard generics. / GPL-2   GPL-3	linux-32, linux-64, osx-64, win-32, win-64

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You can install offline copies of both [docs.anaconda.com](#) and [enterprise-docs.anaconda.com](#) by installing the conda package `anaconda-docs`:

```
conda install anaconda-docs
```

This will install a PDF copy and a zipped HTML copy of each site into the directory `share/doc` for your currently active conda environment.

EXAMPLE: If your conda install directory is `~/miniconda3`, and your environment is named `my-env`, the documentation will be installed into `~/miniconda3/envs/my-env/share/doc/`.

### Open-source package documentation downloads

You can download a package of documentation for many of Anaconda’s open-source packages with this command:

```
conda install anaconda-oss-docs
```

This will install documentation for the open-source packages into the directory `share/doc/anaconda-oss` for your currently active conda environment.

EXAMPLE: If your conda install directory is `~/miniconda3`, and your environment is named `my-env`, the documentation will be installed into `~/miniconda3/envs/my-env/share/doc/anaconda-oss`.

This bundle includes documentation for these packages:

- Python
- NumPy

- SciPy
- pandas
- Conda
- Blaze
- Bleach
- botocore
- Certifi
- cryptography
- CFFI
- coverage
- Cython
- Dask
- Dask.distributed
- dateutil
- greenlet
- h5py
- html5lib
- imageio
- IPython
- Jinja
- Jupyter
- JupyterLab
- Jupyter Notebook
- llvmlite
- msgpack
- Odo
- OpenSSL
- Pillow
- pip
- psutil
- pyOpenSSL
- python-tblib
- PyWavelets
- PyZMQ
- Requests
- ruamel.yaml

- Setuptools
- six
- toolz
- Tornado
- Traitlets
- wheel
- Zict

## Old package lists

You can download previous versions of Anaconda from the [Anaconda installer archive](#).

Older versions of packages can usually be downloaded from the [package repository](#) or from <https://anaconda.org/anaconda/PackageName>.

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**Note:** Replace `PackageName` with the name of the desired package.

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EXAMPLE: At <https://anaconda.org/anaconda/beautifulsoup4>, previous versions of beautifulsoup4 are shown on the **Files** tab.

You can also search for packages from the command line with `conda search PackageName`.

Packages included in previous versions of Anaconda:

## Packages included in Anaconda v.1.0

<ul style="list-style-type: none"> <li>• anaconda launcher</li> <li>• bitarray 0.8.0</li> <li>• bitey</li> <li>• cython 0.16</li> <li>• dateutil 1.5</li> <li>• disco 0.4.2 (Linux only)</li> <li>• erlang (Linux only)</li> <li>• flask 0.9</li> <li>• gevent 0.13.7</li> <li>• gevent-websocket 0.3.6</li> <li>• gevent_zeromq 0.2.5</li> <li>• greenlet0.4.0</li> <li>• h5py 2.0.1</li> <li>• hdf5 1.8.9</li> <li>• PIL 1.1.7</li> </ul>	<ul style="list-style-type: none"> <li>• iopro 1.0 *</li> <li>• ipython 0.13</li> <li>• jinja2 2.6</li> <li>• llvm 3.1</li> <li>• llvmpy 0.8.2.dev</li> <li>• matplotlib 1.1.1</li> <li>• mpi4py 1.3</li> <li>• mpich2 1.4.1p1</li> <li>• networkx 1.7</li> <li>• nose 1.1.2</li> <li>• numba 0.1.dev</li> <li>• numbapro 1.0 *</li> <li>• numexpr 2.0.1</li> <li>• numpy 1.7.dev</li> <li>• opencv 2.4.2</li> </ul>	<ul style="list-style-type: none"> <li>• openssl 1.0.1c</li> <li>• pandas 0.8.1</li> <li>• pip 1.1</li> <li>• pixman 0.26.2</li> <li>• py2cairo 1.10.0</li> <li>• pycurl 7.19.0</li> <li>• pygments 1.5</li> <li>• pysal 1.4.0</li> <li>• pysam 0.6</li> <li>• pytables 2.4.0</li> <li>• python 2.7.3</li> <li>• pytz 2012c</li> <li>• pyyaml 3.10</li> <li>• pyzmq 2.2.0</li> </ul>	<ul style="list-style-type: none"> <li>• redis 2.4.15 (Linux only)</li> <li>• redis py-2.4.13</li> <li>• requests 0.13.5</li> <li>• scikit-learn 0.11</li> <li>• scikits-image 0.6.1</li> <li>• scipy 0.11.0rc2</li> <li>• sqlalchemy 0.7.8</li> <li>• sqlite 3.7.13</li> <li>• statsmodels 0.4.3</li> <li>• sympy 0.7.1</li> <li>• theano 0.5.0</li> <li>• tornado 2.3</li> <li>• werkzeug 0.8.3</li> <li>• wiseRF *</li> </ul>
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\* Included in Anaconda Pro Only



# CONTINUUM<sup>®</sup>

## ANALYTICS

## Packages included in Anaconda v.1.1

• anaconda launcher	• iopro 1.0 *	• openssl 1.0.1c	• redis 2.4.15 (Linux only)
• bitarray 0.8.0	• ipython 0.13	• pandas 0.8.1	• redis py-2.4.13
• bitey	• jinja2 2.6	• pip 1.1	• requests 0.13.5
• cython 0.16	• llvm 3.1	• pixman 0.26.2	• scikit-learn 0.11
• dateutil 1.5	• llvmpy 0.8.2.dev	• py2cairo 1.10.0	• scikits-image 0.6.1
• disco 0.4.2 (Linux only)	• matplotlib 1.1.1	• pycurl 7.19.0	• scipy 0.11.0rc2
• erlang (Linux only)	• mpi4py 1.3	• pygments 1.5	• spyder
• flask 0.9	• mpich2 1.4.1p1	• pysal 1.4.0	• sqlalchemy 0.7.8
• gevent 0.13.7	• networkx 1.7	• pysam 0.6	• sqlite 3.7.13
• gevent-websocket 0.3.6	• nose 1.1.2	• pytables 2.4.0	• statsmodels 0.4.3
• gevent_zeromq 0.2.5	• numba 0.1.dev	• python 2.7.3	• sympy 0.7.1
• greenlet 0.4.0	• numbapro 1.0 *	• pytz 2012c	• theano 0.5.0
• h5py 2.0.1	• numexpr 2.0.1	• pyyaml 3.10	• tornado 2.3
• hdf5 1.8.9	• numpy 1.7.dev	• pyzmq 2.2.0	• werkzeug 0.8.3
• PIL 1.1.7	• opencv 2.4.2		• wiseRF *

\* Included in Anaconda Pro Only

**Note:** Packages may vary on different platforms.

## Packages included in Anaconda 1.2.1

<ul style="list-style-type: none"> <li>• bitarray 0.8.0</li> <li>• bitey 0.0</li> <li>• boto 2.6.0</li> <li>• cairo 1.12.2 <i>L</i></li> <li>• chaco 4.2.1.dev <i>M</i></li> <li>• conda 1.2.1</li> <li>• cython 0.17.1</li> <li>• dateutil 1.5</li> <li>• disco 0.4.2 <i>L</i></li> <li>• distribute 0.6.30</li> <li>• docutils 0.9.1</li> <li>• erlang R15B01 <i>L</i></li> <li>• flask 0.9</li> <li>• freetype 2.4.10</li> <li>• gevent 0.13.7</li> <li>• gevent-websocket 0.3.6</li> <li>• gevent_zeromq 0.2.5</li> <li>• greenlet 0.4.0</li> <li>• grin 1.2.1</li> <li>• h5py 2.1.0</li> <li>• hdf5 1.8.9</li> </ul>	<ul style="list-style-type: none"> <li>• imaging 1.1.7</li> <li>• iopro 1.2.2 <i>P</i></li> <li>• ipython 0.13.1</li> <li>• jinja2 2.6</li> <li>• jpeg 8d</li> <li>• libevent 2.0.20</li> <li>• libpng 1.5.13</li> <li>• llvm 3.1</li> <li>• llvmpy 0.9</li> <li>• matplotlib 1.2.0</li> <li>• mdp 3.3</li> <li>• meta 0.4.2.dev</li> <li>• mingw 4.7 <i>W</i></li> <li>• mkl 10.3 <i>LP</i></li> <li>• mpi4py 1.3 <i>L</i></li> <li>• mpich2 1.4.1p1 <i>L</i></li> <li>• networkx 1.7</li> <li>• nltk 2.0.3</li> <li>• nose 1.1.2</li> <li>• numba 0.3.2</li> <li>• numbapro 0.7.3 <i>P</i></li> </ul>	<ul style="list-style-type: none"> <li>• numexpr 2.0.1</li> <li>• numpy 1.6.2 <i>W</i></li> <li>• numpy 1.7.0b2 <i>U</i></li> <li>• opencv 2.4.2 <i>L</i></li> <li>• pandas 0.9.0</li> <li>• pip 1.2.1</li> <li>• psutil 0.6.1</li> <li>• py 1.4.12</li> <li>• py2cairo 1.10.0 <i>L</i></li> <li>• pyaudio 0.2.6 <i>M</i></li> <li>• pycurl 7.19.0</li> <li>• pyflakes 0.5.0</li> <li>• pyreadline 1.7.1 <i>W</i></li> <li>• pysal 1.4.0</li> <li>• pysam 0.6 <i>U</i></li> <li>• pyside 1.1.2</li> <li>• pytables 2.4.0</li> <li>• pytest 2.3.3</li> <li>• python 2.7.3</li> <li>• pytz 2012d</li> </ul>	<ul style="list-style-type: none"> <li>• pyyaml 3.10</li> <li>• pyzmq 2.2.0.1</li> <li>• qt 4.7.4</li> <li>• redis 2.4.15 <i>L</i></li> <li>• redis-py 2.4.13 <i>L</i></li> <li>• requests 0.13.9</li> <li>• scikit-learn 0.11</li> <li>• scikits-image 0.6.1</li> <li>• scipy 0.11.0</li> <li>• sphinx 1.1.3</li> <li>• spyder 2.1.11</li> <li>• sqlalchemy 0.7.8</li> <li>• statsmodels 0.4.3</li> <li>• sympy 0.7.1</li> <li>• theano 0.5.0 <i>L</i></li> <li>• tornado 2.3</li> <li>• werkzeug 0.8.3</li> <li>• wisef 1.1 <i>UP</i></li> <li>• yaml 0.1.4</li> <li>• zeromq 2.2.0</li> <li>• zlib 1.2.7</li> </ul>
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*U*: Unix - *L*: Linux - *M*: macOS - *W*: Windows - *P*: not in CE

## Packages included in Anaconda 1.3.1

<ul style="list-style-type: none"> <li>• biopython 1.60</li> <li>• bitarray 0.8.0</li> <li>• bitey 0.0</li> <li>• boto 2.7.0</li> <li>• cairo 1.12.2 <i>L</i></li> <li>• conda 1.3.5</li> <li>• cubes 0.10.1</li> <li>• cython 0.17.4</li> <li>• dateutil 1.5</li> <li>• disco 0.4.4 <i>L</i></li> <li>• distribute 0.6.34</li> <li>• docutils 0.10</li> <li>• erlang R15B01 <i>L</i></li> <li>• flask 0.9</li> <li>• freetype 2.4.10</li> <li>• gdata 2.0.17</li> <li>• gevent 0.13.8</li> <li>• gevent-websocket 0.3.6</li> <li>• gevent_zeromq 0.2.5</li> <li>• googlecl 0.9.12</li> <li>• greenlet 0.4.0</li> <li>• grin 1.2.1</li> </ul>	<ul style="list-style-type: none"> <li>• h5py 2.1.1</li> <li>• hdf5 1.8.9</li> <li>• imaging 1.1.7</li> <li>• iopro 1.3.2 <i>P</i></li> <li>• ipython 0.13.1</li> <li>• jinja2 2.6</li> <li>• libevent 2.0.20</li> <li>• libnvvm 1.0 <i>P</i></li> <li>• libpng 1.5.13</li> <li>• llvm 3.2</li> <li>• llvmpy 0.10.2</li> <li>• matplotlib 1.2.0</li> <li>• mdp 3.3</li> <li>• meta 0.4.2.dev</li> <li>• mingw 4.7 <i>W</i></li> <li>• mkl 10.3 <i>LP</i></li> <li>• mpi4py 1.3 <i>L</i></li> <li>• mpich2 1.4.1p1 <i>L</i></li> <li>• networkx 1.7</li> <li>• nltk 2.0.4</li> <li>• nose 1.2.1</li> <li>• numba 0.6.0</li> </ul>	<ul style="list-style-type: none"> <li>• numbapro 0.8.1 <i>P</i></li> <li>• numexpr 2.0.1</li> <li>• numpy 1.6.2 <i>W</i></li> <li>• numpy 1.7.0rc1 <i>U</i></li> <li>• opencv 2.4.2 <i>L</i></li> <li>• pandas 0.10.1</li> <li>• pip 1.2.1</li> <li>• ply 3.4</li> <li>• psutil 0.6.1</li> <li>• py 1.4.12</li> <li>• py2cairo 1.10.0 <i>L</i></li> <li>• pyaudio 0.2.7 <i>M</i></li> <li>• pycrypto 2.6</li> <li>• pycurl 7.19.0</li> <li>• pyflakes 0.5.0</li> <li>• pygments 1.5</li> <li>• pyparsing 1.5.6</li> <li>• pysal 1.4.0</li> <li>• pysam 0.6 <i>U</i></li> <li>• pyside 1.1.2</li> <li>• pytables 2.4.0</li> <li>• pytest 2.3.4</li> </ul>	<ul style="list-style-type: none"> <li>• python 2.7.3</li> <li>• pytz 2012d</li> <li>• pyyaml 3.10</li> <li>• pyzmq 2.2.0.1</li> <li>• qt 4.7.4</li> <li>• redis 2.6.9 <i>U</i></li> <li>• redis-py 2.7.2 <i>U</i></li> <li>• requests 0.13.9</li> <li>• scikit-learn 0.13</li> <li>• scikits-image 0.7.1</li> <li>• scipy 0.11.0</li> <li>• sphinx 1.1.3</li> <li>• spyder 2.1.13</li> <li>• sqlalchemy 0.7.8</li> <li>• statsmodels 0.4.3</li> <li>• sympy 0.7.1</li> <li>• theano 0.5.0 <i>L</i></li> <li>• tornado 2.4.1</li> <li>• werkzeug 0.8.3</li> <li>• wisef 1.1 <i>UP</i></li> <li>• zeromq 2.2.0</li> <li>• zlib 1.2.7</li> </ul>
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*U*: Unix - *L*: Linux - *M*: macOS - *W*: Windows - *P*: not in CE

## Packages included in Anaconda 1.4.0

**Python 2.7 (what is included in the installers):**

<ul style="list-style-type: none"> <li>• astropy 0.2</li> <li>• biopython 1.60</li> <li>• bitarray 0.8.0</li> <li>• bitey 0.0</li> <li>• boto 2.8.0</li> <li>• cairo 1.12.2 <i>L</i></li> <li>• conda 1.4.4</li> <li>• cubes 0.10.2</li> <li>• cython 0.18</li> <li>• dateutil 2.1</li> <li>• disco 0.4.4 <i>L</i></li> <li>• distribute 0.6.34</li> <li>• docutils 0.10</li> <li>• erlang R15B01 <i>L</i></li> <li>• flask 0.9</li> <li>• freetype 2.4.10</li> <li>• gdata 2.0.17</li> <li>• gevent 0.13.8</li> <li>• gevent-websocket 0.3.6</li> <li>• gevent_zeromq 0.2.5</li> <li>• googlecl 0.9.12</li> <li>• greenlet 0.4.0</li> </ul>	<ul style="list-style-type: none"> <li>• grin 1.2.1</li> <li>• h5py 2.1.1</li> <li>• hdf5 1.8.9</li> <li>• imaging 1.1.7</li> <li>• ipython 0.13.1</li> <li>• jinja2 2.6</li> <li>• libevent 2.0.20</li> <li>• libpng 1.5.13</li> <li>• llvm 3.2</li> <li>• llvmpy 0.11.1</li> <li>• lxml 3.0.2</li> <li>• matplotlib 1.2.0</li> <li>• mdp 3.3</li> <li>• menuinst 1.0.0 <i>W</i></li> <li>• meta 0.4.2.dev</li> <li>• mingw 4.7 <i>W</i></li> <li>• mpi4py 1.3 <i>L</i></li> <li>• mpich2 1.4.1p1 <i>L</i></li> <li>• networkx 1.7</li> <li>• nltk 2.0.4</li> <li>• nose 1.2.1</li> <li>• numba 0.7.0</li> </ul>	<ul style="list-style-type: none"> <li>• numexpr 2.0.1</li> <li>• numpy 1.7.0</li> <li>• opencv 2.4.2 <i>L</i></li> <li>• pandas 0.10.1</li> <li>• pip 1.2.1</li> <li>• ply 3.4</li> <li>• psutil 0.6.1</li> <li>• py 1.4.12</li> <li>• py2cairo 1.10.0 <i>L</i></li> <li>• pyaudio 0.2.7 <i>M</i></li> <li>• pycparser 2.9.1</li> <li>• pycrypto 2.6</li> <li>• pycurl 7.19.0 <i>LM</i></li> <li>• pyflakes 0.6.1</li> <li>• pygments 1.6</li> <li>• pyparsing 1.5.6</li> <li>• pysal 1.5.0</li> <li>• pysam 0.6 <i>LM</i></li> <li>• pyside 1.1.2</li> <li>• pytables 2.4.0</li> <li>• pytest 2.3.4</li> <li>• python 2.7.3</li> </ul>	<ul style="list-style-type: none"> <li>• pytz 2012j</li> <li>• pyyaml 3.10</li> <li>• pyzmq 2.2.0.1</li> <li>• qt 4.7.4</li> <li>• redis 2.6.9 <i>LM</i></li> <li>• redis-py 2.7.2 <i>LM</i></li> <li>• requests 0.13.9</li> <li>• scikit-image 0.8.2</li> <li>• scikit-learn 0.13</li> <li>• scipy 0.11.0</li> <li>• six 1.2.0</li> <li>• sphinx 1.1.3</li> <li>• spyder 2.1.13</li> <li>• sqlalchemy 0.7.8</li> <li>• statsmodels 0.4.3</li> <li>• sympy 0.7.1</li> <li>• theano 0.5.0 <i>L</i></li> <li>• tornado 2.4.1</li> <li>• werkzeug 0.8.3</li> <li>• xlrd 0.9.0</li> <li>• xlwt 0.7.4</li> <li>• zlib 1.2.7</li> </ul>
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Only available on: *L* (Linux) - *M* (macOS) - *W* (Windows)

**Python 3.3 (available through conda):**

<ul style="list-style-type: none"> <li>• astropy 0.2</li> <li>• bitarray 0.8.0</li> <li>• cython 0.18</li> <li>• dateutil 2.1</li> <li>• distribute 0.6.34</li> <li>• docutils 0.10</li> <li>• freetype 2.4.10</li> <li>• greenlet 0.4.0</li> <li>• ipython 0.13.1</li> <li>• jinja2 2.6</li> <li>• libpng 1.5.13</li> </ul>	<ul style="list-style-type: none"> <li>• llvm 3.2</li> <li>• llvmpy 0.11.1</li> <li>• lxml 3.0.2</li> <li>• matplotlib 1.2.0</li> <li>• mdp 3.3</li> <li>• mingw 4.7 <i>W</i></li> <li>• networkx 1.7</li> <li>• nose 1.2.1</li> <li>• numpy 1.7.0</li> <li>• pandas 0.10.1 <i>LM</i></li> <li>• pip 1.2.1</li> </ul>	<ul style="list-style-type: none"> <li>• ply 3.4</li> <li>• psutil 0.6.1</li> <li>• pycparser 2.9.1</li> <li>• pycrypto 2.6</li> <li>• pyflakes 0.6.1</li> <li>• pygments 1.6</li> <li>• python 3.3.0</li> <li>• pytz 2012j</li> <li>• pyyaml 3.10</li> <li>• pyzmq 2.2.0.1</li> <li>• requests 0.13.9</li> </ul>	<ul style="list-style-type: none"> <li>• scikit-image 0.8.2 <i>LM</i></li> <li>• scipy 0.11.0 <i>LM</i></li> <li>• six 1.2.0</li> <li>• sphinx 1.1.3</li> <li>• sqlalchemy 0.7.8</li> <li>• tornado 2.4.1</li> <li>• xlrd 0.9.0</li> <li>• zlib 1.2.7</li> </ul>
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**Python 2.6 (available through conda):**

<ul style="list-style-type: none"><li>• argparse 1.2.1</li><li>• astropy 0.2</li><li>• biopython 1.60</li><li>• bitarray 0.8.0</li><li>• boto 2.8.0</li><li>• cairo 1.12.2 <i>L</i></li><li>• cython 0.18</li><li>• dateutil 2.1</li><li>• disco 0.4.4 <i>L</i></li><li>• distribute 0.6.34</li><li>• docutils 0.10</li><li>• erlang R15B01 <i>L</i></li><li>• flask 0.9</li><li>• freetype 2.4.10</li><li>• gdata 2.0.17</li><li>• gevent 0.13.8</li><li>• gevent-websocket 0.3.6</li><li>• gevent_zeromq 0.2.5</li><li>• googlecl 0.9.12</li><li>• greenlet 0.4.0</li></ul>	<ul style="list-style-type: none"><li>• grin 1.2.1</li><li>• h5py 2.1.1</li><li>• hdf5 1.8.9</li><li>• imaging 1.1.7</li><li>• ipython 0.13.1</li><li>• jinja2 2.6</li><li>• libevent 2.0.20</li><li>• libpng 1.5.13</li><li>• llvm 3.2</li><li>• llvmpy 0.11.1</li><li>• lxml 3.0.2</li><li>• matplotlib 1.2.0 <i>LM</i></li><li>• mdp 3.3</li><li>• mingw 4.7 <i>W</i></li><li>• mpi4py 1.3 <i>L</i></li><li>• mpich2 1.4.1p1 <i>L</i></li><li>• networkx 1.7</li><li>• nltk 2.0.4</li><li>• nose 1.2.1</li><li>• numba 0.7.0</li></ul>	<ul style="list-style-type: none"><li>• numexpr 2.0.1</li><li>• numpy 1.7.0</li><li>• opencv 2.4.2 <i>L</i></li><li>• pandas 0.10.1</li><li>• pip 1.2.1</li><li>• ply 3.4</li><li>• psutil 0.6.1</li><li>• py 1.4.12</li><li>• py2cairo 1.10.0 <i>L</i></li><li>• pycparser 2.9.1</li><li>• pycrypto 2.6</li><li>• pycurl 7.19.0 <i>LM</i></li><li>• pyflakes 0.6.1</li><li>• pygments 1.6</li><li>• pyparsing 1.5.6</li><li>• pysam 0.6 <i>LM</i></li><li>• pytables 2.4.0 <i>LM</i></li><li>• pytest 2.3.4</li><li>• python 2.6.8</li><li>• pytz 2012j</li></ul>	<ul style="list-style-type: none"><li>• pyyaml 3.10</li><li>• pyzmq 2.2.0.1</li><li>• redis 2.6.9 <i>LM</i></li><li>• redis-py 2.7.2 <i>LM</i></li><li>• requests 0.13.9</li><li>• scikit-image 0.8.2</li><li>• scikit-learn 0.13</li><li>• scipy 0.11.0</li><li>• six 1.2.0</li><li>• sphinx 1.1.3</li><li>• sqlalchemy 0.7.8</li><li>• statsmodels 0.4.3</li><li>• sympy 0.7.1 <i>LM</i></li><li>• theano 0.5.0 <i>L</i></li><li>• tornado 2.4.1</li><li>• werkzeug 0.8.3</li><li>• xlrd 0.9.0</li><li>• xlwt 0.7.4</li><li>• zlib 1.2.7</li></ul>
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Only available on: *L* (Linux) - *M* (macOS) - *W* (Windows)

## Packages included in Anaconda 1.5.0

<ul style="list-style-type: none"> <li>• astropy 0.2.1</li> <li>• atom 0.2.3</li> <li>• biopython 1.61</li> <li>• bitarray 0.8.1</li> <li>• boto 2.9.2</li> <li>• cairo 1.12.2 <i>L</i></li> <li>• casuarious 1.1</li> <li>• conda 1.5.2</li> <li>• cubes 0.10.2</li> <li>• curl 7.30.0 <i>LM</i></li> <li>• cython 0.19</li> <li>• dateutil 2.1</li> <li>• disco 0.4.4 <i>L</i></li> <li>• distribute 0.6.36</li> <li>• docutils 0.10</li> <li>• dynd-python 0.3.0</li> <li>• enaml 0.7.6</li> <li>• erlang R15B01 <i>L</i></li> <li>• flask 0.9</li> <li>• freetype 2.4.10</li> <li>• gevent 0.13.8</li> <li>• gevent-websocket 0.3.6</li> <li>• gevent_zeromq 0.2.5</li> </ul>	<ul style="list-style-type: none"> <li>• greenlet 0.4.0</li> <li>• grin 1.2.1</li> <li>• h5py 2.1.1</li> <li>• hdf5 1.8.9</li> <li>• imaging 1.1.7</li> <li>• ipython 0.13.2</li> <li>• jinja2 2.6</li> <li>• libevent 2.0.20</li> <li>• libnetcdf 4.2.1.1 <i>LM</i></li> <li>• libpng 1.5.13</li> <li>• llvm 3.2</li> <li>• llvmpy 0.11.2</li> <li>• lxml 3.2.0</li> <li>• matplotlib 1.2.1</li> <li>• mdp 3.3</li> <li>• menuinst 1.0.0 <i>W</i></li> <li>• meta 0.4.2.dev</li> <li>• mingw 4.7 <i>W</i></li> <li>• mpi4py 1.3 <i>L</i></li> <li>• mpich2 1.4.1p1 <i>L</i></li> <li>• netcdf4 1.0.4 <i>LM</i></li> <li>• networkx 1.7</li> <li>• nltk 2.0.4</li> </ul>	<ul style="list-style-type: none"> <li>• nose 1.3.0</li> <li>• numba 0.8.1</li> <li>• numexpr 2.0.1</li> <li>• numpy 1.7.1</li> <li>• opencv 2.4.2 <i>L</i></li> <li>• pandas 0.11.0</li> <li>• pip 1.3.1</li> <li>• ply 3.4</li> <li>• psutil 0.7.1</li> <li>• py 1.4.12</li> <li>• py2cairo 1.10.0 <i>L</i></li> <li>• pyaudio 0.2.7 <i>M</i></li> <li>• pycosat 0.6.0</li> <li>• pycparser 2.9.1</li> <li>• pycrypto 2.6</li> <li>• pycurl 7.19.0 <i>LM</i></li> <li>• pyflakes 0.7.2</li> <li>• pygments 1.6</li> <li>• pyparsing 1.5.6</li> <li>• pysal 1.5.0</li> <li>• pysam 0.6 <i>LM</i></li> <li>• pyside 1.1.2</li> <li>• pytables 2.4.0</li> </ul>	<ul style="list-style-type: none"> <li>• pytest 2.3.4</li> <li>• python 2.7.4</li> <li>• pytz 2013b</li> <li>• pyyaml 3.10</li> <li>• pyzmq 2.2.0.1</li> <li>• qt 4.7.4</li> <li>• redis-py 2.7.2 <i>LM</i></li> <li>• requests 1.2.0</li> <li>• scikit-image 0.8.2</li> <li>• scikit-learn 0.13.1</li> <li>• scipy 0.12.0</li> <li>• six 1.3.0</li> <li>• sphinx 1.1.3</li> <li>• spyder 2.2.0</li> <li>• sqlalchemy 0.8.1</li> <li>• statsmodels 0.4.3</li> <li>• sympy 0.7.2</li> <li>• theano 0.5.0 <i>L</i></li> <li>• tornado 3.0.1</li> <li>• werkzeug 0.8.3</li> <li>• xlrd 0.9.2</li> <li>• xlwt 0.7.5</li> <li>• zlib 1.2.7</li> </ul>
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Only available on: *L* (Linux) - *M* (macOS) - *W* (Windows)

## Python 3.3 (available through conda):

<ul style="list-style-type: none"> <li>• astropy 0.2.1</li> <li>• bitarray 0.8.1</li> <li>• curl 7.30.0 <i>LM</i></li> <li>• cython 0.19</li> <li>• dateutil 2.1</li> <li>• distribute 0.6.36</li> <li>• docutils 0.10</li> <li>• dynd-python 0.3.0</li> <li>• freetype 2.4.10</li> <li>• greenlet 0.4.0</li> <li>• hdf5 1.8.9</li> <li>• ipython 0.13.2</li> <li>• jinja2 2.6</li> </ul>	<ul style="list-style-type: none"> <li>• libnetcdf 4.2.1.1 <i>LM</i></li> <li>• libpng 1.5.13</li> <li>• llvm 3.2</li> <li>• llvmpy 0.11.2</li> <li>• lxml 3.2.0</li> <li>• matplotlib 1.2.1</li> <li>• mdp 3.3</li> <li>• mingw 4.7 <i>W</i></li> <li>• netcdf4 1.0.4 <i>LM</i></li> <li>• networkx 1.7</li> <li>• nose 1.3.0</li> <li>• numba 0.8.1</li> <li>• numpy 1.7.1</li> </ul>	<ul style="list-style-type: none"> <li>• pandas 0.11.0</li> <li>• pip 1.3.1</li> <li>• ply 3.4</li> <li>• psutil 0.7.1</li> <li>• pycosat 0.6.0</li> <li>• pycparser 2.9.1</li> <li>• pycrypto 2.6</li> <li>• pyflakes 0.7.2</li> <li>• pygments 1.6</li> <li>• pyside 1.1.2 <i>W</i></li> <li>• python 3.3.1</li> <li>• pytz 2013b</li> <li>• pyyaml 3.10</li> </ul>	<ul style="list-style-type: none"> <li>• pyzmq 2.2.0.1</li> <li>• requests 1.2.0</li> <li>• scikit-image 0.8.2</li> <li>• scipy 0.12.0</li> <li>• six 1.3.0</li> <li>• sphinx 1.1.3</li> <li>• sqlalchemy 0.8.1</li> <li>• sympy 0.7.2</li> <li>• tornado 3.0.1</li> <li>• xlrd 0.9.2</li> <li>• zlib 1.2.7</li> </ul>
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## Python 2.6 (available through conda):

<ul style="list-style-type: none"> <li>• argparse 1.2.1</li> <li>• astropy 0.2.1</li> <li>• atom 0.2.3</li> <li>• biopython 1.61</li> <li>• bitarray 0.8.1</li> <li>• boto 2.9.2</li> <li>• cairo 1.12.2 <i>L</i></li> <li>• casuarious 1.1</li> <li>• curl 7.30.0 <i>LM</i></li> <li>• cython 0.19</li> <li>• dateutil 2.1</li> <li>• disco 0.4.4 <i>L</i></li> <li>• distribute 0.6.36</li> <li>• docutils 0.10</li> <li>• dynd-python 0.3.0</li> <li>• erlang R15B01 <i>L</i></li> <li>• flask 0.9</li> <li>• freetype 2.4.10</li> <li>• gevent 0.13.8</li> <li>• gevent-websocket 0.3.6</li> <li>• gevent_zeromq 0.2.5</li> </ul>	<ul style="list-style-type: none"> <li>• greenlet 0.4.0</li> <li>• grin 1.2.1</li> <li>• h5py 2.1.1</li> <li>• hdf5 1.8.9</li> <li>• imaging 1.1.7</li> <li>• ipython 0.13.2</li> <li>• jinja2 2.6</li> <li>• libevent 2.0.20</li> <li>• libnetcdf 4.2.1.1 <i>LM</i></li> <li>• libpng 1.5.13</li> <li>• llvm 3.2</li> <li>• llvmpy 0.11.2</li> <li>• lxml 3.2.0</li> <li>• matplotlib 1.2.1 <i>LM</i></li> <li>• mdp 3.3</li> <li>• mingw 4.7 <i>W</i></li> <li>• mpi4py 1.3 <i>L</i></li> <li>• mpich2 1.4.1p1 <i>L</i></li> <li>• netcdf4 1.0.4 <i>LM</i></li> <li>• networkx 1.7</li> <li>• nltk 2.0.4</li> </ul>	<ul style="list-style-type: none"> <li>• nose 1.3.0</li> <li>• numba 0.8.1</li> <li>• numexpr 2.0.1</li> <li>• numpy 1.7.1</li> <li>• opencv 2.4.2 <i>L</i></li> <li>• ordereddict 1.1</li> <li>• pandas 0.11.0</li> <li>• pip 1.3.1</li> <li>• ply 3.4</li> <li>• psutil 0.7.1</li> <li>• py 1.4.12</li> <li>• py2cairo 1.10.0 <i>L</i></li> <li>• pycosat 0.6.0</li> <li>• pycparser 2.9.1</li> <li>• pycrypto 2.6</li> <li>• pycurl 7.19.0 <i>LM</i></li> <li>• pyflakes 0.7.2</li> <li>• pygments 1.6</li> <li>• pyparsing 1.5.6</li> <li>• pysam 0.6 <i>LM</i></li> <li>• pytables 2.4.0 <i>LM</i></li> </ul>	<ul style="list-style-type: none"> <li>• pytest 2.3.4</li> <li>• python 2.6.8</li> <li>• pytz 2013b</li> <li>• pyyaml 3.10</li> <li>• pyzmq 2.2.0.1</li> <li>• redis-py 2.7.2 <i>LM</i></li> <li>• requests 1.2.0</li> <li>• scikit-image 0.8.2</li> <li>• scikit-learn 0.13.1</li> <li>• scipy 0.12.0</li> <li>• six 1.3.0</li> <li>• sphinx 1.1.3</li> <li>• sqlalchemy 0.8.1</li> <li>• statsmodels 0.4.3</li> <li>• sympy 0.7.2 <i>LM</i></li> <li>• theano 0.5.0 <i>L</i></li> <li>• tornado 3.0.1</li> <li>• werkzeug 0.8.3</li> <li>• xlrd 0.9.2</li> <li>• xlwt 0.7.5</li> <li>• zlib 1.2.7</li> </ul>
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Only available on: *L* (Linux) - *M* (macOS) - *W* (Windows)



## Packages included in Anaconda 1.6.1

<ul style="list-style-type: none"> <li>• astropy 0.2.3</li> <li>• atom 0.2.3</li> <li>• binstar 0.1.2</li> <li>• biopython 1.61</li> <li>• bitarray 0.8.1</li> <li>• boto 2.9.6</li> <li>• cairo 1.12.2 <i>L</i></li> <li>• casuarious 1.1</li> <li>• conda 1.7.2</li> <li>• cubes 0.10.2</li> <li>• curl 7.30.0 <i>LM</i></li> <li>• cython 0.19.1</li> <li>• dateutil 2.1</li> <li>• disco 0.4.4 <i>L</i></li> <li>• distribute 0.6.45</li> <li>• docutils 0.10</li> <li>• dynd-python 0.4.0</li> <li>• enaml 0.7.6</li> <li>• erlang R15B01 <i>L</i></li> <li>• flask 0.10.1</li> <li>• freetype 2.4.10</li> <li>• gevent 0.13.8</li> <li>• gevent-websocket 0.3.6</li> <li>• gevent_zeromq 0.2.5</li> <li>• greenlet 0.4.1</li> </ul>	<ul style="list-style-type: none"> <li>• grin 1.2.1</li> <li>• h5py 2.1.1</li> <li>• hdf5 1.8.9</li> <li>• imaging 1.1.7</li> <li>• ipython 0.13.2</li> <li>• itsdangerous 0.21</li> <li>• jinja2 2.6</li> <li>• keyring 1.4</li> <li>• launcher 0.1.2</li> <li>• libevent 2.0.20</li> <li>• libnetcdf 4.2.1.1 <i>LM</i></li> <li>• libpng 1.5.13</li> <li>• llvm 3.2</li> <li>• llvmmath 0.1.0</li> <li>• llvmpy 0.11.3</li> <li>• lxml 3.2.1</li> <li>• matplotlib 1.2.1</li> <li>• mdp 3.3</li> <li>• menuinst 1.0.1 <i>W</i></li> <li>• meta 0.4.2.dev</li> <li>• mingw 4.7 <i>W</i></li> <li>• mpi4py 1.3 <i>L</i></li> <li>• mpich2 1.4.1p1 <i>L</i></li> <li>• netcdf4 1.0.4 <i>LM</i></li> <li>• networkx 1.7</li> </ul>	<ul style="list-style-type: none"> <li>• nltk 2.0.4</li> <li>• nose 1.3.0</li> <li>• numba 0.9.0</li> <li>• numexpr 2.0.1</li> <li>• numpy 1.7.1</li> <li>• opencv 2.4.2 <i>L</i></li> <li>• pandas 0.11.0</li> <li>• pep8 1.4.5</li> <li>• pip 1.3.1</li> <li>• ply 3.4</li> <li>• psutil 0.7.1</li> <li>• py 1.4.14</li> <li>• py2cairo 1.10.0 <i>L</i></li> <li>• pyaudio 0.2.7 <i>M</i></li> <li>• pycosat 0.6.0</li> <li>• pycparser 2.9.1</li> <li>• pycrypto 2.6</li> <li>• pycurl 7.19.0 <i>LM</i></li> <li>• pyflakes 0.7.2</li> <li>• pygments 1.6</li> <li>• pyparsing 1.5.6</li> <li>• pysal 1.5.0</li> <li>• pysam 0.6 <i>LM</i></li> <li>• pyside 1.1.2</li> <li>• pytables 2.4.0</li> </ul>	<ul style="list-style-type: none"> <li>• pytest 2.3.5</li> <li>• python 2.7.5</li> <li>• pytz 2013b</li> <li>• pywin32 218.4 <i>W</i></li> <li>• pyyaml 3.10</li> <li>• pyzmq 2.2.0.1</li> <li>• qt 4.7.4</li> <li>• redis-py 2.7.2 <i>LM</i></li> <li>• requests 1.2.3</li> <li>• rope 0.9.4</li> <li>• scikit-image 0.8.2</li> <li>• scikit-learn 0.13.1</li> <li>• scipy 0.12.0</li> <li>• six 1.3.0</li> <li>• sphinx 1.1.3</li> <li>• spyder 2.2.0</li> <li>• sqlalchemy 0.8.1</li> <li>• statsmodels 0.4.3</li> <li>• sympy 0.7.2</li> <li>• theano 0.5.0 <i>L</i></li> <li>• tornado 3.1</li> <li>• werkzeug 0.9.1</li> <li>• xlrd 0.9.2</li> <li>• xlwt 0.7.5</li> <li>• zlib 1.2.7</li> </ul>
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Only available on: *L* (Linux) - *M* (macOS) - *W* (Windows)

## Python 3.3 (available through conda):

<ul style="list-style-type: none"> <li>• astropy 0.2.3</li> <li>• bitarray 0.8.1</li> <li>• curl 7.30.0 <i>LM</i></li> <li>• cython 0.19.1</li> <li>• dateutil 2.1</li> <li>• distribute 0.6.45</li> <li>• docutils 0.10</li> <li>• dynd-python 0.4.0</li> <li>• freetype 2.4.10</li> <li>• greenlet 0.4.1</li> <li>• hdf5 1.8.9</li> <li>• ipython 0.13.2</li> <li>• jinja2 2.6</li> </ul>	<ul style="list-style-type: none"> <li>• libnetcdf 4.2.1.1 <i>LM</i></li> <li>• libpng 1.5.13</li> <li>• llvm 3.2</li> <li>• llvmmath 0.1.0</li> <li>• llvmpy 0.11.3</li> <li>• lxml 3.2.1</li> <li>• matplotlib 1.2.1</li> <li>• mdp 3.3</li> <li>• mingw 4.7 <i>W</i></li> <li>• netcdf4 1.0.4 <i>LM</i></li> <li>• networkx 1.7</li> <li>• nose 1.3.0</li> <li>• numba 0.9.0</li> </ul>	<ul style="list-style-type: none"> <li>• numpy 1.7.1</li> <li>• pandas 0.11.0</li> <li>• pip 1.3.1</li> <li>• ply 3.4</li> <li>• psutil 0.7.1</li> <li>• pycosat 0.6.0</li> <li>• pycparser 2.9.1</li> <li>• pycrypto 2.6</li> <li>• pyflakes 0.7.2</li> <li>• pygments 1.6</li> <li>• pyside 1.1.2 <i>W</i></li> <li>• python 3.3.2</li> <li>• pytz 2013b</li> </ul>	<ul style="list-style-type: none"> <li>• pyyaml 3.10</li> <li>• pyzmq 2.2.0.1</li> <li>• requests 1.2.3</li> <li>• scikit-image 0.8.2</li> <li>• scipy 0.12.0</li> <li>• six 1.3.0</li> <li>• sphinx 1.1.3</li> <li>• sqlalchemy 0.8.1</li> <li>• sympy 0.7.2</li> <li>• tornado 3.1</li> <li>• xlrd 0.9.2</li> <li>• zlib 1.2.7</li> </ul>
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## Python 2.6 (available through conda):

<ul style="list-style-type: none"> <li>• argparse 1.2.1</li> <li>• astropy 0.2.3</li> <li>• atom 0.2.3</li> <li>• biopython 1.61</li> <li>• bitarray 0.8.1</li> <li>• boto 2.9.6</li> <li>• cairo 1.12.2 <i>L</i></li> <li>• casuarious 1.1</li> <li>• curl 7.30.0 <i>LM</i></li> <li>• cython 0.19.1</li> <li>• dateutil 2.1</li> <li>• disco 0.4.4 <i>L</i></li> <li>• distribute 0.6.45</li> <li>• docutils 0.10</li> <li>• dynd-python 0.4.0</li> <li>• erlang R15B01 <i>L</i></li> <li>• flask 0.10.1</li> <li>• freetype 2.4.10</li> <li>• gevent 0.13.8</li> <li>• gevent-websocket 0.3.6</li> <li>• gevent_zeromq 0.2.5</li> <li>• greenlet 0.4.1</li> </ul>	<ul style="list-style-type: none"> <li>• grin 1.2.1</li> <li>• h5py 2.1.1</li> <li>• hdf5 1.8.9</li> <li>• imaging 1.1.7</li> <li>• ipython 0.13.2</li> <li>• itsdangerous 0.21</li> <li>• jinja2 2.6</li> <li>• libevent 2.0.20</li> <li>• libnetcdf 4.2.1.1 <i>LM</i></li> <li>• libpng 1.5.13</li> <li>• llvm 3.2</li> <li>• llvmmath 0.1.0</li> <li>• llvmpy 0.11.3</li> <li>• lxml 3.2.1</li> <li>• matplotlib 1.2.1 <i>LM</i></li> <li>• mdp 3.3</li> <li>• mingw 4.7 <i>W</i></li> <li>• mpi4py 1.3 <i>L</i></li> <li>• mpich2 1.4.1p1 <i>L</i></li> <li>• netcdf4 1.0.4 <i>LM</i></li> <li>• networkx 1.7</li> <li>• nltk 2.0.4</li> </ul>	<ul style="list-style-type: none"> <li>• nose 1.3.0</li> <li>• numba 0.9.0</li> <li>• numexpr 2.0.1</li> <li>• numpy 1.7.1</li> <li>• opencv 2.4.2 <i>L</i></li> <li>• ordereddict 1.1</li> <li>• pandas 0.11.0</li> <li>• pep8 1.4.5</li> <li>• pip 1.3.1</li> <li>• ply 3.4</li> <li>• psutil 0.7.1</li> <li>• py 1.4.14</li> <li>• py2cairo 1.10.0 <i>L</i></li> <li>• pycosat 0.6.0</li> <li>• pycparser 2.9.1</li> <li>• pycrypto 2.6</li> <li>• pycurl 7.19.0 <i>LM</i></li> <li>• pyflakes 0.7.2</li> <li>• pygments 1.6</li> <li>• pyparsing 1.5.6</li> <li>• pysam 0.6 <i>LM</i></li> <li>• pytables 2.4.0 <i>LM</i></li> </ul>	<ul style="list-style-type: none"> <li>• pytest 2.3.5</li> <li>• python 2.6.8</li> <li>• pytz 2013b</li> <li>• pyyaml 3.10</li> <li>• pyzmq 2.2.0.1</li> <li>• redis-py 2.7.2 <i>LM</i></li> <li>• requests 1.2.3</li> <li>• scikit-image 0.8.2</li> <li>• scikit-learn 0.13.1</li> <li>• scipy 0.12.0</li> <li>• six 1.3.0</li> <li>• sphinx 1.1.3</li> <li>• sqlalchemy 0.8.1</li> <li>• statsmodels 0.4.3</li> <li>• sympy 0.7.2 <i>LM</i></li> <li>• theano 0.5.0 <i>L</i></li> <li>• tornado 3.1</li> <li>• werkzeug 0.9.1</li> <li>• xlrd 0.9.2</li> <li>• xlwt 0.7.5</li> <li>• zlib 1.2.7</li> </ul>
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Only available on: *L* (Linux) - *M* (macOS) - *W* (Windows)

## Packages included in Anaconda 1.7.0

<ul style="list-style-type: none"> <li>• apptools 4.2.0</li> <li>• astropy 0.2.4</li> <li>• atom 0.3.2</li> <li>• binstar 0.3.1</li> <li>• biopython 1.61</li> <li>• bitarray 0.8.1</li> <li>• bokeh 0.1.1</li> <li>• boto 2.12.0</li> <li>• cairo 1.12.2 <i>L</i></li> <li>• casuarious 1.1</li> <li>• chaco 4.3.0</li> <li>• configobj 4.7.2</li> <li>• cubes 0.10.2</li> <li>• curl 7.30.0 <i>LM</i></li> <li>• cython 0.19.1</li> <li>• dateutil 2.1</li> <li>• disco 0.4.4 <i>L</i></li> <li>• distribute 0.6.45</li> <li>• docutils 0.11</li> <li>• dynd-python 0.4.2</li> <li>• enable 4.3.0</li> <li>• enaml 0.7.19</li> <li>• envisage 4.3.0</li> <li>• erlang R15B01 <i>L</i></li> <li>• flask 0.10.1</li> <li>• freetype 2.4.10</li> <li>• gevent 0.13.8</li> <li>• gevent-websocket 0.3.6</li> <li>• gevent_zeromq 0.2.5</li> </ul>	<ul style="list-style-type: none"> <li>• greenlet 0.4.1</li> <li>• grin 1.2.1</li> <li>• h5py 2.2.0</li> <li>• hdf5 1.8.9</li> <li>• imaging 1.1.7</li> <li>• ipython 1.0.0</li> <li>• itsdangerous 0.23</li> <li>• jinja2 2.7.1</li> <li>• keyring 3.0.1</li> <li>• launcher 0.1.2</li> <li>• libevent 2.0.20</li> <li>• libnetcdf 4.2.1.1 <i>LM</i></li> <li>• libpng 1.5.13 <i>LM</i></li> <li>• libtiff 4.0.2 <i>LM</i></li> <li>• libxml2 2.9.0 <i>LM</i></li> <li>• libxslt 1.1.28 <i>LM</i></li> <li>• llvm 3.3</li> <li>• llvmmath 0.1.1</li> <li>• llvmpy 0.12.0</li> <li>• lxml 3.2.3</li> <li>• markupsafe 0.18</li> <li>• matplotlib 1.3.0</li> <li>• mayavi 4.3.0</li> <li>• mdp 3.3</li> <li>• menuinst 1.0.1 <i>W</i></li> <li>• meta 0.4.2.dev</li> <li>• mingw 4.7 <i>W</i></li> <li>• mpi4py 1.3 <i>L</i></li> <li>• mpich2 1.4.1p1 <i>L</i></li> </ul>	<ul style="list-style-type: none"> <li>• netcdf4 1.0.5 <i>LM</i></li> <li>• networkx 1.8.1</li> <li>• nltk 2.0.4</li> <li>• nose 1.3.0</li> <li>• numba 0.10.2</li> <li>• numexpr 2.0.1</li> <li>• numpy 1.7.1</li> <li>• opencv 2.4.6 <i>L</i></li> <li>• pandas 0.12.0</li> <li>• patsy 0.2.1</li> <li>• pep8 1.4.6</li> <li>• pip 1.4.1</li> <li>• ply 3.4</li> <li>• psutil 1.0.1</li> <li>• py 1.4.14</li> <li>• py2cairo 1.10.0 <i>L</i></li> <li>• pyaudio 0.2.7 <i>M</i></li> <li>• pycosat 0.6.0</li> <li>• pycparser 2.9.1</li> <li>• pycrypto 2.6</li> <li>• pycurl 7.19.0 <i>LM</i></li> <li>• pyface 4.3.0</li> <li>• pyflakes 0.7.3</li> <li>• pygments 1.6</li> <li>• pyparsing 1.5.6</li> <li>• pyreadline 2.0.dev <i>W</i></li> <li>• pysal 1.6.0</li> <li>• pysam 0.6 <i>LM</i></li> <li>• pyside 1.1.2</li> </ul>	<ul style="list-style-type: none"> <li>• pytables 2.4.0</li> <li>• pytest 2.3.5</li> <li>• python 2.7.5</li> <li>• pytz 2013b</li> <li>• pywin32 218.4 <i>W</i></li> <li>• pyyaml 3.10</li> <li>• pyzmq 2.2.0.1</li> <li>• qt 4.7.4</li> <li>• redis-py 2.7.2 <i>LM</i></li> <li>• requests 1.2.3</li> <li>• rope 0.9.4</li> <li>• scikit-image 0.8.2</li> <li>• scikit-learn 0.14.1</li> <li>• scipy 0.12.0</li> <li>• six 1.4.1</li> <li>• sphinx 1.1.3</li> <li>• spyder 2.2.4</li> <li>• sqlalchemy 0.8.2</li> <li>• statsmodels 0.5.0</li> <li>• sympy 0.7.3</li> <li>• theano 0.5.0 <i>L</i></li> <li>• tornado 3.1.1</li> <li>• traits 4.3.0</li> <li>• traitsui 4.3.0</li> <li>• vtk 5.10.1</li> <li>• werkzeug 0.9.4</li> <li>• xlrd 0.9.2</li> <li>• xlwt 0.7.5</li> <li>• zlib 1.2.7</li> </ul>
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Only available on: *L* (Linux) - *M* (macOS) - *W* (Windows)

## Python 3.3 (available through conda):

<ul style="list-style-type: none"> <li>• astropy 0.2.4</li> <li>• bitarray 0.8.1</li> <li>• curl 7.30.0 <i>LM</i></li> <li>• cython 0.19.1</li> <li>• dateutil 2.1</li> <li>• distribute 0.6.45</li> <li>• docutils 0.11</li> <li>• dynd-python 0.4.2</li> <li>• flask 0.10.1</li> <li>• freetype 2.4.10</li> <li>• greenlet 0.4.1</li> <li>• hdf5 1.8.9</li> <li>• ipython 1.0.0</li> <li>• itsdangerous 0.23</li> <li>• jinja2 2.7.1</li> <li>• libnetcdf 4.2.1.1 <i>LM</i></li> </ul>	<ul style="list-style-type: none"> <li>• libpng 1.5.13 <i>LM</i></li> <li>• libtiff 4.0.2 <i>LM</i></li> <li>• libxml2 2.9.0 <i>LM</i></li> <li>• libxslt 1.1.28 <i>LM</i></li> <li>• llvm 3.3</li> <li>• llvmmath 0.1.1</li> <li>• llvmpy 0.12.0</li> <li>• lxml 3.2.3</li> <li>• markupsafe 0.18</li> <li>• matplotlib 1.3.0</li> <li>• mdp 3.3</li> <li>• mingw 4.7 <i>W</i></li> <li>• netcdf4 1.0.5 <i>LM</i></li> <li>• networkx 1.8.1</li> <li>• nose 1.3.0</li> <li>• numba 0.10.2</li> </ul>	<ul style="list-style-type: none"> <li>• numpy 1.7.1</li> <li>• pandas 0.12.0</li> <li>• patsy 0.2.1</li> <li>• pillow 2.1.0</li> <li>• pip 1.4.1</li> <li>• ply 3.4</li> <li>• psutil 1.0.1</li> <li>• pycosat 0.6.0</li> <li>• pycparser 2.9.1</li> <li>• pycrypto 2.6</li> <li>• pyflakes 0.7.3</li> <li>• pygments 1.6</li> <li>• pyparsing 1.5.6</li> <li>• pyreadline 2.0.dev <i>W</i></li> <li>• pyside 1.1.2 <i>W</i></li> <li>• python 3.3.2</li> </ul>	<ul style="list-style-type: none"> <li>• pytz 2013b</li> <li>• pyyaml 3.10</li> <li>• pyzmq 2.2.0.1</li> <li>• requests 1.2.3</li> <li>• scikit-image 0.8.2</li> <li>• scipy 0.12.0</li> <li>• six 1.4.1</li> <li>• sphinx 1.1.3</li> <li>• sqlalchemy 0.8.2</li> <li>• statsmodels 0.5.0</li> <li>• sympy 0.7.3</li> <li>• tornado 3.1.1</li> <li>• werkzeug 0.9.4</li> <li>• xlrd 0.9.2</li> <li>• zlib 1.2.7</li> </ul>
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## Python 2.6 (available through conda):

<ul style="list-style-type: none"> <li>• argparse 1.2.1</li> <li>• astropy 0.2.4</li> <li>• atom 0.3.2</li> <li>• biopython 1.61</li> <li>• bitarray 0.8.1</li> <li>• boto 2.12.0</li> <li>• cairo 1.12.2 <i>L</i></li> <li>• casuarious 1.1</li> <li>• configobj 4.7.2</li> <li>• curl 7.30.0 <i>LM</i></li> <li>• cython 0.19.1</li> <li>• dateutil 2.1</li> <li>• disco 0.4.4 <i>L</i></li> <li>• distribute 0.6.45</li> <li>• docutils 0.11</li> <li>• dynd-python 0.4.2</li> <li>• erlang R15B01 <i>L</i></li> <li>• flask 0.10.1</li> <li>• freetype 2.4.10</li> <li>• gevent 0.13.8</li> <li>• gevent-websocket 0.3.6</li> <li>• gevent_zeromq 0.2.5</li> <li>• greenlet 0.4.1</li> <li>• grin 1.2.1</li> </ul>	<ul style="list-style-type: none"> <li>• h5py 2.2.0</li> <li>• hdf5 1.8.9</li> <li>• imaging 1.1.7</li> <li>• ipython 1.0.0</li> <li>• itsdangerous 0.23</li> <li>• jinja2 2.7.1</li> <li>• libevent 2.0.20</li> <li>• libnetcdf 4.2.1.1 <i>LM</i></li> <li>• libpng 1.5.13 <i>LM</i></li> <li>• libtiff 4.0.2 <i>LM</i></li> <li>• libxml2 2.9.0 <i>LM</i></li> <li>• libxslt 1.1.28 <i>LM</i></li> <li>• llvm 3.3</li> <li>• llvmmath 0.1.1</li> <li>• llvmpy 0.12.0</li> <li>• lxml 3.2.3</li> <li>• markupsafe 0.18</li> <li>• matplotlib 1.3.0 <i>LM</i></li> <li>• mdp 3.3</li> <li>• mingw 4.7 <i>W</i></li> <li>• mpi4py 1.3 <i>L</i></li> <li>• mpich2 1.4.1p1 <i>L</i></li> <li>• netcdf4 1.0.5 <i>LM</i></li> <li>• networkx 1.8.1</li> </ul>	<ul style="list-style-type: none"> <li>• nltk 2.0.4</li> <li>• nose 1.3.0</li> <li>• numba 0.10.2</li> <li>• numexpr 2.0.1</li> <li>• numpy 1.7.1</li> <li>• opencv 2.4.6 <i>L</i></li> <li>• ordereddict 1.1</li> <li>• pandas 0.12.0</li> <li>• patsy 0.2.1</li> <li>• pep8 1.4.6</li> <li>• pip 1.4.1</li> <li>• ply 3.4</li> <li>• psutil 1.0.1</li> <li>• py 1.4.14</li> <li>• py2cairo 1.10.0 <i>L</i></li> <li>• pycosat 0.6.0</li> <li>• pycparser 2.9.1</li> <li>• pycrypto 2.6</li> <li>• pycurl 7.19.0 <i>LM</i></li> <li>• pyflakes 0.7.3</li> <li>• pygments 1.6</li> <li>• pyparsing 1.5.6</li> <li>• pyreadline 2.0.dev <i>W</i></li> <li>• pysam 0.6 <i>LM</i></li> </ul>	<ul style="list-style-type: none"> <li>• pytables 2.4.0 <i>LM</i></li> <li>• pytest 2.3.5</li> <li>• python 2.6.8</li> <li>• pytz 2013b</li> <li>• pyyaml 3.10</li> <li>• pyzmq 2.2.0.1</li> <li>• redis-py 2.7.2 <i>LM</i></li> <li>• requests 1.2.3</li> <li>• scikit-image 0.8.2</li> <li>• scikit-learn 0.14.1</li> <li>• scipy 0.12.0</li> <li>• six 1.4.1</li> <li>• sphinx 1.1.3</li> <li>• sqlalchemy 0.8.2</li> <li>• statsmodels 0.5.0</li> <li>• sympy 0.7.3 <i>LM</i></li> <li>• theano 0.5.0 <i>L</i></li> <li>• tornado 3.1.1</li> <li>• werkzeug 0.9.4</li> <li>• xlrd 0.9.2</li> <li>• xlwt 0.7.5</li> <li>• zlib 1.2.7</li> </ul>
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Only available on: *L* (Linux) - *M* (macOS) - *W* (Windows)

## Packages included in Anaconda 1.8.0

### Python 2.7 (included in installer):

<ul style="list-style-type: none"> <li>• apptools 4.2.0</li> <li>• astropy 0.2.5</li> <li>• atom 0.3.4</li> <li>• beautiful-soup 4.3.1</li> <li>• binstar 0.3.1</li> <li>• biopython 1.62</li> <li>• bitarray 0.8.1</li> <li>• blaze 0.3</li> <li>• bokeh 0.2</li> <li>• boto 2.15.0</li> <li>• cairo 1.12.2 <i>L</i></li> <li>• casuarious 1.1</li> <li>• chaco 4.3.0</li> <li>• colorama 0.2.7</li> <li>• configobj 4.7.2</li> <li>• cubes 0.10.2</li> <li>• curl 7.30.0 <i>LM</i></li> <li>• cython 0.19.2</li> <li>• dateutil 2.1</li> <li>• disco 0.4.4 <i>L</i></li> <li>• distribute 0.6.45</li> <li>• docutils 0.11</li> <li>• dynd-python 0.5.0</li> <li>• enable 4.3.0</li> <li>• enaml 0.8.3</li> <li>• envisage 4.3.0</li> <li>• erlang R15B01 <i>L</i></li> <li>• flask 0.10.1</li> <li>• freetype 2.4.10</li> <li>• gevent 0.13.8</li> <li>• gevent-websocket 0.3.6</li> </ul>	<ul style="list-style-type: none"> <li>• gevent_zeromq 0.2.5</li> <li>• greenlet 0.4.1</li> <li>• grin 1.2.1</li> <li>• h5py 2.2.0</li> <li>• hdf5 1.8.9</li> <li>• imaging 1.1.7</li> <li>• ipython 1.1.0</li> <li>• itsdangerous 0.23</li> <li>• jinja2 2.7.1</li> <li>• keyring 3.2</li> <li>• launcher 0.1.2</li> <li>• libevent 2.0.20</li> <li>• libnetcdf 4.2.1.1 <i>LM</i></li> <li>• libpng 1.5.13 <i>LM</i></li> <li>• libtiff 4.0.2 <i>LM</i></li> <li>• libxml2 2.9.0 <i>LM</i></li> <li>• libxslt 1.1.28 <i>LM</i></li> <li>• llvm 3.3</li> <li>• llvmmath 0.1.1</li> <li>• llvmpy 0.12.0</li> <li>• lxml 3.2.3</li> <li>• markupsafe 0.18</li> <li>• matplotlib 1.3.1</li> <li>• mayavi 4.3.0</li> <li>• mdp 3.3</li> <li>• menuinst 1.0.3 <i>W</i></li> <li>• meta 0.4.2.dev</li> <li>• mingw 4.7 <i>W</i></li> <li>• mpi4py 1.3 <i>L</i></li> <li>• mpich2 1.4.1p1 <i>L</i></li> <li>• netcdf4 1.0.6 <i>LM</i></li> </ul>	<ul style="list-style-type: none"> <li>• networkx 1.8.1</li> <li>• nltk 2.0.4</li> <li>• nose 1.3.0</li> <li>• numba 0.11.0</li> <li>• numexpr 2.2.2</li> <li>• numpy 1.7.1</li> <li>• opencv 2.4.6 <i>L</i></li> <li>• openpyxl 1.6.2</li> <li>• pandas 0.12.0</li> <li>• patsy 0.2.1</li> <li>• pep8 1.4.6</li> <li>• pip 1.4.1</li> <li>• ply 3.4</li> <li>• psutil 1.1.2</li> <li>• py 1.4.17</li> <li>• py2cairo 1.10.0 <i>L</i></li> <li>• pyaudio 0.2.7 <i>M</i></li> <li>• pycosat 0.6.0</li> <li>• pycparser 2.9.1</li> <li>• pycrypto 2.6.1</li> <li>• pycurl 7.19.0 <i>LM</i></li> <li>• pyface 4.3.0</li> <li>• pyflakes 0.7.3</li> <li>• pygments 1.6</li> <li>• pykit 0.1.0</li> <li>• pyparsing 1.5.6</li> <li>• pyreadline 2.0.dev <i>W</i></li> <li>• pysal 1.6.0</li> <li>• pysam 0.6 <i>LM</i></li> <li>• pyside 1.2.1</li> <li>• pytables 3.0.0</li> </ul>	<ul style="list-style-type: none"> <li>• pytest 2.4.2</li> <li>• python 2.7.5</li> <li>• pytz 2013b</li> <li>• pywin32 218.4 <i>W</i></li> <li>• pyyaml 3.10</li> <li>• pyzmq 2.2.0.1</li> <li>• qt 4.8.5</li> <li>• redis 2.6.9 <i>LM</i></li> <li>• redis-py 2.7.2 <i>LM</i></li> <li>• requests 1.2.3</li> <li>• rope 0.9.4</li> <li>• scikit-image 0.9.3</li> <li>• scikit-learn 0.14.1</li> <li>• scipy 0.13.0</li> <li>• six 1.4.1</li> <li>• sphinx 1.1.3</li> <li>• spyder 2.2.5</li> <li>• sqlalchemy 0.8.3</li> <li>• statsmodels 0.5.0</li> <li>• sympy 0.7.3</li> <li>• theano 0.5.0 <i>L</i></li> <li>• tornado 3.1.1</li> <li>• traits 4.3.0</li> <li>• traitsui 4.3.0</li> <li>• vtk 5.10.1</li> <li>• werkzeug 0.9.4</li> <li>• xlrd 0.9.2</li> <li>• xlwt 0.7.5</li> <li>• yaml 0.1.4 <i>LM</i></li> <li>• zeromq 2.2.0 <i>LM</i></li> <li>• zlib 1.2.7</li> </ul>
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Only available on: *L* (Linux) - *M* (macOS) - *W* (Windows)

**Python 3.3 (available through conda):**

<ul style="list-style-type: none"><li>• astropy 0.2.5</li><li>• beautiful-soup 4.3.1</li><li>• bitarray 0.8.1</li><li>• colorama 0.2.7</li><li>• curl 7.30.0 <i>LM</i></li><li>• cython 0.19.2</li><li>• dateutil 2.1</li><li>• distribute 0.6.45</li><li>• docutils 0.11</li><li>• dynd-python 0.5.0</li><li>• flask 0.10.1</li><li>• freetype 2.4.10</li><li>• greenlet 0.4.1</li><li>• hdf5 1.8.9</li><li>• ipython 1.1.0</li><li>• itsdangerous 0.23</li><li>• jinja2 2.7.1</li><li>• libnetcdf 4.2.1.1 <i>LM</i></li></ul>	<ul style="list-style-type: none"><li>• libpng 1.5.13 <i>LM</i></li><li>• libtiff 4.0.2 <i>LM</i></li><li>• libxml2 2.9.0 <i>LM</i></li><li>• libxslt 1.1.28 <i>LM</i></li><li>• llvm 3.3</li><li>• llvmmath 0.1.1</li><li>• llvmpy 0.12.0</li><li>• lxml 3.2.3</li><li>• markupsafe 0.18</li><li>• matplotlib 1.3.1</li><li>• mdp 3.3</li><li>• mingw 4.7 <i>W</i></li><li>• netcdf4 1.0.6 <i>LM</i></li><li>• networkx 1.8.1</li><li>• nose 1.3.0</li><li>• numba 0.11.0</li><li>• numexpr 2.2.2</li><li>• numpy 1.7.1</li></ul>	<ul style="list-style-type: none"><li>• openpyxl 1.6.2</li><li>• pandas 0.12.0</li><li>• patsy 0.2.1</li><li>• pillow 2.1.0</li><li>• pip 1.4.1</li><li>• ply 3.4</li><li>• psutil 1.1.2</li><li>• pycosat 0.6.0</li><li>• pycparser 2.9.1</li><li>• pycrypto 2.6.1</li><li>• pyflakes 0.7.3</li><li>• pygments 1.6</li><li>• pyparsing 1.5.6</li><li>• pyreadline 2.0.dev <i>W</i></li><li>• pyside 1.2.1 <i>W</i></li><li>• pytables 3.0.0</li><li>• python 3.3.2</li><li>• pytz 2013b</li></ul>	<ul style="list-style-type: none"><li>• pyyaml 3.10</li><li>• pyzmq 2.2.0.1</li><li>• requests 1.2.3</li><li>• scikit-image 0.9.3</li><li>• scipy 0.13.0</li><li>• six 1.4.1</li><li>• sphinx 1.1.3</li><li>• sqlalchemy 0.8.3</li><li>• statsmodels 0.5.0</li><li>• sympy 0.7.3</li><li>• tornado 3.1.1</li><li>• werkzeug 0.9.4</li><li>• xlrd 0.9.2</li><li>• yaml 0.1.4 <i>LM</i></li><li>• zeromq 2.2.0 <i>LM</i></li><li>• zlib 1.2.7</li></ul>
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**Python 2.6 (available through conda):**

<ul style="list-style-type: none"> <li>• argparse 1.2.1</li> <li>• astropy 0.2.5</li> <li>• atom 0.3.4</li> <li>• beautiful-soup 4.3.1</li> <li>• biopython 1.62</li> <li>• bitarray 0.8.1</li> <li>• boto 2.15.0</li> <li>• cairo 1.12.2 <i>L</i></li> <li>• casuarious 1.1</li> <li>• colorama 0.2.7</li> <li>• configobj 4.7.2</li> <li>• curl 7.30.0 <i>LM</i></li> <li>• cython 0.19.2</li> <li>• dateutil 2.1</li> <li>• disco 0.4.4 <i>L</i></li> <li>• distribute 0.6.45</li> <li>• docutils 0.11</li> <li>• dynd-python 0.5.0</li> <li>• erlang R15B01 <i>L</i></li> <li>• flask 0.10.1</li> <li>• freetype 2.4.10</li> <li>• gevent 0.13.8</li> <li>• gevent-websocket 0.3.6</li> <li>• gevent_zeromq 0.2.5</li> <li>• greenlet 0.4.1</li> </ul>	<ul style="list-style-type: none"> <li>• grin 1.2.1</li> <li>• h5py 2.2.0</li> <li>• hdf5 1.8.9</li> <li>• imaging 1.1.7</li> <li>• ipython 1.1.0</li> <li>• itsdangerous 0.23</li> <li>• jinja2 2.7.1</li> <li>• libevent 2.0.20</li> <li>• libnetcdf 4.2.1.1 <i>LM</i></li> <li>• libpng 1.5.13 <i>LM</i></li> <li>• libtiff 4.0.2 <i>LM</i></li> <li>• libxml2 2.9.0 <i>LM</i></li> <li>• libxslt 1.1.28 <i>LM</i></li> <li>• llvm 3.3</li> <li>• llvmmath 0.1.1</li> <li>• llvmpy 0.12.0</li> <li>• lxml 3.2.3</li> <li>• markupsafe 0.18</li> <li>• matplotlib 1.3.1 <i>LM</i></li> <li>• mdp 3.3</li> <li>• mingw 4.7 <i>W</i></li> <li>• mpi4py 1.3 <i>L</i></li> <li>• mpich2 1.4.1p1 <i>L</i></li> <li>• netcdf4 1.0.6 <i>LM</i></li> <li>• networkx 1.8.1</li> </ul>	<ul style="list-style-type: none"> <li>• nltk 2.0.4</li> <li>• nose 1.3.0</li> <li>• numba 0.11.0</li> <li>• numexpr 2.2.2</li> <li>• numpy 1.7.1</li> <li>• opencv 2.4.6 <i>L</i></li> <li>• ordereddict 1.1</li> <li>• pandas 0.12.0</li> <li>• patsy 0.2.1</li> <li>• pep8 1.4.6</li> <li>• pip 1.4.1</li> <li>• ply 3.4</li> <li>• psutil 1.1.2</li> <li>• py 1.4.17</li> <li>• py2cairo 1.10.0 <i>L</i></li> <li>• pycosat 0.6.0</li> <li>• pycparser 2.9.1</li> <li>• pycrypto 2.6.1</li> <li>• pycurl 7.19.0 <i>LM</i></li> <li>• pyflakes 0.7.3</li> <li>• pygments 1.6</li> <li>• pyparsing 1.5.6</li> <li>• pyreadline 2.0.dev <i>W</i></li> <li>• pysam 0.6 <i>LM</i></li> <li>• pytables 3.0.0 <i>LM</i></li> </ul>	<ul style="list-style-type: none"> <li>• pytest 2.4.2</li> <li>• python 2.6.9</li> <li>• pytz 2013b</li> <li>• pyyaml 3.10</li> <li>• pyzmq 2.2.0.1</li> <li>• redis 2.6.9 <i>LM</i></li> <li>• redis-py 2.7.2 <i>LM</i></li> <li>• requests 1.2.3</li> <li>• scikit-image 0.9.3</li> <li>• scikit-learn 0.14.1</li> <li>• scipy 0.13.0</li> <li>• six 1.4.1</li> <li>• sphinx 1.1.3</li> <li>• sqlalchemy 0.8.3</li> <li>• statsmodels 0.5.0</li> <li>• sympy 0.7.3 <i>LM</i></li> <li>• theano 0.5.0 <i>L</i></li> <li>• tornado 3.1.1</li> <li>• werkzeug 0.9.4</li> <li>• xlrd 0.9.2</li> <li>• xlwt 0.7.5</li> <li>• yaml 0.1.4 <i>LM</i></li> <li>• zeromq 2.2.0 <i>LM</i></li> <li>• zlib 1.2.7</li> </ul>
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Only available on: *L* (Linux) - *M* (macOS) - *W* (Windows)

**Packages included in Anaconda 1.9.0**

## Python 2.7 (included in installer):

<ul style="list-style-type: none"> <li>• apptools 4.2.1</li> <li>• argcomplete 0.6.7</li> <li>• astropy 0.3.0</li> <li>• atom 0.3.6</li> <li>• beautiful-soup 4.3.1</li> <li>• binstar 0.4.4</li> <li>• biopython 1.63</li> <li>• bitarray 0.8.1</li> <li>• blaze 0.4.1</li> <li>• blz 0.6.1</li> <li>• bokeh 0.4</li> <li>• boto 2.24.0</li> <li>• cairo 1.12.2 <i>L</i></li> <li>• casuarious 1.1</li> <li>• cdecimal 2.3</li> <li>• chaco 4.4.1</li> <li>• colorama 0.2.7</li> <li>• conda 3.0.3</li> <li>• conda-build 1.1.0</li> <li>• configobj 4.7.2</li> <li>• cubes 0.10.2</li> <li>• curl 7.30.0 <i>LM</i></li> <li>• cython 0.20</li> <li>• datashape 0.1.0</li> <li>• dateutil 2.1</li> <li>• disco 0.4.4 <i>L</i></li> <li>• docutils 0.11</li> <li>• dynd-python 0.6.0</li> <li>• enable 4.3.0</li> <li>• enaml 0.9.0</li> <li>• envisage 4.4.0</li> <li>• erlang R15B01 <i>L</i></li> <li>• flask 0.10.1</li> <li>• freetype 2.4.10</li> </ul>	<ul style="list-style-type: none"> <li>• future 0.11.2</li> <li>• gevent 1.0</li> <li>• gevent-websocket 0.9.2</li> <li>• gevent_zeromq 0.2.5</li> <li>• greenlet 0.4.2</li> <li>• grin 1.2.1</li> <li>• h5py 2.2.1</li> <li>• hdf5 1.8.9</li> <li>• ipython 1.1.0</li> <li>• itsdangerous 0.23</li> <li>• jinja2 2.7.2</li> <li>• keyring 3.3</li> <li>• kiwisolver 0.1.2</li> <li>• launcher 0.1.2</li> <li>• libdynd 0.6.0 <i>LM</i></li> <li>• libnetcdf 4.2.1.1 <i>LM</i></li> <li>• libpng 1.5.13 <i>LM</i></li> <li>• libsodium 0.4.5 <i>L</i></li> <li>• libtiff 4.0.2 <i>LM</i></li> <li>• libxml2 2.9.0 <i>LM</i></li> <li>• libxslt 1.1.28 <i>LM</i></li> <li>• llvm 3.3</li> <li>• llvmpy 0.12.2</li> <li>• lxml 3.2.3</li> <li>• markupsafe 0.18</li> <li>• matplotlib 1.3.1</li> <li>• mayavi 4.3.1</li> <li>• mdp 3.3</li> <li>• menuinst 1.0.3 <i>W</i></li> <li>• mingw 4.7 <i>W</i></li> <li>• mock 1.0.1</li> <li>• mpi4py 1.3 <i>L</i></li> <li>• mpich2 1.4.1p1 <i>L</i></li> <li>• netcdf4 1.0.7 <i>LM</i></li> </ul>	<ul style="list-style-type: none"> <li>• networkx 1.8.1</li> <li>• nltk 2.0.4</li> <li>• nose 1.3.0</li> <li>• numba 0.12.0</li> <li>• numexpr 2.3.0</li> <li>• numpy 1.8.0</li> <li>• opencv 2.4.6 <i>L</i></li> <li>• openpyxl 1.8.2</li> <li>• openssl 1.0.1c <i>LM</i></li> <li>• pandas 0.13.0</li> <li>• patsy 0.2.1</li> <li>• pep8 1.4.6</li> <li>• pil 1.1.7</li> <li>• pip 1.5.2</li> <li>• ply 3.4</li> <li>• psutil 1.2.1</li> <li>• py 1.4.20</li> <li>• py2cairo 1.10.0 <i>L</i></li> <li>• pyaudio 0.2.7 <i>M</i></li> <li>• pycosat 0.6.0</li> <li>• pycparser 2.10</li> <li>• pycrypto 2.6.1</li> <li>• pycurl 7.19.0 <i>LM</i></li> <li>• pyface 4.4.0</li> <li>• pyflakes 0.7.3</li> <li>• pygments 1.6</li> <li>• pykit 0.1.0</li> <li>• pyparsing 2.0.1</li> <li>• pyreadline 2.0 <i>W</i></li> <li>• pysal 1.6.0</li> <li>• pysam 0.6 <i>LM</i></li> <li>• pyside 1.2.1</li> <li>• pytables 3.1.0</li> <li>• pytest 2.5.2</li> </ul>	<ul style="list-style-type: none"> <li>• python 2.7.6</li> <li>• pytz 2013b</li> <li>• pywin32 218.4 <i>W</i></li> <li>• pyyaml 3.10</li> <li>• pyzmq 2.2.0.1</li> <li>• qt 4.8.5</li> <li>• redis 2.6.9 <i>LM</i></li> <li>• redis-py 2.9.1 <i>LM</i></li> <li>• requests 2.2.1</li> <li>• rope 0.9.4</li> <li>• scikit-image 0.9.3</li> <li>• scikit-learn 0.14.1</li> <li>• scipy 0.13.3</li> <li>• setuptools 2.1</li> <li>• six 1.5.2</li> <li>• sphinx 1.2.1</li> <li>• spyder 2.2.5</li> <li>• sqlalchemy 0.9.2</li> <li>•</li> <li>• ssl_match_hostname 3.4.0.2</li> <li>• statsmodels 0.5.0</li> <li>• sympy 0.7.4.1</li> <li>• theano 0.6.0 <i>L</i></li> <li>• tk 8.5.13 <i>LM</i></li> <li>• tornado 3.2.0</li> <li>• traits 4.4.0</li> <li>• traitsui 4.4.0</li> <li>• ujson 1.33</li> <li>• vtk 5.10.1</li> <li>• werkzeug 0.9.4</li> <li>• xlrd 0.9.2</li> <li>• xlwt 0.7.5</li> <li>• yaml 0.1.4 <i>LM</i></li> <li>• zeromq 2.2.0 <i>LM</i></li> <li>• zlib 1.2.7</li> </ul>
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Only available on: *L* (Linux) - *M* (macOS) - *W* (Windows)



**Python 3.3 (available through conda):**

<ul style="list-style-type: none"> <li>• argcomplete 0.6.7</li> <li>• astropy 0.3.0</li> <li>• beautiful-soup 4.3.1</li> <li>• bitarray 0.8.1</li> <li>• blaze 0.4.1</li> <li>• blz 0.6.1</li> <li>• bokeh 0.4</li> <li>• cdecimal 2.3</li> <li>• colorama 0.2.7</li> <li>• curl 7.30.0 <i>LM</i></li> <li>• cython 0.20</li> <li>• datashape 0.1.0</li> <li>• dateutil 2.1</li> <li>• docutils 0.11</li> <li>• dynd-python 0.6.0</li> <li>• flask 0.10.1</li> <li>• freetype 2.4.10</li> <li>• future 0.11.2</li> <li>• greenlet 0.4.2</li> <li>• hdf5 1.8.9</li> <li>• ipython 1.1.0</li> <li>• itsdangerous 0.23</li> </ul>	<ul style="list-style-type: none"> <li>• jinja2 2.7.2</li> <li>• libdynd 0.6.0 <i>LM</i></li> <li>• libnetcdf 4.2.1.1 <i>LM</i></li> <li>• libpng 1.5.13 <i>LM</i></li> <li>• libsodium 0.4.5 <i>L</i></li> <li>• libtiff 4.0.2 <i>LM</i></li> <li>• libxml2 2.9.0 <i>LM</i></li> <li>• libxslt 1.1.28 <i>LM</i></li> <li>• llvm 3.3</li> <li>• llvmpy 0.12.2</li> <li>• lxml 3.2.3</li> <li>• markupsafe 0.18</li> <li>• matplotlib 1.3.1 <i>LM</i></li> <li>• mdp 3.3</li> <li>• mingw 4.7 <i>W</i></li> <li>• mock 1.0.1</li> <li>• netcdf4 1.0.7 <i>LM</i></li> <li>• networkx 1.8.1</li> <li>• nose 1.3.0</li> <li>• numba 0.12.0</li> <li>• numexpr 2.3.0</li> <li>• numpy 1.8.0</li> </ul>	<ul style="list-style-type: none"> <li>• openpyxl 1.8.2</li> <li>• pandas 0.13.0</li> <li>• patsy 0.2.1</li> <li>• pillow 2.1.0</li> <li>• pip 1.5.2</li> <li>• ply 3.4</li> <li>• psutil 1.2.1</li> <li>• py 1.4.20</li> <li>• pycosat 0.6.0</li> <li>• pycparser 2.10</li> <li>• pycrypto 2.6.1</li> <li>• pyflakes 0.7.3</li> <li>• pygments 1.6</li> <li>• pykit 0.1.0</li> <li>• pyparsing 2.0.1</li> <li>• pyreadline 2.0 <i>W</i></li> <li>• pyside 1.1.2 <i>W</i></li> <li>• pytables 3.1.0</li> <li>• pytest 2.5.2</li> <li>• python 3.3.3</li> <li>• pytz 2013b</li> <li>• pyyaml 3.10</li> </ul>	<ul style="list-style-type: none"> <li>• pyzmq 2.2.0.1</li> <li>• redis 2.6.9 <i>LM</i></li> <li>• redis-py 2.9.1 <i>LM</i></li> <li>• requests 2.2.1</li> <li>• scikit-image 0.9.3</li> <li>• scikit-learn 0.14.1</li> <li>• scipy 0.13.3</li> <li>• setuptools 2.1</li> <li>• six 1.5.2</li> <li>• sphinx 1.2.1</li> <li>• sqlalchemy 0.9.2</li> <li>•</li> <li>• ssl_match_hostname 3.4.0.2</li> <li>• statsmodels 0.5.0</li> <li>• sympy 0.7.4.1</li> <li>• tornado 3.2.0</li> <li>• ujson 1.33</li> <li>• werkzeug 0.9.4</li> <li>• xlrd 0.9.2</li> <li>• yaml 0.1.4 <i>LM</i></li> <li>• zeromq 2.2.0 <i>LM</i></li> <li>• zlib 1.2.7</li> </ul>
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## Python 2.6 (available through conda):

<ul style="list-style-type: none"> <li>• argcomplete 0.6.7</li> <li>• argparse 1.2.1</li> <li>• astropy 0.3.0</li> <li>• atom 0.3.6</li> <li>• beautiful-soup 4.3.1</li> <li>• biopython 1.63</li> <li>• bitarray 0.8.1</li> <li>• blaze 0.4.1</li> <li>• blz 0.6.1</li> <li>• boto 2.24.0</li> <li>• cairo 1.12.2 <i>L</i></li> <li>• casuarius 1.1</li> <li>• cdecimal 2.3</li> <li>• colorama 0.2.7</li> <li>• configobj 4.7.2</li> <li>• curl 7.30.0 <i>LM</i></li> <li>• cython 0.20</li> <li>• datashape 0.1.0</li> <li>• dateutil 2.1</li> <li>• disco 0.4.4 <i>L</i></li> <li>• docutils 0.11</li> <li>• dynd-python 0.6.0</li> <li>• erlang R15B01 <i>L</i></li> <li>• flask 0.10.1</li> <li>• freetype 2.4.10</li> <li>• future 0.11.2</li> <li>• gevent 1.0</li> <li>• gevent-websocket 0.9.2</li> </ul>	<ul style="list-style-type: none"> <li>• gevent_zeromq 0.2.5</li> <li>• greenlet 0.4.2</li> <li>• grin 1.2.1</li> <li>• h5py 2.2.1</li> <li>• hdf5 1.8.9</li> <li>• ipython 1.1.0</li> <li>• itsdangerous 0.23</li> <li>• jinja2 2.7.2</li> <li>• kiwisolver 0.1.2</li> <li>• libdynd 0.6.0 <i>LM</i></li> <li>• libnetcdf 4.2.1.1 <i>LM</i></li> <li>• libpng 1.5.13 <i>LM</i></li> <li>• libsodium 0.4.5 <i>L</i></li> <li>• libtiff 4.0.2 <i>LM</i></li> <li>• libxml2 2.9.0 <i>LM</i></li> <li>• libxslt 1.1.28 <i>LM</i></li> <li>• llvm 3.3</li> <li>• llvmpy 0.12.2</li> <li>• lxml 3.2.3</li> <li>• markupsafe 0.18</li> <li>• matplotlib 1.3.1 <i>LM</i></li> <li>• mdp 3.3</li> <li>• mingw 4.7 <i>W</i></li> <li>• mock 1.0.1</li> <li>• mpi4py 1.3 <i>L</i></li> <li>• mpich2 1.4.1p1 <i>L</i></li> <li>• netcdf4 1.0.7 <i>LM</i></li> <li>• networkx 1.8.1</li> </ul>	<ul style="list-style-type: none"> <li>• nltk 2.0.4</li> <li>• nose 1.3.0</li> <li>• numba 0.12.0</li> <li>• numexpr 2.3.0</li> <li>• numpy 1.8.0</li> <li>• opencv 2.4.6 <i>L</i></li> <li>• ordereddict 1.1</li> <li>• pandas 0.13.0</li> <li>• patsy 0.2.1</li> <li>• pep8 1.4.6</li> <li>• pil 1.1.7</li> <li>• pip 1.5.2</li> <li>• ply 3.4</li> <li>• psutil 1.2.1</li> <li>• py 1.4.20</li> <li>• py2cairo 1.10.0 <i>L</i></li> <li>• pycosat 0.6.0</li> <li>• pycparser 2.10</li> <li>• pycrypto 2.6.1</li> <li>• pycurl 7.19.0 <i>LM</i></li> <li>• pyflakes 0.7.3</li> <li>• pygments 1.6</li> <li>• pykit 0.1.0</li> <li>• pyparsing 2.0.1</li> <li>• pyreadline 2.0 <i>W</i></li> <li>• pysam 0.6 <i>LM</i></li> <li>• pytables 3.1.0 <i>LM</i></li> <li>• pytest 2.5.2</li> </ul>	<ul style="list-style-type: none"> <li>• python 2.6.9</li> <li>• pytz 2013b</li> <li>• pyyaml 3.10</li> <li>• pyzmq 2.2.0.1</li> <li>• redis 2.6.9 <i>LM</i></li> <li>• redis-py 2.9.1 <i>LM</i></li> <li>• requests 2.2.1</li> <li>• scikit-image 0.9.3</li> <li>• scikit-learn 0.14.1</li> <li>• scipy 0.13.3</li> <li>• setuptools 2.1</li> <li>• six 1.5.2</li> <li>• sphinx 1.2.1</li> <li>• sqlalchemy 0.9.2</li> <li>•</li> <li>• ssl_match_hostname 3.4.0.2</li> <li>• statsmodels 0.5.0</li> <li>• sympy 0.7.4.1</li> <li>• theano 0.6.0 <i>L</i></li> <li>• tornado 3.2.0</li> <li>• traits 4.4.0</li> <li>• ujson 1.33</li> <li>• unittest2 0.5.1</li> <li>• werkzeug 0.9.4</li> <li>• xlrd 0.9.2</li> <li>• xlwt 0.7.5</li> <li>• yaml 0.1.4 <i>LM</i></li> <li>• zeromq 2.2.0 <i>LM</i></li> <li>• zlib 1.2.7</li> </ul>
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Only available on: *L* (Linux) - *M* (macOS) - *W* (Windows)

## Packages included in Anaconda 1.9.1

**Python 2.7 (included in installer):**

<ul style="list-style-type: none"> <li>• apptools 4.2.1</li> <li>• argcomplete 0.6.7</li> <li>• astropy 0.3.0</li> <li>• atom 0.3.7</li> <li>• beautiful-soup 4.3.1</li> <li>• binstar 0.4.4</li> <li>• biopython 1.63</li> <li>• bitarray 0.8.1</li> <li>• blaze 0.4.2</li> <li>• blz 0.6.1</li> <li>• bokeh 0.4.1</li> <li>• boto 2.25.0</li> <li>• cairo 1.12.2 <i>L</i></li> <li>• casuarious 1.1</li> <li>• cdecimal 2.3</li> <li>• chaco 4.4.1</li> <li>• colorama 0.2.7</li> <li>• conda 3.0.6</li> <li>• conda-build 1.2.0</li> <li>• configobj 4.7.2</li> <li>• cubes 0.10.2</li> <li>• curl 7.30.0 <i>LM</i></li> <li>• cython 0.20.1</li> <li>• datashape 0.1.1</li> <li>• dateutil 2.1</li> <li>• disco 0.4.4 <i>L</i></li> <li>• docutils 0.11</li> <li>• dynd-python 0.6.1</li> <li>• enable 4.3.0</li> <li>• enaml 0.9.1</li> <li>• envisage 4.4.0</li> <li>• erlang R15B01 <i>L</i></li> <li>• flask 0.10.1</li> <li>• freetype 2.4.10</li> </ul>	<ul style="list-style-type: none"> <li>• future 0.11.2</li> <li>• gevent 1.0</li> <li>• gevent-websocket 0.9.2</li> <li>• gevent_zeromq 0.2.5</li> <li>• greenlet 0.4.2</li> <li>• grin 1.2.1</li> <li>• h5py 2.2.1</li> <li>• hdf5 1.8.9</li> <li>• ipython 1.1.0</li> <li>• itsdangerous 0.23</li> <li>• jinja2 2.7.2</li> <li>• keyring 3.3</li> <li>• kiwisolver 0.1.2</li> <li>• launcher 0.1.2</li> <li>• libnetcdf 4.2.1.1 <i>LM</i></li> <li>• libpng 1.5.13 <i>LM</i></li> <li>• libsodium 0.4.5 <i>L</i></li> <li>• libtiff 4.0.2 <i>LM</i></li> <li>• libxml2 2.9.0 <i>LM</i></li> <li>• libxslt 1.1.28 <i>LM</i></li> <li>• llvm 3.3</li> <li>• llvmpy 0.12.3</li> <li>• lxml 3.3.1</li> <li>• markupsafe 0.18</li> <li>• matplotlib 1.3.1</li> <li>• mayavi 4.3.1</li> <li>• mdp 3.3</li> <li>• menuinst 1.0.3 <i>W</i></li> <li>• mingw 4.7 <i>W</i></li> <li>• mock 1.0.1</li> <li>• mpi4py 1.3 <i>L</i></li> <li>• mpich2 1.4.1p1 <i>L</i></li> <li>• netcdf4 1.0.8 <i>LM</i></li> <li>• networkx 1.8.1</li> </ul>	<ul style="list-style-type: none"> <li>• nltk 2.0.4</li> <li>• nose 1.3.0</li> <li>• numba 0.12.1</li> <li>• numexpr 2.3.1</li> <li>• numpy 1.8.0</li> <li>• opencv 2.4.6 <i>L</i></li> <li>• openpyxl 1.8.2</li> <li>• openssl 1.0.1c <i>LM</i></li> <li>• pandas 0.13.1</li> <li>• patsy 0.2.1</li> <li>• pep8 1.4.6</li> <li>• pil 1.1.7</li> <li>• pip 1.5.2</li> <li>• ply 3.4</li> <li>• psutil 1.2.1</li> <li>• py 1.4.20</li> <li>• py2cairo 1.10.0 <i>L</i></li> <li>• pyaudio 0.2.7 <i>M</i></li> <li>• pycosat 0.6.0</li> <li>• pycparser 2.10</li> <li>• pycrypto 2.6.1</li> <li>• pycurl 7.19.0 <i>LM</i></li> <li>• pyface 4.4.0</li> <li>• pyflakes 0.7.3</li> <li>• pygments 1.6</li> <li>• pykit 0.2.0</li> <li>• pyparsing 2.0.1</li> <li>• pyreadline 2.0 <i>W</i></li> <li>• pysal 1.6.0</li> <li>• pysam 0.6 <i>LM</i></li> <li>• pyside 1.2.1</li> <li>• pytables 3.1.0</li> <li>• pytest 2.5.2</li> <li>• python 2.7.6</li> </ul>	<ul style="list-style-type: none"> <li>• pytz 2013b</li> <li>• pywin32 218.4 <i>W</i></li> <li>• pyyaml 3.10</li> <li>• pyzmq 2.2.0.1</li> <li>• qt 4.8.5</li> <li>• redis 2.6.9 <i>LM</i></li> <li>• redis-py 2.9.1 <i>LM</i></li> <li>• requests 2.2.1</li> <li>• rope 0.9.4</li> <li>• scikit-image 0.9.3</li> <li>• scikit-learn 0.14.1</li> <li>• scipy 0.13.3</li> <li>• setuptools 2.2</li> <li>• six 1.5.2</li> <li>• sphinx 1.2.1</li> <li>• spyder 2.2.5</li> <li>• sqlalchemy 0.9.2</li> <li>•</li> <li>• ssl_match_hostname 3.4.0.2</li> <li>• statsmodels 0.5.0</li> <li>• sympy 0.7.4.1</li> <li>• theano 0.6.0 <i>L</i></li> <li>• tk 8.5.13 <i>LM</i></li> <li>• tornado 3.2.0</li> <li>• traits 4.4.0</li> <li>• traitsui 4.4.0</li> <li>• ujson 1.33</li> <li>• vtk 5.10.1</li> <li>• werkzeug 0.9.4</li> <li>• xlrd 0.9.2</li> <li>• xlswriter 0.5.2</li> <li>• xlwt 0.7.5</li> <li>• yaml 0.1.4 <i>LM</i></li> <li>• zeromq 2.2.0 <i>LM</i></li> <li>• zlib 1.2.7</li> </ul>
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Only available on: *L* (Linux) - *M* (macOS) - *W* (Windows)

## Python 3.3 (available through conda):

<ul style="list-style-type: none"> <li>• argcomplete 0.6.7</li> <li>• astropy 0.3.0</li> <li>• beautiful-soup 4.3.1</li> <li>• bitarray 0.8.1</li> <li>• blaze 0.4.2</li> <li>• blz 0.6.1</li> <li>• bokeh 0.4.1</li> <li>• cdecimal 2.3</li> <li>• colorama 0.2.7</li> <li>• curl 7.30.0 <i>LM</i></li> <li>• cython 0.20.1</li> <li>• datashape 0.1.1</li> <li>• dateutil 2.1</li> <li>• docutils 0.11</li> <li>• dynd-python 0.6.1</li> <li>• flask 0.10.1</li> <li>• freetype 2.4.10</li> <li>• future 0.11.2</li> <li>• greenlet 0.4.2</li> <li>• h5py 2.2.1</li> <li>• hdf5 1.8.9</li> <li>• ipython 1.1.0</li> <li>• itsdangerous 0.23</li> </ul>	<ul style="list-style-type: none"> <li>• jinja2 2.7.2</li> <li>• libnetcdf 4.2.1.1 <i>LM</i></li> <li>• libpng 1.5.13 <i>LM</i></li> <li>• libsodium 0.4.5 <i>L</i></li> <li>• libtiff 4.0.2 <i>LM</i></li> <li>• libxml2 2.9.0 <i>LM</i></li> <li>• libxslt 1.1.28 <i>LM</i></li> <li>• llvm 3.3</li> <li>• llvmpy 0.12.3</li> <li>• lxml 3.3.1</li> <li>• markupsafe 0.18</li> <li>• matplotlib 1.3.1 <i>LM</i></li> <li>• mdp 3.3</li> <li>• mingw 4.7 <i>W</i></li> <li>• mock 1.0.1</li> <li>• netcdf4 1.0.8 <i>LM</i></li> <li>• networkx 1.8.1</li> <li>• nose 1.3.0</li> <li>• numba 0.12.1</li> <li>• numexpr 2.3.1</li> <li>• numpy 1.8.0</li> <li>• openpyxl 1.8.2</li> <li>• openssl 1.0.1c <i>LM</i></li> </ul>	<ul style="list-style-type: none"> <li>• pandas 0.13.1</li> <li>• patsy 0.2.1</li> <li>• pillow 2.1.0</li> <li>• pip 1.5.2</li> <li>• ply 3.4</li> <li>• psutil 1.2.1</li> <li>• py 1.4.20</li> <li>• pycosat 0.6.0</li> <li>• pycparser 2.10</li> <li>• pycrypto 2.6.1</li> <li>• pyflakes 0.7.3</li> <li>• pygments 1.6</li> <li>• pykit 0.2.0</li> <li>• pyparsing 2.0.1</li> <li>• pyreadline 2.0 <i>W</i></li> <li>• pyside 1.2.1 <i>W</i></li> <li>• pytables 3.1.0</li> <li>• pytest 2.5.2</li> <li>• python 3.3.4</li> <li>• pytz 2013b</li> <li>• pyyaml 3.10</li> <li>• pyzmq 2.2.0.1</li> <li>• redis 2.6.9 <i>LM</i></li> </ul>	<ul style="list-style-type: none"> <li>• redis-py 2.9.1 <i>LM</i></li> <li>• requests 2.2.1</li> <li>• scikit-image 0.9.3</li> <li>• scikit-learn 0.14.1</li> <li>• scipy 0.13.3</li> <li>• setuptools 2.2</li> <li>• six 1.5.2</li> <li>• sphinx 1.2.1</li> <li>• sqlalchemy 0.9.2</li> <li>•</li> <li>• ssl_match_hostname 3.4.0.2</li> <li>• statsmodels 0.5.0</li> <li>• sympy 0.7.4.1</li> <li>• tk 8.5.13 <i>LM</i></li> <li>• tornado 3.2.0</li> <li>• ujson 1.33</li> <li>• werkzeug 0.9.4</li> <li>• xlrd 0.9.2</li> <li>• xlsxwriter 0.5.2</li> <li>• yaml 0.1.4 <i>LM</i></li> <li>• zeromq 2.2.0 <i>LM</i></li> <li>• zlib 1.2.7</li> </ul>
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**Python 2.6 (available through conda):**

<ul style="list-style-type: none"> <li>• argcomplete 0.6.7</li> <li>• argparse 1.2.1</li> <li>• astropy 0.3.0</li> <li>• atom 0.3.7</li> <li>• beautiful-soup 4.3.1</li> <li>• biopython 1.63</li> <li>• bitarray 0.8.1</li> <li>• blaze 0.4.2 <i>LM</i></li> <li>• blz 0.6.1</li> <li>• boto 2.25.0</li> <li>• cairo 1.12.2 <i>L</i></li> <li>• casuarius 1.1</li> <li>• cdecimal 2.3</li> <li>• colorama 0.2.7</li> <li>• configobj 4.7.2</li> <li>• curl 7.30.0 <i>LM</i></li> <li>• cython 0.20.1</li> <li>• datashape 0.1.1</li> <li>• dateutil 2.1</li> <li>• disco 0.4.4 <i>L</i></li> <li>• docutils 0.11</li> <li>• dynd-python 0.6.1</li> <li>• erlang R15B01 <i>L</i></li> <li>• flask 0.10.1</li> <li>• freetype 2.4.10</li> <li>• future 0.11.2</li> <li>• gevent 1.0</li> <li>• gevent-websocket 0.9.2</li> <li>• gevent_zeromq 0.2.5</li> </ul>	<ul style="list-style-type: none"> <li>• greenlet 0.4.2</li> <li>• grin 1.2.1</li> <li>• h5py 2.2.1</li> <li>• hdf5 1.8.9</li> <li>• ipython 1.1.0</li> <li>• itsdangerous 0.23</li> <li>• jinja2 2.7.2</li> <li>• kiwisolver 0.1.2</li> <li>• libnetcdf 4.2.1.1 <i>LM</i></li> <li>• libpng 1.5.13 <i>LM</i></li> <li>• libsodium 0.4.5 <i>L</i></li> <li>• libtiff 4.0.2 <i>LM</i></li> <li>• libxml2 2.9.0 <i>LM</i></li> <li>• libxslt 1.1.28 <i>LM</i></li> <li>• llvm 3.3</li> <li>• llvmpy 0.12.3</li> <li>• lxml 3.3.1</li> <li>• markupsafe 0.18</li> <li>• matplotlib 1.3.1 <i>LM</i></li> <li>• mdp 3.3</li> <li>• mingw 4.7 <i>W</i></li> <li>• mock 1.0.1</li> <li>• mpi4py 1.3 <i>L</i></li> <li>• mpich2 1.4.1p1 <i>L</i></li> <li>• netcdf4 1.0.8 <i>LM</i></li> <li>• networkx 1.8.1</li> <li>• nltk 2.0.4</li> <li>• nose 1.3.0</li> <li>• numba 0.12.1</li> </ul>	<ul style="list-style-type: none"> <li>• numexpr 2.3.1</li> <li>• numpy 1.8.0</li> <li>• opencv 2.4.6 <i>L</i></li> <li>• openssl 1.0.1c <i>LM</i></li> <li>• ordereddict 1.1</li> <li>• pandas 0.13.1</li> <li>• patsy 0.2.1</li> <li>• pep8 1.4.6</li> <li>• pil 1.1.7</li> <li>• pip 1.5.2</li> <li>• ply 3.4</li> <li>• psutil 1.2.1</li> <li>• py 1.4.20</li> <li>• py2cairo 1.10.0 <i>L</i></li> <li>• pycosat 0.6.0</li> <li>• pycparser 2.10</li> <li>• pycrypto 2.6.1</li> <li>• pycurl 7.19.0 <i>LM</i></li> <li>• pyflakes 0.7.3</li> <li>• pygments 1.6</li> <li>• pykit 0.2.0</li> <li>• pyparsing 2.0.1</li> <li>• pyreadline 2.0 <i>W</i></li> <li>• pysam 0.6 <i>LM</i></li> <li>• pytables 3.1.0 <i>LM</i></li> <li>• pytest 2.5.2</li> <li>• python 2.6.9</li> <li>• pytz 2013b</li> <li>• pyyaml 3.10</li> </ul>	<ul style="list-style-type: none"> <li>• pyzmq 2.2.0.1</li> <li>• redis 2.6.9 <i>LM</i></li> <li>• redis-py 2.9.1 <i>LM</i></li> <li>• requests 2.2.1</li> <li>• scikit-image 0.9.3</li> <li>• scikit-learn 0.14.1</li> <li>• scipy 0.13.3</li> <li>• setuptools 2.2</li> <li>• six 1.5.2</li> <li>• sphinx 1.2.1</li> <li>• sqlalchemy 0.9.2</li> <li>•</li> <li>• ssl_match_hostname 3.4.0.2</li> <li>• statsmodels 0.5.0</li> <li>• sympy 0.7.4.1</li> <li>• theano 0.6.0 <i>L</i></li> <li>• tk 8.5.13 <i>LM</i></li> <li>• tornado 3.2.0</li> <li>• traits 4.4.0</li> <li>• ujson 1.33</li> <li>• unittest2 0.5.1</li> <li>• werkzeug 0.9.4</li> <li>• xlrd 0.9.2</li> <li>• xlswriter 0.5.2</li> <li>• xlwt 0.7.5</li> <li>• yaml 0.1.4 <i>LM</i></li> <li>• zeromq 2.2.0 <i>LM</i></li> <li>• zlib 1.2.7</li> </ul>
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Only available on: *L* (Linux) - *M* (macOS) - *W* (Windows)

**Packages included in Anaconda 1.9.2**

## Python 2.7 (included in installer):

<ul style="list-style-type: none"> <li>• apptools 4.2.1</li> <li>• argcomplete 0.6.7</li> <li>• astropy 0.3.0</li> <li>• atom 0.3.7</li> <li>• beautiful-soup 4.3.1</li> <li>• binstar 0.4.4</li> <li>• biopython 1.63</li> <li>• bitarray 0.8.1</li> <li>• blaze 0.4.2</li> <li>• blz 0.6.1</li> <li>• bokeh 0.4.1</li> <li>• boto 2.25.0</li> <li>• cairo 1.12.2 <i>L</i></li> <li>• casuarious 1.1</li> <li>• cdecimal 2.3</li> <li>• chaco 4.4.1</li> <li>• colorama 0.2.7</li> <li>• conda 3.4.1</li> <li>• conda-build 1.3.1</li> <li>• configobj 4.7.2</li> <li>• cubes 0.10.2</li> <li>• curl 7.30.0 <i>LM</i></li> <li>• cython 0.20.1</li> <li>• datashape 0.1.1</li> <li>• dateutil 2.1</li> <li>• disco 0.4.4 <i>L</i></li> <li>• docutils 0.11</li> <li>• dynd-python 0.6.1</li> <li>• enable 4.3.0</li> <li>• enaml 0.9.1</li> <li>• envisage 4.4.0</li> <li>• erlang R15B01 <i>L</i></li> <li>• flask 0.10.1</li> <li>• freetype 2.4.10</li> </ul>	<ul style="list-style-type: none"> <li>• future 0.11.2</li> <li>• gevent 1.0</li> <li>• gevent-websocket 0.9.2</li> <li>• gevent_zeromq 0.2.5</li> <li>• greenlet 0.4.2</li> <li>• grin 1.2.1</li> <li>• h5py 2.2.1</li> <li>• hdf5 1.8.9</li> <li>• ipython 1.1.0</li> <li>• itsdangerous 0.23</li> <li>• jinja2 2.7.2</li> <li>• keyring 3.3</li> <li>• kiwisolver 0.1.2</li> <li>• launcher 0.1.2</li> <li>• libnetcdf 4.2.1.1 <i>LM</i></li> <li>• libpng 1.5.13 <i>LM</i></li> <li>• libsodium 0.4.5 <i>L</i></li> <li>• libtiff 4.0.2 <i>LM</i></li> <li>• libxml2 2.9.0 <i>LM</i></li> <li>• libxslt 1.1.28 <i>LM</i></li> <li>• llvm 3.3</li> <li>• llvmpy 0.12.3</li> <li>• lxml 3.3.1</li> <li>• markupsafe 0.18</li> <li>• matplotlib 1.3.1</li> <li>• mayavi 4.3.1</li> <li>• mdp 3.3</li> <li>• menuinst 1.0.3 <i>W</i></li> <li>• mingw 4.7 <i>W</i></li> <li>• mock 1.0.1</li> <li>• mpi4py 1.3 <i>L</i></li> <li>• mpich2 1.4.1p1 <i>L</i></li> <li>• netcdf4 1.0.8 <i>LM</i></li> <li>• networkx 1.8.1</li> </ul>	<ul style="list-style-type: none"> <li>• nltk 2.0.4</li> <li>• nose 1.3.0</li> <li>• numba 0.12.1</li> <li>• numexpr 2.3.1</li> <li>• numpy 1.8.0</li> <li>• opencv 2.4.6 <i>L</i></li> <li>• openpyxl 1.8.2</li> <li>• openssl 1.0.1g <i>LM</i></li> <li>• pandas 0.13.1</li> <li>• patsy 0.2.1</li> <li>• pep8 1.4.6</li> <li>• pil 1.1.7</li> <li>• pip 1.5.2</li> <li>• ply 3.4</li> <li>• psutil 1.2.1</li> <li>• py 1.4.20</li> <li>• py2cairo 1.10.0 <i>L</i></li> <li>• pyaudio 0.2.7 <i>M</i></li> <li>• pycosat 0.6.0</li> <li>• pycparser 2.10</li> <li>• pycrypto 2.6.1</li> <li>• pycurl 7.19.0 <i>LM</i></li> <li>• pyface 4.4.0</li> <li>• pyflakes 0.7.3</li> <li>• pygments 1.6</li> <li>• pykit 0.2.0</li> <li>• pyparsing 2.0.1</li> <li>• pyreadline 2.0 <i>W</i></li> <li>• pysal 1.6.0</li> <li>• pysam 0.6 <i>LM</i></li> <li>• pyside 1.2.1</li> <li>• pytables 3.1.0</li> <li>• pytest 2.5.2</li> <li>• python 2.7.6</li> </ul>	<ul style="list-style-type: none"> <li>• pytz 2013b</li> <li>• pywin32 218.4 <i>W</i></li> <li>• pyyaml 3.10</li> <li>• pyzmq 2.2.0.1</li> <li>• qt 4.8.5</li> <li>• redis 2.6.9 <i>LM</i></li> <li>• redis-py 2.9.1 <i>LM</i></li> <li>• requests 2.2.1</li> <li>• rope 0.9.4</li> <li>• scikit-image 0.9.3</li> <li>• scikit-learn 0.14.1</li> <li>• scipy 0.13.3</li> <li>• setuptools 2.2</li> <li>• six 1.5.2</li> <li>• sphinx 1.2.1</li> <li>• spyder 2.2.5</li> <li>• sqlalchemy 0.9.2</li> <li>•</li> <li>• ssl_match_hostname 3.4.0.2</li> <li>• statsmodels 0.5.0</li> <li>• sympy 0.7.4.1</li> <li>• theano 0.6.0 <i>L</i></li> <li>• tk 8.5.13 <i>LM</i></li> <li>• tornado 3.2.0</li> <li>• traits 4.4.0</li> <li>• traitsui 4.4.0</li> <li>• ujson 1.33</li> <li>• vtk 5.10.1</li> <li>• werkzeug 0.9.4</li> <li>• xlrd 0.9.2</li> <li>• xlswriter 0.5.2</li> <li>• xlwt 0.7.5</li> <li>• yaml 0.1.4 <i>LM</i></li> <li>• zeromq 2.2.0 <i>LM</i></li> <li>• zlib 1.2.7</li> </ul>
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Only available on: *L* (Linux) - *M* (macOS) - *W* (Windows)

**Python 3.3 (available through conda):**

<ul style="list-style-type: none"> <li>• argcomplete 0.6.7</li> <li>• astropy 0.3.0</li> <li>• beautiful-soup 4.3.1</li> <li>• bitarray 0.8.1</li> <li>• blaze 0.4.2</li> <li>• blz 0.6.1</li> <li>• bokeh 0.4.1</li> <li>• cdecimal 2.3</li> <li>• colorama 0.2.7</li> <li>• curl 7.30.0 <i>LM</i></li> <li>• cython 0.20.1</li> <li>• datashape 0.1.1</li> <li>• dateutil 2.1</li> <li>• docutils 0.11</li> <li>• dynd-python 0.6.1</li> <li>• flask 0.10.1</li> <li>• freetype 2.4.10</li> <li>• future 0.11.2</li> <li>• greenlet 0.4.2</li> <li>• h5py 2.2.1</li> <li>• hdf5 1.8.9</li> <li>• ipython 1.1.0</li> <li>• itsdangerous 0.23</li> </ul>	<ul style="list-style-type: none"> <li>• jinja2 2.7.2</li> <li>• libnetcdf 4.2.1.1 <i>LM</i></li> <li>• libpng 1.5.13 <i>LM</i></li> <li>• libsodium 0.4.5 <i>L</i></li> <li>• libtiff 4.0.2 <i>LM</i></li> <li>• libxml2 2.9.0 <i>LM</i></li> <li>• libxslt 1.1.28 <i>LM</i></li> <li>• llvm 3.3</li> <li>• llvmpy 0.12.3</li> <li>• lxml 3.3.1</li> <li>• markupsafe 0.18</li> <li>• matplotlib 1.3.1 <i>LM</i></li> <li>• mdp 3.3</li> <li>• mingw 4.7 <i>W</i></li> <li>• mock 1.0.1</li> <li>• netcdf4 1.0.8 <i>LM</i></li> <li>• networkx 1.8.1</li> <li>• nose 1.3.0</li> <li>• numba 0.12.1</li> <li>• numexpr 2.3.1</li> <li>• numpy 1.8.0</li> <li>• openpyxl 1.8.2</li> <li>• openssl 1.0.1g <i>LM</i></li> </ul>	<ul style="list-style-type: none"> <li>• pandas 0.13.1</li> <li>• patsy 0.2.1</li> <li>• pillow 2.1.0</li> <li>• pip 1.5.2</li> <li>• ply 3.4</li> <li>• psutil 1.2.1</li> <li>• py 1.4.20</li> <li>• pycosat 0.6.0</li> <li>• pycparser 2.10</li> <li>• pycrypto 2.6.1</li> <li>• pyflakes 0.7.3</li> <li>• pygments 1.6</li> <li>• pykit 0.2.0</li> <li>• pyparsing 2.0.1</li> <li>• pyreadline 2.0 <i>W</i></li> <li>• pyside 1.2.1 <i>W</i></li> <li>• pytables 3.1.0</li> <li>• pytest 2.5.2</li> <li>• python 3.3.4</li> <li>• pytz 2013b</li> <li>• pyyaml 3.10</li> <li>• pyzmq 2.2.0.1</li> <li>• redis 2.6.9 <i>LM</i></li> </ul>	<ul style="list-style-type: none"> <li>• redis-py 2.9.1 <i>LM</i></li> <li>• requests 2.2.1</li> <li>• scikit-image 0.9.3</li> <li>• scikit-learn 0.14.1</li> <li>• scipy 0.13.3</li> <li>• setuptools 2.2</li> <li>• six 1.5.2</li> <li>• sphinx 1.2.1</li> <li>• sqlalchemy 0.9.2</li> <li>•</li> <li>• ssl_match_hostname 3.4.0.2</li> <li>• statsmodels 0.5.0</li> <li>• sympy 0.7.4.1</li> <li>• tk 8.5.13 <i>LM</i></li> <li>• tornado 3.2.0</li> <li>• ujson 1.33</li> <li>• werkzeug 0.9.4</li> <li>• xlrd 0.9.2</li> <li>• xlsxwriter 0.5.2</li> <li>• yaml 0.1.4 <i>LM</i></li> <li>• zeromq 2.2.0 <i>LM</i></li> <li>• zlib 1.2.7</li> </ul>
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## Python 2.6 (available through conda):

<ul style="list-style-type: none"> <li>• argcomplete 0.6.7</li> <li>• argparse 1.2.1</li> <li>• astropy 0.3.0</li> <li>• atom 0.3.7</li> <li>• beautiful-soup 4.3.1</li> <li>• biopython 1.63</li> <li>• bitarray 0.8.1</li> <li>• blaze 0.4.2 <i>LM</i></li> <li>• blz 0.6.1</li> <li>• boto 2.25.0</li> <li>• cairo 1.12.2 <i>L</i></li> <li>• casuarius 1.1</li> <li>• cdecimal 2.3</li> <li>• colorama 0.2.7</li> <li>• configobj 4.7.2</li> <li>• curl 7.30.0 <i>LM</i></li> <li>• cython 0.20.1</li> <li>• datashape 0.1.1</li> <li>• dateutil 2.1</li> <li>• disco 0.4.4 <i>L</i></li> <li>• docutils 0.11</li> <li>• dynd-python 0.6.1</li> <li>• erlang R15B01 <i>L</i></li> <li>• flask 0.10.1</li> <li>• freetype 2.4.10</li> <li>• future 0.11.2</li> <li>• gevent 1.0</li> <li>• gevent-websocket 0.9.2</li> <li>• gevent_zeromq 0.2.5</li> </ul>	<ul style="list-style-type: none"> <li>• greenlet 0.4.2</li> <li>• grin 1.2.1</li> <li>• h5py 2.2.1</li> <li>• hdf5 1.8.9</li> <li>• ipython 1.1.0</li> <li>• itsdangerous 0.23</li> <li>• jinja2 2.7.2</li> <li>• kiwisolver 0.1.2</li> <li>• libnetcdf 4.2.1.1 <i>LM</i></li> <li>• libpng 1.5.13 <i>LM</i></li> <li>• libsodium 0.4.5 <i>L</i></li> <li>• libtiff 4.0.2 <i>LM</i></li> <li>• libxml2 2.9.0 <i>LM</i></li> <li>• libxslt 1.1.28 <i>LM</i></li> <li>• llvm 3.3</li> <li>• llvmpy 0.12.3</li> <li>• lxml 3.3.1</li> <li>• markupsafe 0.18</li> <li>• matplotlib 1.3.1 <i>LM</i></li> <li>• mdp 3.3</li> <li>• mingw 4.7 <i>W</i></li> <li>• mock 1.0.1</li> <li>• mpi4py 1.3 <i>L</i></li> <li>• mpich2 1.4.1p1 <i>L</i></li> <li>• netcdf4 1.0.8 <i>LM</i></li> <li>• networkx 1.8.1</li> <li>• nltk 2.0.4</li> <li>• nose 1.3.0</li> <li>• numba 0.12.1</li> </ul>	<ul style="list-style-type: none"> <li>• numexpr 2.3.1</li> <li>• numpy 1.8.0</li> <li>• opencv 2.4.6 <i>L</i></li> <li>• openssl 1.0.1g <i>LM</i></li> <li>• ordereddict 1.1</li> <li>• pandas 0.13.1</li> <li>• patsy 0.2.1</li> <li>• pep8 1.4.6</li> <li>• pil 1.1.7</li> <li>• pip 1.5.2</li> <li>• ply 3.4</li> <li>• psutil 1.2.1</li> <li>• py 1.4.20</li> <li>• py2cairo 1.10.0 <i>L</i></li> <li>• pycosat 0.6.0</li> <li>• pycparser 2.10</li> <li>• pycrypto 2.6.1</li> <li>• pycurl 7.19.0 <i>LM</i></li> <li>• pyflakes 0.7.3</li> <li>• pygments 1.6</li> <li>• pykit 0.2.0</li> <li>• pyparsing 2.0.1</li> <li>• pyreadline 2.0 <i>W</i></li> <li>• pysam 0.6 <i>LM</i></li> <li>• pytables 3.1.0 <i>LM</i></li> <li>• pytest 2.5.2</li> <li>• python 2.6.9</li> <li>• pytz 2013b</li> <li>• pyyaml 3.10</li> </ul>	<ul style="list-style-type: none"> <li>• pyzmq 2.2.0.1</li> <li>• redis 2.6.9 <i>LM</i></li> <li>• redis-py 2.9.1 <i>LM</i></li> <li>• requests 2.2.1</li> <li>• scikit-image 0.9.3</li> <li>• scikit-learn 0.14.1</li> <li>• scipy 0.13.3</li> <li>• setuptools 2.2</li> <li>• six 1.5.2</li> <li>• sphinx 1.2.1</li> <li>• sqlalchemy 0.9.2</li> <li>•</li> <li>• ssl_match_hostname 3.4.0.2</li> <li>• statsmodels 0.5.0</li> <li>• sympy 0.7.4.1</li> <li>• theano 0.6.0 <i>L</i></li> <li>• tk 8.5.13 <i>LM</i></li> <li>• tornado 3.2.0</li> <li>• traits 4.4.0</li> <li>• ujson 1.33</li> <li>• unittest2 0.5.1</li> <li>• werkzeug 0.9.4</li> <li>• xlrd 0.9.2</li> <li>• xlswriter 0.5.2</li> <li>• xlwt 0.7.5</li> <li>• yaml 0.1.4 <i>LM</i></li> <li>• zeromq 2.2.0 <i>LM</i></li> <li>• zlib 1.2.7</li> </ul>
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Only available on: *L* (Linux) - *M* (macOS) - *W* (Windows)

## Packages included in Anaconda 2.0.1 for Python version 2.6

Python version: 2.6

Number of supported packages: 171

Name	Version	License	In Installer
argcomplete	0.6.7	Apache Software License	False
argparse	1.2.1	PSF	False
astroid	1.1.1	LGPL	False
astropy	0.3.2	BSD	False
atom	0.3.7	BSD	False
basemap <sup>Linux Mac</sup>	1.0.7	PSF	False

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beautiful-soup	4.3.1	PSF/MIT	False
biopython	1.63	BSD-like	False
bitarray	0.8.1	PSF	False
blaze <sup>Linux Mac</sup>	0.5.0	BSD	False
blist	1.3.6	BSD	False
blz	0.6.2	BSD	False
boto	2.28.0	MIT	False
bsdiff4	1.1.4	BSD	False
cairo <sup>Linux</sup>	1.12.2	LGPL 2.1 and MPL 1.1	False
casuarius	1.1	LGPL	False
cdecimal	2.3	BSD	False
cffi <sup>Linux Mac</sup>	0.8.2	MIT	False
cheetah	2.4.4	MIT	False
chrpath <sup>Linux</sup>	0.13	GPL	False
colorama	0.2.7	BSD	False
conda-api	1.1.0	BSD	False
configobj	5.0.5	BSD	False
coverage	3.7.1	BSD	False
curl <sup>Linux Mac</sup>	7.30.0	MIT/X derivate	False
cython	0.20.1	Apache 2.0	False
datashape	0.2.0	BSD	False
dateutil	2.1	BSD	False
decorator	3.4.0	BSD	False
distribute <sup>Linux</sup>	0.6.45	PSF or ZPL	False
dnspython	1.10.0	as-is	False
docutils	0.11	Public-Domain, PSF, 2-clause BSD, GPL3	False
dynd-python	0.6.2	BSD	False
ecdsa	0.11	MIT	False
faulthandler	2.3	BSD	False
feedparser	5.1.3	MIT	False
flake8	2.1.0	MIT	False
flask	0.10.1	BSD	False
freetype <sup>Linux Mac</sup>	2.4.10	FreeType License	False
future	0.12.1	MIT	False
futures	2.1.6	BSD	False
gdal	1.10.1	MIT	False
gdata	2.0.18	Apache 2.0	False
geos <sup>Linux Mac</sup>	3.3.3	LGPL	False
gevent	1.0.1	MIT	False
gevent-websocket	0.9.3	Apache	False
googlecl	0.9.12	Apache 2.0	False
greenlet	0.4.2	MIT	False
grin	1.2.1	BSD	False
gunicorn <sup>Linux Mac</sup>	18.0	MIT	False
h5py	2.3.0	New BSD	False
hdf5 <sup>Linux Mac</sup>	1.8.9	BSD-style	False
html5lib	0.999	MIT	False
iopro	1.6.5	proprietary - Continuum Analytics, Inc.	False
itsdangerous	0.24	BSD License	False
jdcal	1.0	BSD	False

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Table 60 – continued from previous page

jinja2	2.7.2	BSD	False
jpeg <sup>Linux Mac</sup>	8d	Custom free software license	False
kiwisolver	0.1.2	BSD	False
lcms <sup>Linux Mac</sup>	1.19	MIT	False
libdynd <sup>Linux Mac</sup>	0.6.2	BSD	False
libffi <sup>Linux</sup>	3.0.13	MIT	False
libnetcdf <sup>Linux Mac</sup>	4.2.1.1	MIT	False
libpng <sup>Linux Mac</sup>	1.5.13	Open Source	False
libsodium <sup>Linux Mac</sup>	0.4.5	MIT	False
libtiff <sup>Linux Mac</sup>	4.0.2	as-is	False
libxml2 <sup>Linux Mac</sup>	2.9.0	MIT	False
libxslt <sup>Linux Mac</sup>	1.1.28	MIT	False
llvm <sup>Linux Mac</sup>	3.3	Open Source	False
llvmpy	0.12.6	New BSD License	False
logilab-common	0.61.0	LGPL	False
lxml	3.3.5	BSD	False
markdown <sup>Linux Mac</sup>	2.4	BSD	False
markupsafe	0.18	BSD	False
mathjax	2.2	Apache	False
matplotlib	1.3.1	PSF-based	False
mccabe	0.2.1	Expat	False
mdp	3.3	BSD	False
mercurial	3.0	GPLv2	False
mingw <sup>Windows</sup>	4.7	GPL	False
mock	1.0.1	BSD	False
mpi4py <sup>Linux</sup>	1.3	BSD	False
mpich2 <sup>Linux</sup>	1.4.1p1	mpich license	False
multipledispatch	0.4.3	BSD	False
netcdf4	1.0.8	MIT	False
networkx	1.8.1	BSD	False
nlTK	2.0.4	Apache 2.0	False
nose	1.3.3	LGPL	False
numba	0.13.2	numba license	False
numexpr	2.3.1	MIT	False
numpy	1.8.1	BSD	False
numpydoc	0.4	BSD	False
openssl <sup>Linux Mac</sup>	1.0.1h	Apache-style	False
ordereddict	1.1	MIT	False
pandas	0.14.0	BSD	False
pandasql	0.4.2	BSD	False
paramiko	1.14.0	LGPL	False
pastedeploy <sup>Linux Mac</sup>	1.5.2	MIT	False
patchelf <sup>Linux</sup>	0.6	GPL3	False
patsy	0.2.1	BSD License	False
pep8	1.5.6	MIT License	False
pil	1.1.7	PIL license	False
pillow <sup>Linux Mac</sup>	2.4.0	Standard PIL license	False
pip	1.5.6	MIT	False
pixmap <sup>Linux</sup>	0.26.2	MIT	False
ply	3.4	BSD	False

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Table 60 – continued from previous page

psutil	2.1.1	BSD	False
py	1.4.20	MIT	False
py2cairo <sup>Linux</sup>	1.10.0	LGPL 2.1 and MPL 1.1	False
pyasn1 <sup>Linux</sup>	0.1.6	BSD	False
pycosat	0.6.1	MIT	False
pycparser	2.10	BSD	False
pycrypto	2.6.1	Public Domain	False
pycurl <sup>Linux Mac</sup>	7.19.3.1	LGPL and MIT/X	False
pyflakes	0.8.1	MIT	False
pygments	1.6	BSD	False
pylint	1.2.1	GPL	False
pymc <sup>Linux</sup>	2.3.2	<a href="#">Academic Free License</a>	False
pyodbc	3.0.7	MIT	False
pyparsing	2.0.1	MIT	False
pyqt	4.10.4	GPL	False
pyreadline <sup>Windows</sup>	2.0	BSD	False
pysam <sup>Linux Mac</sup>	0.6	MIT	False
pytables <sup>Linux Mac</sup>	3.1.1	BSD	False
pytest	2.5.2	MIT	False
python	2.6.9	PSF	False
pytz	2014.3	MIT	False
pyyaml	3.11	MIT	False
pyzmq	14.3.0	LGPL and BSD	False
qt <sup>Linux Mac</sup>	4.8.5	LGPL	False
readline <sup>Linux Mac</sup>	6.2	GPL 3	False
redis <sup>Linux Mac</sup>	2.6.9	3-clause BSD	False
redis-py <sup>Linux Mac</sup>	2.9.1	<a href="#">MIT</a>	False
requests	2.3.0	ISC	False
rope	0.9.4	GPL	False
scikit-image	0.10.0	<a href="#">Modified BSD</a>	False
scikit-learn	0.14.1	3-clause BSD	False
scipy	0.14.0	BSD	False
setuptools	3.6	PSF or ZPL	False
shapely <sup>Linux Mac</sup>	1.3.2	BSD	False
sip <sup>Linux Mac</sup>	4.15.5	GPL	False
six	1.6.1	MIT	False
sphinx	1.2.2	BSD	False
sqlalchemy	0.9.4	MIT	False
sqlite <sup>Linux Mac</sup>	3.8.4.1	<a href="#">Public Domain</a>	False
sqlparse	0.1.11	BSD	False
ssh	1.8.0	LGPL	False
ssl_match_hostname	3.4.0.2	PSF	False
starcluster <sup>Linux</sup>	0.93.3	LGPL	False
statsmodels	0.5.0	3-clause Modified BSD	False
sympy	0.7.5	New BSD	False
theano <sup>Linux</sup>	0.6.0	BSD	False
tk <sup>Linux Mac</sup>	8.5.15	BSD-style	False
tornado	3.2.1	Apache	False
traits	4.4.0	BSD	False
twisted	14.0.0	MIT	False

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Table 60 – continued from previous page

ujson	1.33	BSD	False
unittest2	0.5.1	BSD	False
unixodbc <sup>Linux</sup>	2.3.1	???	False
util-linux <sup>Linux</sup>	2.21	GPL	False
w3lib	1.5	BSD	False
werkzeug	0.9.6	BSD	False
whoosh	2.5.7	BSD	False
workerpool <sup>Linux</sup>	0.9.2	MIT	False
xlrd	0.9.3	BSD	False
xlswriter	0.5.5	BSD	False
xlwt	0.7.5	BSD	False
yaml <sup>Linux Mac</sup>	0.1.4	MIT	False
zeromq <sup>Linux Mac</sup>	4.0.4	LGPL	False
zlib <sup>Linux Mac</sup>	1.2.7	zlib	False
zope.interface	4.1.1	Zope Public License	False

### Packages included in Anaconda 2.0.1 for Python version 2.7

Python version: 2.7

Number of supported packages: 197

Name	Version	License	In Installer
apptools	4.2.1	BSD	False
argcomplete	0.6.7	Apache Software License	True
astroid	1.1.1	LGPL	False
astropy	0.3.2	BSD	True
atom	0.3.7	BSD	True
basemap	1.0.7	PSF	False
beautiful-soup	4.3.1	PSF/MIT	True
binstar	0.5.3	BSD	True
biopython	1.63	BSD-like	False
bitarray	0.8.1	PSF	True
blaze	0.5.0	BSD	True
blist	1.3.6	BSD	False
blz	0.6.2	BSD	True
bokeh	0.4.4	New BSD	True
boto	2.28.0	MIT	True
bsdiff4	1.1.4	BSD	False
cairo <sup>Linux</sup>	1.12.2	LGPL 2.1 and MPL 1.1	True
casuarious	1.1	LGPL	True
cdecimal	2.3	BSD	True
cffil <sup>Linux Mac</sup>	0.8.2	MIT	False
chaco	4.4.1	BSD	True
cheetah	2.4.4	MIT	False
chrpath <sup>Linux</sup>	0.13	GPL	False
colorama	0.2.7	BSD	True
conda	3.5.5	BSD	True
conda-api	1.1.0	BSD	False
conda-build	1.3.5	BSD	True

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Table 61 – continued from previous page

configobj	5.0.5	BSD	True
coverage	3.7.1	BSD	False
cubes	0.10.2	MIT	True
curl <sup>Linux Mac</sup>	7.30.0	MIT/X derivate	True
cython	0.20.1	Apache 2.0	True
datashape	0.2.0	BSD	True
dateutil	2.1	BSD	True
decorator	3.4.0	BSD	False
distribute <sup>Linux Mac</sup>	0.6.45	PSF or ZPL	False
dnspython	1.10.0	as-is	False
docutils	0.11	Public-Domain, PSF, 2-clause BSD, GPL3	True
dynd-python	0.6.2	BSD	True
ecdsa	0.11	MIT	False
enable	4.3.0	BSD	True
enaml	0.9.1	BSD	True
envisage	4.4.0	BSD	False
faulthandler	2.3	BSD	False
feedparser	5.1.3	MIT	False
fiona	1.1.4	BSD	False
flake8	2.1.0	MIT	False
flask	0.10.1	BSD	True
freetype <sup>Linux Mac</sup>	2.4.10	FreeType License	True
future	0.12.1	MIT	True
futures	2.1.6	BSD	False
gdal	1.10.1	MIT	False
gdata	2.0.18	Apache 2.0	False
geos <sup>Linux Mac</sup>	3.3.3	LGPL	False
gevent	1.0.1	MIT	True
gevent-websocket	0.9.3	Apache	True
googlecl	0.9.12	Apache 2.0	False
greenlet	0.4.2	MIT	True
grin	1.2.1	BSD	True
gunicorn <sup>Linux Mac</sup>	18.0	MIT	False
h5py	2.3.0	New BSD	True
hdf5 <sup>Linux Mac</sup>	1.8.9	BSD-style	True
html5lib	0.999	MIT	False
hyde <sup>Linux Mac</sup>	0.8.5	MIT	False
iopro	1.6.5	proprietary - Continuum Analytics, Inc.	False
ipython	2.1.0	BSD	True
itsdangerous	0.24	BSD License	True
jdcalf	1.0	BSD	True
jinja2	2.7.2	BSD	True
jpeg <sup>Linux Mac</sup>	8d	Custom free software license	True
keyring	3.7	PSF	False
kiwisolver	0.1.2	BSD	True
launcher	0.1.5	proprietary - Continuum Analytics, Inc.	True
lcms <sup>Linux Mac</sup>	1.19	MIT	True
libdynd <sup>Linux Mac</sup>	0.6.2	BSD	True
libffi <sup>Linux</sup>	3.0.13	MIT	False
libnetcdf <sup>Linux Mac</sup>	4.2.1.1	MIT	False

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Table 61 – continued from previous page

libpng <small>Linux Mac</small>	1.5.13	Open Source	True
libsodium <small>Linux Mac</small>	0.4.5	MIT	True
libtiff <small>Linux Mac</small>	4.0.2	as-is	True
libxml2 <small>Linux Mac</small>	2.9.0	MIT	True
libxslt <small>Linux Mac</small>	1.1.28	MIT	True
llvm <small>Linux Mac</small>	3.3	Open Source	True
llvmpy	0.12.6	New BSD License	True
logilab-common	0.61.0	LGPL	False
lxml	3.3.5	BSD	True
markdown <small>Linux Mac</small>	2.4	BSD	False
markupsafe	0.18	BSD	True
mathjax	2.2	Apache	False
matplotlib	1.3.1	PSF-based	True
mayavi	4.3.1	BSD	False
mccabe	0.2.1	Expat	False
mdp	3.3	BSD	False
menuinst <small>Windows</small>	1.0.3	BDF	True
mercurial	3.0	GPLv2	False
mingw <small>Windows</small>	4.7	GPL	True
mock	1.0.1	BSD	True
mpi4py <small>Linux</small>	1.3	BSD	True
mpich2 <small>Linux</small>	1.4.1p1	mpich license	True
multipledispatch	0.4.3	BSD	True
netcdf4	1.0.8	MIT	False
networkx	1.8.1	BSD	True
nlTK	2.0.4	Apache 2.0	True
nose	1.3.3	LGPL	True
numba	0.13.2	numba license	True
numexpr	2.3.1	MIT	True
numpy	1.8.1	BSD	True
numpydoc	0.4	BSD	False
openpyxl	1.8.5	MIT/Expat	True
openssl <small>Linux Mac</small>	1.0.1h	Apache-style	True
pandas	0.14.0	BSD	True
pandasql	0.4.2	BSD	False
paramiko	1.14.0	LGPL	False
pastedeploy <small>Linux Mac</small>	1.5.2	MIT	False
patchelf <small>Linux</small>	0.6	GPL3	False
patsy	0.2.1	BSD License	True
pep8	1.5.6	MIT License	True
pil	1.1.7	PIL license	True
pillow <small>Linux Mac</small>	2.4.0	Standard PIL license	False
pip	1.5.6	MIT	True
pixman <small>Linux</small>	0.26.2	MIT	True
ply	3.4	BSD	True
psutil	2.1.1	BSD	True
py	1.4.20	MIT	True
py2cairo <small>Linux</small>	1.10.0	LGPL 2.1 and MPL 1.1	True
pyasn1 <small>Linux</small>	0.1.6	BSD	False
pyaudio <small>Mac</small>	0.2.7	MIT	True

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Table 61 – continued from previous page

pycosat	0.6.1	MIT	True
pycparser	2.10	BSD	True
pycrypto	2.6.1	Public Domain	True
pycurl <sup>Linux Mac</sup>	7.19.3.1	LGPL and MIT/X	True
pyface	4.4.0	BSD	True
pyflakes	0.8.1	MIT	True
pygments	1.6	BSD	True
pylint	1.2.1	GPL	False
pymc <sup>Linux</sup>	2.3.2	<a href="#">Academic Free License</a>	False
pyodbc	3.0.7	MIT	False
yparsing	2.0.1	MIT	True
pyqt	4.10.4	GPL	True
pyreadline <sup>Windows</sup>	2.0	BSD	True
pysal	1.6.0	New BSD License	False
pysam <sup>Linux Mac</sup>	0.6	MIT	False
pytables	3.1.1	BSD	True
pytest	2.5.2	MIT	True
python	2.7.7	PSF	True
pytz	2014.3	MIT	True
pywin32 <sup>Windows</sup>	218.4	PSF	True
pyyaml	3.11	MIT	True
pyzmq	14.3.0	LGPL and BSD	True
qt <sup>Linux Mac</sup>	4.8.5	LGPL	True
readline <sup>Linux Mac</sup>	6.2	GPL 3	True
redis <sup>Linux Mac</sup>	2.6.9	3-clause BSD	True
redis-py <sup>Linux Mac</sup>	2.9.1	<a href="#">MIT</a>	True
reportlab	3.1.8	BSD	False
requests	2.3.0	ISC	True
rope	0.9.4	GPL	True
runipy	0.1.0	BSD	True
scikit-image	0.10.0	<a href="#">Modified BSD</a>	True
scikit-learn	0.14.1	3-clause BSD	True
scipy	0.14.0	BSD	True
setuptools	3.6	PSF or ZPL	True
shapely <sup>Linux Mac</sup>	1.3.2	BSD	False
sip <sup>Linux Mac</sup>	4.15.5	GPL	True
six	1.6.1	MIT	True
sphinx	1.2.2	BSD	True
spyder	2.3.0rc1	MIT	True
sqlalchemy	0.9.4	MIT	True
sqlite <sup>Linux Mac</sup>	3.8.4.1	<a href="#">Public Domain</a>	True
sqlparse	0.1.11	BSD	False
ssh	1.8.0	LGPL	False
ssl_match_hostname	3.4.0.2	PSF	True
starcluster <sup>Linux</sup>	0.93.3	LGPL	False
statsmodels	0.5.0	3-clause Modified BSD	True
sympy	0.7.5	New BSD	True
theano <sup>Linux</sup>	0.6.0	BSD	True
tk <sup>Linux Mac</sup>	8.5.15	BSD-style	True
tornado	3.2.1	Apache	True

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Table 61 – continued from previous page

traits	4.4.0	BSD	True
traitsui	4.4.0	BSD	True
twisted	14.0.0	MIT	False
ujson	1.33	BSD	True
unixodbc <sup>Linux</sup>	2.3.1	???	False
util-linux <sup>Linux</sup>	2.21	GPL	True
vtk	5.10.1	BSD	False
w3lib	1.5	BSD	False
werkzeug	0.9.6	BSD	True
whoosh	2.5.7	BSD	False
workerpool <sup>Linux</sup>	0.9.2	MIT	False
xlrd	0.9.3	BSD	True
xlsxwriter	0.5.5	BSD	True
xlwings <sup>Windows</sup>	0.1.0	BSD 3-clause	True
xlwt	0.7.5	BSD	True
yaml <sup>Linux Mac</sup>	0.1.4	MIT	True
yt <sup>Linux Mac</sup>	2.6.2	BSD	False
zeromq <sup>Linux Mac</sup>	4.0.4	LGPL	True
zlib <sup>Linux Mac</sup>	1.2.7	zlib	True
zope.interface	4.1.1	Zope Public License	False

### Packages included in Anaconda 2.0.1 for Python version 3.3

Python version: 3.3

Number of supported packages: 141

Name	Version	License	In Installer
argcomplete	0.6.7	Apache Software License	False
astroid	1.1.1	LGPL	False
astropy	0.3.2	BSD	False
basemap <sup>Linux Mac</sup>	1.0.7	PSF	False
beautiful-soup	4.3.1	PSF/MIT	False
binstar	0.5.3	BSD	False
biopython	1.63	BSD-like	False
bitarray	0.8.1	PSF	False
blaze	0.5.0	BSD	False
blist	1.3.6	BSD	False
blz	0.6.2	BSD	False
bokeh	0.4.4	New BSD	False
bsdiff4	1.1.4	BSD	False
cdecimal	2.3	BSD	False
cffi <sup>Linux</sup>	0.8.2	MIT	False
chrpath <sup>Linux</sup>	0.13	GPL	False
colorama	0.2.7	BSD	False
conda	3.5.5	BSD	False
conda-api	1.1.0	BSD	False
conda-build	1.3.5	BSD	False
configobj	5.0.5	BSD	False
coverage	3.7.1	BSD	False

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Table 62 – continued from previous page

curl <sup>Linux Mac</sup>	7.30.0	MIT/X derivate	False
cython	0.20.1	Apache 2.0	False
datashape	0.2.0	BSD	False
dateutil	2.1	BSD	False
docutils	0.11	Public-Domain, PSF, 2-clause BSD, GPL3	False
dynd-python	0.6.2	BSD	False
ecdsa	0.11	MIT	False
feedparser	5.1.3	MIT	False
fiona	1.1.4	BSD	False
flake8	2.1.0	MIT	False
flask	0.10.1	BSD	False
freetype <sup>Linux Mac</sup>	2.4.10	FreeType License	False
future	0.12.1	MIT	False
futures	2.1.6	BSD	False
gdal	1.10.1	MIT	False
geos <sup>Linux Mac</sup>	3.3.3	LGPL	False
greenlet	0.4.2	MIT	False
unicorn <sup>Linux Mac</sup>	18.0	MIT	False
h5py	2.3.0	New BSD	False
hdf5 <sup>Linux Mac</sup>	1.8.9	BSD-style	False
html5lib	0.999	MIT	False
ipython	2.1.0	BSD	False
itsdangerous	0.24	BSD License	False
jdcal	1.0	BSD	False
jinja2	2.7.2	BSD	False
jpeg <sup>Linux Mac</sup>	8d	Custom free software license	False
libdynd <sup>Linux Mac</sup>	0.6.2	BSD	False
libffi <sup>Linux</sup>	3.0.13	MIT	False
libnetcdf <sup>Linux Mac</sup>	4.2.1.1	MIT	False
libpng <sup>Linux Mac</sup>	1.5.13	Open Source	False
libsodium <sup>Linux Mac</sup>	0.4.5	MIT	False
libtiff <sup>Linux Mac</sup>	4.0.2	as-is	False
libxml2 <sup>Linux Mac</sup>	2.9.0	MIT	False
libxslt <sup>Linux Mac</sup>	1.1.28	MIT	False
llvm <sup>Linux Mac</sup>	3.3	Open Source	False
llvmpy	0.12.6	New BSD License	False
logilab-common	0.61.0	LGPL	False
lxml	3.3.5	BSD	False
markdown <sup>Linux Mac</sup>	2.4	BSD	False
markupsafe	0.18	BSD	False
mathjax	2.2	Apache	False
matplotlib	1.3.1	PSF-based	False
mccabe	0.2.1	Expat	False
mdp	3.3	BSD	False
mingw <sup>Windows</sup>	4.7	GPL	False
mock	1.0.1	BSD	False
multipledispatch	0.4.3	BSD	False
netcdf4	1.0.8	MIT	False
networkx	1.8.1	BSD	False
nose	1.3.3	LGPL	False

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Table 62 – continued from previous page

numba	0.13.2	numba license	False
numexpr	2.3.1	MIT	False
numpy	1.8.1	BSD	False
openpyxl	1.8.5	MIT/Expat	False
openssl <sup>Linux Mac</sup>	1.0.1h	Apache-style	False
pandas	0.14.0	BSD	False
pandasql	0.4.2	BSD	False
paramiko <sup>Linux Mac</sup>	1.14.0	LGPL	False
pastedeploy <sup>Linux Mac</sup>	1.5.2	MIT	False
patchelf <sup>Linux</sup>	0.6	GPL3	False
patsy	0.2.1	BSD License	False
pep8	1.5.6	MIT License	False
pillow <sup>Linux Mac</sup>	2.4.0	Standard PIL license	False
pip	1.5.6	MIT	False
ply	3.4	BSD	False
psutil	2.1.1	BSD	False
py	1.4.20	MIT	False
pyasn1 <sup>Linux</sup>	0.1.6	BSD	False
pycosat	0.6.1	MIT	False
pycparser	2.10	BSD	False
pycrypto	2.6.1	Public Domain	False
pyflakes	0.8.1	MIT	False
pygments	1.6	BSD	False
pylint	1.2.1	GPL	False
pyodbc	3.0.7	MIT	False
pyparsing	2.0.1	MIT	False
pyqt	4.10.4	GPL	False
pyreadline <sup>Windows</sup>	2.0	BSD	False
pytables	3.1.1	BSD	False
pytest	2.5.2	MIT	False
python	3.3.5	PSF	False
pytz	2014.3	MIT	False
pyyaml	3.11	MIT	False
pyzmq	14.3.0	LGPL and BSD	False
qt <sup>Linux Mac</sup>	4.8.5	LGPL	False
readline <sup>Linux Mac</sup>	6.2	GPL 3	False
redis <sup>Linux Mac</sup>	2.6.9	3-clause BSD	False
redis-py <sup>Linux Mac</sup>	2.9.1	MIT	False
reportlab	3.1.8	BSD	False
requests	2.3.0	ISC	False
rope	0.9.4	GPL	False
runipy	0.1.0	BSD	False
scikit-image	0.10.0	Modified BSD	False
scikit-learn	0.14.1	3-clause BSD	False
scipy	0.14.0	BSD	False
setuptools	3.6	PSF or ZPL	False
shapely <sup>Linux Mac</sup>	1.3.2	BSD	False
sip <sup>Linux Mac</sup>	4.15.5	GPL	False
six	1.6.1	MIT	False
sphinx	1.2.2	BSD	False

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Table 62 – continued from previous page

sqlalchemy	0.9.4	MIT	False
sqlite <small>Linux Mac</small>	3.8.4.1	Public Domain	False
sqlparse	0.1.11	BSD	False
ssl_match_hostname	3.4.0.2	PSF	False
statsmodels	0.5.0	3-clause Modified BSD	False
sympy	0.7.5	New BSD	False
tk <small>Linux Mac</small>	8.5.15	BSD-style	False
tornado	3.2.1	Apache	False
ujson	1.33	BSD	False
unixodbc <small>Linux</small>	2.3.1	???	False
util-linux <small>Linux</small>	2.21	GPL	False
werkzeug	0.9.6	BSD	False
whoosh	2.5.7	BSD	False
xlrd	0.9.3	BSD	False
xlsxwriter	0.5.5	BSD	False
yaml <small>Linux Mac</small>	0.1.4	MIT	False
zeromq <small>Linux Mac</small>	4.0.4	LGPL	False
zlib <small>Linux Mac</small>	1.2.7	zlib	False
zope.interface	4.1.1	Zope Public License	False

### Packages included in Anaconda 2.0.1 for Python version 3.4

Python version: 3.4

Number of supported packages: 141

Name	Version	License	In Installer
argcomplete	0.6.7	Apache Software License	True
astroid	1.1.1	LGPL	False
astropy	0.3.2	BSD	True
basemap <small>Linux Mac</small>	1.0.7	PSF	False
beautiful-soup	4.3.1	PSF/MIT	True
binstar	0.5.3	BSD	True
biopython	1.63	BSD-like	False
bitarray	0.8.1	PSF	True
blaze	0.5.0	BSD	True
blist	1.3.6	BSD	False
blz	0.6.2	BSD	True
bokeh	0.4.4	New BSD	True
bsdiff4	1.1.4	BSD	False
cdecimal	2.3	BSD	True
cffi <small>Linux</small>	0.8.2	MIT	False
chrpath <small>Linux</small>	0.13	GPL	False
colorama	0.2.7	BSD	True
conda	3.5.5	BSD	True
conda-api	1.1.0	BSD	False
conda-build	1.3.5	BSD	True
configobj	5.0.5	BSD	True
coverage	3.7.1	BSD	False
curl <small>Linux Mac</small>	7.30.0	MIT/X derivate	True

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Table 63 – continued from previous page

cython	0.20.1	Apache 2.0	True
datashape	0.2.0	BSD	True
dateutil	2.1	BSD	True
docutils	0.11	Public-Domain, PSF, 2-clause BSD, GPL3	True
dynd-python	0.6.2	BSD	True
ecdsa	0.11	MIT	False
feedparser	5.1.3	MIT	False
fiona	1.1.4	BSD	False
flake8	2.1.0	MIT	False
flask	0.10.1	BSD	True
freetype <small>Linux Mac</small>	2.4.10	FreeType License	True
future	0.12.1	MIT	True
futures	2.1.6	BSD	False
gdal	1.10.1	MIT	False
geos <small>Linux Mac</small>	3.3.3	LGPL	False
greenlet	0.4.2	MIT	True
gunicorn <small>Linux Mac</small>	18.0	MIT	False
h5py	2.3.0	New BSD	True
hdf5 <small>Linux Mac</small>	1.8.9	BSD-style	True
html5lib	0.999	MIT	False
ipython	2.1.0	BSD	True
itsdangerous	0.24	BSD License	True
jdcalf	1.0	BSD	True
jinj2	2.7.2	BSD	True
jpeg <small>Linux Mac</small>	8d	Custom free software license	True
libdynd <small>Linux Mac</small>	0.6.2	BSD	True
libffi <small>Linux</small>	3.0.13	MIT	False
libnetcdf <small>Linux Mac</small>	4.2.1.1	MIT	False
libpng <small>Linux Mac</small>	1.5.13	Open Source	True
libsodium <small>Linux Mac</small>	0.4.5	MIT	True
libtiff <small>Linux Mac</small>	4.0.2	as-is	True
libxml2 <small>Linux Mac</small>	2.9.0	MIT	True
libxslt <small>Linux Mac</small>	1.1.28	MIT	True
llvm <small>Linux Mac</small>	3.3	Open Source	True
llvmpy	0.12.6	New BSD License	True
logilab-common	0.61.0	LGPL	False
lxml	3.3.5	BSD	True
markdown <small>Linux Mac</small>	2.4	BSD	False
markupsafe	0.18	BSD	True
mathjax	2.2	Apache	False
matplotlib	1.3.1	PSF-based	True
mccabe	0.2.1	Expat	False
mdp	3.3	BSD	False
menuinst <small>Windows</small>	1.0.3	BDF	True
mingw <small>Windows</small>	4.7	GPL	True
mock	1.0.1	BSD	True
multipledispatch	0.4.3	BSD	True
netcdf4	1.0.8	MIT	False
networkx	1.8.1	BSD	True
nose	1.3.3	LGPL	True

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Table 63 – continued from previous page

numba	0.13.2	numba license	True
numexpr	2.3.1	MIT	True
numpy	1.8.1	BSD	True
openpyxl	1.8.5	MIT/Expat	True
openssl <sup>Linux Mac</sup>	1.0.1h	Apache-style	True
pandas	0.14.0	BSD	True
pandasql	0.4.2	BSD	False
paramiko <sup>Linux Mac</sup>	1.14.0	LGPL	False
pastedeploy <sup>Linux Mac</sup>	1.5.2	MIT	False
patchelf <sup>Linux</sup>	0.6	GPL3	False
patsy	0.2.1	BSD License	True
pep8	1.5.6	MIT License	False
pillow <sup>Linux Mac</sup>	2.4.0	Standard PIL license	True
pip	1.5.6	MIT	True
ply	3.4	BSD	True
psutil	2.1.1	BSD	True
py	1.4.20	MIT	True
pyasn1 <sup>Linux</sup>	0.1.6	BSD	False
pycosat	0.6.1	MIT	True
pycparser	2.10	BSD	True
pycrypto	2.6.1	Public Domain	True
pyflakes	0.8.1	MIT	True
pygments	1.6	BSD	True
pylint	1.2.1	GPL	False
pyodbc	3.0.7	MIT	False
pyparsing	2.0.1	MIT	True
pyqt	4.10.4	GPL	True
pyreadline <sup>Windows</sup>	2.0	BSD	True
pytables	3.1.1	BSD	True
pytest	2.5.2	MIT	True
python	3.4.1	PSF	True
pytz	2014.3	MIT	True
pyyaml	3.11	MIT	True
pyzmq	14.3.0	LGPL and BSD	True
qt <sup>Linux Mac</sup>	4.8.5	LGPL	True
readline <sup>Linux Mac</sup>	6.2	GPL 3	True
redis <sup>Linux Mac</sup>	2.6.9	3-clause BSD	True
redis-py <sup>Linux Mac</sup>	2.9.1	MIT	True
reportlab	3.1.8	BSD	False
requests	2.3.0	ISC	True
rope	0.9.4	GPL	True
runipy	0.1.0	BSD	True
scikit-image	0.10.0	Modified BSD	True
scipy	0.14.0	BSD	True
setuptools	3.6	PSF or ZPL	True
shapely <sup>Linux Mac</sup>	1.3.2	BSD	False
sip <sup>Linux Mac</sup>	4.15.5	GPL	True
six	1.6.1	MIT	True
sphinx	1.2.2	BSD	True
spyder	2.3.0rc1	MIT	True

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sqlalchemy	0.9.4	MIT	True
sqlite <sup>Linux Mac</sup>	3.8.4.1	Public Domain	True
sqlparse	0.1.11	BSD	False
ssl_match_hostname	3.4.0.2	PSF	True
sympy	0.7.5	New BSD	True
tk <sup>Linux Mac</sup>	8.5.15	BSD-style	True
tornado	3.2.1	Apache	True
ujson	1.33	BSD	True
unixodbc <sup>Linux</sup>	2.3.1	???	False
util-linux <sup>Linux</sup>	2.21	GPL	True
werkzeug	0.9.6	BSD	True
whoosh	2.5.7	BSD	False
xlrd	0.9.3	BSD	True
xlswriter	0.5.5	BSD	True
yaml <sup>Linux Mac</sup>	0.1.4	MIT	True
zeromq <sup>Linux Mac</sup>	4.0.4	LGPL	True
zlib <sup>Linux Mac</sup>	1.2.7	zlib	True
zope.interface	4.1.1	Zope Public License	False

### Packages included in Anaconda 2.1.0 for Python version 2.6

Python version: 2.6

Number of supported packages: 194

Name	Version	License	In Installer
abstract-rendering <sup>Linux Mac</sup>	0.5.1	3rd-clause BSD	False
argcomplete	0.8.1	Apache Software License	False
argparse	1.2.1	PSF	False
astroid	1.2.1	LGPL	False
astropy	0.4.2	BSD	False
atom	0.3.9	BSD	False
basemap <sup>Linux Mac</sup>	1.0.7	PSF	False
bcolz	0.7.1	BSD	False
beautiful-soup	4.3.2	PSF/MIT	False
biopython	1.64	BSD-like	False
bitarray	0.8.1	PSF	False
blaze <sup>Linux Mac</sup>	0.6.3	BSD	False
blist	1.3.6	BSD	False
blz	0.6.2	BSD	False
boto	2.32.1	MIT	False
bsddb <sup>Linux Mac</sup>	1.0	PSF	False
bsdiff4	1.1.4	BSD	False
cairo <sup>Linux</sup>	1.12.2	LGPL 2.1 and MPL 1.1	False
casuarious	1.1	LGPL	False
cdecimal	2.3	BSD	False
cffi	0.8.6	MIT	False
chameleon	2.16	BSD-like	False
cheetah	2.4.4	MIT	False
chrpath <sup>Linux</sup>	0.13	GPL	False

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Table 64 – continued from previous page

colorama	0.3.1	BSD	False
conda-api	1.1.0	BSD	False
configobj	5.0.6	BSD	False
coverage	3.7.1	BSD	False
cryptography	0.5.4	Apache 2.0	False
cssselect	0.9.1	BSD	False
curl <sup>Linux Mac</sup>	7.38.0	MIT/X derivate	False
cython	0.21	Apache 2.0	False
cytoolz	0.7.0	BSD	False
datashape	0.3.0	BSD	False
dateutil	2.1	BSD	False
db <sup>Linux Mac</sup>	5.3.28	AGPLv3	False
decorator	3.4.0	BSD	False
dnspython	1.10.0	as-is	False
docutils	0.12	Public-Domain, PSF, 2-clause BSD, GPL3	False
dynd-python	0.6.5	BSD	False
ecdsa	0.11	MIT	False
ephem	3.7.5.3	LGPL	False
faulthandler	2.3	BSD	False
feedparser	5.1.3	MIT	False
flake8	2.2.3	MIT	False
flask	0.10.1	BSD	False
freetype <sup>Linux Mac</sup>	2.4.10	FreeType License	False
future	0.13.1	MIT	False
futures	2.1.6	BSD	False
gdal	1.11.0	MIT	False
gdata	2.0.18	Apache 2.0	False
gensim	0.10.2	LGPL	False
geos <sup>Linux Mac</sup>	3.3.3	LGPL	False
gevent	1.0.1	MIT	False
gevent-websocket	0.9.3	Apache	False
googlecl	0.9.12	Apache 2.0	False
greenlet	0.4.4	MIT	False
grin	1.2.1	BSD	False
gunicorn <sup>Linux Mac</sup>	19.1.0	MIT	False
h5py	2.3.1	New BSD	False
hdf5 <sup>Linux Mac</sup>	1.8.13	BSD-style	False
html5lib	0.999	MIT	False
iopro	1.6.7	proprietary - Continuum Analytics, Inc.	False
itsdangerous	0.24	BSD License	False
jdcal	1.0	BSD	False
jinja2	2.7.3	BSD	False
jpeg <sup>Linux Mac</sup>	8d	Custom free software license	False
kiwisolver	0.1.3	BSD	False
lcms <sup>Linux Mac</sup>	1.19	MIT	False
libdynd <sup>Linux Mac</sup>	0.6.5	BSD	False
libffi <sup>Linux</sup>	3.0.13	MIT	False
libnetcdf <sup>Linux Mac</sup>	4.3.2	MIT	False
libpng <sup>Linux Mac</sup>	1.5.13	Open Source	False
libsodium <sup>Linux Mac</sup>	0.4.5	MIT	False

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Table 64 – continued from previous page

libtiff <small>Linux Mac</small>	4.0.2	as-is	False
libxml2 <small>Linux Mac</small>	2.9.0	MIT	False
libxslt <small>Linux Mac</small>	1.1.28	MIT	False
llvm <small>Linux Mac</small>	3.3	Open Source	False
llvmpy	0.12.7	New BSD License	False
logilab-common	0.62.1	LGPL	False
lxml	3.4.0	BSD	False
markupsafe	0.23	BSD	False
mathjax	2.2	Apache	False
matplotlib	1.4.0	PSF-based	False
mccabe	0.2.1	Expat	False
mdp	3.3	BSD	False
mercurial	3.1	GPLv2	False
mingw <small>Windows</small>	4.7	GPL	False
mock	1.0.1	BSD	False
mpi4py <small>Linux</small>	1.3	BSD	False
mpich2 <small>Linux</small>	1.4.1p1	mpich license	False
multimethods	1.0.0	MIT	False
multipledispatch	0.4.7	BSD	False
natsort	3.5.0	MIT	False
netcdf4	1.1.1	MIT	False
networkx	1.9.1	BSD	False
nlTK	3.0.0	Apache 2.0	False
nose	1.3.4	LGPL	False
numba	0.14.0	numba license	False
numexpr	2.3.1	MIT	False
numpy	1.9.0	BSD	False
numpydoc	0.4	BSD	False
openssl <small>Linux Mac</small>	1.0.1h	Apache-style	False
ordereddict	1.1	MIT	False
pandas	0.14.1	BSD	False
pandasql	0.6.1	BSD	False
paramiko	1.14.1	LGPL	False
passlib	1.6.2	BSD	False
pastedeploy <small>Linux Mac</small>	1.5.2	MIT	False
patchelf <small>Linux</small>	0.6	GPL3	False
patsy	0.3.0	BSD License	False
pep381client	1.5	Academic Free License, version 3	False
pep8	1.5.7	MIT License	False
pil	1.1.7	PIL license	False
pillow <small>Linux Mac</small>	2.5.1	Standard PIL license	False
pip	1.5.6	MIT	False
pixmap <small>Linux</small>	0.26.2	MIT	False
ply	3.4	BSD	False
psutil	2.1.1	BSD	False
py	1.4.25	MIT	False
py2cairo <small>Linux</small>	1.10.0	LGPL 2.1 and MPL 1.1	False
pyasn1 <small>Linux</small>	0.1.6	BSD	False
pycosat	0.6.1	MIT	False
pyparser	2.10	BSD	False

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Table 64 – continued from previous page

pycrypto	2.6.1	Public Domain	False
pycurl <sup>Linux Mac</sup>	7.19.5	LGPL and MIT/X	False
pyflakes	0.8.1	MIT	False
pygments	1.6	BSD	False
pylint	1.3.1	GPL	False
pymc <sup>Linux</sup>	2.3.3	Academic Free License	False
pymongo	2.7.2	Apache 2.0	False
pyodbc	3.0.7	MIT	False
pyopenssl	0.14	APL2	False
pyparsing	2.0.1	MIT	False
pyqt	4.10.4	GPL	False
pyreadline <sup>Windows</sup>	2.0	BSD	False
pysam <sup>Linux Mac</sup>	0.6	MIT	False
pyserial	2.7	PSF	False
pytables <sup>Linux Mac</sup>	3.1.1	BSD	False
pytest	2.6.3	MIT	False
python	2.6.9	PSF	False
pytz	2014.7	MIT	False
pywin32 <sup>Windows</sup>	219	PSF	False
pyyaml	3.11	MIT	False
pyzmq	14.3.1	LGPL and BSD	False
qt <sup>Linux Mac</sup>	4.8.5	LGPL	False
queuelib	1.2.2	BSD	False
readline <sup>Linux Mac</sup>	6.2	GPL 3	False
redis <sup>Linux Mac</sup>	2.6.9	3-clause BSD	False
redis-py <sup>Linux Mac</sup>	2.9.1	MIT	False
repoze.lru	0.6	BSD	False
requests	2.4.1	ISC	False
rope	0.9.4	GPL	False
scikit-image	0.10.1	Modified BSD	False
scikit-learn	0.15.2	3-clause BSD	False
scipy	0.14.0	BSD	False
setuptools	5.8	PSF or ZPL	False
shapely <sup>Linux Mac</sup>	1.4.1	BSD	False
sip <sup>Linux Mac</sup>	4.15.5	GPL	False
six	1.8.0	MIT	False
sockjs-tornado	1.0.1	MIT	False
sphinx	1.2.3	BSD	False
sqlalchemy	0.9.7	MIT	False
sqlite <sup>Linux Mac</sup>	3.8.4.1	Public Domain	False
sqlparse	0.1.12	BSD	False
ssh	1.8.0	LGPL	False
ssl_match_hostname	3.4.0.2	PSF	False
starcluster <sup>Linux</sup>	0.93.3	LGPL	False
statsmodels	0.5.0	3-clause Modified BSD	False
sympy	0.7.5	New BSD	False
theano <sup>Linux</sup>	0.6.0	BSD	False
tk <sup>Linux Mac</sup>	8.5.15	BSD-style	False
toolz	0.7.0	BSD	False
tornado	4.0.2	Apache	False

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traits	4.4.0	BSD	False
twisted	14.0.2	MIT	False
ujson	1.33	BSD	False
unicodecsv	0.9.4	BSD	False
unittest2	0.5.1	BSD	False
unixodbc <sup>Linux</sup>	2.3.1	???	False
util-linux <sup>Linux</sup>	2.21	GPL	False
uuid	1.30	???	False
venusian	1.0	BSD	False
werkzeug	0.9.6	BSD	False
whoosh	2.5.7	BSD	False
workerpool <sup>Linux</sup>	0.9.2	MIT	False
xlrd	0.9.3	BSD	False
xlswriter	0.5.7	BSD	False
xlutils	1.7.1	MIT	False
xlwt	0.7.5	BSD	False
yaml <sup>Linux Mac</sup>	0.1.4	MIT	False
zeromq <sup>Linux Mac</sup>	4.0.4	LGPL	False
zlib <sup>Linux Mac</sup>	1.2.7	zlib	False
zope.interface	4.1.1	Zope Public License	False

### Packages included in Anaconda 2.1.0 for Python version 2.7

Python version: 2.7

Number of supported packages: 224

Name	Version	License	In Installer
abstract-rendering <sup>Linux Mac</sup>	0.5.1	3rd-clause BSD	True
apptools	4.2.1	BSD	False
argcomplete	0.8.1	Apache Software License	True
astroid	1.2.1	LGPL	False
astropy	0.4.2	BSD	True
atom	0.3.9	BSD	True
basemap	1.0.7	PSF	False
bcolz	0.7.1	BSD	False
beautiful-soup	4.3.2	PSF/MIT	True
binstar	0.7.1	BSD	True
biopython	1.64	BSD-like	False
bitarray	0.8.1	PSF	True
blaze	0.6.3	BSD	True
blist	1.3.6	BSD	False
blz	0.6.2	BSD	True
bokeh	0.6.1	New BSD	True
boto	2.32.1	MIT	True
bsddb <sup>Linux Mac</sup>	1.0	PSF	False
bsdiff4	1.1.4	BSD	False
cairo <sup>Linux</sup>	1.12.2	LGPL 2.1 and MPL 1.1	True
casuarious	1.1	LGPL	True
cdecimal	2.3	BSD	True

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cffi	0.8.6	MIT	True
chaco	4.4.1	BSD	True
chameleon	2.16	BSD-like	False
cheetah	2.4.4	MIT	False
chrpath <sup>Linux</sup>	0.13	GPL	False
colorama	0.3.1	BSD	True
conda	3.7.0	BSD	True
conda-api	1.1.0	BSD	False
conda-build	1.8.2	BSD	True
configobj	5.0.6	BSD	True
coverage	3.7.1	BSD	False
cryptography	0.5.4	Apache 2.0	True
cssselect	0.9.1	BSD	False
cubes	0.10.2	MIT	False
curl <sup>Linux Mac</sup>	7.38.0	MIT/X <i>derivate</i>	True
cython	0.21	Apache 2.0	True
cytoolz	0.7.0	BSD	True
datashape	0.3.0	BSD	True
dateutil	2.1	BSD	True
db <sup>Linux Mac</sup>	5.3.28	AGPLv3	False
decorator	3.4.0	BSD	True
django	1.7	BSD	False
dnspython	1.10.0	<i>as-is</i>	False
docutils	0.12	Public-Domain, PSF, 2-clause BSD, GPL3	True
dynd-python	0.6.5	BSD	True
ecdsa	0.11	MIT	False
enable	4.3.0	BSD	True
enaml	0.9.8	BSD	True
envisage	4.4.0	BSD	False
ephem	3.7.5.3	LGPL	False
faulthandler	2.3	BSD	False
feedparser	5.1.3	MIT	False
fiona	1.1.6	BSD	False
flake8	2.2.3	MIT	False
flask	0.10.1	BSD	True
freetype <sup>Linux Mac</sup>	2.4.10	<i>FreeType License</i>	True
future	0.13.1	MIT	True
futures	2.1.6	BSD	True
gdal	1.11.0	MIT	False
gdata	2.0.18	Apache 2.0	False
gensim	0.10.2	LGPL	False
geos <sup>Linux Mac</sup>	3.3.3	LGPL	False
gevent	1.0.1	MIT	True
gevent-websocket	0.9.3	Apache	True
googlecl	0.9.12	Apache 2.0	False
greenlet	0.4.4	MIT	True
grin	1.2.1	BSD	True
unicorn <sup>Linux Mac</sup>	19.1.0	MIT	False
h5py	2.3.1	<i>New BSD</i>	True
hdf5 <sup>Linux Mac</sup>	1.8.13	<i>BSD-style</i>	True

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Table 65 – continued from previous page

html5lib	0.999	MIT	False
hyde <small>Linux Mac</small>	0.8.5	MIT	False
iopro	1.6.7	proprietary - Continuum Analytics, Inc.	False
ipython	2.2.0	BSD	True
itsdangerous	0.24	BSD License	True
jdcal	1.0	BSD	True
jinja2	2.7.3	BSD	True
jpeg <small>Linux Mac</small>	8d	Custom free software license	True
kiwisolver	0.1.3	BSD	True
launcher <small>Mac Windows</small>	1.0.0	proprietary - Continuum Analytics, Inc.	True
lcms <small>Linux Mac</small>	1.19	MIT	True
libdynd <small>Linux Mac</small>	0.6.5	BSD	True
libffi <small>Linux</small>	3.0.13	MIT	True
libnetcdf <small>Linux Mac</small>	4.3.2	MIT	False
libpng <small>Linux Mac</small>	1.5.13	Open Source	True
libsodium <small>Linux Mac</small>	0.4.5	MIT	True
libtiff <small>Linux Mac</small>	4.0.2	as-is	True
libxml2 <small>Linux Mac</small>	2.9.0	MIT	True
libxslt <small>Linux Mac</small>	1.1.28	MIT	True
llvm <small>Linux Mac</small>	3.3	Open Source	True
llvmpy	0.12.7	New BSD License	True
logilab-common	0.62.1	LGPL	False
lxml	3.4.0	BSD	True
markdown <small>Linux Mac</small>	2.5	BSD	False
markupsafe	0.23	BSD	True
mathjax	2.2	Apache	False
matplotlib	1.4.0	PSF-based	True
mayavi	4.3.1	BSD	False
mccabe	0.2.1	Expat	False
mdp	3.3	BSD	False
menuinst <small>Windows</small>	1.0.4	BDF	True
mercurial	3.1	GPLv2	False
mingw <small>Windows</small>	4.7	GPL	True
mock	1.0.1	BSD	True
mpi4py <small>Linux</small>	1.3	BSD	True
mpich2 <small>Linux</small>	1.4.1p1	mpich license	True
multimethods	1.0.0	MIT	False
multiplatform	0.4.7	BSD	True
natsort	3.5.0	MIT	False
netcdf4	1.1.1	MIT	False
networkx	1.9.1	BSD	True
nltk	3.0.0	Apache 2.0	True
node-webkit <small>Mac Windows</small>	0.10.1	MIT	True
nose	1.3.4	LGPL	True
numba	0.14.0	numba license	True
numexpr	2.3.1	MIT	True
numpy	1.9.0	BSD	True
numpydoc	0.4	BSD	False
openpyxl	1.8.5	MIT/Expat	True
openssl <small>Linux Mac</small>	1.0.1h	Apache-style	True

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Table 65 – continued from previous page

pandas	0.14.1	BSD	True
pandasql	0.6.1	BSD	False
paramiko	1.14.1	LGPL	False
passlib	1.6.2	BSD	False
pastedeploy <sup>Linux Mac</sup>	1.5.2	MIT	False
patchelf <sup>Linux</sup>	0.6	GPL3	False
patsy	0.3.0	BSD License	True
pep381client	1.5	Academic Free License, version 3	False
pep8	1.5.7	MIT License	True
pil	1.1.7	<a href="#">PIL license</a>	True
pillow <sup>Linux Mac</sup>	2.5.1	Standard PIL license	False
pip	1.5.6	MIT	True
pixman <sup>Linux</sup>	0.26.2	MIT	True
ply	3.4	BSD	True
psutil	2.1.1	BSD	True
py	1.4.25	MIT	True
py2cairo <sup>Linux</sup>	1.10.0	LGPL 2.1 and MPL 1.1	True
pyasn1 <sup>Linux</sup>	0.1.6	BSD	False
pyaudio <sup>Mac</sup>	0.2.7	MIT	True
pycosat	0.6.1	MIT	True
pycparser	2.10	BSD	True
pycrypto	2.6.1	Public Domain	True
pycurl <sup>Linux Mac</sup>	7.19.5	LGPL and MIT/X	True
pyface	4.4.0	BSD	True
pyflakes	0.8.1	MIT	True
pygments	1.6	BSD	True
pylint	1.3.1	GPL	False
pymc <sup>Linux</sup>	2.3.3	<a href="#">Academic Free License</a>	False
pymongo	2.7.2	Apache 2.0	False
pyodbc	3.0.7	MIT	False
pyopenssl	0.14	APL2	True
pyparsing	2.0.1	MIT	True
pyqt	4.10.4	GPL	True
pyreadline <sup>Windows</sup>	2.0	BSD	True
pysal	1.6.0	New BSD License	False
pysam <sup>Linux Mac</sup>	0.6	MIT	False
pyserial	2.7	PSF	False
pytables	3.1.1	BSD	True
pytest	2.6.3	MIT	True
python	2.7.8	PSF	True
pytz	2014.7	MIT	True
pywin32 <sup>Windows</sup>	219	PSF	True
pyyaml	3.11	MIT	True
pyzmq	14.3.1	LGPL and BSD	True
qt <sup>Linux Mac</sup>	4.8.5	LGPL	True
queuelib	1.2.2	BSD	False
readline <sup>Linux Mac</sup>	6.2	GPL 3	True
redis <sup>Linux Mac</sup>	2.6.9	3-clause BSD	True
redis-py <sup>Linux Mac</sup>	2.9.1	<a href="#">MIT</a>	True
reportlab	3.1.8	BSD	False

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repoze.lru	0.6	BSD	False
requests	2.4.1	ISC	True
rope	0.9.4	GPL	True
runipy	0.1.1	BSD	True
scikit-bio <sup>Linux Mac</sup>	0.2.0	BSD	False
scikit-image	0.10.1	Modified BSD	True
scikit-learn	0.15.2	3-clause BSD	True
scipy	0.14.0	BSD	True
scrappy	0.24.4	BSD	False
setuptools	5.8	PSF or ZPL	True
shapely <sup>Linux Mac</sup>	1.4.1	BSD	False
sip <sup>Linux Mac</sup>	4.15.5	GPL	True
six	1.8.0	MIT	True
sockjs-tornado	1.0.1	MIT	True
sphinx	1.2.3	BSD	True
spyder	2.3.1	MIT	True
sqlalchemy	0.9.7	MIT	True
sqlite <sup>Linux Mac</sup>	3.8.4.1	Public Domain	True
sqlparse	0.1.12	BSD	False
ssh	1.8.0	LGPL	False
ssl_match_hostname	3.4.0.2	PSF	True
starcluster <sup>Linux</sup>	0.93.3	LGPL	False
statsmodels	0.5.0	3-clause Modified BSD	True
sympy	0.7.5	New BSD	True
theano <sup>Linux</sup>	0.6.0	BSD	True
tk <sup>Linux Mac</sup>	8.5.15	BSD-style	True
toolz	0.7.0	BSD	True
tornado	4.0.2	Apache	True
traits	4.4.0	BSD	True
traitsui	4.4.0	BSD	True
twisted	14.0.2	MIT	False
ujson	1.33	BSD	True
unicodcsv	0.9.4	BSD	True
unixodbc <sup>Linux</sup>	2.3.1	???	False
util-linux <sup>Linux</sup>	2.21	GPL	True
uuid	1.30	???	False
venusian	1.0	BSD	False
vtk	5.10.1	BSD	False
w3lib	1.8.1	BSD	False
werkzeug	0.9.6	BSD	True
whoosh	2.5.7	BSD	False
workerpool <sup>Linux</sup>	0.9.2	MIT	False
xldr	0.9.3	BSD	True
xlsxwriter	0.5.7	BSD	True
xlutils	1.7.1	MIT	False
xlwings <sup>Windows</sup>	0.2.2	BSD 3-clause	True
xlwt	0.7.5	BSD	True
yaml <sup>Linux Mac</sup>	0.1.4	MIT	True
yt <sup>Linux Mac</sup>	3.0.1	BSD	False
zeromq <sup>Linux Mac</sup>	4.0.4	LGPL	True

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zlib <sup>Linux Mac</sup>	1.2.7	zlib	True
zope.interface	4.1.1	Zope Public License	False

### Packages included in Anaconda 2.1.0 for Python version 3.3

Python version: 3.3

Number of supported packages: 167

Name	Version	License	In Installer
abstract-rendering <sup>Linux Mac</sup>	0.5.1	3rd-clause BSD	False
argcomplete	0.8.1	Apache Software License	False
astroid	1.2.1	LGPL	False
astropy	0.4.2	BSD	False
basemap <sup>Linux Mac</sup>	1.0.7	PSF	False
bcolz	0.7.1	BSD	False
beautiful-soup	4.3.2	PSF/MIT	False
binstar	0.7.1	BSD	False
biopython	1.64	BSD-like	False
bitarray	0.8.1	PSF	False
blaze	0.6.3	BSD	False
blist	1.3.6	BSD	False
blz	0.6.2	BSD	False
bokeh	0.6.1	New BSD	False
boto	2.32.1	MIT	False
bsdiff4	1.1.4	BSD	False
cffi	0.8.6	MIT	False
chameleon	2.16	BSD-like	False
chrpath <sup>Linux</sup>	0.13	GPL	False
colorama	0.3.1	BSD	False
conda	3.7.0	BSD	False
conda-api	1.1.0	BSD	False
conda-build	1.8.2	BSD	False
configobj	5.0.6	BSD	False
coverage	3.7.1	BSD	False
cryptography	0.5.4	Apache 2.0	False
cssselect <sup>Linux Mac</sup>	0.9.1	BSD	False
curl <sup>Linux Mac</sup>	7.38.0	MIT/X derivate	False
cython	0.21	Apache 2.0	False
cytoolz	0.7.0	BSD	False
datashape	0.3.0	BSD	False
dateutil	2.1	BSD	False
decorator	3.4.0	BSD	False
django	1.7	BSD	False
docutils	0.12	Public-Domain, PSF, 2-clause BSD, GPL3	False
dynd-python	0.6.5	BSD	False
ecdsa	0.11	MIT	False
ephem	3.7.5.3	LGPL	False
feedparser	5.1.3	MIT	False
fiona	1.1.6	BSD	False

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flake8	2.2.3	MIT	False
flask	0.10.1	BSD	False
freetype <small>Linux Mac</small>	2.4.10	<a href="#">FreeType License</a>	False
future	0.13.1	MIT	False
futures	2.1.6	BSD	False
gdal	1.11.0	MIT	False
gensim	0.10.2	LGPL	False
geos <small>Linux Mac</small>	3.3.3	LGPL	False
greenlet	0.4.4	MIT	False
gunicorn <small>Linux Mac</small>	19.1.0	MIT	False
h5py	2.3.1	<a href="#">New BSD</a>	False
hdf5 <small>Linux Mac</small>	1.8.13	<a href="#">BSD-style</a>	False
html5lib	0.999	MIT	False
ipython	2.2.0	BSD	False
itsdangerous	0.24	BSD License	False
jdcal	1.0	BSD	False
jinja2	2.7.3	BSD	False
jpeg <small>Linux Mac</small>	8d	Custom free software license	False
libdynd <small>Linux Mac</small>	0.6.5	BSD	False
libffi <small>Linux</small>	3.0.13	MIT	False
libnetcdf <small>Linux Mac</small>	4.3.2	MIT	False
libpng <small>Linux Mac</small>	1.5.13	<a href="#">Open Source</a>	False
libsodium <small>Linux Mac</small>	0.4.5	MIT	False
libtiff <small>Linux Mac</small>	4.0.2	<a href="#">as-is</a>	False
libxml2 <small>Linux Mac</small>	2.9.0	MIT	False
libxslt <small>Linux Mac</small>	1.1.28	MIT	False
llvm <small>Linux Mac</small>	3.3	<a href="#">Open Source</a>	False
llvmpy	0.12.7	New BSD License	False
logilab-common	0.62.1	LGPL	False
lxml	3.4.0	BSD	False
markdown <small>Linux Mac</small>	2.5	BSD	False
markupsafe	0.23	BSD	False
mathjax	2.2	Apache	False
matplotlib	1.4.0	<a href="#">PSF-based</a>	False
mccabe	0.2.1	Expat	False
mdp	3.3	BSD	False
mingw <small>Windows</small>	4.7	<a href="#">GPL</a>	False
mock	1.0.1	BSD	False
multimethods	1.0.0	MIT	False
multiplatform	0.4.7	BSD	False
natsort	3.5.0	MIT	False
netcdf4	1.1.1	MIT	False
networkx	1.9.1	BSD	False
nltk	3.0.0	Apache 2.0	False
nose	1.3.4	LGPL	False
numba	0.14.0	numba license	False
numexpr	2.3.1	MIT	False
numpy	1.9.0	BSD	False
openpyxl	1.8.5	MIT/Expat	False
openssl <small>Linux Mac</small>	1.0.1h	<a href="#">Apache-style</a>	False

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pandas	0.14.1	BSD	False
paramiko	1.14.1	LGPL	False
passlib	1.6.2	BSD	False
pastedeploy <sup>Linux Mac</sup>	1.5.2	MIT	False
patchelf <sup>Linux</sup>	0.6	GPL3	False
patsy	0.3.0	BSD License	False
pep8	1.5.7	MIT License	False
pillow <sup>Linux Mac</sup>	2.5.1	Standard PIL license	False
pip	1.5.6	MIT	False
ply	3.4	BSD	False
psutil	2.1.1	BSD	False
py	1.4.25	MIT	False
pyasn1 <sup>Linux</sup>	0.1.6	BSD	False
pycosat	0.6.1	MIT	False
pycparser	2.10	BSD	False
pycrypto	2.6.1	Public Domain	False
pycurl <sup>Linux Mac</sup>	7.19.5	LGPL and MIT/X	False
pyflakes	0.8.1	MIT	False
pygments	1.6	BSD	False
pylint	1.3.1	GPL	False
pymongo	2.7.2	Apache 2.0	False
pyodbc	3.0.7	MIT	False
pyopenssl	0.14	APL2	False
pyarsing	2.0.1	MIT	False
pyqt	4.10.4	GPL	False
pyreadline <sup>Windows</sup>	2.0	BSD	False
pyserial	2.7	PSF	False
pytables	3.1.1	BSD	False
pytest	2.6.3	MIT	False
python	3.3.5	PSF	False
pytz	2014.7	MIT	False
pywin32 <sup>Windows</sup>	219	PSF	False
pyyaml	3.11	MIT	False
pyzmq	14.3.1	LGPL and BSD	False
qt <sup>Linux Mac</sup>	4.8.5	LGPL	False
queuelib	1.2.2	BSD	False
readline <sup>Linux Mac</sup>	6.2	GPL 3	False
redis <sup>Linux Mac</sup>	2.6.9	3-clause BSD	False
redis-py <sup>Linux Mac</sup>	2.9.1	MIT	False
reportlab	3.1.8	BSD	False
repoze.lru	0.6	BSD	False
requests	2.4.1	ISC	False
rope	0.9.4	GPL	False
runipy	0.1.1	BSD	False
scikit-bio <sup>Linux Mac</sup>	0.2.0	BSD	False
scikit-image	0.10.1	Modified BSD	False
scikit-learn	0.15.2	3-clause BSD	False
scipy	0.14.0	BSD	False
setuptools	5.8	PSF or ZPL	False
shapely <sup>Linux Mac</sup>	1.4.1	BSD	False

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Table 66 – continued from previous page

sip <sup>Linux Mac</sup>	4.15.5	GPL	False
six	1.8.0	MIT	False
sockjs-tornado	1.0.1	MIT	False
sphinx	1.2.3	BSD	False
sqlalchemy	0.9.7	MIT	False
sqlite <sup>Linux Mac</sup>	3.8.4.1	Public Domain	False
sqlparse	0.1.12	BSD	False
statsmodels	0.5.0	3-clause Modified BSD	False
sympy	0.7.5	New BSD	False
tk <sup>Linux Mac</sup>	8.5.15	BSD-style	False
toolz	0.7.0	BSD	False
tornado	4.0.2	Apache	False
twisted	14.0.2	MIT	False
ujson	1.33	BSD	False
unixodbc <sup>Linux</sup>	2.3.1	???	False
util-linux <sup>Linux</sup>	2.21	GPL	False
venusian	1.0	BSD	False
w3lib	1.8.1	BSD	False
werkzeug	0.9.6	BSD	False
whoosh	2.5.7	BSD	False
xlrd	0.9.3	BSD	False
xlswriter	0.5.7	BSD	False
xz <sup>Linux Mac</sup>	5.0.5	Public Domain and GPL	False
yaml <sup>Linux Mac</sup>	0.1.4	MIT	False
zeromq <sup>Linux Mac</sup>	4.0.4	LGPL	False
zlib <sup>Linux Mac</sup>	1.2.7	zlib	False
zope.interface	4.1.1	Zope Public License	False

### Packages included in Anaconda 2.1.0 for Python version 3.4

Python version: 3.4

Number of supported packages: 171

Name	Version	License	In Installer
abstract-rendering <sup>Linux Mac</sup>	0.5.1	3rd-clause BSD	True
argcomplete	0.8.1	Apache Software License	True
astroid	1.2.1	LGPL	False
astropy	0.4.2	BSD	True
basemap <sup>Linux Mac</sup>	1.0.7	PSF	False
bcolz	0.7.1	BSD	False
beautiful-soup	4.3.2	PSF/MIT	True
binstar	0.7.1	BSD	True
biopython	1.64	BSD-like	False
bitarray	0.8.1	PSF	True
blaze	0.6.3	BSD	True
blist	1.3.6	BSD	False
blz	0.6.2	BSD	True
bokeh	0.6.1	New BSD	True
boto	2.32.1	MIT	True

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Table 67 – continued from previous page

bsdiff4	1.1.4	BSD	False
cffi	0.8.6	MIT	True
chameleon	2.16	BSD-like	False
chrpath <sup>Linux</sup>	0.13	GPL	False
colorama	0.3.1	BSD	True
conda	3.7.0	BSD	True
conda-api	1.1.0	BSD	False
conda-build	1.8.2	BSD	True
configobj	5.0.6	BSD	True
coverage	3.7.1	BSD	False
cryptography	0.5.4	Apache 2.0	True
cssselect <sup>Linux Mac</sup>	0.9.1	BSD	False
curl <sup>Linux Mac</sup>	7.38.0	MIT/X derivate	True
cython	0.21	Apache 2.0	True
cytoolz	0.7.0	BSD	True
datashape	0.3.0	BSD	True
dateutil	2.1	BSD	True
decorator	3.4.0	BSD	True
django	1.7	BSD	False
docutils	0.12	Public-Domain, PSF, 2-clause BSD, GPL3	True
dynd-python	0.6.5	BSD	True
ecdsa	0.11	MIT	False
ephem	3.7.5.3	LGPL	False
feedparser	5.1.3	MIT	False
fiona	1.1.6	BSD	False
flake8	2.2.3	MIT	False
flask	0.10.1	BSD	True
freetype <sup>Linux Mac</sup>	2.4.10	FreeType License	True
future	0.13.1	MIT	True
futures	2.1.6	BSD	False
gdal	1.11.0	MIT	False
gensim	0.10.2	LGPL	False
geos <sup>Linux Mac</sup>	3.3.3	LGPL	False
greenlet	0.4.4	MIT	True
gunicorn <sup>Linux Mac</sup>	19.1.0	MIT	False
h5py	2.3.1	New BSD	True
hdf5 <sup>Linux Mac</sup>	1.8.13	BSD-style	True
html5lib	0.999	MIT	False
ipython	2.2.0	BSD	True
itsdangerous	0.24	BSD License	True
jdcal	1.0	BSD	True
jinja2	2.7.3	BSD	True
jpeg <sup>Linux Mac</sup>	8d	Custom free software license	True
launcher <sup>Mac Windows</sup>	1.0.0	proprietary - Continuum Analytics, Inc.	True
libdynd <sup>Linux Mac</sup>	0.6.5	BSD	True
libffi <sup>Linux</sup>	3.0.13	MIT	True
libnetcdf <sup>Linux Mac</sup>	4.3.2	MIT	False
libpng <sup>Linux Mac</sup>	1.5.13	Open Source	True
libsodium <sup>Linux Mac</sup>	0.4.5	MIT	True
libtiff <sup>Linux Mac</sup>	4.0.2	as-is	True

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Table 67 – continued from previous page

libxml2 <sup>Linux Mac</sup>	2.9.0	MIT	True
libxslt <sup>Linux Mac</sup>	1.1.28	MIT	True
llvm <sup>Linux Mac</sup>	3.3	<a href="#">Open Source</a>	True
llvmpy	0.12.7	New BSD License	True
logilab-common	0.62.1	LGPL	False
lxml	3.4.0	BSD	True
markdown <sup>Linux Mac</sup>	2.5	BSD	False
markupsafe	0.23	BSD	True
mathjax	2.2	Apache	False
matplotlib	1.4.0	<a href="#">PSF-based</a>	True
mccabe	0.2.1	Expat	False
mdp	3.3	BSD	False
menuinst <sup>Windows</sup>	1.0.4	BDF	True
mingw <sup>Windows</sup>	4.7	<a href="#">GPL</a>	True
mock	1.0.1	BSD	True
multimethods	1.0.0	MIT	False
multipledispatch	0.4.7	BSD	True
natsort	3.5.0	MIT	False
netcdf4	1.1.1	MIT	False
networkx	1.9.1	BSD	True
nlTK	3.0.0	Apache 2.0	True
node-webkit <sup>Mac Windows</sup>	0.10.1	MIT	True
nose	1.3.4	LGPL	True
numba	0.14.0	numba license	True
numexpr	2.3.1	MIT	True
numpy	1.9.0	BSD	True
openpyxl	1.8.5	MIT/Expat	True
openssl <sup>Linux Mac</sup>	1.0.1h	<a href="#">Apache-style</a>	True
pandas	0.14.1	BSD	True
paramiko	1.14.1	LGPL	False
passlib	1.6.2	BSD	False
pastedeploy <sup>Linux Mac</sup>	1.5.2	MIT	False
patchelf <sup>Linux</sup>	0.6	GPL3	False
patsy	0.3.0	BSD License	True
pep8	1.5.7	MIT License	False
pillow <sup>Linux Mac</sup>	2.5.1	Standard PIL license	True
pip	1.5.6	MIT	True
ply	3.4	BSD	True
psutil	2.1.1	BSD	True
py	1.4.25	MIT	True
pyasn1 <sup>Linux</sup>	0.1.6	BSD	False
pycosat	0.6.1	MIT	True
pycparser	2.10	BSD	True
pycrypto	2.6.1	Public Domain	True
pycurl <sup>Linux Mac</sup>	7.19.5	LGPL and MIT/X	True
pyflakes	0.8.1	MIT	True
pygments	1.6	BSD	True
pylint	1.3.1	GPL	False
pymongo	2.7.2	Apache 2.0	False
pyodbc	3.0.7	MIT	False

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Table 67 – continued from previous page

pyopenssl	0.14	APL2	True
yparsing	2.0.1	MIT	True
pyqt	4.10.4	GPL	True
pyreadline <sup>Windows</sup>	2.0	BSD	True
pyserial	2.7	PSF	False
pytables	3.1.1	BSD	True
pytest	2.6.3	MIT	True
python	3.4.1	PSF	True
pytz	2014.7	MIT	True
pywin32 <sup>Windows</sup>	219	PSF	True
pyyaml	3.11	MIT	True
pyzmq	14.3.1	LGPL and BSD	True
qt <sup>Linux Mac</sup>	4.8.5	LGPL	True
queuelib	1.2.2	BSD	False
readline <sup>Linux Mac</sup>	6.2	GPL 3	True
redis <sup>Linux Mac</sup>	2.6.9	3-clause BSD	True
redis-py <sup>Linux Mac</sup>	2.9.1	MIT	True
reportlab	3.1.8	BSD	False
repoze.lru	0.6	BSD	False
requests	2.4.1	ISC	True
rope	0.9.4	GPL	True
runipy	0.1.1	BSD	True
scikit-bio <sup>Linux Mac</sup>	0.2.0	BSD	False
scikit-image	0.10.1	Modified BSD	True
scikit-learn	0.15.2	3-clause BSD	True
scipy	0.14.0	BSD	True
setuptools	5.8	PSF or ZPL	True
shapely <sup>Linux Mac</sup>	1.4.1	BSD	False
sip <sup>Linux Mac</sup>	4.15.5	GPL	True
six	1.8.0	MIT	True
sockjs-tornado	1.0.1	MIT	True
sphinx	1.2.3	BSD	True
spyder	2.3.1	MIT	True
sqlalchemy	0.9.7	MIT	True
sqlite <sup>Linux Mac</sup>	3.8.4.1	Public Domain	True
sqlparse	0.1.12	BSD	False
statsmodels	0.5.0	3-clause Modified BSD	True
sympy	0.7.5	New BSD	True
tk <sup>Linux Mac</sup>	8.5.15	BSD-style	True
toolz	0.7.0	BSD	True
tornado	4.0.2	Apache	True
twisted	14.0.2	MIT	False
ujson	1.33	BSD	True
unixodbc <sup>Linux</sup>	2.3.1	???	False
util-linux <sup>Linux</sup>	2.21	GPL	True
venusian	1.0	BSD	False
w3lib	1.8.1	BSD	False
werkzeug	0.9.6	BSD	True
whoosh	2.5.7	BSD	False
xlrd	0.9.3	BSD	True

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Table 67 – continued from previous page

xlsxwriter	0.5.7	BSD	True
xz <small>Linux Mac</small>	5.0.5	Public Domain and GPL	True
yaml <small>Linux Mac</small>	0.1.4	<a href="#">MIT</a>	True
zeromq <small>Linux Mac</small>	4.0.4	LGPL	True
zlib <small>Linux Mac</small>	1.2.7	<a href="#">zlib</a>	True
zope.interface	4.1.1	Zope Public License	False

**Packages included in Anaconda 2.2.0 for Python version 2.6**

**Packages included in Anaconda 2.2.0 for Python version 2.7**

**Packages included in Anaconda 2.2.0 for Python version 3.3**

**Packages included in Anaconda 2.2.0 for Python version 3.4**

**Packages included in Anaconda 2.3.0 for Python version 2.6**

**Packages included in Anaconda 2.3.0 for Python version 2.7**

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**Packages included in Anaconda 2.3.0 for Python version 3.4**

**Packages included in Anaconda 2.4.0 for Python version 2.7**

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**Packages included in Anaconda 2.4.0 for Python version 3.4**

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**Packages included in Anaconda 2.4.0 for Python version 3.5**

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**Packages included in Anaconda 2.4.1 for Python version 3.5**

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**Packages included in Anaconda 2.5.0 for Python version 2.7**

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**Packages included in Anaconda 4.0.0 for Python version 2.7**

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Packages included in Anaconda 5.0.0 for 32-bit Linux with Python 2.7

Packages included in Anaconda 5.0.0 for 64-bit Linux with Python 2.7

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Packages included in Anaconda 5.3.0 for 64-bit Linux on IBM Power CPUs with Python 3.7

Packages included in Anaconda 5.3.0 for 64-bit macOS with Python 3.7

Packages included in Anaconda 5.3.0 for 32-bit Windows with Python 3.7

Packages included in Anaconda 5.3.0 for 64-bit Windows with Python 3.7

Packages included in Anaconda 2018.12 for 32-bit Linux with Python 2.7

Packages included in Anaconda 2018.12 for 64-bit Linux with Python 2.7

Packages included in Anaconda 2018.12 for 64-bit Linux on IBM Power CPUs with Python 2.7

Packages included in Anaconda 2018.12 for macOS with Python 2.7

Packages included in Anaconda 2018.12 for 32-bit Windows with Python 2.7

Packages included in Anaconda 2018.12 for 64-bit Windows with Python 2.7

Packages included in Anaconda 2018.12 for 32-bit Linux with Python 3.6

Packages included in Anaconda 2018.12 for 64-bit Linux with Python 3.6

Packages included in Anaconda 2018.12 for 64-bit Linux on IBM Power CPUs with Python 3.6

Packages included in Anaconda 2018.12 for macOS with Python 3.6

Packages included in Anaconda 2018.12 for 32-bit Windows with Python 3.6

Packages included in Anaconda 2018.12 for 64-bit Windows with Python 3.6

Packages included in Anaconda 2018.12 for 32-bit Linux with Python 3.7

Packages included in Anaconda 2018.12 for 64-bit Linux with Python 3.7

Packages included in Anaconda 2018.12 for 64-bit Linux on IBM Power CPUs with Python 3.7

Packages included in Anaconda 2018.12 for macOS with Python 3.7

Packages included in Anaconda 2018.12 for 32-bit Windows with Python 3.7

Packages included in Anaconda 2018.12 for 64-bit Windows with Python 3.7

Packages included in Anaconda 2019.03 for 64-bit Linux with Python 2.7

Packages included in Anaconda 2019.03 for 64-bit Linux on IBM Power CPUs with Python 2.7

Packages included in Anaconda 2019.03 for macOS with Python 2.7

Packages included in Anaconda 2019.03 for 32-bit Windows with Python 2.7

Packages included in Anaconda 2019.03 for 64-bit Windows with Python 2.7

Packages included in Anaconda 2019.03 for 64-bit Linux with Python 3.6

Packages included in Anaconda 2019.03 for 64-bit Linux on IBM Power CPUs with Python 3.6

Packages included in Anaconda 2019.03 for macOS with Python 3.6

Packages included in Anaconda 2019.03 for 32-bit Windows with Python 3.6

Packages included in Anaconda 2019.03 for 64-bit Windows with Python 3.6

Packages included in Anaconda 2019.03 for 64-bit Linux with Python 3.7

Packages included in Anaconda 2019.03 for 64-bit Linux on IBM Power CPUs with Python 3.7

Packages included in Anaconda 2019.03 for macOS with Python 3.7

Packages included in Anaconda 2019.03 for 32-bit Windows with Python 3.7

Packages included in Anaconda 2019.03 for 64-bit Windows with Python 3.7

Packages included in Anaconda 2019.07 for 64-bit Linux with Python 2.7

Packages included in Anaconda 2019.07 for 64-bit Linux on IBM Power CPUs with Python 2.7

Packages included in Anaconda 2019.07 for macOS with Python 2.7

Packages included in Anaconda 2019.07 for 32-bit Windows with Python 2.7

Packages included in Anaconda 2019.07 for 64-bit Windows with Python 2.7

Packages included in Anaconda 2019.07 for 64-bit Linux with Python 3.6

Packages included in Anaconda 2019.07 for 64-bit Linux on IBM Power CPUs with Python 3.6

Packages included in Anaconda 2019.07 for macOS with Python 3.6

Packages included in Anaconda 2019.07 for 32-bit Windows with Python 3.6

Packages included in Anaconda 2019.07 for 64-bit Windows with Python 3.6

Packages included in Anaconda 2019.07 for 64-bit Linux with Python 3.7

Packages included in Anaconda 2019.07 for 64-bit Linux on IBM Power CPUs with Python 3.7

Packages included in Anaconda 2019.07 for macOS with Python 3.7

Packages included in Anaconda 2019.07 for 32-bit Windows with Python 3.7

Packages included in Anaconda 2019.07 for 64-bit Windows with Python 3.7

Packages included in Anaconda 2019.10 for 64-bit Linux with Python 2.7

Packages included in Anaconda 2019.10 for 64-bit Linux on IBM Power CPUs with Python 2.7

Packages included in Anaconda 2019.10 for macOS with Python 2.7

Packages included in Anaconda 2019.10 for 32-bit Windows with Python 2.7

Packages included in Anaconda 2019.10 for 64-bit Windows with Python 2.7

Packages included in Anaconda 2019.10 for 64-bit Linux with Python 3.6

Packages included in Anaconda 2019.10 for 64-bit Linux on IBM Power CPUs with Python 3.6

Packages included in Anaconda 2019.10 for macOS with Python 3.6

Packages included in Anaconda 2019.10 for 32-bit Windows with Python 3.6

Packages included in Anaconda 2019.10 for 64-bit Windows with Python 3.6

Packages included in Anaconda 2019.10 for 64-bit Linux with Python 3.7

Packages included in Anaconda 2019.10 for 64-bit Linux on IBM Power CPUs with Python 3.7

Packages included in Anaconda 2019.10 for macOS with Python 3.7

Packages included in Anaconda 2019.10 for 32-bit Windows with Python 3.7

Packages included in Anaconda 2019.10 for 64-bit Windows with Python 3.7

Packages included in Anaconda 2020.02 for 64-bit Linux with Python 3.6

**Packages included in Anaconda 2020.02 for 64-bit Linux on IBM Power CPUs with Python 3.6**

**Packages included in Anaconda 2020.02 for macOS with Python 3.6**

**Packages included in Anaconda 2020.02 for 32-bit Windows with Python 3.6**

**Packages included in Anaconda 2020.02 for 64-bit Windows with Python 3.6**

**Packages included in Anaconda 2020.02 for 64-bit Linux with Python 3.7**

**Packages included in Anaconda 2020.02 for 64-bit Linux on IBM Power CPUs with Python 3.7**

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**Packages included in Anaconda 2020.02 for 64-bit Linux with Python 3.8**

**Packages included in Anaconda 2020.02 for 64-bit Linux on IBM Power CPUs with Python 3.8**

**Packages included in Anaconda 2020.02 for macOS with Python 3.8**

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The following packages are included in the repository accessible through Anaconda® Individual Edition that relate to cryptography:

- `openssl` The OpenSSL Project is a collaborative effort to develop a robust, commercial-grade, full-featured, and Open Source toolkit implementing the Transport Layer Security (TLS) and Secure Sockets Layer (SSL) protocols as well as a full-strength general purpose cryptography library.
- `pycrypto` A collection of both secure hash functions (such as SHA256 and RIPEMD160), and various encryption algorithms (AES, DES, RSA, ElGamal, etc.).
- `pyopenssl` A thin Python wrapper around (a subset of) the OpenSSL library.
- `kerberos` (krb5, non-Windows platforms) A network authentication protocol designed to provide strong authentication for client/server applications by using secret-key cryptography.
- `cryptography` A Python library which exposes cryptographic recipes and primitives.
- `pycryptodome` A fork of PyCrypto. It is a self-contained Python package of low-level cryptographic primitives. (<https://pycryptodome.readthedocs.io/en/latest/src/introduction.html>)
- `pycryptodomex` A stand-alone version of pycryptodome.
- `libsodium` A software library for encryption, decryption, signatures, password hashing and more.
- `pynacl` A Python binding to the Networking and Cryptography library, a crypto library with the stated goal of improving usability, security and speed.

## 4.3 Anaconda Cloud

*What is Anaconda Cloud?*

**Anaconda Cloud** is a package management service by **Anaconda**. Cloud makes it easy to find, access, store and share public notebooks, environments, and conda and PyPI packages. Cloud also makes it easy to stay current with updates made to the packages and environments you are using. Cloud hosts hundreds of useful Python packages, notebooks, projects and environments for a wide variety of applications. You do not need to log in, or even to have a Cloud account, to search for public packages, download and install them.

You can build new conda packages using `conda-build`, then upload the packages to Cloud to quickly share with others or access yourself from anywhere. The Anaconda Cloud command line interface (CLI), `anaconda-client`, allows you to manage your account - including authentication, tokens, upload, download, remove and search.

Connect to and manage your Anaconda Cloud account. Upload packages you have created. Generate access tokens to allow access to private packages.

For developers, Cloud is designed to make software development, release and maintenance easy by providing broad package management support. Cloud allows for free public package hosting, as well as package channels, providing a flexible and scalable service for groups and organizations of all sizes.

Hosting of freely available packages always remains free for individuals and organizations hosting up to 3 GB of packages.

To use Cloud, you should first:

- **Download Anaconda.** The Anaconda installer

includes `conda`, `conda-build` and `anaconda-client`.

- Become familiar with using conda. A good place to start is the [conda cheat sheet](#) and the [conda test drive](#).

### 4.3.1 User guide

Anaconda Cloud is a package management service that makes it easy to find, access, store and share public notebooks, environments, and conda and PyPI packages. Cloud also makes it easy to stay current with updates made to the

packages and environments you are using.

To begin using Cloud, read *Getting started*, then the remaining sections of the user guide.

### Getting started

- *Installing Anaconda Client*
- *Finding, downloading and installing packages*
- *Building and uploading packages*
- *Sharing notebooks*
- *Sharing environments*

### Installing Anaconda Client

You can use Anaconda Client command line interface (CLI) to:

- Connect to and manage your Anaconda Cloud account.
- Upload *packages* you have created.
- Generate access *tokens* to allow access to private packages.

NOTE: Client is not necessary to search for and download packages.

This tool can be installed using an Anaconda Prompt or the Terminal application in three ways: with `conda`, with `pip` or with `pip` from source. We recommend using `conda`.

Option 1, `conda`:

```
conda install anaconda-client
```

Option 2, `pip`:

```
pip install anaconda-client
```

Option 3, installing with `pip` from source:

```
pip install git+https://github.com/Anaconda-Platform/anaconda-client
```

After installing, view the complete list of Client tasks with this command:

```
anaconda -h
```

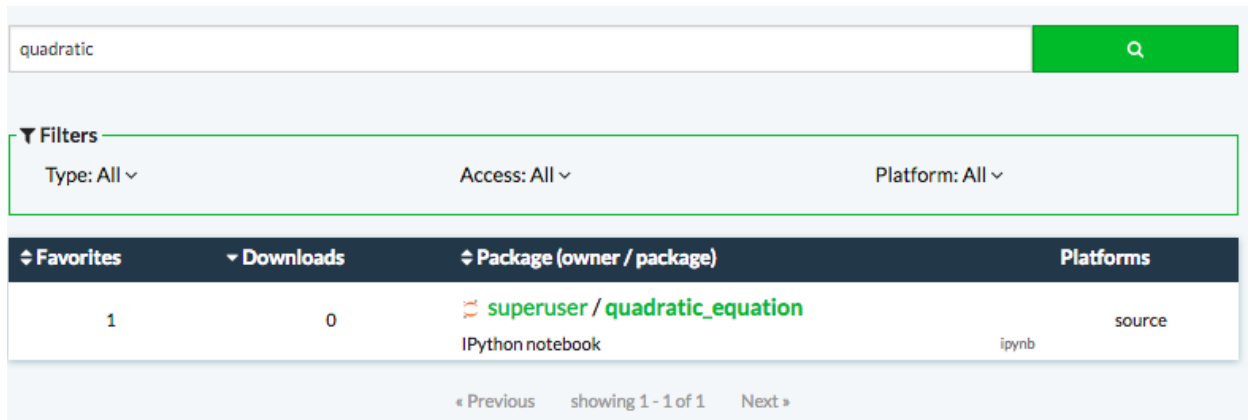
### Finding, downloading and installing packages

#### Searching for public packages

`Cloud` hosts hundreds of useful Python packages for a wide variety of applications. You do not need to be logged in, or even need a Cloud account, to search for public packages, download and install them. You need an account only to access *private packages* without a *token* or to share your packages with others.

To search for packages:

1. In the top Search box, type part or all of the name of a program you are searching for, and then press Enter.
2. Packages that match your search string are displayed. To see more information, click the package name.



For more information, see [Working with packages](#).

## Refining your search results

You can filter search results using 3 filter controls:

- **Type:** All, conda only or PyPI only.
- **Access:** All, Public and/or Private—only available if you are logged in.
- **Platform:** All, source, linux-32, linux-64, linux-armv61, linux-armv71, linux-ppc64le, noarch, osx-32, osx-64, win-32, win-64.

Source packages are source code only, not yet built for any specific platform.

Noarch packages are built to work on all platforms.

## Downloading and installing packages from Cloud

You can download and install packages using [Anaconda Navigator](#), the graphical user interface for Anaconda. Advanced users may prefer a terminal window or command prompt.

## Using Navigator

Navigator is automatically installed when you install Anaconda®.

To download and install a package into its own environment:

1. Start Navigator by clicking its program icon on your desktop or in your programs menu.
2. Sign Navigator into Cloud so you can search for packages marked as private. Click the top right Sign in to Anaconda Cloud button and type your Cloud username and password, then click the Login button.

3. On the **Environments** tab, in the far-right Search packages box, enter the name of the desired package.
4. In the list to the left of Channels, select either Not installed or All, then click the Search button.
5. Select the checkbox of the package you want to install, then click the Apply button.

For more information, see [Navigator](#).

### Using conda in a Terminal window or Anaconda Prompt

To download and install a package into its own environment:

1. Locate a package on Cloud that you want to download, then click on the package name.
2. A detail page displays specific installation instructions for the current operating system. Copy and paste the full command into your terminal window.

For example, the command could be structured as:

```
conda install -c username packagename
```

NOTE: For the following examples to work, you need to have [conda](#) downloaded and installed.

TIP: Conda expands `username` to a URL such as <https://anaconda.org/username>, based on the settings in the `.condarc` file.

### Building and uploading packages

[Open a Cloud account](#) to upload packages or to access private packages without a token.

To build and upload packages, install the Client command line interface (CLI). For more information, see [Installing Anaconda Client](#).

Use the Terminal window or an Anaconda Prompt to perform the following steps.

1. Install Anaconda Client:

```
conda install anaconda-client
```

2. Log into your Cloud account:

```
anaconda login
```

At the prompt, enter your Cloud username and password.

3. Choose the package you would like to build. For this example, download our public test package:

```
git clone https://github.com/Anaconda-Platform/anaconda-client
cd anaconda-client/example-packages/conda/
```

4. To build your test package, first install `conda-build` and turn off automatic Client uploading, then run the `conda build` command:

```
conda install conda-build
conda config --set anaconda_upload no
conda build .
```

5. Find the path to where the newly-built file was placed so you can use it in the next step:

```
conda build . --output
```

6. Upload your newly-built test package to your Cloud account:

```
anaconda login  
anaconda upload /your/path/conda-package.tar.bz2
```

NOTE: Replace `/your/path/` with the actual path that you found in the previous step.

For more information, see [conda packages](#).

## Sharing notebooks

To share a [Jupyter notebook](#)—formerly IPython notebook—on Cloud:

1. To Upload your notebook to Cloud, open the Terminal or an Anaconda Prompt and enter:

```
anaconda upload my-notebook.ipynb
```

NOTE: Replace `my-notebook` with the actual name of your notebook.

2. You can see an HTML version of your notebook stored at:

```
http://notebooks.anaconda.org/<USERNAME>/my-notebook
```

NOTE: Replace `<USERNAME>` with your username, and `my-notebook` with the actual name of your notebook.

3. Anyone who has access to Cloud can download your notebook. To download the notebook, open the Terminal or an Anaconda Prompt and enter:

```
anaconda download username/my-notebook
```

NOTE: Replace `username` with your username, and `my-notebook` with the actual name of your notebook.

## Sharing environments

To share an environment on Cloud:

1. See the [conda user guide](#) to create and save a conda environment. Open the Terminal or an Anaconda Prompt and enter:

```
conda env export -n my-environment -f my-environment.yml
```

NOTE: Replace `my-environment` with the actual name of your environment.

2. Upload it to Cloud either using the web interface or the `anaconda upload` command.

- Using the web interface:

Go to <https://anaconda.org/USERNAME/environments>.

NOTE: Replace `USERNAME` with your username.

In the top right corner use the Upload button to upload your environment.

- Using the `anaconda upload` command from the Terminal window or an Anaconda Prompt:

```
anaconda upload my-environment.yml
```

NOTE: Replace `my-environment` with the actual name of your environment.

3. You can see a list of your uploaded environments at:

```
http://envs.anaconda.org/<USERNAME>
```

NOTE: Replace `<USERNAME>` with your username.

4. Anyone can download and install your environment from Cloud.

- Using the web interface:

Go to `https://anaconda.org/USERNAME/environments`.

NOTE: Replace `USERNAME` with the username.

Select the environment, click the Files tab, and under the Names field click the file to download.

- Using the Terminal or an Anaconda Prompt:

```
conda env create user/my-environment
source activate my-environment
```

NOTE: Replace `my-environment` with the actual name of your environment.

### How to...

- *Use packages*
- *Use the Anaconda Client CLI*
- *Build packages*

## Use packages

### Finding a package

In your browser, you can search Anaconda Cloud for packages by package name. From the top navigation bar of any page, enter the package name in the search box. You can filter your searches to specify only conda or PyPI packages, and you can sort results by number of favorites or number of downloads by clicking the search results column heading.

### Downloading and installing a package from Cloud

To install a conda package, in your Terminal window or Anaconda Prompt run:

```
conda install -c username packagename
```

Conda expands `username` to a URL such as <https://anaconda.org/username> or <https://conda.anaconda.org/username> based on the settings in the `.condarc` file.

NOTE: Replace `username` with your username, and `packagename` with the actual name of the package.



## Downloading and installing a PyPI package from Cloud

To install a PyPI package, in your Terminal window or Anaconda Prompt run:

```
pip install --index-url pypi.anaconda.org/USERNAME/simple packagename
```

NOTE: Replace USERNAME with your username, and packagename with the actual name of the package.

## Use the Anaconda Client CLI

### Installing Client

For installation and setup instructions, see *Install Anaconda Client*.

### Finding my Client login credentials

Your credentials for Client are those you used to create an account on Cloud.

To get help:

1. Go to <https://anaconda.org>.
2. Select the **Sign In** tab.
3. Click either I forgot my password or I forgot my username.

### Logging into Client

After you have downloaded and configured Client, open a Terminal window or an Anaconda Prompt and run:

```
anaconda login
```

### Displaying a list of Client commands

From a Terminal window or an Anaconda Prompt, run:

```
anaconda --help
```

### Finding out more about a Client command

From a Terminal window or an Anaconda Prompt, run:

```
anaconda COMMANDNAME -h
```

NOTE: Replace COMMANDNAME with the name of the command about which you want more information.

### Listing all available Client configuration files

From a Terminal window or an Anaconda Prompt, run:

```
anaconda config --files
```

### Listing all of your Client configuration variables

From a Terminal window or an Anaconda Prompt, run:

```
anaconda config --show
```

### Finding out more about Client

You can learn more about Client using the help command, documentation or community support email group.

### Build packages

#### Building and uploading a package

For a quick example, see *Building and uploading packages* in *Getting started*.

#### Testing a built package

In your Terminal window or Anaconda Prompt run:

```
conda create --use-local -n test PACKAGENAME
```

Specify the `--use-local` option.

NOTE: Replace PACKAGENAME with the actual name of the package.

#### Uploading a package to Cloud

In a Terminal window or Anaconda Prompt, run:

```
anaconda upload PACKAGENAME
```

NOTE: Replace PACKAGENAME with the actual name of the package.

#### Finding help for uploading packages

You can obtain a complete list of upload options, including:

- Package channel.
- Label.
- Availability to other users.

- Metadata.

To list the options, in a Terminal window or Anaconda Prompt run:

```
anaconda upload -h
```

## Tutorial

### Using labels in the development cycle

Anaconda Cloud *labels* can be used to facilitate a development cycle and organize the code that is in development, in testing and in production, without affecting non-development users. With labels you can upload a file to a specific label, so only users who put that label in the URL they search are able to find it.

Using Anaconda Client, *package* developers can create additional labels such as development `labels/dev`, test `labels/test` or other labels that are searched only if the user specifies the label. The following search examples use a *namespace* of `travis`:

- <https://anaconda.org/travis/labels/main> – the label searched by default.
- <https://anaconda.org/travis> – same as default label with `main` implicit.
- <https://anaconda.org/travis/labels/dev> – contains the packages in development.
- <https://anaconda.org/travis/labels/test> – contains packages ready to test.
- <https://anaconda.org/travis/labels/any-custom-label> – any label you want to use.

In this example, we show you how to use a `test` label, so that you can upload files without affecting your production-quality packages. Without a `--label` argument the default label is `main`.

Use the Terminal window or an Anaconda Prompt to perform the following steps:

1. Let us start with a conda package. If you do not have one, use our example conda package. Before you build the package, edit the version in the `meta.yaml` file in `anaconda-client/example-packages/conda/` to be `2.0`:

```
git clone https://github.com/Anaconda-Platform/anaconda-client/
cd anaconda-client/example-packages/conda/
nano meta.yaml # Bump version to 2.0
conda config --set anaconda_upload no
conda build .
```

2. Upload your test package to Cloud using the Client *upload* command.

Adding the `--label` option tells Cloud to make the upload visible only to users who specify that label:

```
anaconda upload /path/to/conda-package-2.0.tar.bz2 --label test
```

NOTE: Replace `/path/to/` with the actual path where you stored the package.

3. You now can see that even when you search conda `main`, you do not see the `2.0` version of the test package. This is because you need to tell conda to look for your new `test` label.
4. The `--override` argument tells conda not to use any channels in your `~/.condarc` file.

No `2.0` results:

```
conda search --override -c USERNAME conda-package
```

NOTE: Replace USERNAME with your username.

Your 2.0 package is here:

```
conda search --override -c USERNAME/label/test conda-package
```

NOTE: Replace USERNAME with your username.

5. You can give the label USERNAME/label/test to your testers.

NOTE: Replace USERNAME with your username.

6. Once they finish testing, you may then want to copy the test packages back to your main label:

```
anaconda label --copy test main
```

You can also manage your package labels from your dashboard: <https://anaconda.org/USERNAME/conda-package>.

Your version 2.0 is now in main:

```
conda search --override -c USERNAME conda-package
```

NOTE: Replace USERNAME with your username.

If you use `anaconda-client` 1.7 or higher, you can use `anaconda move` to move packages from one label to another:

```
anaconda move --from-label OLD --to-label NEW SPEC
```

Replace OLD with the old label, NEW with the new label, and SPEC with the package to move. SPEC can be either “user/package/version/file”, or “user/package/version” in which case it moves all files in that version.

## Tasks

### Working with accounts

- *Personal accounts*
- *Organization accounts*

### Personal accounts

#### Overview

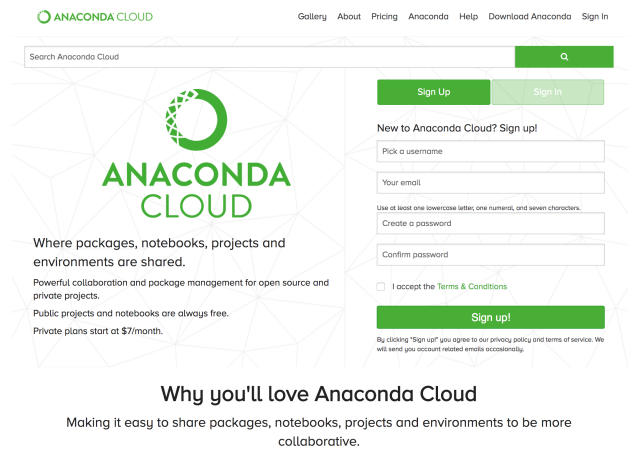
This section explains how to create a free, personal account, log in and out, and access the settings and features of different types of accounts.

#### Creating a free account

All Anaconda Cloud users can find, download and use packages without having a Cloud account.

However, you need to create a Cloud account to:

- Author packages.
- Upload packages, notebooks and environments.
- Access shared, private packages.
- Create organizations.



To sign up for a free Cloud account:

1. In a browser, go to [Anaconda Cloud](#).
2. Make sure the **Sign Up** tab is active.

NOTE: There is also a **Sign In** tab for existing users.

3. Select a username.
4. Enter your email address.

NOTE: Users who register with an .edu email are granted some additional features.

5. Create a password.
6. Enter the password again to confirm it.
7. Read and accept the Terms and Conditions.
8. Click the Sign up button.

The system creates your free account, logs you in and displays your personal dashboard.

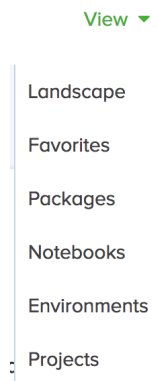
TIP: Cloud displays your profile photo if the email address you used to register on Cloud is associated with a Gravatar account. To associate your email address or to change your Gravatar profile photo, go to [gravatar.com](#).

When you are logged into Cloud, the Profile list appears at the top right of every page. This indicates the name of the currently active user or organization.



The View menu contains these options:

- Landscape: Your home page.
- Favorites: Packages from other users you have starred.
- Packages: Only packages you have created.
- Notebooks: Only notebooks you have created.
- Environments: Only environments you have created.
- Projects: Only projects you have uploaded.



Packages, notebooks and environments that you have created with this account appear on your dashboard. For more information, see [packages](#).

### Resetting your password

The **Sign In** tab provides two links to help regain access to your account:

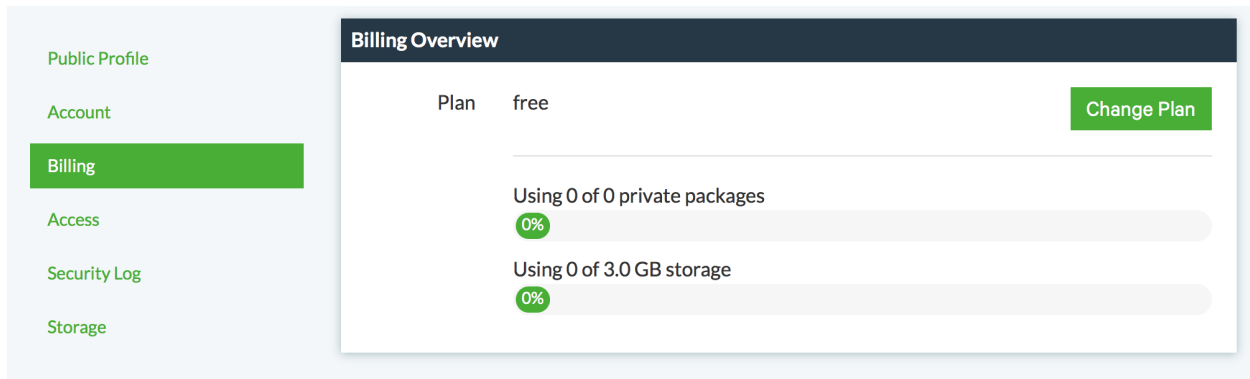
- I forgot my username. Click this link to have the username emailed to the email address of record.
- I forgot my password. Click this link to have a reset password link sent to the email address of record.

NOTE: The reset password link expires within 24 hours. If you no longer have access to the email account, you can create a new account or email [support@anaconda.com](mailto:support@anaconda.com) for assistance.

### Upgrading or downgrading your plan

To change a Cloud plan:

1. Log in to the Cloud account that you want to change.
2. At the top right of the Cloud interface, in the Profile list, select Settings.
3. Select the Billing option.



4. Click the Change Plan button.
5. Select the desired plan.

If you are moving from a free to a charged plan, enter your credit card information, and then click the OK button.

NOTE: If you need more private packages or storage space than is included in a personal plan, [contact Anaconda](#) so we can customize a plan for you.

NOTE: If you need assistance with billing questions, you can [contact Anaconda](#).

## Creating access tokens

The best way to manage access or make packages private is to create [organizations](#) or [groups](#), which allow you to set separate permissions per package, notebook or environment.

You can also control access with the [token](#) system. You can use tokens to control access to private repositories, collections or packages on Cloud. Additionally, the degree of access a token grants is completely configurable at the time of generation. You can generate multiple tokens to control which groups of users have access to certain features if they have the appropriate token.

## Generating tokens

You can generate tokens using the Web UI or Anaconda Client.

NOTE: By default, tokens expire after one year.

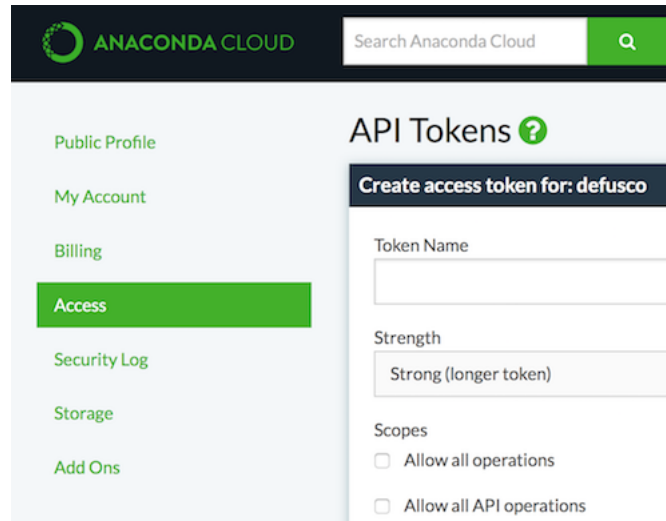
To generate a token using the Web UI:

1. Navigate to:

```
https://anaconda.org/<channel>/settings/access
```

NOTE: Replace `<channel>` with the actual channel name.

2. From here you can select a name for the token and set the required scopes.



To generate a token with Client:

1. In your Terminal window or Anaconda Prompt run:

```
anaconda auth --create --name YOUR-TOKEN-NAME --scopes 'repos conda:download'
```

NOTE: Replace YOUR-TOKEN-NAME with the token name you want.

2. This generates a random alphanumeric token string, which you can then distribute to fellow Cloud users to enable them to download a package that you have marked private. The token produced in this example provides access to download any of your private conda repositories.
3. It can be enabled with the `conda config` command. In your Terminal window or Anaconda Prompt run:

```
conda config --add channels https://conda.anaconda.org/t/<token>/<channel>

Add a channel with a token and a label::

conda config --add channels https://conda.anaconda.org/t/<token>/<channel>/
↪label/<labelname>

NOTE: Replace ``<token>`` with your token string, ``<channel>`` with the channel_
↪name,
``<labelname>`` with the label name used in :ref:`cloud-accounts-generate`.
```

NOTE: If you lose the random alphanumeric string, you need to *revoke the token* and create a new one.

Scopes are provided as a space-separated, quoted list. The available scopes are:

- `all`: Allow all operations.
- `api`: Allow all API operations.
- `api:modify-group`: Allow addition and modification of groups.
- `api:read`: Allow read access to the API site.
- `api:write`: Allow write access to the API site.
- `conda`: Allow all operations on Conda repositories.
- `conda:download`: Allow private downloads from Conda repositories.



- `pypi`: Allow all operations on PyPI repositories.
- `pypi:download`: Allow private downloads from PyPI repositories.
- `pypi:upload`: Allow uploads to PyPI repositories.
- `repos`: Allow access to all package repositories.

NOTE: Tokens provide access to all packages within a specified channel. Separate permissions per package, notebook or environment may be better handled with *organizations* and *groups*.

## Revoking tokens

You can revoke tokens using the Web UI or Anaconda Client.

To revoke a token using the Web UI, navigate to the following URL:

```
https://anaconda.org/<channel>/settings/access
```

NOTE: Replace `<channel>` with the actual channel name.

To revoke a token using Client, in your Terminal window or Anaconda Prompt run:

```
anaconda auth -r YOUR-TOKEN-NAME
```

NOTE: Replace `YOUR-TOKEN-NAME` with the token name you want to revoke.

## Organization accounts

### Overview

You can create a *Cloud organization* to:

- Share packages, environments or notebooks under an organization's account rather than your personal account.
- Assign multiple account administrators.
- Assign different access permissions to groups of users and customize per-package access by group.
- Host more, larger packages.

### Working with organizations

- *Creating an organization*
- *Deleting an organization*
- *Customizing users and groups*
- *Uploading packages to an organization*
- *Creating groups for differing access levels*

Organizations enable you to maintain group-owned repositories and set access levels for various users in the group.

### Creating an organization

To create an organization:

1. Log in to Anaconda Cloud.
2. In the Tools list, select Organizations, and then scroll to the bottom of the page.
3. Supply an organization name.

NOTE: Organization names cannot include spaces or special characters.

4. Supply an email address, then click the Create Organization button.

The system displays the dashboard for the new organization.

As the creator and owner of an organization, you have automatic administrative access to this organization and any packages associated with the organization.

In the Tools list, the Group Membership option shows a list of all organizations to which you belong.

### Deleting an organization

To delete an organization you administer and erase all data associated with it:

1. At the top right of the Cloud interface, in the Profile list, select Switch To.
2. Select the organization you want to delete.
3. In the Profile list, select Settings.
4. Select the Account option. You may be asked to verify your password.
5. In the Delete Account section, click the Delete button.

A confirmation page then requests that you provide the full name of the organization.

### Customizing users and groups

To add, remove, or edit group and user access for an organization you administer:

1. At the top right of the Cloud interface, in the Profile list, select the desired organization profile.
2. In the Tools list, select Groups.
3. You can review and edit the current group and user access for an organization, as well as add new groups and users at this address: <https://anaconda.org/<OrgName>/groups/>

NOTE: Replace <OrgName> with the organization name.

NOTE: Users receive a dashboard notification when you add them to an organization.

### Uploading packages to an organization

To upload a package to an organization, use the `-u/--user` option and in the Terminal window or an Anaconda Prompt, run:

```
anaconda upload --user ORGANIZATION package.tar.bz2
```

NOTE: Replace `ORGANIZATION` with the organization name, and `package.tar.bz2` with the actual name of the package.

NOTE: Only the co-owners of an organization may upload packages to the organization.

### Creating groups for differing access levels

Within an organization, you can create a group to customize access for a group of users. There are four types of permissions you can grant:

- **Read:** Provides access only to the packages. Users in a read-only group can see the list of files within a package and can install them through conda.
- **Read-Write:** Provides access to upload new versions of an existing package, delete files of a package and manage the individual labels of files. Users in a read-write group cannot upload files for non-existing packages, cannot delete or transfer the package and cannot lock and unlock labels.
- **Admin:** Provides access do everything except uploading new packages (admin users can still upload to an existing package) and lock and unlock labels.
- **Owners:** The user has full control over the organization and group.

To create a group and set access levels:

1. Click the +New Group button.
2. Give the group a name, and assign the desired permissions– Read-Only, Read-Write or Administration.
3. Add the desired members by username in the Members box.
4. Add the packages which this group can access in the Packages box.
5. Click the Save Group button.

### Working with packages

- *Overview*
- *Using package managers*
- *Uploading packages*
- *Using private packages*
- *Removing a previous version of a package*
- *Adding a collaborator to a package*
- *Removing a collaborator from a package*
- *Transferring a package to a new owner*
- *Copying a package*
- *Deleting a package*

### Overview

All files uploaded to Anaconda Cloud are stored in packages. Each Cloud package is visible at its own unique URL based on the name of the user who owns the package and the name of the package.

Users can create a Cloud package and then upload files into it.

For more information, see *package*.

---

**Note:** Throughout this task, replace placeholder text like `USERNAME` and `PACKAGENAME` with the text specific to your project.

---

### Namespaces

A namespace is the part of Cloud where a user or organization may host packages. For example, the user namespace <https://anaconda.org/travis> contains packages that were uploaded and shared by a user named `travis`.

For more information, see *namespace*.

### Labels

A label is part of the URLs on Cloud where conda looks for packages.

Each file within a package may be tagged with one or more labels, or not tagged at all to accept the default label of `main`.

For more information, see *label*.

### Using package managers

Cloud supports two package managers, *conda* and *PyPI*. To work with conda or PyPI packages, you must use their corresponding subdomains:

- To install conda packages from the user `travis`, use the repository URL `https://conda.anaconda.org/travis`
- To install PyPI packages from the user `travis`, use the repository URL `https://pypi.anaconda.org/travis`

### Conda packages

#### Uploading conda packages

This example shows how to build and upload a *conda* package to Cloud using `conda build`.

Use the terminal window or an Anaconda Prompt to perform the following steps:

1. Before you start, install `anaconda-client` and `conda-build`:

```
conda install anaconda-client conda-build
```

2. Choose the repository for which you would like to build the package. In this example, we use a simple public *conda test* package:

```
git clone https://github.com/Anaconda-Platform/anaconda-client
cd anaconda-client/example-packages/conda/
```

In this directory, there are two required files, `meta.yaml` and `build.sh`.

macOS and Linux systems are Unix systems. Packages built for Unix systems require a `build.sh` file, packages built for Windows require a `bld.bat` file, and packages built for both Windows and Unix systems require both a `build.sh` file and a `bld.bat` file. All packages require a `meta.yaml` file.

3. To build the package, turn off automatic Client uploading and then run the `conda build` command:

```
conda config --set anaconda_upload no
conda build .
```

All packages built in this way are placed in a subdirectory of the *Anaconda* `conda-bld` directory.

4. You can check where the resulting file was placed with the `--output` option:

```
conda build . --output
```

5. You can upload the test package to Cloud with the Anaconda *upload* command:

```
anaconda login
anaconda upload /path/to/conda-package.tar.bz2
```

---

**Note:** Replace `/path/to/` with the actual path where you stored the package.

---

For more information on conda's overall build framework, you may also want to read the articles [Building conda packages](#).

## Installing conda packages

You can install conda packages from Cloud by adding channels to your conda configuration.

Use the terminal window or an Anaconda Prompt to perform the following steps:

1. Because conda knows how to interact with Cloud, specifying the channel `sean` translates to <https://anaconda.org/sean>:

```
conda config --add channels sean
```

2. You can now install public conda packages from Sean's Cloud account. Try installing the `testci` package at <https://anaconda.org/sean/testci>:

```
conda install testci
```

3. You can install a package from a channel with a token and a label:

```
conda install -c https://conda.anaconda.org/t/token/channel/label/labelname_
↪packagename
```

---

**Note:** Replace `token` with the provided token, `channel` with a user channel, `labelname` with the label name and `packagename` with the package name you want to install.

---

### PyPI packages

#### Uploading PyPI packages

We can test PyPI package uploading with a small public example package saved in the [anaconda-client repository](#).

Use the terminal window or an Anaconda Prompt to perform the following steps:

1. Begin by cloning the repository from the command line:

```
git clone git@github.com:Anaconda-Platform/anaconda-client.git
cd anaconda-client/example-packages/pypi/
```

2. You can now create your PyPI package with the `setup.py` script:

```
python setup.py sdist
```

3. The package has now been built as a source tarball and is ready to be uploaded:

```
anaconda upload dist/*.tar.gz
```

Your package is now available at `http://anaconda.org/USERNAME/PACKAGE`.

#### Installing PyPI packages

The best way to install a PyPI package is using `pip`. For the following command, we use the package we authored in the examples above. In your terminal window or an Anaconda Prompt, run:

```
pip install --extra-index-url https://pypi.anaconda.org/USERNAME/simple pypi-test-
↪package
```

#### Installing private PyPI packages

The best way to manage access or make PyPI and other packages private is to create [organizations](#) or [groups](#), which allow you to set separate permissions per package, notebook or environment.

You can also control access with the token system. All Cloud URLs can be prefixed with `/t/$TOKEN` to access private packages.

In your terminal window or an Anaconda Prompt, run:

```
TOKEN=$(anaconda auth --create --name YOUR-TOKEN-NAME)
pip install --index-url https://pypi.anaconda.org/t/$TOKEN/USERNAME/simple-test-
↪package
```

---

**Note:** Replace `YOUR-TOKEN-NAME` with the name of the token you created, `USERNAME` with your username and `simple-test-package` with the actual test-package name.

---

#### Uploading packages

1. To upload package files to Cloud, use the terminal window or an Anaconda Prompt and the [upload](#) command:

```
anaconda login
anaconda upload PACKAGENAME
```

Cloud automatically detects packages and notebooks, package or notebook types, and their versions.

2. Your package is now available at:

```
https://anaconda.org/USERNAME/PACKAGENAME
```

3. Your package also can be downloaded by anyone using Client from the terminal window or an Anaconda Prompt:

```
anaconda download USERNAME/PACKAGENAME
```

## Using private packages

It is no longer possible to sign up for an individual paid plan with private packages. Anyone who had private packages in the past still has the ability to have those hosted privately.

By default, all packages, notebooks, and environments uploaded to Cloud are accessible to anyone who has access to the repository.

Packages uploaded to your user channel on Cloud can be marked as private using the Web UI:

1. Select the desired package.
2. Select the **Settings** tab.
3. Select Admin in the sidebar.
4. Alternatively, you can reach this page with the following URL:

```
https://anaconda.org/username/packageName/settings/admin
```

---

**Note:** Jupyter notebooks and conda environments can also be marked private using this procedure and URL.

---

---

**Note:** Other Cloud users may access your private packages either with tokens or by logging in.

---

## Private packages with tokens

---

**Note:** Replace `token` with the provided token, `channel` with a user channel, `labelname` with the label name, and `packagename` with a package name you want to install.

---

To make your private packages available to be accessed with tokens:

1. First create an access *token* that includes the following scope for Client:

```
conda:download
```

Or, in the Web UI with:

```
Allow private downloads from conda repositories
```

The token is a random alphanumeric string and this is used to install a package or add a channel from which you want to install private packages.

2. Using the provided token, a user channel can be added to `config` from the terminal window or an Anaconda Prompt with:

```
conda config --add channels https://conda.anaconda.org/t/token/channel
```

3. The token can also be used to install packages without first adding the channel. In the terminal window or an Anaconda Prompt, run:

```
conda install -c https://conda.anaconda.org/t/token/channel packagename
```

To install a package from a channel using token and label name:

```
conda install -c https://conda.anaconda.org/t/token/channel/label/labelname_↵  
↵packagename
```

4. Private PyPI packages can also be installed in the Web UI:

```
https://pypi.anaconda.org/t/token/channel
```

### Private packages with login

To make your private packages available to users who have logged in:

1. Create an *organization*.
2. Create a group in that organization, which may be a read-only group.
3. Add to the group the users that you want to grant access to.
4. Upload the package to the organization, or transfer an existing package to the organization.

After you grant them access, other users can download and install your package using the Web UI or Client.

To download a package:

1. In a browser, navigate to the desired channel.
2. If the organization name is `OrgName` and the package name is `conda-package`, use these commands in the terminal window or an Anaconda Prompt:

```
conda install anaconda-client  
anaconda login  
conda install -c OrgName conda-package
```

Or instead:

```
conda install anaconda-client  
anaconda login  
conda install -c https://conda.anaconda.org/OrgName conda-package
```



## Removing a previous version of a package

To remove a previous version of one of your packages from Cloud:

1. Select the package name.
2. Select the **Files** tab.
3. Select the checkbox to the left of the version you want to remove.
4. In the **Actions** menu, select Remove.

You may instead use the terminal window or an Anaconda Prompt:

1. Run:

```
anaconda remove USERNAME/PACKAGENAME/0.2
```

---

**Note:** Replace USERNAME with your username, PACKAGENAME with the package name and 0.2 with the desired version.

---

2. You can now see the change on your profile page:

```
https://anaconda.org/USERNAME/PACKAGE
```

## Adding a collaborator to a package

You can add other users that are not part of an organization to collaborate on your packages. You will need the usernames of the other users.

1. From your dashboard, select the package by clicking on its name.
2. To display the package settings, select the Settings option.
3. To display the current collaborators, select the Collaborators option.
4. Type the username of the person you want to add as a collaborator, and then click the Add button.

---

**Note:** All collaborators are given full read/write permissions to the package, even private packages.

---

## Removing a collaborator from a package

To revoke package access previously granted to a collaborator:

1. From your dashboard select the package by clicking on its name.
2. To display the package settings, select the Settings option.
3. To display the current collaborators, select the Collaborators option.
4. Click the red X button next to a collaborator to revoke their access.

### Transferring a package to a new owner

By default, when you create or add packages, they are attached to your individual profile. You can transfer ownership to another owner account you control, such as an organization profile you manage.

To transfer a package to a new owner:

1. From your dashboard—or the dashboard of an organization you administer—select the package for which you want to transfer ownership.  
The system displays options for that package.
2. To display the package settings, select the Settings option.
3. Select the Admin option.
4. Under Transfer this package to a new owner, click the Transfer button.
5. Select the organization name for the new owner.
6. Click the Transfer Ownership button.

### Copying a package

To copy a package from the channel `conda-forge` to a personal channel such as `jsmith`:

```
anaconda copy conda-forge/glueviz/0.10.4 --to-owner jsmith
```

`conda-forge/glueviz/0.10.4` is a “spec” and can match either of two formats: `user/package/version` or `user/package/version/filename`.

Previously labels were called “channels”, and the `anaconda copy` command has deprecated options `from-channel` and `to-channel` that expect to operate on labels. These deprecated options should not be used. If you attempt to run `anaconda copy --from-channel conda-forge --to-channel jsmith glueviz`, you will receive an error that Label `conda-forge` does not exist.

### Deleting a package

To delete a package from Cloud, including all of its versions:

1. Select the package name.
2. Select the Settings option.
3. In the left sidebar, select Admin.
4. Click Delete.

You may instead use the terminal window or an Anaconda Prompt:

1. Run:

```
anaconda remove USERNAME/PACKAGENAME
```

2. You can now see the change on your profile page:

```
https://anaconda.org/USERNAME
```

## Working with notebooks

To begin working with Jupyter Notebooks, see the [Official Jupyter Notebook documentation](#).

To share a [Jupyter notebook](#) on Cloud:

1. Save a notebook.
2. Download and check out the handy JupyterLab and Jupyter Notebook cheat sheet to create and save a notebook.
3. To upload your notebook to Cloud, open Anaconda Prompt or Terminal and enter:

```
anaconda upload my-notebook.ipynb
```

NOTE: Replace `my-notebook` with the actual name of your notebook.

4. You can see an HTML version of your notebook stored at:

```
http://notebooks.anaconda.org/<USERNAME>/my-notebook
```

NOTE: Replace `<USERNAME>` with your username, and `my-notebook` with the actual name of your notebook.

5. Anyone who has access to Cloud can download your notebook. To download the notebook, open Anaconda Prompt or Terminal and enter:

```
anaconda download username/my-notebook
```

NOTE: Replace `username` with your username, and `my-notebook` with the actual name of your notebook.

## Working with environments

To share an environment on Anaconda Cloud:

1. See the [conda user guide](#) to create and save a conda environment. Open the Terminal or an Anaconda Prompt and enter:

```
conda env export -n my-environment -f my-environment.yml
```

NOTE: Replace `my-environment` with the actual name of your environment.

2. Upload it to Cloud either using the web interface or the `anaconda upload` command.

- Using the web interface:

Go to <https://anaconda.org/USERNAME/environments>.

NOTE: Replace `USERNAME` with your username.

In the top right corner use the Upload button to upload your environment.

- Using the `anaconda upload` command from the Terminal or an Anaconda Prompt:

```
anaconda upload my-environment.yml
```

NOTE: Replace `my-environment` with the actual name of your environment.

3. You can see a list of your uploaded environments at:

```
http://envs.anaconda.org/USERNAME
```

NOTE: Replace USERNAME with your username.

4. Anyone can download and install your environment from Cloud.

- Using the web interface:

Go to `https://anaconda.org/USERNAME/environments`.

NOTE: Replace USERNAME with the username.

Select the environment, go to Files tab and click the file to download under Names field.

- Using the Terminal or an Anaconda Prompt:

```
conda env create user/my-environment
source activate my-environment
```

NOTE: Replace my-environment with the actual name of your environment.

### Working with other file types

In addition to packages and notebooks, Anaconda Cloud can be used to store and share data science files of any type.

### Uploading other file types

You can upload any type of file with the Anaconda Client command line interface (CLI) by using the steps below.

PyPI package files, conda package files and notebook files are automatically detected. There is no auto-detect for other types of files, so you must explicitly specify the package, package-type and version fields.

In the following example, we upload a spreadsheet named baby-names in comma separated value (CSV) format.

Use the Terminal window or an Anaconda Prompt to upload the spreadsheet:

1. Create a new package, which creates a *namespace* that can hold multiple files:

```
anaconda login
anaconda package --create jsmith/baby-names
```

2. Upload the file to the new namespace:

```
anaconda upload --user jsmith --package baby-names --package-type file --version 1
↪ 1 baby-names1.csv
```

NOTE: In this example, the user-or organization-name is jsmith, the package name is baby-names, the package type is file, the version is 1 and the full filename is baby-names1.csv.

### Downloading other file types

Files, such as the one created above, are available at:

```
https://anaconda.org/<USERNAME>/<PACKAGENAME>
```

Anyone can download these files using Client from the Terminal window or an Anaconda Prompt:

```
anaconda download <USERNAME>/<PACKAGENAME>
```

NOTE: Replace `<USERNAME>` with the desired username, and `<PACKAGENAME>` with the desired package name.

If the repository has multiple files with the same name and different extensions, `anaconda download` will download all of them by default. If you use `anaconda-client` 1.7 or higher, you can use `anaconda download` with the option `--package-type` or `-t` to specify only one of these files. This option can work with the values `pypi`, `conda`, `ipynb`, and `env`.

### 4.3.2 FAQs

- *What is Anaconda Cloud?*
- *What kind of packages does Cloud support?*
- *Who can find and install my packages?*
- *What is Anaconda, Inc.?*
- *What are Cloud's terms of service?*
- *How much does Cloud cost?*
- *How do I get started with Cloud?*
- *What kind of account do I have?*
- *What is included in the free version of Cloud?*
- *What is an organization account, and how is it different from an individual account?*

#### What is Anaconda Cloud?

Anaconda Cloud is a package management service by [Anaconda](#). For more information, see [Anaconda Cloud](#).

#### What kind of packages does Cloud support?

Cloud supports any type of package. Today, it is primarily used for conda and PyPI packages, as well as notebooks and environments.

#### Who can find and install my packages?

If you have a free account, all of your packages are public. After you upload them to Cloud, anyone can search for and download them.

#### What is Anaconda, Inc.?

Anaconda is a software development and consulting company of passionate open source advocates based in Austin, Texas, USA. We are committed to the open source community. We created the Anaconda Python distribution and contribute to many other open source-based data analytics tools. You can find out more about us by reading [our story](#).

### What are Cloud's terms of service?

Our terms of service are available at <https://anaconda.org/about/legal/terms> . For any additional questions, contact us by [email](#).

### How much does Cloud cost?

Cloud is free for downloading and uploading public packages.

### How do I get started with Cloud?

You can search, download and install hundreds of public packages without having an account. If you want to upload packages, you need to sign up for a [Cloud account](#). For more information, see [sign up for a free Cloud account](#).

### What kind of account do I have?

By default your account is a personal, free account. All packages you upload to Cloud are public, and you are the only person with administrative access to your account.

### What is included in the free version of Cloud?

The free plan allows you to search for, create and host public packages, and provides up to 3 GB storage space.

### What is an organization account, and how is it different from an individual account?

An organization account allows multiple individual users to administer packages and have more control of package access by other users. An individual account is for use by one person.

## 4.3.3 Help and support

### Joining community support

We invite you to join our community support mailing lists for both [Anaconda](#) and [conda](#). On these lists you can ask questions, answer questions and discuss ways to use Cloud. You also can submit requests for new features and make any other comments you may have.

### Reporting a bug

Please use the Anaconda Cloud page [Report a Bug](#) to find the correct point of contact to report the bug you are experiencing. When reporting bugs on GitHub, please search to see if anyone else has reported it, and make a new issue if no one else has.

## 4.3.4 Command Reference

See also: [API Reference](#)

Anaconda client is the command line interface (CLI) to Anaconda Cloud, and can be used for logging in, logging out, managing your account, uploading files, generating access tokens, viewing tokens, and other tasks as shown by running:

```
anaconda -h
```

Full command reference:

## anaconda

```
usage: anaconda [-h] [--disable-ssl-warnings] [--show-traceback] [-v] [-q]
               [-V] [-t TOKEN] [-s SITE]
               ...

Anaconda Cloud command line manager

optional arguments:
  -h, --help            show this help message and exit
  -V, --version          show program's version number and exit

output:
  --disable-ssl-warnings  Disable SSL warnings (default: False)
  --show-traceback       Show the full traceback for chalmers user errors
                        (default: False)
  -v, --verbose          print debug information ot the console
  -q, --quiet            Only show warnings or errors the console

anaconda-client options:
  -t TOKEN, --token TOKEN
                        Authentication token to use. May be a token or a path
                        to a file containing a token
  -s SITE, --site SITE  select the anaconda-client site to use

Commands:

  auth                Manage Authorization Tokens
  label               Manage your Anaconda Cloud labels
  channel              [DEPRECATED in favor of label] Manage your Anaconda
                        Cloud channels
  config              Anaconda client configuration
  copy                Copy packages from one account to another
  download             Download notebooks from Anaconda Cloud
  groups              Manage Groups
  login               Authenticate a user
  logout              Log out from Anaconda Cloud
  notebook             [DEPRECATED in favor of upload/download] Interact
                        with notebooks in anaconda.org
  package              Package utils
  remove              Remove an object from Anaconda Cloud. Must refer to
                        the formal package name as it appears in the URL of
                        the package. Also use anaconda show <USERNAME> to see
                        list of package names. Example: anaconda remove
                        continuumio/empty-example-notebook
  search              Search Anaconda Cloud
  show                Show information about an object
  upload              Upload packages to Anaconda Cloud
  whoami              Print the information of the current user
  build               Anaconda build client for continuous integration,
                        testing and building packages
```

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worker	Anaconda build client <b>for</b> continuous integration, testing <b>and</b> building packages
--------	---

## Authentication

### auth

```
usage: anaconda auth [-h] [-n NAME] [-o ORGANIZATION]
                    [--strength {strong,weak}] [--strong] [-w] [--url URL]
                    [--max-age MAX_AGE] [-s SCOPES] [--out OUT]
                    (-x | -l | -r NAME [NAME ...] | -c | -i)
```

Manage Authorization Tokens

optional arguments:

```
-h, --help            show this help message and exit
-n NAME, --name NAME  A unique name so you can identify this token later.
                     View your tokens at anaconda.org/settings/access
-o ORGANIZATION, --org ORGANIZATION, --organization ORGANIZATION
                     Set the token owner (must be an organization)
```

token creation arguments:

These arguments are only valid with the `--create` action

```
--strength {strong,weak}
--strong            Create a longer token (default)
-w, --weak          Create a shorter token
--url URL           The url of the application that will use this token
--max-age MAX_AGE   The maximum age in seconds that this token will be
                    valid for
-s SCOPES, --scopes SCOPES
                    Scopes for token. For example if you want to limit
                    this token to conda downloads only you would use
                    --scopes "repo conda:download"
--out OUT
```

actions:

```
-x, --list-scopes    list all authentication scopes
-l, --list           list all user authentication tokens
-r NAME [NAME ...], --remove NAME [NAME ...]
                    remove authentication tokens
-c, --create         Create an authentication token
-i, --info, --current-info
                    Show information about the current authentication
                    token
```

Manage Authentication tokens

See also: *Using Anaconda Cloud Tokens*



## login

```
usage: anaconda login [-h] [--hostname HOSTNAME] [--username LOGIN_USERNAME]
                    [--password LOGIN_PASSWORD]

Authenticate a user

optional arguments:
  -h, --help            show this help message and exit
  --hostname HOSTNAME   Specify the host name of this login, this should be
                        unique (default: hq-phone-114.corp.continuum.io)
  --username LOGIN_USERNAME
                        Specify your username. If this is not given, you will
                        be prompted
  --password LOGIN_PASSWORD
                        Specify your password. If this is not given, you will
                        be prompted
```

## logout

```
usage: anaconda logout [-h]

Log out from Anaconda Cloud

optional arguments:
  -h, --help  show this help message and exit
```

## whoami

Print the information of the current user

```
usage: anaconda whoami [-h]

Print the information of the current user

optional arguments:
  -h, --help  show this help message and exit
```

## Informational

### show

```
usage: anaconda show [-h] spec

Show information about an object

positional arguments:
  spec          Package written as USER[/PACKAGE[/VERSION[/FILE]]]

optional arguments:
  -h, --help  show this help message and exit
```

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Show information about an `object`

Examples:

```

anaconda show continuumio
anaconda show continuumio/python
anaconda show continuumio/python/2.7.5
anaconda show sean/meta/1.2.0/meta.tar.gz

```

## search

```

usage: anaconda search [-h] [-t {conda,pypi}]
                        [-p {osx-32,osx-64,win-32,win-64,linux-32,linux-64,linux-
↳ armv61,linux-armv71,linux-ppc64le,noarch}]
                        name

```

Search Anaconda Cloud

positional arguments:

name                      Search string

optional arguments:

```

-h, --help                show this help message and exit
-t {conda,pypi}, --package-type {conda,pypi}
                           only search for packages of this type
-p {osx-32,osx-64,win-32,win-64,linux-32,linux-64,linux-armv61,linux-armv71,linux-
↳ ppc64le,noarch}, --platform {osx-32,osx-64,win-32,win-64,linux-32,linux-64,linux-
↳ armv61,linux-armv71,linux-ppc64le,noarch}
                           only search for packages of the chosen platform

```

Search Anaconda Cloud **for** packages

## config

```

usage: anaconda config [-h] [--type TYPE] [--set name value] [--get name]
                       [--remove REMOVE] [--show] [-f] [--show-sources] [-u]
                       [-s]

```

Anaconda client configuration

optional arguments:

```

-h, --help                show this help message and exit
--type TYPE               The type of the values in the set commands

```

actions:

```

--set name value          sets a new variable: name value
--get name                get value: name
--remove REMOVE           removes a variable
--show                    show all variables
-f, --files               show the config file names
--show-sources            Display all identified config sources

```

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```
location:
    -u, --user           set a variable for this user
    -s, --system, --site set a variable for all users on this machine

anaconda-client configuration

Get, Set, Remove or Show the anaconda-client configuration.

##### anaconda-client sites

anaconda-client sites are a mechanism to allow users to quickly switch
between Anaconda Cloud instances. This is primarily used for testing
the anaconda alpha site. But also has applications for the
on-site [Anaconda Enterprise] (http://continuum.io/anaconda-server).

anaconda-client comes with two pre-configured sites `alpha` and
`binstar` you may use these in one of two ways:

    * Invoke the anaconda command with the `-s/--site` option
      e.g. to use the alpha testing site:

          anaconda -s alpha whoami

    * Set a site as the default:

          anaconda config --set default_site alpha
          anaconda whoami

##### Add an anaconda-client site

After installing Anaconda Enterprise
you can add a site named site_name like this:

    anaconda config --set sites.site_name.url "http://<anaconda-enterprise-ip>:<port>/
↪api"
    anaconda config --set default_site site_name

##### Site Options VS Global Options

All options can be set as global options - affecting all sites,
or site options - affecting only one site

By default options are set globally e.g.:

    anaconda config --set OPTION VALUE

If you want the option to be limited to a single site,
prefix the option with `sites.site_name` e.g.

    anaconda config --set sites.site_name.OPTION VALUE

##### Common anaconda-client configuration options

    * `url`: Set the anaconda api url (default: https://api.anaconda.org)
    * `ssl_verify`: Perform ssl validation on the https requests.
      ssl_verify may be `True`, `False` or a path to a root CA pem file.
```

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```
##### Toggle auto_register when doing anaconda upload
```

The default is yes, automatically create a new package when uploading.  
If no, then an upload will fail if the package name does not already exist on the `server`.

```
anaconda config --set auto_register yes|no
```

## Managing Packages

### package

```
usage: anaconda package [-h]
                        (--add-collaborator user | --list-collaborators | --create)
                        [--summary SUMMARY] [--license LICENSE]
                        [--license-url LICENSE_URL] [--personal | --private]
                        USER/PACKAGE
```

Anaconda Cloud package utilities

positional arguments:

USER/PACKAGE Package to operate on

optional arguments:

-h, --help show this help message **and** exit

actions:

```
--add-collaborator user
                        username of the collaborator you want to add
--list-collaborators  list all of the collaborators in a package
--create              Create a package
```

metadata arguments:

```
--summary SUMMARY      Set the package short summary
--license LICENSE       Set the package license
--license-url LICENSE_URL
                        Set the package license url
```

privacy:

```
--personal             Set the package access to personal This package will
                        be available only on your personal registries
--private              Set the package access to private This package will
                        require authorized and authenticated access to install
```

### upload

```
usage: anaconda upload [-h] [-c CHANNELS] [-l LABELS] [--no-progress]
                        [-u USER] [--all] [-p PACKAGE] [-v VERSION]
                        [-s SUMMARY] [-t PACKAGE_TYPE] [-d DESCRIPTION]
                        [--thumbnail THUMBNAIL] [--private]
                        [--no-register | --register] [--build-id BUILD_ID]
```

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```

        [-i | -f | --force]
        files [files ...]

Upload packages to Anaconda Cloud

positional arguments:
  files                Distributions to upload

optional arguments:
  -h, --help            show this help message and exit
  -c CHANNELS, --channel CHANNELS
                        [DEPRECATED] Add this file to a specific channel.
                        Warning: if the file channels do not include "main",
                        the file will not show up in your user channel
  -l LABELS, --label LABELS
                        Add this file to a specific label. Warning: if the
                        file labels do not include "main", the file will not
                        show up in your user label
  --no-progress          Don't show upload progress
  -u USER, --user USER  User account or Organization, defaults to the current
                        user
  --all                  Use conda convert to generate packages for all
                        platforms and upload them
  --no-register          Don't create a new package namespace if it does not
                        exist
  --register             Create a new package namespace if it does not exist
  --build-id BUILD_ID    Anaconda Cloud Build ID (internal only)
  -i, --interactive      Run an interactive prompt if any packages are missing
  -f, --fail             Fail if a package or release does not exist (default)
  --force               Force a package upload regardless of errors

metadata options:
  -p PACKAGE, --package PACKAGE
                        Defaults to the package name in the uploaded file
  -v VERSION, --version VERSION
                        Defaults to the package version in the uploaded file
  -s SUMMARY, --summary SUMMARY
                        Set the summary of the package
  -t PACKAGE_TYPE, --package-type PACKAGE_TYPE
                        Set the package type [ipynb, env]. Defaults to
                        autodetect
  -d DESCRIPTION, --description DESCRIPTION
                        description of the file(s)
  --thumbnail THUMBNAIL
                        Notebook's thumbnail image
  --private              Create the package with private access

  anaconda upload CONDA_PACKAGE_1.bz2
  anaconda upload notebook.ipynb
  anaconda upload environment.yml

```

See Also:

- [Uploading a Conda Package](#)
- [Uploading a PyPI Package](#)

### download

```
usage: anaconda download [-h] [-f] [-o OUTPUT] handle

Download packages from Anaconda Cloud

positional arguments:
  handle                user/notebook

optional arguments:
  -h, --help            show this help message and exit
  -f, --force            Overwrite
  -o OUTPUT, --output OUTPUT
                        Download as

Usage:
  anaconda download notebook
  anaconda download user/notebook
```

### remove

```
usage: anaconda remove [-h] [-f] specs [specs ...]

Remove an object from Anaconda Cloud

example::

  anaconda remove sean/meta/1.2.0/meta.tar.gz

positional arguments:
  specs                Package written as <user>[/<package>[/<version>[/<filename>]]]

optional arguments:
  -h, --help          show this help message and exit
  -f, --force          Do not prompt removal
```

### groups

```
usage: anaconda groups [-h] [--perms {read,write,admin}]
                        {add,show,members,add_member,remove_member,packages,add_
↵package,remove_package}
                        spec

positional arguments:
  {add,show,members,add_member,remove_member,packages,add_package,remove_package}
                        The group management command to execute
  spec                  <organization>/<group_name>/<member>

optional arguments:
  -h, --help            show this help message and exit
  --perms {read,write,admin}
                        The permission the group should provide
```

## label

```
usage: anaconda label [-h] [-o ORGANIZATION]
                        (--copy LABEL LABEL | --list | --show LABEL | --lock LABEL | --
->unlock LABEL | --remove LABEL)
```

Manage your Anaconda Cloud channels

optional arguments:

```
-h, --help            show this help message and exit
-o ORGANIZATION, --organization ORGANIZATION
                        Manage an organizations labels
--copy LABEL LABEL
--list                list all labels for a user
--show LABEL          Show all of the files in a label
--lock LABEL          Lock a label
--unlock LABEL        Unlock a label
--remove LABEL        Remove a label
```

## copy

```
usage: anaconda copy [-h] [--to-owner TO_OWNER] [--from-label FROM_LABEL]
                    [--to-label TO_LABEL]
                    spec
```

Copy packages from one account to another

positional arguments:

```
spec                Package - written as user/package/version[/filename]
                    If filename is not given, copy all files in the
                    version
```

optional arguments:

```
-h, --help            show this help message and exit
--to-owner TO_OWNER   User account to copy package to (default: your
                        account)
--from-label FROM_LABEL
                        Label to copy packages from
--to-label TO_LABEL   Label to put all packages into
```

## move

```
usage: anaconda move [-h] [--from-label FROM_LABEL] [--to-label TO_LABEL] spec
```

Move packages between labels.

positional arguments:

```
spec                Package - written as user/package/version[/filename]
                    If filename is not given, move all files in the
                    version
```

optional arguments:

```
-h, --help            show this help message and exit
```

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```
--from-label FROM_LABEL      Label to move packages from
--to-label TO_LABEL          Label to move packages to
```

### 4.3.5 Glossary

- *Anaconda*
- *Anaconda Cloud*
- *Anaconda Client CLI*
- *Binstar*
- *conda*
- *conda build*
- *conda package*
- *label*
- *Miniconda*
- *namespace*
- *noarch package*
- *on-site repository*
- *organization account*
- *package*
- *package manager*
- *repository*
- *source package*
- *token*

## Anaconda

An easy-to-install, free collection of open source packages, including Python and the conda package manager, with free community support. Over 150 packages are installed with Anaconda. After installing Anaconda, you can install or update over 250 additional open source packages contained in the Anaconda repository using the `conda install PACKAGENAME` command.

NOTE: Replace `PACKAGENAME` with the name of the desired package.

## Anaconda Cloud

[Anaconda Cloud](#) is a package management service by [Anaconda](#). Cloud makes it easy to find, access, store and share public notebooks, environments, and conda and PyPI packages. Cloud also makes it easy to stay current with updates made to the packages and environments you are using.



Cloud hosts hundreds of useful Python packages, notebooks and environments for a wide variety of applications. You do not need a Cloud account, or to be logged in, to search for public packages, download and install them.

For more information, see the [introduction to Anaconda Cloud](#).

## Anaconda Client CLI

The Anaconda Client command line interface (CLI) allows you to log into Cloud directly from your terminal window and manage your account. It is not necessary for downloading or installing packages from Cloud.

## Binstar

Binstar was an early project name for Cloud. You may still see the term Binstar in certain command and directory names.

## conda

The conda package manager and environment manager program that installs and updates packages and their dependencies, and lets you easily switch between environments on your local computer.

## conda build

The command line interface that lets you build packages for your local operating system.

## conda package

A compressed file containing system-level libraries, Python modules, executable programs or other components. The file uses the tarball format.

## label

Part of the URLs on Cloud where conda looks for packages. Labels are searched only if you specify a label.

The default label is `main`, so packages that are uploaded without specifying a label are automatically labeled `main`. The version labeled `main` is also downloaded by default, unless a user specifies a different label.

So, if a file is labeled `main`, then the label name may be omitted from the URL. For example, the following repositories are equivalent:

```
https://anaconda.org/sean/labels/main
https://anaconda.org/sean
```

Commands such as `conda install` can be used with a channel or used with a channel and a label:

```
conda install --channel sean selenium
conda install --channel sean/label/dev selenium
conda install --channel sean/label/stable selenium
```

### Miniconda

A minimal installer for *conda*. Like *Anaconda*, Miniconda is a software package that includes the conda package manager and Python and its dependencies. However, Miniconda does not include any other packages. Once conda is installed by installing either Anaconda or Miniconda, you can install other software packages directly from the command line using `conda install`.

### namespace

Each user and organization has their own location called a “namespace” where they may host packages. You can view the public packages in a user or organization’s namespace by navigating to their user page.

EXAMPLE: The `travis` user namespace located at <https://anaconda.org/travis> contains packages that were uploaded and shared by the user whose account is named `travis`.

### noarch package

A conda package that contains nothing specific to any system architecture, so it may be installed on any system. When conda searches for packages on any system in a channel, conda always checks both the system-specific subdirectory, for example, `linux-64` and the `noarch` directory.

### on-site repository

Cloud is powered by Anaconda Repository by Anaconda, Inc. You can run your own private repository behind firewalls or in air-gapped environments. For more information, contact [sales@anaconda.com](mailto:sales@anaconda.com).

### organization account

An organization account is a type of account on Cloud that allows multiple individual users to administer packages and control package access to different user groups. It also includes a large amount of storage space.

### package

All files uploaded to Cloud are stored in packages. Each Cloud package is visible at its own unique URL based on the name of the user who owns the package and the name of the package.

For example, if a user `travis` uploads a test package named `testpkg`, it is visible at:

`https://anaconda.org/travis/testpkg`

Cloud packages may contain multiple files, and these files may be data files such as comma separated value (CSV), tab separated value (TSV), or text (TXT), or package files such as conda packages, PyPI packages or R packages.

NOTE: All packages are public if uploaded by users of free accounts. Packages may be designated as private by upgrading to a paid account.

### package manager

A package manager is a tool that facilitates the process of installing, upgrading, configuring and removing packages, including the packages on Cloud. Cloud supports two package managers, *conda* and *PyPI*.

For more information, see *using package managers*.

## repository

A storage location from which software packages may be retrieved and installed on a computer.

## source package

“Source” packages are source code only, not yet built for any specific platform, and might be compatible with all, some or only one of the platforms.

## token

A token—or authentication token—is the mechanism by which anonymous users can download private packages without using a Cloud account. It is an alpha-numeric code that is inserted into a URL that allows access by anyone who has the URL. You can use Client to generate new tokens to give other users specifically scoped access to packages and collections.

## 4.4 Archive

This is the archive of Anaconda products that are no longer in production. This documentation is provided as a courtesy for customers who still use them.

### 4.4.1 Anaconda Accelerate

#### *High Performance Computing*

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**Note:** This product is discontinued. This archived copy of the product documentation is provided for those customers who are still using it. SEE <https://www.anaconda.com/blog/developer-blog/open-sourcing-anaconda-accelerate/>

---

Anaconda Accelerate is a package that provides the Anaconda® platform access to several numerical libraries that are optimized for performance on Intel CPUs and NVidia GPUs.

The current version, 2.3.1, was released on January 30, 2017.

Anyone can now use the functionality from Accelerate without purchasing a license!

On July 27, 2017, Accelerate was split into the [Intel Distribution for Python](#) and the open source [Numba](#) project’s sub-projects [pyculib](#), [pyculib\\_sorting](#) and [data\\_profiler](#). Numba and all its sub-projects are available under a BSD license.

More information is available in the post [Open Sourcing Anaconda Accelerate](#).

## Features

- **Bindings to the following *CUDA* libraries:**

- *cuBLAS*
- *cuFFT*
- *cuSPARSE*
- *cuRAND*

- *CUDA Sorting* algorithms from the CUB and Modern GPU libraries
- Speed-boosted linear algebra operations in NumPy, SciPy, scikit-learn and NumExpr libraries using Intel’s Math Kernel Library (*MKL*).
- Accelerated variants of Numpy’s built-in *UFuncs*.
- Increased-speed Fast Fourier Transformations (*FFT*) in NumPy.

## Installation

This section contains information related to:

### Requirements

- 64-bit operating system—Windows, macOS or Linux
- **Supported Python and Numpy combinations:**
  - Python 2.7 with Numpy 1.9, 1.10 or 1.11
  - Python 3.4 with Numpy 1.9, 1.10 or 1.11
  - Python 3.5 with Numpy 1.9, 1.10 or 1.11
  - Python 3.6 with Numpy 1.11
- Numba 0.30

### CUDA feature requirements

- NVidia driver version 349.00 or later
- CUDA toolkit 7.0
- At least one CUDA GPU with compute capability 2.0 or above

## Installing Accelerate

Accelerate is included with Anaconda Workgroup and Anaconda Enterprise [subscriptions](#).

To start a 30-day free trial, download and install the Anaconda Accelerate package.

## Installing with Anaconda

If you already have the *Anaconda free Python distribution* <<http://anaconda.com/downloads.html>>, take the following steps to install Accelerate:

1. Run the command `conda update conda`.
2. Run the command `conda install accelerate`.

If you do not have Anaconda installed, see [Downloads](#).

NOTE: Accelerate can also be installed into your own non-Anaconda Python environment.

For more information, contact [sales@anaconda.com](mailto:sales@anaconda.com).

## Updating Accelerate

To update Accelerate, take the following steps:

1. Run the command `conda update conda`.
2. Run the command `conda update accelerate`.

## Updating NumbaPro

If you have NumbaPro installed, you must manually upgrade NumbaPro to install the NumbaPro compatibility layer by taking the following steps:

1. Run the command `conda update conda`.
2. Run the command `conda update numbapro`.

## Managing your Accelerate license

You can install, view or remove your Accelerate license with the graphical Anaconda Navigator license manager, or manually with your operating system.

For more information, see </anaconda/user-guide/tasks/install-licenses>.

## User guide

This section contains information related to:

## CUDA libraries

The following CUDA libraries have bindings and algorithms that are available for use with Accelerate:

### cuBLAS

Provides basic linear algebra building blocks. See [NVIDIA cuBLAS](#).

The cuBLAS binding provides an interface that accepts NumPy arrays and Numba's CUDA device arrays. The binding automatically transfers NumPy array arguments to the device as required. This automatic transfer may generate some unnecessary transfers, so optimal performance is likely to be obtained by the manual transfer for NumPy arrays into device arrays and using the cuBLAS to manipulate device arrays where possible.

No special naming convention is used to identify the data type, unlike in the BLAS C and Fortran APIs. Arguments for array storage information which are part of the cuBLAS C API are also not necessary since NumPy arrays and device arrays contain this information.

All functions are accessed through the `accelerate.cuda.blas.Blas` class:

### BLAS Level 1

`accelerate.cuda.blas.Blas.nrm2(x)`

Computes the L2 norm for array *x*. Same as *numpy.linalg.norm(x)*.

**Parameters** **x** (*python.array*) – input vector

**Returns** resulting norm.

`accelerate.cuda.blas.Blas.dot(x, y)`

Compute the dot product of array *x* and array *y*. Same as *np.dot(x, y)*.

**Parameters**

- **x** (*python.array*) – vector
- **y** (*python.array*) – vector

**Returns** dot product of *x* and *y*

`accelerate.cuda.blas.Blas.dotc(x, y)`

Uses the conjugate of the element of the vectors to compute the dot product of array *x* and array *y* for complex dtype only. Same as *np.vdot(x, y)*.

**Parameters**

- **x** (*python.array*) – vector
- **y** (*python.array*) – vector

**Returns** dot product of *x* and *y*

`accelerate.cuda.blas.Blas.scal(alpha, x)`

Scale *x* inplace by *alpha*. Same as *x = alpha \* x*

**Parameters**

- **alpha** – scalar
- **x** (*python.array*) – vector

`accelerate.cuda.blas.Blas.axpy(alpha, x)`

Compute *y = alpha \* x + y* inplace.

**Parameters**

- **alpha** – scalar
- **x** (*python.array*) – vector

`accelerate.cuda.blas.Blas.amax(x)`

Find the index of the first largest element in array *x*. Same as *np.argmax(x)*

**Parameters** **x** (*python.array*) – vector

**Returns** index (start from 0).

`accelerate.cuda.blas.Blas.amin(x)`

Find the index of the first largest element in array *x*. Same as *np.argmin(x)*

**Parameters** **x** (*python.array*) – vector

**Returns** index (start from 0).

`accelerate.cuda.blas.Blas.asum(x)`

Compute the sum of all element in array *x*.

**Parameters** **x** (*python.array*) – vector

**Returns** *x.sum()*

`accelerate.cuda.blas.Blas.rot(x, y, c, s)`

Apply the Givens rotation matrix specified by the cosine element  $c$  and the sine element  $s$  inplace on vector element  $x$  and  $y$ .

Same as  $x, y = c * x + s * y, -s * x + c * y$

#### Parameters

- **x** (`python.array`) – vector
- **y** (`python.array`) – vector

`accelerate.cuda.blas.Blas.rotg(a, b)`

Constructs the Givens rotation matrix with the column vector (a, b).

#### Parameters

- **a** – first element of the column vector
- **b** – second element of the column vector

#### Returns

a tuple (r, z, c, s)

$r - r = a^{**2} + b^{**2}$

**z** – Use to reconstruct  $c$  and  $s$ . Refer to cuBLAS documentation for detail.

**c** – The consine element.

**s** – The sine element.

`accelerate.cuda.blas.Blas.rotm(x, y, param)`

Applies the modified Givens transformation inplace.

Same as:

```
param = flag, h11, h21, h12, h22
x[i] = h11 * x[i] + h12 * y[i]
y[i] = h21 * x[i] + h22 * y[i]
```

Refer to the cuBLAS documentation for the use of *flag*.

#### Parameters

- **x** (`python.array`) – vector
- **y** (`python.array`) – vector

`accelerate.cuda.blas.Blas.rotmg(d1, d2, x1, y1)`

Constructs the modified Givens transformation  $H$  that zeros out the second entry of a column vector ( $d1 * x1, d2 * y1$ ).

#### Parameters

- **d1** – scaling factor for the x-coordinate of the input vector
- **d2** – scaling factor for the y-coordinate of the input vector
- **x1** – x-coordinate of the input vector
- **y1** – y-coordinate of the input vector

**Returns** A 1D array that is usable in *rotm*. The first element is the flag for *rotm*. The rest of the elements corresponds to the *h11, h21, h12, h22* elements of  $H$ .

## BLAS Level 2

All level 2 routines follow the following naming convention for all arguments:

- **A, B, C, AP – (2D array) Matrix argument.** *AP* implies packed storage for banded matrix.
- *x, y, z* – (1D arrays) Vector argument.
- *alpha, beta* – (scalar) Can be floats or complex numbers depending.
- *m* – (scalar) Number of rows of matrix *A*.
- ***n* – (scalar) Number of columns of matrix *A*. If *m* is not needed, *n* also means the number of rows of the matrix *A*; thus, implying a square matrix.**
- ***trans, transa, transb* – (string)** Select the operation *op* to apply to a matrix:
  - ‘N’:  $op(X) = X$ , the identity operation;
  - ‘T’:  $op(X) = X^{**T}$ , the transpose;
  - ‘C’:  $op(X) = X^{**H}$ , the conjugate transpose.

*trans* only applies to the only matrix argument. *transa* and *transb* apply to matrix *A* and matrix *B*, respectively.
- ***uplo* – (string) Can be ‘U’ for filling the upper triangular matrix; or ‘L’ for filling the lower triangular matrix.**
- *diag* – (boolean) Whether the matrix diagonal has unit elements.
- ***mode* – (string) ‘L’ means the matrix is on the left side in the equation.** ‘R’ means the matrix is on the right side in the equation.

---

**Note:** The last array argument is always overwritten with the result.

---

`accelerate.cuda.blas.Blas.gbmv(trans, m, n, kl, ku, alpha, A, x, beta, y)`  
banded matrix-vector multiplication  $y = \alpha * op(A) * x + \beta * y$  where *A* has *kl* sub-diagonals and *ku* super-diagonals.

`accelerate.cuda.blas.Blas.gemv(trans, m, n, alpha, A, x, beta, y)`  
matrix-vector multiplication  $y = \alpha * op(A) * x + \beta * y$

`accelerate.cuda.blas.Blas.trmv(uplo, trans, diag, n, A, x)`  
triangular matrix-vector multiplication  $x = op(A) * x$

`accelerate.cuda.blas.Blas.tbmv(uplo, trans, diag, n, k, A, x)`  
triangular banded matrix-vector  $x = op(A) * x$

`accelerate.cuda.blas.Blas.tpmv(uplo, trans, diag, n, AP, x)`  
triangular packed matrix-vector multiplication  $x = op(A) * x$

`accelerate.cuda.blas.Blas.trsv(uplo, trans, diag, n, A, x)`  
Solves the triangular linear system with a single right-hand-side.  $op(A) * x = b$

`accelerate.cuda.blas.Blas.tpsv(uplo, trans, diag, n, AP, x)`  
Solves the packed triangular linear system with a single right-hand-side.  $op(A) * x = b$

`accelerate.cuda.blas.Blas.tbsv(uplo, trans, diag, n, k, A, x)`  
Solves the triangular banded linear system with a single right-hand-side.  $op(A) * x = b$

`accelerate.cuda.blas.Blas.symv(uplo, n, alpha, A, x, beta, y)`  
symmetric matrix-vector multiplication  $y = \alpha * A * x + \beta * y$



```

accelerate.cuda.blas.Blas.hemv(uplo, n, alpha, A, x, beta, y)
    Hermitian matrix-vector multiplication  $y = \alpha * A * x + \beta * y$ 

accelerate.cuda.blas.Blas.sbmv(uplo, n, k, alpha, A, x, beta, y)
    symmetric banded matrix-vector multiplication  $y = \alpha * A * x + \beta * y$ 

accelerate.cuda.blas.Blas.hbmV(uplo, n, k, alpha, A, x, beta, y)
    Hermitian banded matrix-vector multiplication  $y = \alpha * A * x + \beta * y$ 

accelerate.cuda.blas.Blas.spmv(uplo, n, alpha, AP, x, beta, y)
    symmetric packed matrix-vector multiplication  $y = \alpha * A * x + \beta * y$ 

accelerate.cuda.blas.Blas.hpmv(uplo, n, alpha, AP, x, beta, y)
    Hermitian packed matrix-vector multiplication  $y = \alpha * A * x + \beta * y$ 

accelerate.cuda.blas.Blas.ger(m, n, alpha, x, y, A)
    the rank-1 update  $A := \alpha * x * y ** T + A$ 

accelerate.cuda.blas.Blas.geru(m, n, alpha, x, y, A)
    the rank-1 update  $A := \alpha * x * y ** T + A$ 

accelerate.cuda.blas.Blas.gerc(m, n, alpha, x, y, A)
    the rank-1 update  $A := \alpha * x * y ** H + A$ 

accelerate.cuda.blas.Blas.syr(uplo, n, alpha, x, A)
    symmetric rank 1 operation  $A := \alpha * x * x ** T + A$ 

accelerate.cuda.blas.Blas.her(uplo, n, alpha, x, A)
    hermitian rank 1 operation  $A := \alpha * x * x ** H + A$ 

accelerate.cuda.blas.Blas.spr(uplo, n, alpha, x, AP)
    the symmetric rank 1 operation  $A := \alpha * x * x ** T + A$ 

accelerate.cuda.blas.Blas.hpr(uplo, n, alpha, x, AP)
    hermitian rank 1 operation  $A := \alpha * x * x ** H + A$ 

accelerate.cuda.blas.Blas.syr2(uplo, n, alpha, x, y, A)
    symmetric rank-2 update  $A = \alpha * x * y ** T + y * x ** T + A$ 

accelerate.cuda.blas.Blas.her2(uplo, n, alpha, x, y, A)
    Hermitian rank-2 update  $A = \alpha * x * y ** H + \alpha * y * x ** H + A$ 

accelerate.cuda.blas.Blas.spr2(uplo, n, alpha, x, y, A)
    packed symmetric rank-2 update  $A = \alpha * x * y ** T + y * x ** T + A$ 

accelerate.cuda.blas.Blas.hpr2(uplo, n, alpha, x, y, A)
    packed Hermitian rank-2 update  $A = \alpha * x * y ** H + \alpha * y * x ** H + A$ 

```

### BLAS Level 3

All level 3 routines follow the same naming convention for arguments as in level 2 routines.

```

accelerate.cuda.blas.Blas.gemm(transa, transb, m, n, k, alpha, A, B, beta, C)
    matrix-matrix multiplication  $C = \alpha * op(A) * op(B) + \beta * C$ 

accelerate.cuda.blas.Blas.syrk(uplo, trans, n, k, alpha, A, beta, C)
    symmetric rank- k update  $C = \alpha * op(A) * op(A) ** T + \beta * C$ 

accelerate.cuda.blas.Blas.herk(uplo, trans, n, k, alpha, A, beta, C)
    Hermitian rank- k update  $C = \alpha * op(A) * op(A) ** H + \beta * C$ 

```

`accelerate.cuda.blas.Blas.symm(side, uplo, m, n, alpha, A, B, beta, C)`  
symmetric matrix-matrix multiplication:

```
if side == 'L':
    C = alpha * A * B + beta * C
else: # side == 'R'
    C = alpha * B * A + beta * C
```

`accelerate.cuda.blas.Blas.hemm(side, uplo, m, n, alpha, A, B, beta, C)`  
Hermitian matrix-matrix multiplication:

```
if side == 'L':
    C = alpha * A * B + beta * C
else: # side == 'R':
    C = alpha * B * A + beta * C
```

`accelerate.cuda.blas.Blas.trsm(side, uplo, trans, diag, m, n, alpha, A, B)`  
Solves the triangular linear system with multiple right-hand-sides:

```
if side == 'L':
    op(A) * X = alpha * B
else: # side == 'R'
    X * op(A) = alpha * B
```

`accelerate.cuda.blas.Blas.trmm(side, uplo, trans, diag, m, n, alpha, A, B, C)`  
triangular matrix-matrix multiplication:

```
if side == ':':
    C = alpha * op(A) * B
else: # side == 'R'
    C = alpha * B * op(A)
```

`accelerate.cuda.blas.Blas.dgmm(side, m, n, A, x, C)`  
matrix-matrix multiplication:

```
if mode == 'R':
    C = A * x * diag(X)
else: # mode == 'L'
    C = diag(X) * x * A
```

`accelerate.cuda.blas.Blas.geam(transa, transb, m, n, alpha, A, beta, B, C)`  
matrix-matrix addition/transposition  $C = \alpha * op(A) + \beta * op(B)$

## cuSPARSE

Provides basic linear algebra operations for sparse matrices. See [NVIDIA cuSPARSE](#) for an in-depth description of the cuSPARSE library and its methods and data types. All functions are accessed through the `accelerate.cuda.sparse.Sparse` class:

Similarly to the cuBLAS interface, no special naming convention is used for functions to operate on different datatypes - all datatypes are handled by each function, and dispatch of the corresponding library function is handled by Accelerate. However, it is often necessary to provide a *matrix descriptor* to functions, which provides some information about the format and properties of a matrix. A matrix descriptor can be obtained from the `accelerate.cuda.sparse.Sparse.matdescr()` method:

`accelerate.cuda.sparse.Sparse.matdescr (indexbase, diagtype, fillmode, matrixtype)`

Creates a matrix descriptor that describes a matrix with the given *indexbase*, *diagtype*, *fillmode*, and *matrixtype*. Note that not all of these options are relevant to every matrix storage format.

#### Parameters

- **indexbase** – Optional. 0 for 0-based indexing, or 1 for 1-based indexing. If not specified, the default given to the `accelerate.cuda.sparse.Sparse` constructor is used instead.
- **diagtype** – Optional. Defaults to 'N'. 'N' signifies that the matrix diagonal has non-unit elements. 'U' signifies that the matrix diagonal only contains unit elements.
- **fillmode** – Optional. Defaults to 'L'. 'L' indicates that the lower triangular part of the matrix is stored. 'U' indicates that the upper triangular part of the matrix is stored.
- **matrixtype** – Optional. Defaults to 'G'. 'S' indicates that the matrix is symmetric. 'H' indicates that the matrix is Hermitian. 'T' indicates that the matrix is triangular. 'G' is used for a *general* matrix, which is not symmetric, Hermitian, or triangular.

**Returns** A matrix descriptor.

Many of the methods of the `accelerate.cuda.sparse.Sparse` class accept the individual data structures that make up a sparse representation of a matrix (for example the values, the row pointers and the column indices for a CSR format matrix). However, some methods (such as `accelerate.cuda.sparse.Sparse.csr_gemm_ez()`), accept an instance of the `accelerate.cuda.sparse.CudaSparseMatrix` class:

**class** `accelerate.cuda.sparse.CudaSparseMatrix`

Base class for a representation of a sparse matrix on a CUDA device. The constructor takes no arguments.

**from\_host\_matrix** (*matrix*, *stream*)

Initialise the matrix structure and values from an instance of a matrix on the host. The host matrix must be of the corresponding host type, which is documented for each subclass below.

**copy\_to\_host** (*stream*)

Create an instance of the corresponding host matrix type and copy the matrix structure and data into it from the device. See subclass documentation for an indication of the corresponding matrix type.

Subclasses of the sparse matrix type are:

**class** `accelerate.cuda.sparse.CudaBSRMatrix`

CUDA sparse matrix for which the corresponding type is a `scipy.sparse.bsr_matrix`.

**class** `accelerate.cuda.sparse.CudaCSRMatrix`

CUDA sparse matrix for which the corresponding type is a `scipy.sparse.csr_matrix`.

**class** `accelerate.cuda.sparse.CudaCSCMatrix`

CUDA sparse matrix for which the corresponding type is a `scipy.sparse.csc_matrix`.

There are also some convenience methods for constructing CUDA sparse matrices in a similar manner to Scipy sparse matrices:

## BLAS Level 1

`accelerate.cuda.sparse.Sparse.axpyi (alpha, xVal, xInd, y)`

Multiplies the sparse vector *x* by *alpha* and adds the result to the dense vector *y*.

#### Parameters

- **alpha** – scalar
- **xVal** – vector of non-zero values of *x*

- **xInd** – vector of indices of non-zero values of  $x$
- **y** – dense vector

**Returns** dense vector

`accelerate.cuda.sparse.Sparse.doti(xVal, xInd, y)`

Computes the dot product of the sparse vector  $x$  and dense vector  $y$ .

**Parameters**

- **xVal** – vector of non-zero values of  $x$
- **xInd** – vector of indices of non-zero values of  $x$
- **y** – dense vector

**Returns** scalar

`accelerate.cuda.sparse.Sparse.dotci(xVal, xInd, y)`

Computes the dot product of the complex conjugate of the sparse vector  $x$  and the dense vector  $y$ .

**Parameters**

- **xVal** – vector of non-zero values of  $x$
- **xInd** – vector of indices of non-zero values of  $x$
- **y** – dense vector

**Returns** scalar

`accelerate.cuda.sparse.Sparse.gthr(y, xVal, xInd)`

Gathers the elements of  $y$  at the indices  $xInd$  into the array  $xVal$

**Parameters**

- **xVal** – vector of non-zero values of  $x$
- **xInd** – vector of indices of non-zero values of  $x$
- **y** – dense vector

**Returns** None

`accelerate.cuda.sparse.Sparse.gthrz(y, xVal, xInd)`

Gathers the elements of  $y$  at the indices  $xInd$  into the array  $xVal$  and zeroes out the gathered elements of  $y$ .

**Parameters**

- **xVal** – vector of non-zero values of  $x$
- **xInd** – vector of indices of non-zero values of  $x$
- **y** – dense vector

**Returns** None

`accelerate.cuda.sparse.Sparse.sctr(xVal, xInd, y)`

Scatters the elements of the sparse vector  $x$  into the dense vector  $y$ . Elements of  $y$  whose indices are not listed in  $xInd$  are unmodified.

**Parameters**

- **xVal** – vector of non-zero values of  $x$
- **xInd** – vector of indices of non-zero values of  $x$
- **y** – dense vector

**Returns** None

## BLAS Level 2

All level 2 routines follow the following naming convention for the following arguments:

- **alpha, beta** – (scalar) Can be real or complex numbers.
- **descr, descrA, descrB** – (descriptor) Matrix descriptor. An appropriate descriptor may be obtained by calling `accelerate.cuda.sparse.Sparse.matdescr()`. *descr* only applies to the only matrix argument. *descrA* and *descrB* apply to matrix *A* and matrix *B*, respectively.
- **dir** – (string) Can be 'C' to indicate column-major block storage or 'R' to indicate row-major block storage.
- **trans, transa, transb** – (string) Select the operation *op* to apply to a matrix:
  - 'N':  $op(X) = X$ , the identity operation;
  - 'T':  $op(X) = X^{**T}$ , the transpose;
  - 'C':  $op(X) = X^{**H}$ , the conjugate transpose.

*trans* only applies to the only matrix argument. *transa* and *transb* apply to matrix *A* and matrix *B*, respectively.

`accelerate.cuda.sparse.Sparse.bsrnv_matrix(dir, trans, alpha, descr, bsrmat, x, beta, y)`  
 Matrix-vector multiplication  $y = \alpha * op(A) * x + \beta * y$  with a BSR-format matrix.

### Parameters

- **dir** – block storage direction
- **trans** – operation to apply to the matrix
- **alpha** – scalar
- **descr** – matrix descriptor
- **bsrmat** – the matrix *A*
- **x** – dense vector
- **beta** – scalar
- **y** – dense vector

**Returns** None

`accelerate.cuda.sparse.Sparse.bsrnv(dir, trans, mb, nb, nnzb, alpha, descr, bsrVal, bsrRowPtr, bsrColInd, blockDim, x, beta, y)`

Matrix-vector multiplication  $y = \alpha * op(A) * x + \beta * y$  with a BSR-format matrix. This function accepts the individual arrays that make up the structure of a BSR matrix - if a `accelerate.cuda.sparse.CudaBSRMatrix` instance is to hand, it is recommended to use the `bsrnv_matrix()` method instead.

### Parameters

- **dir** – block storage direction
- **trans** – operation to apply to the matrix
- **mb** – Number of block rows of the matrix
- **nb** – Number of block columns of the matrix
- **nnzb** – Number of nonzero blocks of the matrix
- **alpha** – scalar

- **descr** – matrix descriptor
- **bsrVal** – vector of nonzero values of the matrix
- **bsrRowPtr** – vector of block row pointers of the matrix
- **bsrColInd** – vector of block column indices of the matrix
- **blockDim** – block dimension of the matrix
- **x** – dense vector
- **beta** – scalar
- **y** – dense vector

**Returns** None

`accelerate.cuda.sparse.Sparse.bsrxmvm(dir, trans, sizeOfMask, mb, nb, nnzb, alpha, descr, bsrVal, bsrMaskPtr, bsrRowPtr, bsrEndPtr, bsrColInd, blockDim, x, beta, y)`

Matrix-vector multiplication similar to `bsrmv()`, but including a mask operation:  $y(mask) = (\alpha * op(A) * x + \beta * y)(mask)$ . The blocks of  $y$  to be updated are specified in `bsrMaskPtr`. Blocks whose indices are not specified in `bsrMaskPtr` are left unmodified.

#### Parameters

- **dir** – block storage direction
- **trans** – operation to apply to the matrix
- **sizeOfMask** – number of updated blocks of rows of  $y$
- **mb** – Number of block rows of the matrix
- **nb** – Number of block columns of the matrix
- **nnzb** – Number of nonzero blocks of the matrix
- **alpha** – scalar
- **descr** – matrix descriptor
- **bsrVal** – vector of nonzero values of the matrix
- **bsrMaskPtr** – vector of indices of the block elements to be updated
- **bsrRowPtr** – vector of block row pointers of the matrix
- **bsrEndPtr** – vector of pointers to the end of every block row plus one
- **bsrColInd** – vector of block column indices of the matrix
- **blockDim** – block dimension of the matrix
- **x** – dense vector
- **beta** – scalar
- **y** – dense vector

**Returns** None

`accelerate.cuda.sparse.Sparse.csrmv(trans, m, n, nnz, alpha, descr, csrVal, csrRowPtr, csrColInd, x, beta, y)`

Matrix-vector multiplication  $y = \alpha * op(A) * x + \beta * y$  with a CSR-format matrix.

#### Parameters

- **trans** – operation to apply to the matrix

- **m** – Number of rows of the matrix
- **n** – Number of columns of the matrix
- **nnz** – Number of nonzeros of the matrix
- **alpha** – scalar
- **descr** – matrix descriptor
- **csrVal** – vector of nonzero values of the matrix
- **csrRowPtr** – vector of row pointers of the matrix
- **csrColInd** – vector of column indices of the matrix
- **x** – dense vector
- **beta** – scalar
- **y** – dense vector

**Returns** None

`accelerate.cuda.sparse.Sparse.csrsv_analysis(trans, m, nnz, descr, csrVal, csrRowPtr, csrColInd)`

Performs the analysis phase of the solution of the sparse triangular linear system  $op(A) * y = alpha * x$ . This needs to be executed only once for a given matrix and operation type.

#### Parameters

- **trans** – operation to apply to the matrix
- **m** – number of rows of the matrix
- **nnz** – number of nonzeros of the matrix
- **descr** – matrix descriptor
- **csrVal** – vector of nonzero values of the matrix
- **csrRowPtr** – vector of row pointers of the matrix
- **csrColInd** – vector of column indices of the matrix

**Returns** the analysis result, which can be used as input to the solve phase

`accelerate.cuda.sparse.Sparse.csrsv_solve(trans, m, alpha, descr, csrVal, csrRowPtr, csrColInd, info, x, y)`

Performs the analysis phase of the solution of the sparse triangular linear system  $op(A) * y = alpha * x$ .

#### Parameters

- **trans** – operation to apply to the matrix
- **m** – number of rows of the matrix
- **alpha** – scalar
- **descr** – matrix descriptor
- **csrVal** – vector of nonzero values of the matrix
- **csrRowPtr** – vector of row pointers of the matrix
- **csrColInd** – vector of column indices of the matrix
- **info** – the analysis result from `csrsv_analysis()`
- **x** – dense vector

- **y** – dense vector into which the solve result is stored

**Returns** None

### BLAS Level 3

`accelerate.cuda.sparse.Sparse.csrmm` (*transA, m, n, k, nnz, alpha, descrA, csrValA, csrRowPtrA, csrColIndA, B, ldb, beta, C, ldc*)

Matrix-matrix multiplication  $C = \alpha * op(A) * B + \beta * C$  where  $A$  is a sparse matrix in CSR format and  $B$  and  $C$  are dense matrices.

#### Parameters

- **transA** – operation to apply to  $A$
- **m** – number of rows of  $A$
- **n** – number of columns of  $B$  and  $C$
- **k** – number of columns of  $A$
- **nnz** – number of nonzeros in  $A$
- **alpha** – scalar
- **descrA** – matrix descriptor
- **csrValA** – vector of nonzero values of  $A$
- **csrRowPtrA** – vector of row pointers of  $A$
- **csrColIndA** – vector of column indices of  $A$
- **B** – dense matrix
- **ldb** – leading dimension of  $B$
- **beta** – scalar
- **C** – dense matrix
- **ldc** – leading dimension of  $C$

**Returns** None

`accelerate.cuda.sparse.Sparse.csrmm2` (*transA, transB, m, n, k, nnz, alpha, descrA, csrValA, csrRowPtrA, csrColIndA, B, ldb, beta, C, ldc*)

Matrix-matrix multiplication  $C = \alpha * op(A) * op(B) + \beta * C$  where  $A$  is a sparse matrix in CSR format and  $B$  and  $C$  are dense matrices.

#### Parameters

- **transA** – operation to apply to  $A$
- **transB** – operation to apply to  $B$
- **m** – number of rows of  $A$
- **n** – number of columns of  $B$  and  $C$
- **k** – number of columns of  $A$
- **nnz** – number of nonzeros in  $A$
- **alpha** – scalar
- **descrA** – matrix descriptor



- **csrValA** – vector of nonzero values of  $A$
- **csrRowPtrA** – vector of row pointers of  $A$
- **csrColIndA** – vector of column indices of  $A$
- **B** – dense matrix
- **ldb** – leading dimension of  $B$
- **beta** – scalar
- **C** – dense matrix
- **ldc** – leading dimension of  $C$

**Returns** None

`accelerate.cuda.sparse.Sparse.csrsm_analysis(transA, m, nnz, descrA, csrValA, csrRowPtrA, csrColIndA)`

Performs the analysis phase of the solution of a sparse triangular linear system  $op(A) * Y = alpha * X$  with multiple right-hand sides where  $A$  is a sparse matrix in CSR format, and  $X$  and  $Y$  are dense matrices.

#### Parameters

- **transA** – operation to apply to  $A$
- **m** – number of rows of  $A$
- **nnz** – number of nonzeros in  $A$
- **descrA** – matrix descriptor
- **csrValA** – vector of nonzero values of  $A$
- **csrRowPtrA** – vector of row pointers of  $A$
- **csrColIndA** – vector of column indices of  $A$

**Returns** the analysis result

`accelerate.cuda.sparse.Sparse.csrsm_solve(transA, m, n, alpha, descrA, csrValA, csrRowPtrA, csrColIndA, info, X, ldx, Y, ldy)`

Performs the analysis phase of the solution of a sparse triangular linear system  $op(A) * Y = alpha * X$  with multiple right-hand sides where  $A$  is a sparse matrix in CSR format, and  $X$  and  $Y$  are dense matrices.

#### Parameters

- **transA** – operation to apply to  $A$
- **m** – number of rows of  $A$
- **n** – number of columns of  $B$  and  $C$
- **alpha** – scalar
- **descrA** – matrix descriptor
- **csrValA** – vector of nonzero values of  $A$
- **csrRowPtrA** – vector of row pointers of  $A$
- **csrColIndA** – vector of column indices of  $A$
- **info** – the analysis result from `csrsm_analysis()`
- **X** – dense matrix
- **ldx** – leading dimension of  $X$

- **Y** – dense matrix
- **ldy** – leading dimension of *Y*

**Returns** None

## Extra Functions

`accelerate.cuda.sparse.Sparse.XcsrgeamNnz` (*m*, *n*, *descrA*, *nnzA*, *csrRowPtrA*, *csrColIndA*,  
*descrB*, *nnzB*, *csrRowPtrB*, *csrColIndB*, *descrC*,  
*csrRowPtrC*)

Set up the sparsity pattern for the matrix operation  $C = \alpha * A + \beta * B$  where *A*, *B*, and *C* are all sparse matrices in CSR format.

### Parameters

- **m** – number of rows of all matrices
- **n** – number of columns of all matrices
- **descrA** – matrix descriptor for *A*
- **nnzA** – number of nonzeros in *A*
- **csrRowPtrA** – vector of row pointers of *A*
- **csrColIndA** – vector of column indices of *A*
- **descrB** – matrix descriptor for *B*
- **nnzB** – number of nonzeros in *B*
- **csrRowPtrB** – vector of row pointers of *B*
- **csrColIndB** – vector of column indices of *B*
- **descrC** – matrix descriptor for *B*
- **csrRowPtrC** – vector of row pointers of *C*, written to by this method

**Returns** number of nonzeros in *C*

`accelerate.cuda.sparse.Sparse.csrgeam` (*m*, *n*, *alpha*, *descrA*, *nnzA*, *csrValA*, *csrRowPtrA*, *csrColIndA*, *beta*, *descrB*, *nnzB*, *csrValB*, *csrRowPtrB*, *csrColIndB*, *descrC*, *csrValC*, *csrRowPtrC*, *csrColIndC*)

Performs the the matrix operation  $C = \alpha * A + \beta * B$  where *A*, *B*, and *C* are all sparse matrices in CSR format.

### Parameters

- **m** – number of rows of all matrices
- **n** – number of columns of all matrices
- **alpha** – scalar
- **descrA** – matrix descriptor for *A*
- **nnzA** – number of nonzeros in *A*
- **csrValA** – vector of nonzero values of *A*
- **csrRowPtrA** – vector of row pointers of *A*
- **csrColIndA** – vector of column indices of *A*

- **beta** – scalar
- **descrB** – matrix descriptor for  $B$
- **nnzB** – number of nonzeros in  $B$
- **csrValB** – vector of nonzero values of  $B$
- **csrRowPtrB** – vector of row pointers of  $B$
- **csrColIndB** – vector of column indices of  $B$
- **descrC** – matrix descriptor for  $C$
- **csrValC** – vector of nonzero values of  $C$
- **csrRowPtrC** – vector of row pointers of  $C$
- **csrColIndC** – vector of column indices of  $C$

**Returns** None

`accelerate.cuda.sparse.Sparse.XcsrgermmNnz` (*transA, transB, m, n, k, descrA, nnzA, csrRowPtrA, csrColIndA, descrB, nnzB, csrRowPtrB, csrColIndB, descrC, csrRowPtrC*)

Set up the sparsity pattern for the matrix operation  $C = op(A) * op(B)$  where  $A$ ,  $B$ , and  $C$  are all sparse matrices in CSR format.

**Parameters**

- **transA** – operation to apply to  $A$
- **transB** – operation to apply to  $B$
- **m** – number of rows of  $A$  and  $C$
- **n** – number of columns of  $B$  and  $C$
- **k** – number of columns/rows of  $A/B$
- **descrA** – matrix descriptor for  $A$
- **nnzA** – number of nonzeros in  $A$
- **csrRowPtrA** – vector of row pointers of  $A$
- **csrColIndA** – vector of column indices of  $A$
- **descrB** – matrix descriptor for  $B$
- **nnzB** – number of nonzeros in  $B$
- **csrRowPtrB** – vector of row pointers of  $B$
- **csrColIndB** – vector of column indices of  $B$
- **descrC** – matrix descriptor for  $C$
- **csrRowPtrC** – vector of row pointers of  $C$ , written by this function

**Returns** number of nonzeros in  $C$

`accelerate.cuda.sparse.Sparse.csrgermm` (*transA, transB, m, n, k, descrA, nnzA, csrValA, csrRowPtrA, csrColIndA, descrB, nnzB, csrValB, csrRowPtrB, csrColIndB, descrC, csrValC, csrRowPtrC, csrColIndC*)

Perform the matrix operation  $C = op(A) * op(B)$  where  $A$ ,  $B$ , and  $C$  are all sparse matrices in CSR format.

**Parameters**

- **transA** – operation to apply to *A*
- **transB** – operation to apply to *B*
- **m** – number of rows of *A* and *C*
- **n** – number of columns of *B* and *C*
- **k** – number of columns/rows of *A/B*
- **descrA** – matrix descriptor for *A*
- **nnzA** – number of nonzeros in *A*
- **csrValA** – vector of nonzero values in *A*
- **csrRowPtrA** – vector of row pointers of *A*
- **csrColIndA** – vector of column indices of *A*
- **descrB** – matrix descriptor for *B*
- **nnzB** – number of nonzeros in *B*
- **csrValB** – vector of nonzero values in *B*
- **csrRowPtrB** – vector of row pointers of *B*
- **csrColIndB** – vector of column indices of *B*
- **descrC** – matrix descriptor for *C*
- **csrValC** – vector of nonzero values in *C*
- **csrRowPtrC** – vector of row pointers of *C*
- **csrColIndC** – vector of column indices of *C*

**Returns** None

```
accelerate.cuda.sparse.Sparse.csrgermm_ez(A, B, transA='N', transB='N', descrA=None, descrB=None, descrC=None)
```

Performs the matrix operation  $C = op(A) * op(B)$  where *A*, *B* and *C* are all sparse matrices in CSR format. This function accepts and returns `accelerate.cuda.sparse.CudaCSRMatrix` matrices, and makes calls to `XcsrgermmNnz()` and `csrgermm()`.

**Parameters**

- **A** – `accelerate.cuda.sparse.CudaCSRMatrix`
- **B** – `accelerate.cuda.sparse.CudaCSRMatrix`
- **transA** – optional, operation to apply to *A*
- **transB** – optional, operation to apply to *B*
- **descrA** – optional, matrix descriptor for *A*
- **descrB** – optional, matrix descriptor for *B*
- **descrC** – optional, matrix descriptor for *C*

**Returns** `accelerate.cuda.sparse.CudaCSRMatrix`

## Preconditioners

`accelerate.cuda.sparse.Sparse.csric0(trans, m, descr, csrValA, csrRowPtrA, csrColIndA, info)`

Computes incomplete Cholesky factorization of a sparse matrix in CSR format with 0 fill-in and no pivoting:  $op(A) = R^{**T} * R$ . This method must follow a call to `csrsv_analysis()`. The matrix  $A$  is overwritten with the upper or lower triangular factors  $R$  or  $R^{**T}$ .

### Parameters

- **trans** – operation to apply to the matrix
- **m** – number of rows and columns of the matrix
- **descr** – matrix descriptor
- **csrValA** – vector of nonzero values in  $A$
- **csrRowPtrA** – vector of row pointers of  $A$
- **csrColIndA** – vector of column indices of  $A$
- **info** – analysis result

**Returns** None

`accelerate.cuda.sparse.Sparse.csrilu0(trans, m, descr, csrValA, csrRowPtrA, csrColIndA, info)`

Computes incomplete-LU factorization of a sparse matrix in CSR format with 0 fill-in and no pivoting:  $op(A) = L * U$ . This method must follow a call to `csrsv_analysis()`. The matrix  $A$  is overwritten with the lower and upper triangular factors  $L$  and  $U$ .

### Parameters

- **trans** – operation to apply to the matrix
- **m** – number of rows and columns of the matrix
- **descr** – matrix descriptor
- **csrValA** – vector of nonzero values in  $A$
- **csrRowPtrA** – vector of row pointers of  $A$
- **csrColIndA** – vector of column indices of  $A$
- **info** – analysis result

**Returns** None

`accelerate.cuda.sparse.Sparse.gtsv(m, n, dl, d, du, B, ldb)`

Computes the solution of a tridiagonal linear system with multiple right-hand sides:  $A * Y = alpha * X$ .

### Parameters

- **m** – the size of the linear system
- **n** – the number of right-hand sides in the system
- **dl** – dense vector storing the lower-diagonal elements
- **d** – dense vector storing the diagonal elements
- **du** – dense vector storing the upper-diagonal elements
- **B** – dense matrix holding the right-hand sides of the system
- **ldb** – the leading dimension of  $B$

**Returns** None

`accelerate.cuda.sparse.Sparse.gtsv_nopivot(m, n, dl, d, du, B, ldb)`  
Similar to `gtsv()`, but computes the solution without performing any pivoting.

**Parameters**

- **m** – the size of the linear system
- **n** – the number of right-hand sides in the system
- **dl** – dense vector storing the lower-diagonal elements
- **d** – dense vector storing the diagonal elements
- **du** – dense vector storing the upper-diagonal elements
- **B** – dense matrix holding the right-hand sides of the system
- **ldb** – the leading dimension of *B*

**Returns** None

`accelerate.cuda.sparse.Sparse.gtsvStridedBatch(m, dl, d, du, x, batchCount, batchStride)`  
Computes the solution of *i* tridiagonal linear systems:  $A(i) * y(i) = \alpha * x(i)$ .

**Parameters**

- **m** – the size of the linear systems
- **dl** – stacked dense vector storing the lower-diagonal elements of each system
- **d** – stacked dense vector storing the diagonal elements of each system
- **du** – stacked dense vector storing the upper-diagonal elements of each system
- **x** – dense matrix holding the right-hand sides of the systems
- **batchCount** – number of systems to solve
- **batchStride** – number of elements separating the vectors of each system

**Returns** None

## Format Conversion

`accelerate.cuda.sparse.Sparse.bsr2csr(dirA, mb, nb, descrA, bsrValA, bsrRowPtrA, bsrColIndA, blockDim, descrC, csrValC, csrRowPtrC, csrColIndC)`

Convert the sparse matrix *A* in BSR format to CSR format, stored in *C*.

**Parameters**

- **dirA** – row ('R') or column ('C') orientation of block storage
- **mb** – number of block rows of *A*
- **nb** – number of block columns of *A*
- **descrA** – matrix descriptor for *A*
- **bsrValA** – vector of nonzero values of *A*
- **bsrRowPtrA** – vector of block row pointers of *A*
- **bsrColIndA** – vector of block column indices of *A*
- **blockDim** – block dimension of *A*

- **descrC** – matrix descriptor for *C*
- **csrValA** – vector of nonzero values in *C*
- **csrRowPtrA** – vector of row pointers of *C*
- **csrColIndA** – vector of column indices of *C*

**Returns** None

`accelerate.cuda.sparse.Sparse.Xcoo2csr (cooRowInd, nnz, m, csrRowPtr)`

Converts an array containing uncompressed row indices corresponding to the COO format into an array of compressed row pointers corresponding to the CSR format.

**Parameters**

- **cooRowInd** – integer array of uncompressed row indices
- **nnz** – number of nonzeros
- **m** – number of matrix rows
- **csrRowPtr** – vector of row pointers to be written to

**Returns** None

`accelerate.cuda.sparse.Sparse.csc2dense (m, n, descrA, cscValA, cscRowIndA, cscColPtrA, A, lda)`

Convert the sparse matrix *A* in CSC format into a dense matrix.

**Parameters**

- **m** – number of rows of *A*
- **n** – number of columns of *A*
- **descrA** – matrix descriptor for *A*
- **cscValA** – values in the CSC representation of *A*
- **cscRowIndA** – row indices in the CSC representation of *A*
- **cscColPtrA** – column pointers in the CSC representation of *A*
- **A** – dense matrix representation of *A* to be written by this function.
- **lda** – leading dimension of *A*

**Returns** None

`accelerate.cuda.sparse.Sparse.Xcsr2bsrNnz (dirA, m, n, descrA, csrRowPtrA, csrColIndA, blockDim, descrC, bsrRowPtrC)`

Performs the analysis necessary for converting a matrix in CSR format into BSR format.

**Parameters**

- **dirA** – row ('R') or column ('C') orientation of block storage
- **m** – number of rows of matrix
- **n** – number of columns of matrix
- **descrA** – matrix descriptor for input matrix *A*
- **csrRowPtrA** – row pointers of matrix
- **csrColIndA** – column indices of matrix
- **blockDim** – block dimension of output matrix *C*

- **descrC** – matrix descriptor for output matrix *C*

**Returns** number of nonzeros of matrix

`accelerate.cuda.sparse.Sparse.csr2bsr` (*dirA, m, n, descrA, csrValA, csrRowPtrA, csrColIndA, blockDim, descrC, bsrValC, bsrRowPtrC, bsrColIndC*)

Performs conversion of a matrix from CSR format into BSR format.

**Parameters**

- **dirA** – row ('R') or column ('C') orientation of block storage
- **m** – number of rows of matrix
- **n** – number of columns of matrix
- **descrA** – matrix descriptor for input matrix *A*
- **csrValA** – nonzero values of matrix
- **csrRowPtrA** – row pointers of matrix
- **csrColIndA** – column indices of matrix
- **blockDim** – block dimension of output matrix *C*
- **descrC** – matrix descriptor for output matrix *C*
- **bsrValC** – nonzero values of output matrix *C*
- **bsrRowPtrC** – block row pointers of output matrix *C*
- **bsrColIndC** – block column indices of output matrix *C*

**Returns** number of nonzeros of matrix

`accelerate.cuda.sparse.Sparse.Xcsr2coo` (*csrRowPtr, nnz, m, cooRowInd*)

Converts an array of compressed row pointers corresponding to the CSR format into an array of uncompressed row indices corresponding to the COO format.

**Parameters**

- **csrRowPtr** – vector of row pointers
- **nnz** – number of nonzeros
- **m** – number of rows of matrix
- **cooRowInd** – vector of uncompressed row indices written by this function

**Returns** None

`accelerate.cuda.sparse.Sparse.csr2csc` (*m, n, nnz, csrVal, csrRowPtr, csrColInd, cscVal, cscRowInd, cscColPtr, copyValues*)

Converts a sparse matrix in CSR format into a sparse matrix in CSC format.

**Parameters**

- **m** – number of rows of matrix
- **n** – number of columns of matrix
- **nnz** – number of nonzeros of the matrix
- **csrVal** – values in the CSR representation
- **csrRowPtr** – row indices in the CSR representation
- **csrColInd** – column pointers in the CSR representation



- **cscVal** – values in the CSC representation
- **cscRowInd** – row indices in the CSC representation
- **cscColPtr** – column pointers in the CSC representation
- **copyValues** – ‘N’ or ‘S’ for symbolic or numeric copy of values

**Returns** None

`accelerate.cuda.sparse.Sparse.csr2dense(m, n, descr, csrVal, csrRowPtr, csrColInd, A, lda)`  
 Convert a sparse matrix in CSR format into dense format.

**Parameters**

- **m** – number of rows of matrix
- **n** – number of columns of matrix
- **descr** – matrix descriptor
- **csrVal** – values in the CSR representation
- **csrRowPtr** – row indices in the CSR representation
- **csrColInd** – column pointers in the CSR representation
- **A** – the dense representation, written to by this function
- **lda** – leading dimension of the matrix

**Returns** None

`accelerate.cuda.sparse.Sparse.dense2csc(m, n, descrA, A, lda, nnzPerCol, cscVal, cscRowInd, cscColPtr)`

Convert a dense matrix into a sparse matrix in CSC format. The *nnzPerCol* parameter may be computed with a call to `nnz()`.

**Parameters**

- **m** – number of rows of matrix
- **n** – number of columns of matrix
- **descrA** – matrix descriptor
- **A** – the matrix in dense format
- **lda** – leading dimension of the matrix
- **nnzPerCol** – array containing the number of nonzero elements per column
- **cscVal** – values in the CSC representation
- **cscRowInd** – row indices in the CSC representation
- **cscColPtr** – column pointers in the CSC representation

**Returns** None

`accelerate.cuda.sparse.Sparse.dense2csr(m, n, descrA, A, lda, nnzPerRow, csrVal, csrRowPtr, csrColInd)`

Convert a dense matrix into a sparse matrix in CSR format. The *nnzPerRow* parameter may be computed with a call to `nnz()`.

**Parameters**

- **m** – number of rows of matrix
- **n** – number of columns of matrix

- **descrA** – matrix descriptor
- **A** – the matrix in dense format
- **lda** – leading dimension of the matrix
- **nnzPerRow** – array containing the number of nonzero elements per row
- **csrVal** – values in the CSR representation
- **csrRowPtr** – row indices in the CSR representation
- **csrColInd** – column pointers in the CSR representation

**Returns** None

`accelerate.cuda.sparse.Sparse.nnz(dirA, m, n, descrA, A, lda, nnzPerRowCol)`

Computes the number of nonzero elements per row or column of a dense matrix, and the total number of nonzero elements in the matrix.

**Parameters**

- **dirA** – ‘R’ for the number of nonzeros per row, or ‘C’ for per column.
- **m** – number of rows of matrix
- **n** – number of columns of matrix
- **descrA** – matrix descriptor
- **A** – the matrix
- **lda** – leading dimension of the matrix
- **nnzPerRowCol** – array to contain the number of nonzeros per row or column

**Returns** total number of nonzeros in the matrix

## cuFFT

Provides FFT and inverse FFT for 1D, 2D and 3D arrays. See [NVIDIA cuFFT](#).

---

**Note:** cuFFT only supports FFT operations on `numpy.float32`, `numpy.float64`, `numpy.complex64`, `numpy.complex128` with C-contiguous datalayout.

---

## Forward FFT

`accelerate.cuda.fft.fft(ary, out[, stream])`

`accelerate.cuda.fft.fft_inplace(ary[, stream])`

**Parameters**

- **ary** – The input array. The inplace version stores the result in here.
- **out** – The output array for non-inplace versions.
- **stream** – The CUDA stream in which all operations will take place.

## Inverse FFT

```
accelerate.cuda.fft.ifft(ary, out[, stream])  
accelerate.cuda.fft.ifft_inplace(ary[, stream])
```

### Parameters

- **ary** – The input array. The inplace version stores the result in here.
- **out** – The output array for non-inplace versions.
- **stream** – The CUDA stream in which all operations will take place.

## FFTPlan

## cuRAND

Provides *pseudo-random number generator* (PRNG) and *quasi-random generator* (QRNG). See [NVIDIA cuRAND](#).

## CUDA Sorting

Accelerate provides routines for sorting arrays on CUDA GPUs.

### Sorting Large Arrays

The `accelerate.cuda.sorting.RadixSort` class is recommended for sorting large (approx. more than 1 million items) arrays of numeric types.

### Sorting Many Small Arrays

Using `accelerate.cuda.sorting.RadixSort` on small (approx. less than 1 million items) arrays has significant overhead due to multiple kernel launches.

A better alternative is to use `accelerate.cuda.sorting.segmented_sort()` -which launches a single kernel for sorting a batch of many small arrays.

## Math Kernel Library

The Math Kernel Library provides BLAS, LAPACK, and other math routines. For more information, see [Intel's site](#).

The following functions, FFT variants and accelerated UFuncs are available for use with Accelerate:

### MKL utility functions

The `accelerate.mkl` module contains a set of functions to configure and retrieve information about the underlying Intel MKL library.

## Reference

`accelerate.mkl.set_num_threads(n)`

Set the number of threads Intel MKL should use. This is only a hint, and no guarantee is made this number of threads will actually be used. This function takes precedence over the environment variable `MKL_NUM_THREADS`.

This function wraps the Intel MKL function `mkl_set_num_threads`.

`accelerate.mkl.get_max_threads()` → int

Return the number of threads Intel MKL is targeting for parallelism.

This function wraps the Intel MKL function `mkl_get_max_threads`.

`accelerate.mkl.get_version_string()` → str

Return the Intel MKL version information as a string.

This function wraps the Intel MKL function `mkl_get_version_string`.

`accelerate.mkl.mem_stat()` → int, int

Return a (bytes, blocks) tuple of memory usage statistics about the underlying Intel MKL memory allocator. The return tuple contains:

- The total number of bytes allocated (bytes).
- The number of allocated blocks (blocks).

This function wraps the Intel MKL function `mkl_mem_stat`.

`accelerate.mkl.get_cpu_clocks()` → int

Return elapsed CPU clocks as an integer. This may be useful when timing short intervals with high resolution. Note the result is limited to unsigned 64 bit integers, so wrapping of elapsed time is possible.

This function wraps the Intel MKL function `mkl_get_cpu_clocks`.

`accelerate.mkl.get_cpu_frequency()` → int

Return CPU frequency in GHz as a float. Note the result may vary from run to run as it returns the current frequency. That frequency can change in some systems due to several factors (i.e. power management).

This function wraps the Intel MKL function `mkl_get_cpu_frequency`.

## MKL BLAS functions

The `accelerate.mkl.blas` module contains a subset of BLAS functions implemented by means of the underlying Intel MKL library.

## Reference

`accelerate.mkl.blas.dot(x, y)`

Compute and return the vector dot product of *x* and *y*.

### Parameters

- **x** – one-dimensional array
- **y** – one-dimensional array

### Return type

 result

**Note** the input arguments may be copied to adjust their types.

## Example

```
alpha = 1.+1.j
A = np.arange(16, dtype=np.float64).reshape(4,4)
x = np.arange(4, dtype=np.float64)
beta = 0.
y = np.arange(4, dtype=np.float64)
result = blas.gemv('N', alpha, A, x, beta, y)
```

## MKL FFT

The speed-boosted variants of NumPy's FFT operations are accessible in the `numpy.fft` package, and the `accelerate.mkl.fftpack` package. The following functions in these packages are accelerated using MKL:

Function	Description
<code>fft(a, n=None, axis=-1)</code>	1-dimensional forward transform
<code>ifft(a, n=None, axis=-1)</code>	1-dimensional inverse transform
<code>rfft(a, n=None, axis=-1)</code>	1-dimensional forward transform of purely real data
<code>irfft(a, n=None, axis=-1)</code>	1-dimensional inverse transform of purely real data
<code>hfft(a, n=None, axis=-1)</code>	Hermite transform
<code>ihfft(a, n=None, axis=-1)</code>	Inverse Hermite transform
<code>fftn(a, s=None, axes=None)</code>	N-dimensional forward transform
<code>ifftn(a, s=None, axes=None)</code>	N-dimensional inverse transform
<code>fft2(a, s=None, axes=(-2, -1))</code>	2-dimensional forward transform
<code>ifft2(a, s=None, axes=(-2, -1))</code>	2-dimensional inverse transform
<code>rfftn(a, s=None, axes=None)</code>	N-dimensional forward transform of purely real data
<code>rfft2(a, s=None, axes=(-2, -1))</code>	2-dimensional forward transform of purely real data
<code>irfftn(a, s=None, axes=None)</code>	N-dimensional inverse transform of purely real data
<code>irfft2(a, s=None, axes=(-2, -1))</code>	2-dimensional inverse transform of purely real data

For further information on these functions, please refer to the Numpy documentation: `numpy.fft`.

## Accelerated UFuncs

Variants of some Numpy UFuncs that use Intel's Vector Math Library (VML) are found in the `accelerate.mkl` package in the `ufuncs` object. In comparison to Numpy's built-in UFuncs, Accelerated UFuncs have the following properties:

**Performance** Because Accelerated UFuncs call functions from VML, which is a library optimised for high performance using multiple threads and SIMD instructions, performance may be increased when calling Accelerated UFuncs in comparison to calling Numpy UFuncs. The performance increase will only be obtained for contiguous arguments. For non-contiguous arguments, performance comparable to Numpy's will be observed.

### Accuracy

- Accelerated UFuncs produce similar results to their Numpy equivalents for the range of finite values, up to a given relative tolerance.
- The tolerance varies between functions and data types, and is specified for each combination in the following section.
- For the range of infinite and NaN values, the majority of results computed by Accelerated UFuncs will be equal to those computed by their Numpy counterparts. However, this is not guaranteed; for example, an

input for which the Numpy UFunc produces a result of  $x + \text{inf} \cdot j$ , the equivalent Accelerated UFunc may produce a result of  $y + \text{inf} \cdot j$ , where  $x \neq y$ .

- Towards the edge of the domain of a data type (e.g. near  $3.4\text{e}+38$  for `float` and  $1.79\text{e}+308$  for `double` and values of similar magnitude at the negative end of the domain) some Accelerated UFuncs may produce results which differ from Numpy UFuncs, or may raise `FloatingPointError` or `ZeroDivisionError` exceptions. These functions are marked *domain edge warning* in the *Accuracy* column of the tables in the following sections.
- Some numpy implementations of functions that operate in the complex domain have branch cuts which differ from those in MKL, where this has been identified in testing these functions are marked *branch cut warning* in the *Accuracy* column of the tables in the following sections. This warning may also be present in the case of implementations which contain incorrect branch cuts.
- Denormal input values may be treated as zero by Accelerated UFuncs, and denormal output values may be flushed to zero.
- The accuracy reported is approximate and related to the least accurate value encountered when testing with contiguous input arguments. Non-contiguous arguments are more directly exposed to system math library implementations and so their accuracy is not commented on.

**Exception handling** For the range of finite values, exceptions will not be raised by Accelerated UFuncs, just as they would not by Numpy. For the infinite and NaN ranges, Accelerated UFuncs may raise `FloatingPointError` or `ZeroDivisionError` exceptions in cases when Numpy would not, and vice-versa.

Supported functions are described in the following sections.

## Arithmetic Functions

Function	Type	Accuracy
add(x, y)	f4	rtol=1.0e-7
	f8	rtol=1.0e-15
	c8	rtol=1.0e-7
	c16	rtol=1.0e-15
subtract(x, y)	f4	rtol=1.e-7
	f8	rtol=1.e-15
	c8	rtol=1.e-7
	c16	rtol=1.e-15
square(x)	f4	rtol=1.e-7
	f8	rtol=1.e-15
multiply(x, y)	f4	rtol=1.e-7
	f8	rtol=1.e-15
	c8	rtol=1.e-6
	c16	rtol=1.e-15
absolute(x)	f4	rtol=1.e-6
	f8	rtol=1.e-15

## Power and Root Functions

Function	Type	Accuracy
reciprocal(x)	f4	rtol=1.e-7
	f8	rtol=1.e-15
true_divide(x, y)	f4	rtol=1.e-7
	f8	rtol=1.e-15
	c8	rtol=1.e-6
	c16	rtol=1.e-15
sqrt(x, y)	f4	rtol=1.e-6
	f8	rtol=1.e-15
	c8	rtol=1.e-6, domain edge warning
	c16	rtol=1.e-15, domain edge warning
power(x, y)	f4	rtol=1.e-7
	f8	rtol=1.e-15
hypot(x, y)	f4	rtol=1.e-6
	f8	rtol=1.e-15

## Exponential and Logarithmic Functions

Function	Type	Accuracy
exp(x)	f4	rtol=1.e-6
	f8	rtol=1.e-15
	c8	rtol=1.e-6, domain edge warning
	c16	rtol=1.e-15, domain edge warning
expm1(x)	f4	rtol=1.e-6
	f8	rtol=1.e-15
log(x)	f4	rtol=1.e-6
	f8	rtol=1.e-15
	c8	rtol=1.e-5
	c16	rtol=1.e-13
log10(x)	f4	rtol=1.e-6
	f8	rtol=1.e-15
	c8	rtol=1.e-5, domain edge warning
	c16	rtol=1.e-13, domain edge warning
log1p(x)	f4	rtol=1.e-6
	f8	rtol=1.e-15

## Trigonometric Functions

Function	Type	Accuracy
cos (x)	f4	rtol=1.e-6, domain edge warning
	f8	rtol=1.e-15, domain edge warning
	c8	rtol=1.e-6, domain edge warning
	c16	rtol=1.e-15, domain edge warning
sin (x)	f4	rtol=1.e-5, domain edge warning
	f8	rtol=1.e-15, domain edge warning
	c8	rtol=1.e-6, domain edge warning
	c16	rtol=1.e-15, domain edge warning
tan (x)	f4	rtol=1.e-6, domain edge warning
	f8	rtol=1.e-15, domain edge warning
	c8	rtol=5.e-4, domain edge warning
	c16	rtol=5.e-14, domain edge warning
arccos (x)	f4	rtol=1.e-6, branch cut warning
	f8	rtol=1.e-15, branch cut warning
	c8	<b>rtol=1.e-5, domain edge warning,</b> branch cut warning
	c16	<b>rtol=1.e-14, domain edge warning,</b> branch cut warning
arcsin (x)	f4	rtol=1.e-6, branch cut warning
	f8	rtol=1.e-15, branch cut warning
	c8	<b>rtol=1.e-3, domain edge warning,</b> branch cut warning
	c16	<b>rtol=1.e-12, domain edge warning,</b> branch cut warning
arctan (x)	f4	rtol=1.e-6
	f8	rtol=1.e-15
	c8	rtol=1.e-6
	c16	rtol=1.e-15
arctan2 (x)	f4	rtol=1.e-6
	f8	rtol=1.e-15



## Hyperbolic Functions

Function	Type	Accuracy
cosh (x)	f4	rtol=1.e-6, domain edge warning
	f8	rtol=1.e-15, domain edge warning
	c8	rtol=1.e-6, domain edge warning
	c16	rtol=1.e-15, domain edge warning
sinh (x)	f4	rtol=1.e-6, domain edge warning
	f8	rtol=1.e-15, domain edge warning
	c8	rtol=1.e-6, domain edge warning
	c16	rtol=1.e-15, domain edge warning
tanh (x)	f4	rtol=1.e-6, domain edge warning
	f8	rtol=1.e-15, domain edge warning
	c8	rtol=1.e-6, domain edge warning
	c16	rtol=1.e-15, domain edge warning
arccosh (x)	f4	rtol=1.e-6
	f8	rtol=1.e-15
	c8	rtol=1.e-5, domain edge warning
	c16	rtol=1.e-14, domain edge warning
arcsinh (x)	f4	rtol=1.e-6
	f8	rtol=1.e-15
	c8	rtol=5.e-5, domain edge warning
	c16	rtol=1.e-13, domain edge warning
arctanh (x)	f4	rtol=1.e-5, branch cut warning
	f8	rtol=5.e-11, branch cut warning
	c8	<b>rtol=1.e-4, domain edge warning,</b> branch cut warning
	c16	<b>rtol=5.e-14, domain edge warning,</b> branch cut warning

## Profiling

The Python standard library includes code profiling functionality. When active, function invocations and the time spent on them are recorded.

The `accelerate.profiler` module extends this functionality by also recording the functions' signatures, which are useful because often the precise control flow—and thus function performance—depends on the argument types. For NumPy array types, this includes not only the `dtype` attribute, but also the array's shape.

### Profiling example

The following code defines a simple dot function and profiles it without signatures to match the behaviour of the Python standard library profile module:

```
from accelerate import profiler
import numpy as np

def dot(a, b):
    sum=0
    for i in range(len(a)):
        sum += a[i]*b[i]
    return sum

a = np.arange(16, dtype=np.float32)
b = np.arange(16, dtype=np.float32)

p = profiler.Profile(signatures=False)
p.enable()
dot(a, b)
p.disable()
p.print_stats()
```

This generates the following output:

```
3 function calls in 0.000 seconds

Ordered by: standard name

ncalls  tottime  percall  cumtime  percall filename:lineno(function)
1      0.000    0.000    0.000    0.000 builtins.len
1      0.000    0.000    0.000    0.000 dot.py:7(dot)
1      0.000    0.000    0.000    0.000 {method 'disable' of 'prof.Profiler'
↳objects}
```

NOTE: By default, the Profile constructor's signature flag is set to True, resulting in the following output:

```
3 function calls (2 primitive calls) in 0.000 seconds

Ordered by: standard name

ncalls  tottime  percall  cumtime  percall filename:lineno(function)
1      0.000    0.000    0.000    0.000 dot.py:1(disable())
2/1     0.000    0.000    0.000    0.000 dot.py:7(dot(a:ndarray(dtype=float32,
↳shape=(16,)), b:ndarray(dtype=float32, shape=(16,)))
```

In the results for more realistic code, the call graph—and thus the table of function calls—is much bigger, making working with data in tabular form inconvenient.

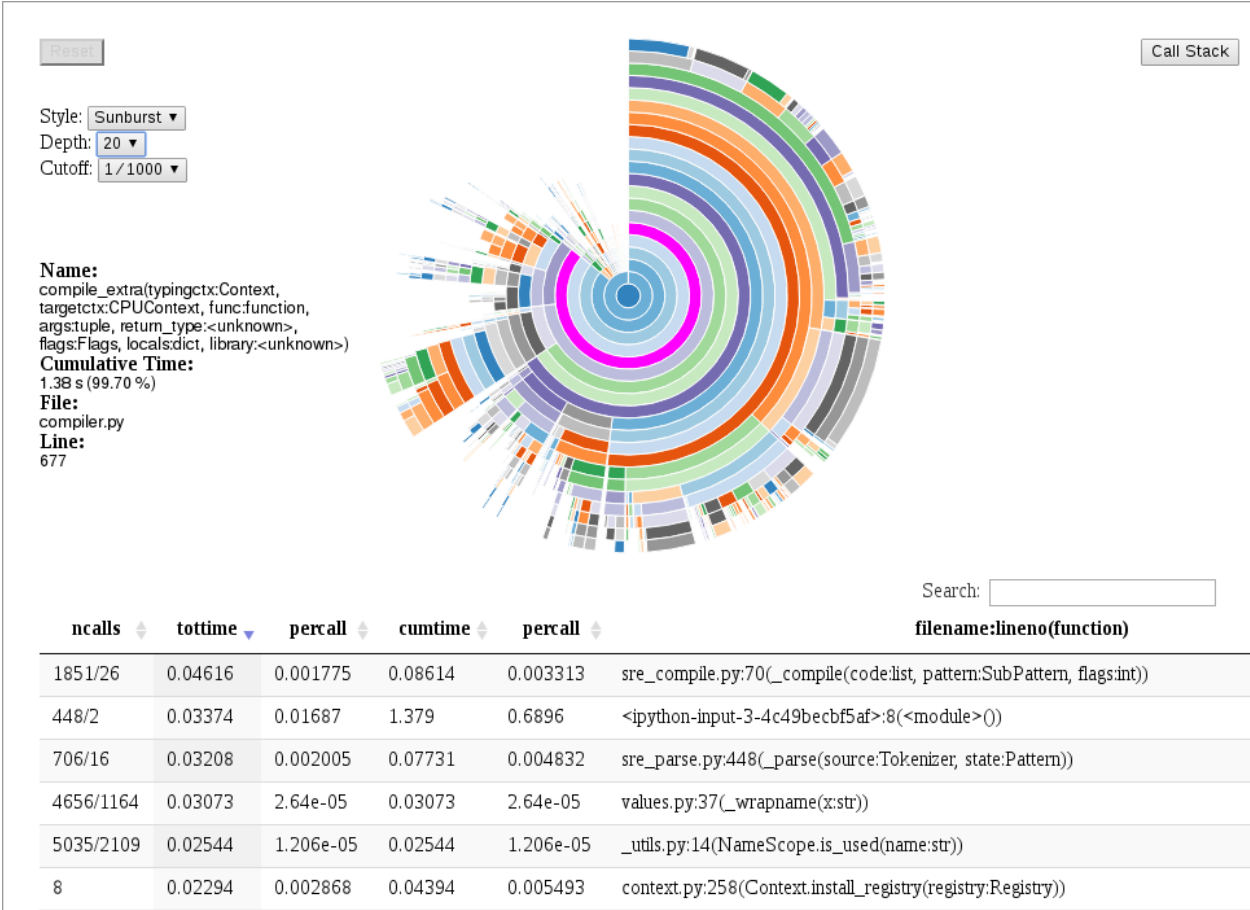
To solve this, the `accelerate.profiler` module also provides functionality to visualize the data. Instead of calling the `print_stats()` method, call the `accelerate.profiler.plot()` function.

NOTE: At this time, the `accelerate.profiler.plot()` function may only be called from inside a notebook.

If the code above was executed from inside a notebook, run the following code:

```
In [3]: profiler.plot(p)
```

Which generates the following output:



Accelerate.profiler API

Environment variables

ACCELERATE\_WARNINGS

If set to anything but 0 (zero), Accelerate may issue performance warnings, such as when input arguments need to be copied to adjust their data layout, or types, to match particular backend requirements.

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## Release notes

## Release notes

### Version 2.3.1

This is a minor update to bump the required version of Numba to 0.30 and to support Python 3.6.

### Version 2.3.0

This release of Accelerate is a feature release, containing these additions:

- A new BLAS wrapper API on top of MKL.
- MKL 11.3.3 is now supported.
- Numba 0.26 is supported-and is required.

### Version 2.2.0

This release of Accelerate is a feature release, containing two additions:

- Expanded the support of Intel MKL accelerated ufuncs with trigonometric and hyperbolic functions.
- Numba 0.25 is supported, and is a requirement.

### Version 2.1.0

This release of Accelerate is a feature release, containing 2 additions:

- Profiling tools
  - An enhanced version of the Python profiler that captures function arguments, including shapes and dtypes of Numpy arrays.
  - Integration of tools for visualising profiles in Jupyter notebooks, allowing interactive experimentation.
- Accelerated UFuncs, which provide a speed improvement over Numpy's built-in UFuncs by using Intel MKL.

### Version 2.0.2

This update adds support for updated versions of Numba and MKL:

- Numba 0.23 is now supported, and is a requirement.
- MKL 11.3.1, standard in Anaconda 2.5, is now supported.

### Version 2.0.1

This minor update to Accelerate adds no functional changes, but provides additional clarification of the the relationship between the Accelerate and NumbaPro conda packages upon installation.

## Version 2.0

NumbaPro has been deprecated, and its code generation features have been moved into open-source Numba. The CUDA library functions have been moved into Accelerate, along with some Intel MKL functionality. High-level functions and access to additional native library implementations will be added in future releases of Accelerate, and there will be no further updates to NumbaPro.

A NumbaPro compatibility layer (listed as release 0.22.0 of NumbaPro) provides access to the new Accelerate packages through the old NumbaPro package names. This avoids the need to change any existing code immediately for use with Accelerate. A warning will be generated upon import of the compatibility layer, to highlight the deprecation of the NumbaPro package.

## CUDA libraries

CUDA library functionality is equivalent to that in NumbaPro 0.21, with the following packages renamed:

NumbaPro Package	Accelerate package
<code>numbapro.cudalib.cublas</code>	<code>accelerate.cuda.blas</code>
<code>numbapro.cudalib.cuffft</code>	<code>accelerate.cuda.fft</code>
<code>numbapro.cudalib.curand</code>	<code>accelerate.cuda.rand</code>
<code>numbapro.cudalib.cusparse</code>	<code>accelerate.cuda.sparse</code>
<code>numbapro.cudalib.sorting</code>	<code>accelerate.cuda.sorting</code>

## Code generation

The `vectorize` targets `parallel` and `cuda` can now be accessed with Numba, as can the `cuda.reduce` decorator. Printing of integers and floating point values from CUDA kernels is also possible in Numba, and no longer requires NumbaPro or Accelerate to be imported.

## Intel MKL

The MKL FFT implementation is available in the package `accelerate.mkl.fftpack`, and MKL service functions are available in the `accelerate.mkl` package.

## Previous versions

The following documentation is provided for users who have not yet upgraded to the current version of Accelerate:

### Anaconda Accelerate

#### cuBLAS

#### CUDA Libraries

#### cuFFT



**cuRAND**

**cuSPARSE**

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**MKL**

**MKL utility functions**

**MKL FFT**

**Accelerated UFuncs**

**Profiling**

**Release Notes**

**CUDA Sorting**

**Anaconda Accelerate**

**cuBLAS**

**CUDA Libraries**

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[MKL](#)

[MKL utility functions](#)

[MKL FFT](#)

[Release Notes](#)

[CUDA Sorting](#)

[Previous versions](#)

The following documentation is provided for users who have not yet upgraded to the current version:

### 4.4.2 Anaconda Adam

*Server & Cluster Installer & Manager*

---

**Note:** This product is discontinued. This archived copy of the product documentation is provided for those customers who are still using it.

---

Anaconda Adam is a command line interface (CLI) utility for Linux that lets you:

- Install and manage these Anaconda® platform components:

Platform component	Description
Anaconda Enterprise Notebooks	Collaborative multi-user notebooks and projects
Anaconda Repository	On-premise repository for conda packages and environments
Anaconda Scale	Distributed package management and computation framework

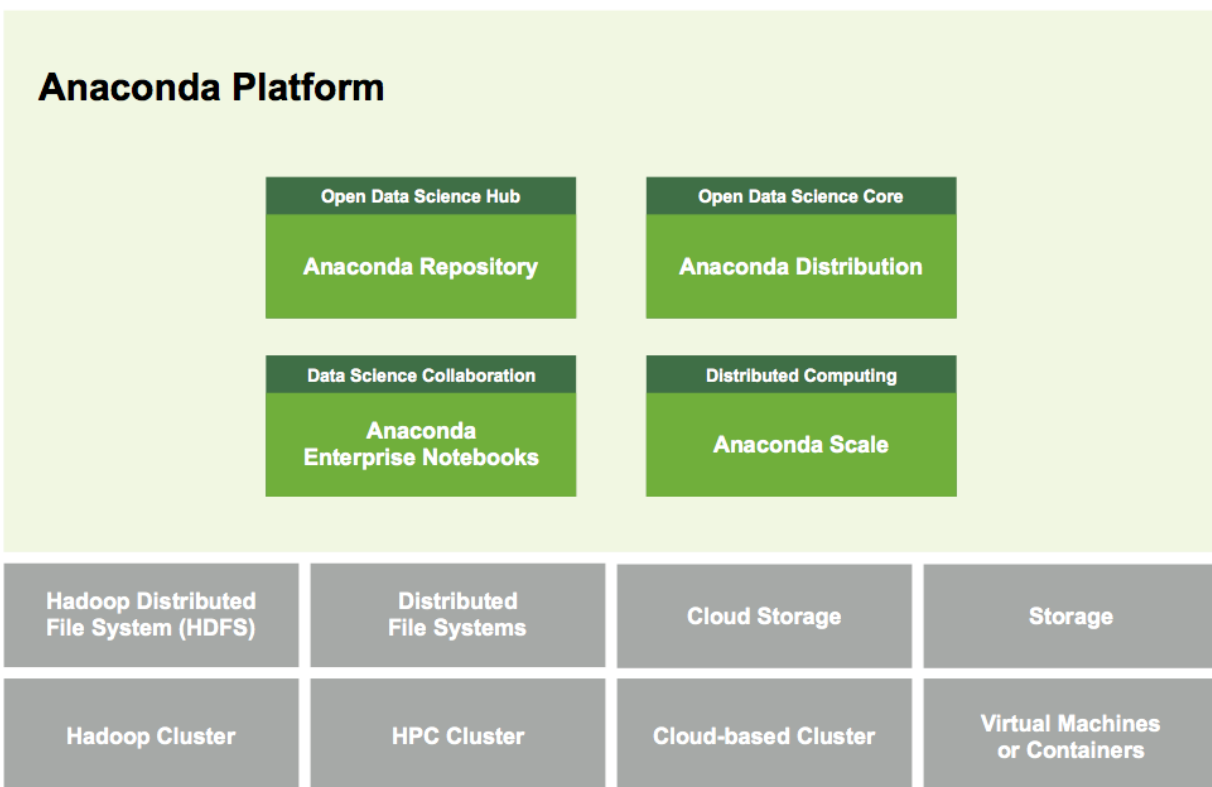
- Create, provision and remove clusters.

- Perform administration tasks on Amazon Elastic Compute Cloud (EC2) servers.
- Manage Anaconda packages.
- Execute commands on multiple nodes.

You must have an [Anaconda Enterprise](#) license to install Anaconda platform components. If you would like to purchase Anaconda platform, please contact [sales@anaconda.com](mailto:sales@anaconda.com).

You can use Adam with:

- Distributed computation frameworks such as Spark or Dask.
- Enterprise Hadoop distributions such as Cloudera CDH or Hortonworks HDP.
- HPC clusters.
- A collection of virtual machines or containers.



## Installation

### Installation requirements

Make sure your system meets the requirements below before installing and using Anaconda Adam.

### Hardware and operating system

To install Adam, you must have one or more 64-bit Linux machines with one of the following Linux distributions:

- RHEL/CentOS 6 or 7
- Ubuntu 14.04 or 16.04

and the following commands installed:

- `ssh`
- `openssl`
- `curl`
- `md5sum`

### License

To install Adam, you must have a valid [Anaconda Enterprise](#) license.

### Account access and security

To install Adam, you need one of the following access options on the target machines:

- Access to the root user with the root password.
- Access to the root user with an SSH key pair.
- Passwordless SSH/sudo enabled for a user account.
- Password-based SSH and passwordless sudo enabled for a user account.

The root or user credentials used for installation must be the same on all of the target nodes.

### Network

You must configure network and security settings to allow access to and from each node—for example, using IPTables or SELinux.

Anaconda platform components use the default network ports listed below. You can configure these ports when you define a cluster profile.

Platform Component	Port
Anaconda Adam (SSH)	22
Anaconda Adam (Salt)	14505
Anaconda Adam (Salt)	14506
Anaconda Adam (Salt REST API)	18000
Anaconda Enterprise Notebooks (UI)	80
Anaconda Enterprise Notebooks (Gateway)	8089
Anaconda Repository (UI)	8080
Anaconda Scale (Dask/Distributed)	8786
Anaconda Scale (Dask/Distributed UI)	8787
Anaconda Scale (Jupyter Notebook UI)	8888

Network ports with a browser user interface (UI) must be accessible by machines outside of the network of Anaconda platform nodes.

Network ports without a browser UI must be accessible between the other Anaconda platform nodes.

## Platform components

See the documentation below for information on CPU, memory and disk space requirements for Anaconda platform components.

- [Anaconda Enterprise Notebooks](#).
- [Anaconda Repository](#).
- [Anaconda Scale](#).

## Python considerations

Adam and Anaconda platform components do not affect existing framework installations of Python. Adam operates independently from the system installation of Python, while Anaconda platform components install their own versions of Python via Anaconda or Miniconda.

## Standard installation

### Downloading the Adam installer

To download the installer, run one of the commands below on the host machine where you want to manage the Anaconda platform:

```
wget https://anaconda.org/anaconda-adam/adam-installer/4.4.0/download/adam-installer-4.4.0-Linux-x86_64.sh
```

Or:

```
curl -LO https://anaconda.org/anaconda-adam/adam-installer/4.4.0/download/adam-installer-4.4.0-Linux-x86_64.sh
```

## Installing Adam

1. Run the installer, specifying the installation directory:

```
bash adam-installer-4.4.0-Linux-x86_64.sh -b -p ~/adam
```

NOTE: Replace ~/adam with the actual installation directory.

2. Add the adam command to your path by modifying the ~/.bashrc file:

```
echo -e '\n# Anaconda Adam\nexport PATH=~/.adam/bin:$PATH' >> ~/.bashrc
```

3. To activate the changes, source your ~/.bashrc file:

```
source ~/.bashrc
```

## Verifying the installation

To verify that the installation succeeded and to create configuration files in ~/.continuum/adam, run the adam command, which outputs the Adam help text:

```

$ adam
Usage: adam [OPTIONS] COMMAND [ARGS]...

Options:
  --version            Show the version and exit.
  -l, --log-level [info|debug|error]
                        Logging level [default: debug]
  -h, --help          Show this message and exit.

Commands:
  cmd                Execute a command on the nodes
  describe           Describe an Adam cluster or profile
  ec2                EC2 options
  enterprise-notebooks
                    Anaconda Enterprise Notebooks options
  info               Display Adam version, system, and
                        license information
  jupyter            Jupyter options
  kubernetes         Kubernetes options
  list               List Adam clusters and profiles
  platform           Anaconda Platform options
  provision          Provision options
  remove             Remove a cluster
  repository         Anaconda Repository options
  salt               Execute a Salt module
  scale              Anaconda Scale options
  ssh                SSH to one of the nodes (0-based
                        index)
  up                 Create a cluster from a profile

```

## Installing your Anaconda Enterprise license file

Copy your Anaconda Enterprise license file to any of the following directories:

- `~/adam/licenses/`.
- `~/continuum/`.
- Any other directory shown by the command `~/adam/bin/conda info --license`.

Adam searches all of these directories for license files named `license*.txt`.

EXAMPLE: `~/adam/licenses/license_bundle_20170428044737.txt`.

## Defining a cluster profile

1. Switch to root user and create a file with this name and path `~/continuum/adam/profile.d/profile.yaml` and the following contents:

```

name: profile
provider: bare

bare:
  username: centos
  \# password: password \# Optional
  port: 22
  keypair: ~/.ssh/my-private-key

```

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```

nodes:
- host: node1.company.com
- host: node2.company.com
- host: node3.company.com
- host: node4.company.com

security:
flush_iptables: false
selinux_context: false
selinux_permissive: false

```

2. Replace `centos` with an actual username. Verify that the username has `sudo` privileges.
3. Replace `22` with the appropriate *SSH port number*.
4. Replace `~/.ssh/my-private-key` with the location of the private SSH key (key pair) to be used. Verify that you have SSH access to all of the cluster nodes.
5. Edit the IP addresses or hostnames of the nodes in the cluster. Each host must be able to connect to the other hosts using the specified FQDN or IP address.

**TIP:** We recommend using the nodes' FQDN that matches the hostname on each machine.

**NOTE:** The first node in the list of nodes is the head node. The remaining nodes are compute nodes.

By default, the `anaconda` user/group is created across the cluster and owns the directory and files located in the root installation directory. If desired, you can *customize the cluster profile* to change these and other settings.

## Creating a cluster

To create a cluster, run:

```
adam up -n [cluster-name] [profile-name]
```

**EXAMPLE:** To create a cluster named “cluster” from a cluster profile named “profile”:

```
adam up -n cluster profile
```

## Installing platform components

After creating or *provisioning a cluster*, you can install platform components by running:

```
adam [platform-component] -n [cluster-name] install
```

**EXAMPLE:** To install Repository, Enterprise Notebooks, and Scale on a cluster named “cluster”:

```

$ adam repository -n cluster install
$ adam enterprise-notebooks -n cluster install
$ adam scale -n cluster cluster install
$ adam scale -n cluster dask install

```

## Opening a platform component

To open a platform component’s user interface in your browser, run:

```
$ adam [platform-component] -n [cluster-name] open
```

EXAMPLE: To open Repository and Enterprise Notebooks on a cluster named “cluster”:

```
$ adam repository -n cluster open
$ adam enterprise-notebooks -n cluster open
```

For more information see *Working with platform components*.

## Installing into an air gapped environment

Currently, Adam can install the remote conda management functionality in an *air gapped* environment using artifacts from Repository. In future versions of Adam, air gapped installations of all Anaconda platform components will be fully supported.

1. *Install Repository*.
2. Configure Repository for the Adam installation on the nodes:
  1. Mirror the `anaconda` and `anaconda-adam` channels onto your local Repository.
  2. Copy the latest versions of the [Anaconda](#) and [Miniconda](#) installers to the `/static/extras/` folder on the Repository web server.
3. Switch to root user and create a cluster profile at `~/.continuum/adam/profile.d/profile.yaml` with the following contents:

```
name: profile
provider: bare

bare:
  username: centos
  # password: password # Optional
  port: 22
  keypair: ~/.ssh/my-private-key
  nodes:
    - host: node1.company.com
    - host: node2.company.com
    - host: node3.company.com
    - host: node4.company.com

plugins:
  conda:
    anaconda_hash: md5=d72add23bc937ccdfc7de4f47deff843
    anaconda_url: http://local.anaconda.repository.address:8080/static/extras/
    ↪Anaconda2-4.4.0-Linux-x86_64.sh
    channel_alias: http://local.anaconda.repository.address:8080/conda/
    channels:
      - http://local.anaconda.repository.address:8080/conda/anaconda
      - http://local.anaconda.repository.address:8080/conda/anaconda-adam
    enabled: true
    miniconda_hash: md5=7097150146dd3b83c805223663ebffcc
    miniconda_url: http://local.anaconda.repository.address:8080/static/extras/
    ↪Miniconda2-4.3.21-Linux-x86_64.sh
    rootdir: /opt/continuum
    ssl_verify: False
```

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```
security:
  flush_iptables: false
  selinux_context: false
  selinux_permissive: false
```

4. Replace `centos` with an actual username. Verify that the username has `sudo` privileges.
5. Replace `22` with the appropriate *SSH port number*.
6. Replace `~/ .ssh/my-private-key` with the location of the private SSH key (`keypair`) to be used. Verify that you have SSH access to all of the cluster nodes.
7. Edit the port and IP addresses or hostnames of the nodes in the cluster.  
NOTE: The first node in the list of nodes is the head node. The remaining nodes are compute nodes.
8. Replace the `anaconda_hash` value with the hash of your Anaconda installer.
9. Replace the `miniconda_hash` value with the hash of your Miniconda installer.
10. Replace `local.anaconda.repository.address` with the address of your Repository.

## Installing into a cloud environment

Adam can be used to create cloud-based instances and install Anaconda platform components on the nodes.

Currently, Adam fully supports Amazon Elastic Compute Cloud (EC2).

To use Adam with instances that already exist on Amazon EC2, or with other cloud providers, follow the *primary installation instructions*.

Refer to the *Installation requirements* page for more information about system requirements, including networking and security requirements.

- *Downloading the Adam installer*
- *Installing Adam*
- *Verifying the installation*
- *Installing your Anaconda Enterprise license file*
- *Creating an EC2 cluster*
- *Installing platform components*
- *Opening a platform component*
- *Removing an EC2 cluster*

## Downloading the Adam installer

To download the installer, run one of the commands below on the host machine where you want to manage the Anaconda platform:

```
wget https://anaconda.org/anaconda-adam/adam-installer/4.4.0/download/adam-installer-
↳ 4.4.0-Linux-x86_64.sh
```

Or:

```
curl -LO https://anaconda.org/anaconda-adam/adam-installer/4.4.0/download/adam-  
↪installer-4.4.0-Linux-x86_64.sh
```

## Installing Adam

1. Run the installer, specifying the installation directory:

```
bash adam-installer-4.4.0-Linux-x86_64.sh -b -p ~/adam
```

NOTE: Replace ~/adam with the actual installation directory.

2. Add the adam command to your path by modifying the ~/.bashrc file:

```
echo -e '\n# Anaconda Adam\nexport PATH=~/adam/bin:$PATH' >> ~/.bashrc
```

3. To activate the changes, source your ~/.bashrc file:

```
source ~/.bashrc
```

## Verifying the installation

To verify that the installation succeeded and to create configuration files in ~/.continuum/adam, run the adam command, which outputs the Adam help text:

```
$ adam  
Usage: adam [OPTIONS] COMMAND [ARGS]...  
  
Options:  
  --version                Show the version and exit.  
  -l, --log-level [info|debug|error]  Logging level [default: debug]  
  -h, --help                Show this message and exit.  
  
Commands:  
  cmd                    Execute a command on the nodes  
  describe               Describe an Adam cluster or profile  
  ec2                    EC2 options  
  enterprise-notebooks   Anaconda Enterprise Notebooks options  
  info                   Display Adam version, system, and  
                        license information  
  jupyter                Jupyter options  
  kubernetes             Kubernetes options  
  list                   List Adam clusters and profiles  
  platform               Anaconda Platform options  
  provision               Provision options  
  remove                 Remove a cluster  
  repository             Anaconda Repository options  
  salt                   Execute a Salt module  
  scale                  Anaconda Scale options  
  ssh                    SSH to one of the nodes (0-based  
                        index)  
  up                     Create a cluster from a profile
```

## Installing your Anaconda Enterprise license file

Copy your Anaconda Enterprise license file to any of the following directories:

- `~/adam/licenses/`.
- `~/continuum/`.
- Any other directory shown by the command `~/adam/bin/conda info --license`.

Adam searches all of these directories for license files named `license*.txt`.

EXAMPLE: `~/adam/licenses/license_bundle_20170428044737.txt`.

## Creating an EC2 cluster

1. Create a file named `~/aws/credentials` that contains your AWS credentials:

```
[default]
aws_access_key_id = your-access-key
aws_secret_access_key = your-secret-key
region = us-east-1
```

NOTE: Replace `your-access-key`, `your-secret-key`, and `us-east-1` with your actual AWS access key ID, your AWS secret access key, and your default region. Region is optional. For more information about configuring your AWS credentials, see the [Boto documentation](#).

2. Create a cluster on EC2 by running:

```
adam ec2 -n mycluster up --keyname my_keypair --keypair ~/.ssh/my_keypair.pem
```

NOTE: Replace “mycluster” with the name you wish to give the new cluster. Replace “my\_keypair” with the keyname on the EC2 console. Replace `~/ssh/my_keypair.pem` with the path to the keypair that matches the keyname.

keyname and keypair are required.

OPTIONAL: You can also specify the AMI, number of nodes, instance types and more. To see the available options, run `adam ec2 up --help`:

```
$ adam ec2 -n cluster up --help
Usage: adam ec2 up [OPTIONS]

Options:
  --keyname TEXT           Keyname on EC2 console
                           [required]
  --keypair PATH           Path to the keypair that
                           matches the keyname
                           [required]
  --vpc-id TEXT            EC2 VPC ID
  --subnet-id TEXT         EC2 Subnet ID on the VPC
  --region-name TEXT       AWS region [default:
                           us-east-1]
  --ami TEXT               EC2 AMI [default:
                           ami-d05e75b8]
  --username TEXT          User to SSH to the AMI
                           [default: ubuntu]
  --type TEXT              EC2 Instance Type
```

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```

                                [default: m4.xlarge]
--count INTEGER                Number of nodes
                                [default: 4]
--security-group TEXT          Security Group Name
                                [default: adam-default]
--volume-type TEXT             Root volume type
                                [default: gp2]
--volume-size INTEGER          Root volume size (GB)
                                [default: 500]
-t, --tag TEXT                 Extra tags to add to the
                                instances
--check-ami / --no-check-ami   Whether or not to check
                                the AMI [default: True]
--provision / --no-provision   Provision salt on the
                                nodes [default: True]
-y, --yes                      Answers yes to questions
-h, --help                    Show this message and exit.
```

## Installing platform components

After creating or *provisioning a cluster*, you can install platform components by running:

```
adam [platform-component] -n [cluster-name] install
```

EXAMPLE: To install Repository, Enterprise Notebooks, and Scale on a cluster named “cluster”:

```
$ adam repository -n cluster install
$ adam enterprise-notebooks -n cluster install
$ adam scale -n cluster cluster install
$ adam scale -n cluster dask install
```

## Opening a platform component

To open a platform component’s user interface in your browser, run:

```
adam [platform-component] -n [cluster-name] open
```

EXAMPLE: To open Repository and Enterprise Notebooks on a cluster named “cluster”:

```
$ adam repository -n cluster open
$ adam enterprise-notebooks -n cluster open
```

For more information see *Working with platform components*.

## Removing an EC2 cluster

To remove an EC2 cluster and terminate the corresponding instances:

1. Run:

```
adam ec2 -n [cluster-name] destroy
```

2. When prompted, type `y`.

EXAMPLE: To remove the cluster named “cluster”:

```
$ adam ec2 -n cluster destroy
Are you sure you want to destroy the cluster cluster?
[y/N]: y
```

The installation process described in the pages above is appropriate for most environments and use cases. However, if you want to customize Anaconda platform settings related to security, network, installation paths, or other settings, please see [Customizing a cluster profile](#).

## User guide

### Concepts

Anaconda platform components run on clusters, which are groups of machines listed in a cluster profile.

### Cluster profile

A cluster profile defines the cluster’s name, its machine nodes and other options such as security and network settings.

One or more cluster profiles are defined during Adam [installation](#), just before creating the cluster.

Cluster profiles are located in the `~/.continuum/adam/profile.d/` directory.

### Cluster definition

A cluster definition identifies information about a running cluster, including the cluster name, nodes in the cluster and other platform component options. Cluster definitions are located in the `~/.continuum/adam/cluster.d/` directory.

### Air gap installation

Installation in an environment without connectivity to the internet for security reasons.

### Getting started

Running the `adam` command shows the options and subcommands that you can use:

```
$ adam
Usage: adam [OPTIONS] COMMAND [ARGS]...

Options:
  --version                Show the version and exit.
  -l, --log-level [info|debug|error]
                           Logging level [default: debug]
  -h, --help                Show this message and exit.

Commands:
  cmd                      Execute a command on the nodes
```

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describe	Describe an Adam cluster or profile
ec2	EC2 options
enterprise-notebooks	Anaconda Enterprise Notebooks options
info	Display Adam version, system, and license information
list	List Adam clusters and profiles
provision	Provision options
remove	Remove a cluster
repository	Anaconda Repository options
salt	Execute a Salt module
scale	Anaconda Scale options
ssh	SSH to one of the nodes (0-based index)
up	Create a cluster from a profile

To see more information about a subcommand, add the `-h` or `--help` option after the subcommand.

EXAMPLE: `adam up --help`.

For details on using the various subcommands, see [Tasks](#).

For information on installing Adam, creating a cluster, and installing and managing platform components, see the [installation guide](#).

## Tasks

### Working with cluster profiles

After installing Anaconda Adam and before creating clusters, you must define one or more cluster profiles.

NOTE: An *air gapped machine* needs additional setup and a special cluster profile.

### Customizing a cluster profile

Although the default cluster profile described in the [installation guide](#) is appropriate for most environments and use cases, you can customize profile settings as needed.

**Cluster profiles** are used to define information about a cluster before it is created, including the cluster name, nodes in the cluster, and other platform component options. Cluster files are located in the `~/.continuum/adam/profile.d/` directory.

**Cluster definitions** are used to identify information about a running cluster, including the cluster name, nodes in the cluster, and other platform component options. Cluster definitions are located in the `~/.continuum/adam/cluster.d/` directory.

- *Sample profile showing all settings*
- *Cluster name*
- *SSH authentication*
- *Node specification*
- *Security settings*

- *Network settings—proxy configuration*
- *Conda settings*
- *Salt settings*
- *System settings*

## Sample profile showing all settings

A cluster profile located at `~/.continuum/adam/profile.d/cluster.yaml` with all configurable settings is shown below:

```
name: cluster
provider: bare

bare:
  username: centos
  # password: anaconda # Optional
  port: 22
  keypair: ~/.ssh/my-private-key
  nodes:
    - host: node1.company.com
    - host: node2.company.com
    - host: node3.company.com
    - host: node4.company.com

security:
  flush_iptables: false
  selinux_context: false
  selinux_permissive: false

network:
  http_proxy: http://server:port/
  # https_proxy: http://server:port/

system:
  tmp_dir: /tmp

plugins:
  conda:
    anaconda_hash: md5=d72add23bc937ccdfc7de4f47deff843
    anaconda_url: http://repo.anaconda.com/archive/Anaconda2-4.4.0-Linux-x86_64.sh
    channel_alias: https://conda.anaconda.org/
    channels:
      - defaults
      - anaconda-adam
    conda_canary: false
    enabled: true
    miniconda_hash: md5=7097150146dd3b83c805223663ebffcc
    miniconda_url: http://repo.anaconda.com/miniconda/Miniconda2-4.3.21-Linux-x86_64.
  ↪ sh
    rootdir: /opt/continuum
    ssl_verify: False

dask:
```

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```
bokeh_port: 8787
bokeh_whitelist: '*'
enabled: false
host: 0.0.0.0
http_port: 9786
nprocs: 1
port: 8786

enterprise-notebooks:
  admin_email: admin@yourdomain.com
  admin_password: anaconda
  admin_user: wakari
  directory: /opt/wakari
  elasticsearch_fn: elasticsearch-1.7.2.noarch.rpm
  enabled: false
  enterprise_notebooks_version: 4.0.0
  gateway_port: 8089
  java_fn: jre-8u65-linux-x64.rpm
  mongodb_fn: mongodb-org-2.6.8-1.x86_64.rpm
  mongodb_mongos_fn: mongodb-org-mongos-2.6.8-1.x86_64.rpm
  mongodb_server_fn: mongodb-org-server-2.6.8-1.x86_64.rpm
  mongodb_shell_fn: mongodb-org-shell-2.6.8-1.x86_64.rpm
  mongodb_tools_fn: mongodb-org-tools-2.6.8-1.x86_64.rpm
  mongodb_version: 2.6.8
  nginx_fn: nginx-1.6.2-1.el6ngx.x86_64.rpm
  root_download_url: https://820451f3d8380952ce65-4cc6343b423784e82fd202bb87cf87cf.
    ↪ssl.cf1.rackcdn.com/
  user: wakari

jupyter:
  dashboards_server:
    enabled: false
    ip: 0.0.0.0
    port: 3000
    user: anaconda
  enabled: false
  kernel_gateway:
    enabled: false
    ip: 0.0.0.0
    port: 7000
    user: anaconda
  notebook:
    directory: ~/notebooks
    enabled: false
    ip: 0.0.0.0
    password: 'anaconda'
    port: 8888
    user: anaconda

repository:
  binstar_server_version: 2.21.0
  channel: main
  email: youremail@anaconda.com
  enabled: false
  mongodb_fn: mongodb-org-2.6.8-1.x86_64.rpm
  mongodb_mongos_fn: mongodb-org-mongos-2.6.8-1.x86_64.rpm
  mongodb_server_fn: mongodb-org-server-2.6.8-1.x86_64.rpm
```

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```

mongodb_shell_fn: mongodb-org-shell-2.6.8-1.x86_64.rpm
mongodb_tools_fn: mongodb-org-tools-2.6.8-1.x86_64.rpm
mongodb_version: 2.6.9
password: anaconda
port: 8080
root_download_url: https://820451f3d8380952ce65-4cc6343b423784e82fd202bb87cf87cf.
↪ssl.cf1.rackcdn.com/
server_user: anaconda-server
superuser: superuser
token: qu-a49e2e69-1047-4eab-a879-a2ee9c198381

salt_settings:
  acl:
    - anaconda
  job_pub_port: 14505
  minion_pub_port: 14510
  minion_pull_port: 14511
  minion_ret_port: 14506
  rest_port: 18000
  salt_groupname: anaconda
  salt_password: anaconda
  salt_username: anaconda
  service_scripts: false

```

## Cluster name

The name setting specifies the name of the cluster and is used by the `-n` option in Anaconda Adam commands.

EXAMPLE: To create a new cluster named “cluster” from a profile named “profile”:

```
$ adam up -n cluster profile
```

## SSH authentication

To connect to remote machines via SSH, Adam requires a valid username, port—default is 22—and an authentication method. Adam supports the following SSH authentication methods:

- Password.
- Key pair—full path to your private key.
- Encrypted key pair—full path to your public key and ssh-agent. The private key must first be added to a running ssh-agent. Use the `agent_pubkey` setting to specify the full path to the associated public key.

For more information about system and account requirements, see [Account access and security](#).

EXAMPLE: To use SSH with a username and password:

```

bare:
  username: centos
  password: anaconda

```

EXAMPLE: To use SSH with a key pair:

```
bare:
  username: centos
  keypair: /full/path/to/key.rsa
```

EXAMPLE: To use SSH with an encrypted key pair:

```
bare:
  username: centos
  agent_pubkey: /full/path/to/key.pub
```

### Node specification

The `nodes` setting defines the nodes that exist within the cluster. By default, the first node in the list of nodes is defined as the head node and the remaining nodes are defined as compute nodes.

Each host must be able to connect to the other hosts via the specified FQDN or IP address.

TIP: We recommended using the node's FQDN that matches the hostname on each machine:

EXAMPLE:

```
bare:
  nodes:
    - host: node1.company.com
    - host: node2.company.com
    - host: node3.company.com
    - host: node4.company.com
```

### Security settings

The `security` settings let you configure IPTables and SELinux.

To flush iptables, reset `flush_iptables` to `true`. Default value: `false`.

```
security:
  flush_iptables: false
```

To set SELinux to permissive, reset `selinux_permissive` to `true`. Default value: `false`.

```
security:
  selinux_permissive: false
```

To set SELinux contexts, reset `selinux_context` to `true`. Default value: `false`.

```
security:
  selinux_context: false
```

### Network settings—proxy configuration

The `network` settings let you install Adam to nodes that access the internet via an HTTP or HTTPS proxy.

To specify an HTTP proxy:

```
network:
  http_proxy: http://server:port/
```

NOTE: Replace `server:port` with the actual server and port.

To specify an HTTPS proxy:

```
network:
  https_proxy: http://server:port/
```

NOTE: Replace `server:port` with the actual server and port.

## Conda settings

These are the default settings for configuring conda:

```
conda:
  anaconda_hash: md5=d72add23bc937ccdfc7de4f47deff843
  anaconda_url: http://repo.anaconda.com/archive/Anaconda2-4.4.0-Linux-x86_64.sh
  channel_alias: https://conda.anaconda.org/
  channels:
    - defaults
    - anaconda-adam
  enabled: true
  miniconda_hash: md5=7097150146dd3b83c805223663ebffcc
  miniconda_url: http://repo.anaconda.com/miniconda/Miniconda2-4.3.21-Linux-x86_64.
↪ sh
  rootdir: /opt/continuum
  ssl_verify: False
```

You can set `ssl_verify` to:

- `False`—no SSL verification—default.
- `True`—SSL verification is used and conda verifies certificates for SSL connections.
- `[cert path]`—the string path to a certificate to be used to verify SSL connections.

## Salt settings

Salt is the configuration management system used by Adam. The `salt_settings` let you configure the network options, access control list and API user credentials used by Salt.

Use the settings below to specify the ports used by the Salt master, minions and REST API:

```
plugins:
  salt_settings:
    job_pub_port: 14505
    minion_pub_port: 14510
    minion_pull_port: 14511
    minion_ret_port: 14506
    rest_port: 18000
```

Use the `acl` setting to specify an access control list that defines non-root system users who can execute Salt commands:

```
plugins:
  salt_settings:
    acl:
      - anaconda
```

Use the settings below to specify the username, password and group that gets created across the cluster and owns the directory and files located in the root installation directory—default: `/opt/continuum`:

```
plugins:
  salt_settings:
    salt_username: anaconda
    salt_password: anaconda
    salt_groupname: anaconda
```

If you do not want to store a clear text password in the cluster profile or cluster definition file, set `salt_password` to an empty string:

```
plugins:
  salt_settings:
    salt_username: anaconda
    salt_password: ''
    salt_groupname: anaconda
```

In this case, Adam prompts for a password in the CLI and only stores the password in memory for the duration of the command or job.

### System settings

The `tmp_dir` setting lets you specify the download directory where temporary installers are downloaded—default: `/tmp`:

```
system:
  tmp_dir: /tmp
```

### Viewing cluster profile information

To view a list of cluster profiles, run `adam list profiles`:

```
$ adam list profiles
profile
second-profile
third-profile
```

To view more detailed information about a profile, run:

```
$ adam describe -p [profile-name]
```

You may also use the `--verbose` flag for increased detail.

EXAMPLE: To view verbose information about the profile named “profile”:

```
$ adam describe -p profile --verbose
bare:
  keypair: ~/.ssh/my_keypair.pem
```

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```

nodes:
- host: 192.168.1.1
- host: 192.168.1.2
- host: 192.168.1.3
- host: 192.168.1.4
port: 22
username: centos
name: cluster
provider: bare
security:
  flush_iptables: false
  selinux_context: false
  selinux_permissive: false

```

## Working with clusters

Defining one or more cluster profiles and creating clusters are described in the *installation guide*.

## Provisioning a cluster

To provision or reprovision an existing cluster, run:

```
$ adam provision -n [cluster-name]
```

EXAMPLE: To provision the cluster named “cluster”:

```
$ adam provision -n cluster
```

## Customizing the provision command—advanced

By default, the `adam provision` command:

- Checks SSH connectivity.
- Creates a default user.
- Installs Salt.
- Syncs formulas.
- Provisions enabled plugins and security settings that are defined in the cluster’s profile.

To run only a portion of this provisioning process, use `adam provision` options and subcommands to control what happens during provisioning.

Run `adam provision --help` to see the available options and subcommands:

```

$ adam provision --help
Usage: adam provision [OPTIONS] COMMAND [ARGS]...

Execute all the provisioning steps for a cluster

See subcommands help for more info. Usage: adam provision -n

```

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```
Options:
  -n, --cluster TEXT      Cluster name [required]
  --flush-iptables        Flush IPTables [default: False]
  --selinux-permissive    Set SELinux to permissive [default:
                          False]
  --selinux-context       Set SELinux contexts [default: False]
  --plugins               Install enabled plugins on provision
                          [default: False]
  -h, --help              Show this message and exit.

Commands:
  anaconda-user           Create the default anaconda user in all
                          the nodes
  check-ssh               Check SSH connection to the nodes
  flush-iptables          Flush IPTables
  plugins                 Provision enabled plugins
  roles                   Set roles on the cluster nodes
  salt                    Provision Salt
  security-settings       Execute the security settings
  selinux-context         Set SELinux contexts
  selinux-permissive      Set SELinux to permissive
  sync                    Sync formulas and settings
```

**EXAMPLE:** To check SSH connectivity to all of the nodes in an existing cluster:

```
$ adam provision -n cluster check-ssh
Checking SSH connection to nodes
2016-10-03 22:10:49,327 - adam.models - DEBUG - Checking ssh
connection for 54.88.20.164
2016-10-03 22:10:50,905 - adam.models - DEBUG - SSH
connection to 54.88.20.164: OK
2016-10-03 22:10:51,008 - adam.models - DEBUG - Checking ssh
connection for 52.90.168.130
2016-10-03 22:10:51,996 - adam.models - DEBUG - SSH
connection to 52.90.168.130: OK
+-----+-----+
| Node IP      | SSH Available |
+-----+-----+
| 54.88.20.164 | True          |
| 52.90.168.130 | True          |
+-----+-----+
| All nodes    | True          |
+-----+-----+
```

## Viewing cluster information

To view a list of running clusters, run `adam list`:

```
$ adam list
cluster
second-cluster
third-cluster
```

To view detailed information about a cluster, run:

```
$ adam describe -n [cluster-name]
```

EXAMPLE: To view information about the cluster named “cluster”:

```
$ adam describe -n cluster
conda:
  anaconda_hash: md5=7097150146dd3b83c805223663ebffcc
  anaconda_url: https://repo.anaconda.com/miniconda/Miniconda2-4.3.21-Linux-x86_64.sh
↪ #adam-ci
  enabled: true
  rootdir: /opt/continuum
name: cluster
nodes:
- host: ci_head_1
  keypair: ~/.ssh/my_private_key
  port: 22
  username: root
- host: ci_compute_1
  keypair: ~/.ssh/my_private_key
  port: 22
  username: root
```

## Adding nodes to an existing cluster

1. In the existing cluster profile, add `host` lines to specify the additional node(s).

EXAMPLE: You have this existing cluster profile, `~/.continuum/adam/profile.d/profile.yaml`:

```
name: profile
provider: bare

bare:
  username: centos
  # password: password # Optional
  port: 22
  keypair: ~/.ssh/my-private-key
  nodes:
  - host: node1.company.com
  - host: node2.company.com
  - host: node3.company.com
  - host: node4.company.com
```

You want to add the following nodes:

- node10.company.com
- node11.company.com
- node12.company.com

Assuming these nodes use the same authentication mode as the existing nodes, add a `host` line for each node:

```
name: profile
provider: bare

bare:
  username: centos
```

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```
# password: password # Optional
port: 22
keypair: ~/.ssh/my-private-key
nodes:
- host: node1.company.com
- host: node2.company.com
- host: node3.company.com
- host: node4.company.com
- host: node10.company.com
- host: node11.company.com
- host: node12.company.com
```

2. Run the `adam up` command to provision the cluster.

EXAMPLE: To use the profile named “profile” to provision the cluster named “cluster”, run:

```
$ adam up -n cluster profile
```

You are prompted to overwrite the cluster definition file located at `~/.continuum/adam/cluster.d/cluster.yaml` to include the newly defined nodes.

During the provisioning process, Adam will install on the new nodes and will not reinstall on the previously defined nodes.

## Managing Anaconda across a cluster

Using Anaconda Scale, you can create and manage conda packages, including Python and R, in multiple conda environments across your nodes.

For more information about installing and managing Anaconda across a cluster, see [Anaconda Scale](#).

## Using SSH to connect to nodes

To SSH to the head node in a cluster, run:

```
$ adam ssh -n [cluster-name]
```

EXAMPLE: To SSH to the head node in a cluster named “cluster”:

```
$ adam ssh -n cluster
Last login: Wed Jun 29 03:08:49 2016 from 172.18.0.1
[root@192.168.1.1 ~]#
```

To connect to a specific node, include the node number after the cluster name. Node 0 is the head node, node 1 is the first compute node, and so on.

EXAMPLE: To SSH to the second compute node in a cluster named “cluster”:

```
$ adam ssh -n cluster 2
Last login: Wed Jun 29 03:10:14 2016 from 172.18.0.1
[root@192.168.1.3 ~]#
```



## Running remote commands

To execute remote commands on a cluster, run:

```
$ adam cmd -n [cluster-name] -t [target-nodes] [command]
```

EXAMPLE: To run the `date` command on all nodes in a cluster named “cluster”:

```
$ adam cmd -n cluster date
192.168.1.1: Wed Jun 29 03:08:10 UTC 2016
192.168.1.2: Wed Jun 29 03:08:10 UTC 2016
192.168.1.3: Wed Jun 29 03:08:10 UTC 2016
192.168.1.4: Wed Jun 29 03:08:10 UTC 2016
```

## Executing Salt modules

To execute Salt modules, run:

```
$ adam salt -n [cluster-name] [nodes] [module-name]
```

EXAMPLE: To execute the “test.ping” Salt module on all nodes in a cluster named “cluster”:

```
$ adam salt -n cluster '*' test.ping
192.168.1.1: true
192.168.1.2: true
192.168.1.3: true
192.168.1.4: true
```

## Removing a cluster

To remove the cluster definition file for an existing bare-metal cluster:

1. Run:

```
$ adam remove -n [cluster-name]
```

2. When prompted, type `y`.

EXAMPLE: To remove the cluster named “cluster”:

```
$ adam remove -n cluster
Are you sure you want to remove the cluster cluster? [y/N]: y
```

To remove an EC2 cluster, see the removal instructions at the end of the [cloud installation guide](#).

## Working with platform components

- [Overview](#)
- [Viewing a platform component’s status](#)
- [Stopping services for a platform component](#)

- *Restarting services for a platform component*

### Overview

Using Anaconda Adam, you can install and manage the Anaconda platform components listed below. An Adam command for managing an Anaconda component has the format:

```
$ adam [platform-component] [command]
```

Platform component	Adam Command Prefix
Anaconda Enterprise Notebooks	adam enterprise-notebooks
Anaconda Repository	adam repository
Anaconda Scale	adam scale

You can also use Adam to install and manage the Anaconda platform on *Amazon EC2 cloud-based nodes* and *air gapped machines*.

### Default usernames and passwords

The default administrator usernames and passwords for each platform component are:

Platform component	Username	Password
Anaconda Enterprise Notebooks	wakari	anaconda
Anaconda Repository	superuser	anaconda
Jupyter Notebook	-	anaconda

### Platform component documentation

For more information on a platform component, see:

- *Anaconda Enterprise Notebooks*.
- *Anaconda Repository*.
- *Anaconda Scale*.

### Viewing a platform component's status

To view the status of a platform component, run:

```
$ adam [platform-component] -n [cluster-name] status
```

EXAMPLE: To view the status of Repository on a cluster named “cluster”:

```
$ adam repository -n cluster status
```

## Stopping services for a platform component

To stop services related to a platform component, run:

```
$ adam [platform-component] -n [cluster-name] stop
```

EXAMPLE: To stop Repository services on a cluster named “cluster”:

```
$ adam repository -n cluster stop
```

## Restarting services for a platform component

To restart services related to a platform component, run:

```
$ adam [platform-component] -n [cluster-name] restart
```

EXAMPLE: To restart Repository services on a cluster named “cluster”:

```
$ adam repository -n cluster restart
```

## Viewing your Adam version and license

To view version and license information, run `adam info`:

```
$ adam info
Adam version: 4.1.0
Plugins:
  adam_enterprise_notebooks: 4.1.0
  adam_repository: 4.1.0
  adam_notebook: 4.1.0
  adam_dask: 4.1.0

Platform: Darwin-15.6.0-x86_64
Darwin Kernel Version 15.6.0: Thu Jun 23 18:25:34 PDT 2016;
root:xnu-3248.60.10~1/RELEASE_X86_64
Python version: 3.5.1 |Continuum Analytics, Inc.| (default,
Dec 7 2015, 11:24:55)
[GCC 4.2.1 (Apple Inc. build 5577)]
Processor: i386
Byte-ordering: little

License information:
Number of nodes currently in use: 14
Number of licensed nodes: 16
Number of managed clusters: 2

Valid platform component licenses:
1: Anaconda Repository Enterprise. End date: 2018-05-24
2: Anaconda Cluster. End date: 2018-05-24
3: Wakari Enterprise. End date: 2018-05-24
4: MKL Optimizations. End date: 2018-05-24
5: IOPro. End date: 2018-05-24
6: Accelerate. End date: 2018-05-24
```

### Updating Adam

To update Anaconda Adam to a newer version:

1. Delete the existing Adam installation directory. By default, this is `~/adam`.

NOTE: *Cluster profile* and *cluster definition* files are stored in `~/.continuum/adam`, which is preserved during the update process.

2. *Re-install Adam.*

### Troubleshooting

- *Errors when creating or provisioning a cluster*
- *Error: unsupported or unrecognized field*

### Errors when creating or provisioning a cluster

You get errors when you run `adam up` to create a cluster or `adam provision` to provision a cluster.

#### Cause

These errors may be caused by an invalid SSH private key or incorrect settings in a cluster profile.

#### Solution

Verify the following:

- The contents of your SSH private key are correct and, on Mac/Linux, set to 600 permissions.
- The user name in the cluster profile, such as `username: centos`, is defined correctly.
- The cluster profile settings are defined correctly in `~/.continuum/adam/profile.d/<profile_name>.yaml`.

### Error: unsupported or unrecognized field

When running Adam commands, you get an error similar to the following:

```
2016-12-05 11:09:50,120 - adam.config - ERROR - {'notebook':  
'Rogue field'}  
Error: One or more fields is not supported or recognized by  
this version of Anaconda Adam. Correct or remove the  
unsupported field in the cluster YAML profile or cluster  
definition YAML file, and try the operation again. See the  
above errors for more details: {'notebook': 'Rogue field'}
```

## Cause

There is an unsupported or unrecognized field in a cluster profile or definition file. If you have updated to a newer version of Adam, some fields in the cluster profile or cluster definition file may have been renamed or removed between versions.

## Solution

1. In the cluster profile file in the `~/ .continuum/adam/profile.d` directory or the cluster definition file in the `~/ .continuum/adam/cluster.d` directory, remove or rename the field shown in the error.
2. Retry the command.

## FAQs

- *Does Anaconda Adam work with a cluster that already has a managed Spark/Hadoop stack?*
- *Which cloud providers does Adam support?*
- *Can I use Adam with a different cloud provider?*
- *Which network ports need to be accessible from the client machine and cluster nodes?*

### Does Anaconda Adam work with a cluster that already has a managed Spark/Hadoop stack?

Yes, you can install Adam alongside existing Hadoop distributions such as Cloudera CDH or Hortonworks HDP. You can use Adam to manage Python and R conda packages and environments across a cluster.

### Which cloud providers does Adam support?

Currently, Adam offers full support for Amazon Elastic Compute Cloud (EC2).

### Can I use Adam with a different cloud provider?

Yes, you can manually create instances on another cloud provider and then provision the nodes. For more information, see [Tasks](#).

### Which network ports need to be accessible from the client machine and cluster nodes?

For communication between the cluster nodes, ports 22, 4505 and 4506 are used to provision the cluster via SSH and Salt.

## Help and support

Priority support is included with the purchase of an Anaconda subscription. Visit the [support](#) section of our website for documentation and contact information for support.

### Training and consulting

Training and consulting are available for the Anaconda platform and all Anaconda platform components. For more information, contact [sales@anaconda.com](mailto:sales@anaconda.com).

### Release notes

Below is a summary of platform component updates, features, bug fixes, and backend improvements for each Anaconda Adam release.

- *Anaconda Adam 4.4.0*
- *Anaconda Adam 4.2.14*
- *Anaconda Adam 4.2.13*
- *Anaconda Adam 4.2.12*
- *Anaconda Adam 4.2.11*
- *Anaconda Adam 4.2.10*
- *Anaconda Adam 4.2.9*
- *Anaconda Adam 4.2.8*
- *Anaconda Adam 4.2.7*
- *Anaconda Adam 4.2.6*
- *Anaconda Adam 4.2.5*
- *Anaconda Adam 4.2.4*
- *Anaconda Adam 4.2.3*
- *Anaconda Adam 4.2.2*
- *Anaconda Adam 4.2.1*
- *Anaconda Adam 4.2.0*
- *Anaconda Adam 4.1.2*
- *Anaconda Adam 4.1.1*
- *Anaconda Adam 4.1.0*
- *Anaconda Adam 4.0.1*
- *Anaconda Adam 4.0.0*
- *Anaconda Adam 1.6.2*
- *Anaconda Adam 1.6.0*
- *Anaconda Adam 1.5.5*
- *Anaconda Adam 1.5.4*
- *Anaconda Adam 1.5.3*
- *Anaconda Adam 1.5.1*
- *Anaconda Adam 1.5.0*

- *Anaconda Adam 1.4.2*
- *Anaconda Adam 1.4.1*
- *Anaconda Adam 1.4.0*

## Anaconda Adam 4.4.0

Released: June 20, 2017

Platform Component	Version	Plugin Version
Anaconda/Miniconda	4.4.0/4.3.21	-
Anaconda Enterprise Notebooks	4.1.2	4.2.14
Anaconda Repository	2.30.3	4.4.0
Anaconda Scale (Dask/Distributed)	0.15.0/1.17.1	4.4.0
Anaconda Scale (Jupyter Notebook)	5.0.0	4.2.14

Download Anaconda Adam:

- Link: [https://anaconda.org/anaconda-adam/adam-installer/4.4.0/download/adam-installer-4.4.0-Linux-x86\\_64.sh](https://anaconda.org/anaconda-adam/adam-installer/4.4.0/download/adam-installer-4.4.0-Linux-x86_64.sh)
- MD5: 64cc02dcaaf7829144cd82db786ab775
- SHA256: 663e2f93177830badadf5dea6647cb0e3d5376770999b85bb02d535d13cfac6d

Platform Component Updates:

- Updated to Anaconda 4.4.0 (conda 4.3.21)
- Updated to Miniconda 4.3.21 (conda 4.3.21)
- Updated to Anaconda Repository 2.30.3
- Updated to Dask 0.15.0 and Distributed 1.17.1

## Anaconda Adam 4.2.14

Released: April 28, 2017

Platform Component	Version	Plugin Version
Anaconda/Miniconda	4.2.0/4.2.12	-
Anaconda Enterprise Notebooks	4.1.2	4.2.14
Anaconda Repository	2.29.1	4.2.14
Anaconda Scale (Dask/Distributed)	0.14.1/1.16.1	4.2.14
Anaconda Scale (Jupyter Notebook)	5.0.0	4.2.14

Download Anaconda Adam:

- Link: [https://anaconda.org/anaconda-adam/adam-installer/4.2.14/download/adam-installer-4.2.14-Linux-x86\\_64.sh](https://anaconda.org/anaconda-adam/adam-installer/4.2.14/download/adam-installer-4.2.14-Linux-x86_64.sh)
- MD5: 3fd72336d12ee635323d3f3541cce1c0
- SHA256: 43275084838a698fee7329651d55b20b3087037cc14bec04e27d6d985d402fbd

Platform Component Updates:

- Updated to Anaconda Enterprise Notebooks 4.1.2
- Updated to Anaconda Repository 2.29.1
- Updated to Dask 0.14.1 and Distributed 1.16.1
- Updated to Jupyter Notebook 5.0.0

### Anaconda Adam 4.2.13

Released: March 2, 2017

Platform component	Version	Plugin version
Anaconda/Miniconda	4.2.0/4.2.12	-
Anaconda Enterprise Notebooks	4.1.1	4.2.11
Anaconda Repository	2.27.2	4.2.13
Anaconda Scale (Dask/Distributed)	0.14.0/1.16.0	4.2.13
Anaconda Scale (Jupyter Notebook)	4.3.1	4.2.11

### Platform component updates

- Updated to Anaconda Repository 2.27.2.
- Updated to Dask 0.14.0 and Distributed 1.16.0.

### Download Adam

- Link: [https://anaconda.org/anaconda-adam/adam-installer/4.2.13/download/adam-installer-4.2.13-Linux-x86\\_64.sh](https://anaconda.org/anaconda-adam/adam-installer/4.2.13/download/adam-installer-4.2.13-Linux-x86_64.sh).
- MD5: a49e1a0c16b00deaaff5d33b8663e8a5.
- SHA256: 4d38ea7fca4e8d872bd64bfa80ecd641cfeaf9aac342d00d3e90b46914268c29.

### Anaconda Adam 4.2.12

Released: February 3, 2017

Platform component	Version	Plugin version
Anaconda/Miniconda	4.2.0/4.2.12	-
Anaconda Enterprise Notebooks	4.1.1	4.2.11
Anaconda Repository	2.26.3	4.2.11
Anaconda Scale (Dask/Distributed)	0.13.0/1.15.0	4.2.11
Anaconda Scale (Jupyter Notebook)	4.3.1	4.2.11

### Bug fixes

Fixed Anaconda/Miniconda download links to be compatible with new `repo.anaconda.com` CDN.



## Download Adam

- Link: [https://anaconda.org/anaconda-adam/adam-installer/4.2.12/download/adam-installer-4.2.12-Linux-x86\\_64.sh](https://anaconda.org/anaconda-adam/adam-installer/4.2.12/download/adam-installer-4.2.12-Linux-x86_64.sh).
- MD5: b119e123b563b3c6ad659835afeec9f1.
- SHA256: fd595b2eee304be5949a22e52d5cf2ee7fd41f8dcdded6700ecf525746a846e19.

## Anaconda Adam 4.2.11

Released: January 16, 2017

Platform component	Version	Plugin version
Anaconda/Miniconda	4.2.0/4.2.12	-
Anaconda Enterprise Notebooks	4.1.1	4.2.11
Anaconda Repository	2.26.3	4.2.11
Anaconda Scale (Dask/Distributed)	0.13.0/1.15.0	4.2.11
Anaconda Scale (Jupyter Notebook)	4.3.1	4.2.11

## Features

Implemented default password in Jupyter Notebooks.

## Backend improvements

- Disable automatic updates of conda.
- Updates for compatibility with conda 4.3.x features.

## Platform component updates

- Updated to Anaconda Enterprise Notebooks 4.1.1.
- Updated to Anaconda Repository 2.26.3.
- Updated to Dask 0.13.0 and Distributed 1.15.0.
- Updated to Jupyter Notebook 4.3.1.
- Removed Anaconda Accelerate as a standalone platform component (now installed as part of Anaconda Scale).

## Download Adam

- Link: [https://anaconda.org/anaconda-adam/adam-installer/4.2.11/download/adam-installer-4.2.11-Linux-x86\\_64.sh](https://anaconda.org/anaconda-adam/adam-installer/4.2.11/download/adam-installer-4.2.11-Linux-x86_64.sh).
- MD5: a6e4406c1552ff1e8ee91aff98ed9b3d.
- SHA256: 6a49fa7e6f3d9912bbc3b3986a7b4516a98d2544e6d032242256e6630aea9f28.

## Anaconda Adam 4.2.10

Released: December 5, 2016

Platform component	Version	Plugin version
Anaconda/Miniconda	4.2.0/4.2.12	-
Anaconda Accelerate	2.3.0	4.2.7
Anaconda Enterprise Notebooks	4.1.0	4.2.4
Anaconda Repository	2.25.1	4.2.10
Anaconda Scale (Dask/Distributed)	0.12.0/1.14.3	4.2.10
Anaconda Scale (Jupyter Notebook)	4.2.3	4.2.7

### Platform component updates

- Updated to Anaconda Repository 2.25.1.
- Updated to Dask 0.12.0 and Distributed 1.14.3.
- Removed Anaconda Mosaic.

### Download Adam

- Link: [https://anaconda.org/anaconda-adam/adam-installer/4.2.10/download/adam-installer-4.2.10-Linux-x86\\_64.sh](https://anaconda.org/anaconda-adam/adam-installer/4.2.10/download/adam-installer-4.2.10-Linux-x86_64.sh).
- MD5: 4ec7e5aae0a6913ab8f14498ba657b7b.
- SHA256: 15a843ec115f413167bad2ef6fe1b4aa7752e74ad8816a0f911042a5626c239a.

## Anaconda Adam 4.2.9

Released: November 29, 2016

Platform component	Version	Plugin version
Anaconda/Miniconda	4.2.0/4.2.12	-
Anaconda Accelerate	2.3.0	4.2.7
Anaconda Enterprise Notebooks	4.1.0	4.2.4
Anaconda Mosaic	1.3.1	4.2.7
Anaconda Repository	2.23.1	4.2.4
Anaconda Scale (Dask/Distributed)	0.11.1/1.13.3	4.2.7
Anaconda Scale (Jupyter Notebook)	4.2.3	4.2.7

### Bug fixes

Fixed scripts that were not included in the release bundle (required for `service_scripts` setting).

## Download Adam

- Link: [https://anaconda.org/anaconda-adam/adam-installer/4.2.9/download/adam-installer-4.2.9-Linux-x86\\_64.sh](https://anaconda.org/anaconda-adam/adam-installer/4.2.9/download/adam-installer-4.2.9-Linux-x86_64.sh).
- MD5: c1a5c61c0ae9e37686f9d3fb3670aa18.
- SHA256: 90cb740f04ec5ac78b65c4574b0d4238eb5c8e913ddaec49c27dcb820665bd00.

## Anaconda Adam 4.2.8

Released: November 29, 2016

Platform component	Version	Plugin version
Anaconda/Miniconda	4.2.0/4.2.12	-
Anaconda Accelerate	2.3.0	4.2.7
Anaconda Enterprise Notebooks	4.1.0	4.2.4
Anaconda Mosaic	1.3.1	4.2.7
Anaconda Repository	2.23.1	4.2.4
Anaconda Scale (Dask/Distributed)	0.11.1/1.13.3	4.2.7
Anaconda Scale (Jupyter Notebook)	4.2.3	4.2.7

## Bug fixes

Fixed issue with cluster profile settings not being migrated to cluster definition file.

## Download Adam

- Link: [https://anaconda.org/anaconda-adam/adam-installer/4.2.8/download/adam-installer-4.2.8-Linux-x86\\_64.sh](https://anaconda.org/anaconda-adam/adam-installer/4.2.8/download/adam-installer-4.2.8-Linux-x86_64.sh).
- MD5: f1083e30500b281e8c1d668c02ae8e3c.
- SHA256: 5a4b4391b1743cfc03d7bfa2e5693cc064cbd609f4c4fea7438846f2fa8d27e8.

## Anaconda Adam 4.2.7

Released: November 16, 2016

Platform component	Version	Plugin version
Anaconda/Miniconda	4.2.0/4.2.12	-
Anaconda Accelerate	2.3.0	4.2.7
Anaconda Enterprise Notebooks	4.1.0	4.2.4
Anaconda Mosaic	1.3.1	4.2.7
Anaconda Repository	2.23.1	4.2.4
Anaconda Scale (Dask/Distributed)	0.11.1/1.13.3	4.2.7
Anaconda Scale (Jupyter Notebook)	4.2.3	4.2.7

### Features

Added configuration settings for `salt_username`, `salt_groupname` and `salt_password`, for a user that is created across the cluster and owns the directory and files located in the root installation directory.

### Backend improvements

Added retries for Salt minion/API connection.

### Download Adam

- Link: [https://anaconda.org/anaconda-adam/adam-installer/4.2.7/download/adam-installer-4.2.7-Linux-x86\\_64.sh](https://anaconda.org/anaconda-adam/adam-installer/4.2.7/download/adam-installer-4.2.7-Linux-x86_64.sh).
- MD5: e1efa2a6652ba8bc9cf974a07dbc1df2.
- SHA256: 71f375ca4e7ab92072af71c970080950292e3b663fd3ca42c681651a154d682d.

### Anaconda Adam 4.2.6

Released: November 9, 2016

Platform component	Version	Plugin version
Anaconda/Miniconda	4.2.0/4.2.12	-
Anaconda Accelerate	2.3.0	4.2.1
Anaconda Enterprise Notebooks	4.1.0	4.2.4
Anaconda Mosaic	1.3.1	4.2.6
Anaconda Repository	2.23.1	4.2.4
Anaconda Scale (Dask/Distributed)	0.11.1/1.13.3	4.2.3
Anaconda Scale (Jupyter Notebook)	4.2.3	4.2.1

### Bug fixes

Fixed installation issue with Anaconda Mosaic related to conda environments.

### Backend improvements

Reverted to `requests` for file downloads via Salt HTTP module backend.

### Download Adam

- Link: [https://anaconda.org/anaconda-adam/adam-installer/4.2.6/download/adam-installer-4.2.6-Linux-x86\\_64.sh](https://anaconda.org/anaconda-adam/adam-installer/4.2.6/download/adam-installer-4.2.6-Linux-x86_64.sh).
- MD5: 035ee07ef6add9d60e23509bd91bebdf.
- SHA256: 3a4ca7ce75a8781fac9d7f38ec768b40c39b52091d39267dd898ec33ef299724.

## Anaconda Adam 4.2.5

Released: November 9, 2016

Platform component	Version	Plugin version
Anaconda/Miniconda	4.2.0/4.2.12	-
Anaconda Accelerate	2.3.0	4.2.1
Anaconda Enterprise Notebooks	4.1.0	4.2.4
Anaconda Mosaic	1.3.1	4.2.1
Anaconda Repository	2.23.1	4.2.4
Anaconda Scale (Dask/Distributed)	0.11.1/1.13.3	4.2.3
Anaconda Scale (Jupyter Notebook)	4.2.3	4.2.1

### Platform component updates

Updated to Miniconda 4.2.12 (conda 4.2.12).

### Download Adam

- Link: [https://anaconda.org/anaconda-adam/adam-installer/4.2.5/download/adam-installer-4.2.5-Linux-x86\\_64.sh](https://anaconda.org/anaconda-adam/adam-installer/4.2.5/download/adam-installer-4.2.5-Linux-x86_64.sh).
- MD5: 2614d2f8239aa0f3b8d070bd2a1ea83e.
- SHA256: 5355646e8e143cc5929061422427ee6e1f2fa143c5898865ccd0122803b72fa5.

## Anaconda Adam 4.2.4

Released: November 8, 2016

Platform component	Version	Plugin version
Anaconda/Miniconda	4.2.0/4.1.11	-
Anaconda Accelerate	2.3.0	4.2.1
Anaconda Enterprise Notebooks	4.1.0	4.2.4
Anaconda Mosaic	1.3.1	4.2.1
Anaconda Repository	2.23.1	4.2.4
Anaconda Scale (Dask/Distributed)	0.11.1/1.13.3	4.2.3
Anaconda Scale (Jupyter Notebook)	4.2.3	4.2.1

### Features

- Added support for creating and updating environments using `conda env` YAML files and listing and removing environments with `adam scale env`.
- Added `tmp_dir` setting to cluster profile to configure temporary download location.
- Added support for removing conda environments using `adam scale conda remove -n my-env --all`.

### Backend improvements

- Added support for downloads from CDN by enabling location header redirects when using `curl`.
- Improved handling and catching for errors returned from Salt.

### Bug fixes

- Fixed handling of proxy settings (including `.condarc` files) in cluster configuration/profile.
- Fixed handling of security settings in cluster definition when using Amazon EC2 instances.
- Fixed ownership for license directory in Anaconda Scale `rootdir`; default: `/opt/continuum/anaconda/licenses`.

### Platform component updates

- Updated to Anaconda Enterprise Notebooks 4.1.0.
- Updated to Anaconda Repository 2.23.1.

### Download Adam

- Link: [https://anaconda.org/anaconda-adam/adam-installer/4.2.4/download/adam-installer-4.2.4-Linux-x86\\_64.sh](https://anaconda.org/anaconda-adam/adam-installer/4.2.4/download/adam-installer-4.2.4-Linux-x86_64.sh).
- MD5: 67df6905007d892aa6597c06d3fe0693.
- SHA256: 2630798205a215ce0021db50591e8507c20cd36164eda27d74dcf1eb9a4d58fd.

### Anaconda Adam 4.2.3

Released: October 24, 2016

Platform component	Version	Plugin version
Anaconda/Miniconda	4.2.0/4.1.11	-
Anaconda Accelerate	2.3.0	4.2.1
Anaconda Enterprise Notebooks	4.0.0	4.2.1
Anaconda Mosaic	1.3.1	4.2.1
Anaconda Repository	2.22.0	4.2.3
Anaconda Scale (Dask/Distributed)	0.11.1/1.13.3	4.2.3
Anaconda Scale (Jupyter Notebook)	4.2.3	4.2.1

### Backend improvements

- Updated `ssl_verify` setting to handle various inputs (true, false, or string).
- Switched to `curl` for downloading Anaconda/Miniconda in environments with SSL/proxies.

## Platform component updates

- Updated to Anaconda Repository 2.22.0.
- Updated to Dask 0.11.1 and Distributed 1.13.3.

## Download Adam

- Link: [https://anaconda.org/anaconda-adam/adam-installer/4.2.3/download/adam-installer-4.2.3-Linux-x86\\_64.sh](https://anaconda.org/anaconda-adam/adam-installer/4.2.3/download/adam-installer-4.2.3-Linux-x86_64.sh).
- MD5: a484a933afcebb99bafbc5bde4e63081.
- SHA256: 8beb36f619f9d6177f0815090fa1ba7d41c769e47978d86c0b0c60164d63b996.

## Anaconda Adam 4.2.2

Released: October 19, 2016

Platform component	Version	Plugin version
Anaconda/Miniconda	4.2.0/4.1.11	-
Anaconda Accelerate	2.3.0	4.2.1
Anaconda Enterprise Notebooks	4.0.0	4.2.1
Anaconda Mosaic	1.3.1	4.2.1
Anaconda Repository	2.21.0	4.2.1
Anaconda Scale (Dask/Distributed)	0.11.0/1.12.2	4.2.1
Anaconda Scale (Jupyter Notebook)	4.2.3	4.2.1

## Bug fixes

Implemented various fixes related to conda configuration file (`.condarc`) and environment variable (`CONDARC`).

## Download Adam

- Link: [https://anaconda.org/anaconda-adam/adam-installer/4.2.2/download/adam-installer-4.2.2-Linux-x86\\_64.sh](https://anaconda.org/anaconda-adam/adam-installer/4.2.2/download/adam-installer-4.2.2-Linux-x86_64.sh).
- MD5: b0a7cc3061283c0c2b8b86dc8643190c.
- SHA256: f6ac6a6a1a6434b039d1ead09ddb056a09e07598859eb04eab33e24e9ad6d85c.

## Anaconda Adam 4.2.1

Released: October 14, 2016

Platform component	Version	Plugin version
Anaconda/Miniconda	4.2.0/4.1.11	-
Anaconda Accelerate	2.3.0	4.2.1
Anaconda Enterprise Notebooks	4.0.0	4.2.1
Anaconda Mosaic	1.3.1	4.2.1
Anaconda Repository	2.21.0	4.2.1
Anaconda Scale (Dask/Distributed)	0.11.0/1.12.2	4.2.1
Anaconda Scale (Jupyter Notebook)	4.2.3	4.2.1

## Features

- Improved output when checking node status (using `Salt test.ping`).
- Added configuration settings to cluster profile related to Salt API username, password, and group.

## Download Adam

- Link: [https://anaconda.org/anaconda-adam/adam-installer/4.2.1/download/adam-installer-4.2.1-Linux-x86\\_64.sh](https://anaconda.org/anaconda-adam/adam-installer/4.2.1/download/adam-installer-4.2.1-Linux-x86_64.sh).
- MD5: f8b01e94cf6b114b4d9df0f2074206a2.
- SHA256: 3ce27577757eb576ed7e3863ad35c5ca37755cdcb0de8f634ca6215ee4b6c67a.

## Anaconda Adam 4.2.0

Released: October 6, 2016

Platform component	Version	Plugin version
Anaconda/Miniconda	4.2.0/4.1.11	-
Anaconda Accelerate	2.3.0	4.2.0
Anaconda Enterprise Notebooks	4.0.0	4.2.0
Anaconda Mosaic	1.3.1	4.2.0
Anaconda Repository	2.21.0	4.2.0
Anaconda Scale (Dask/Distributed)	0.11.0/1.12.2	4.2.0
Anaconda Scale (Jupyter Notebook)	4.2.3	4.2.0

## Features

- Improved error messaging for missing/incompatible cluster profile fields.
- Improved handling of state for installed/enabled platform components.
- Simplified `adam describe` output to hide platform components that are not installed.

## Backend improvements

- Renamed `salt` to `salt_settings` in cluster profile and added documentation.
- Added conda canary builds to test framework.



## Bug fixes

- Fixed user/group ownership for platform component license directories.
- Improved validation of SSH key pairs, passwords, or agent public keys.
- Fixed check for existing Anaconda/Supervisor installations.
- Improved hash check for Miniconda downloads.
- Improved retry functionality for commands executed in parallel across multiple nodes.
- Improved handling of returned states from remote conda commands.
- Print URL when opening/viewing platform components if no browser is available.

## Platform component updates

- Updated to Anaconda 4.2.0 (conda 4.2.9).
- Updated to Anaconda Repository 2.21.0.
- Updated to Dask 0.11.0 and Distributed 1.12.2.
- Updated to Jupyter Notebook 4.2.3.

## Download Adam

- Link: [https://anaconda.org/anaconda-adam/adam-installer/4.2.0/download/adam-installer-4.2.0-Linux-x86\\_64.sh](https://anaconda.org/anaconda-adam/adam-installer/4.2.0/download/adam-installer-4.2.0-Linux-x86_64.sh).
- MD5: 4c6e685615d58486911f06c264bc1990.
- SHA256: 0556ee1b7e8bcd379faf6c2089e7fb525d2845187361a2a96d99a281ba207108.

## Anaconda Adam 4.1.2

Released: August 24, 2016

Platform component	Version	Plugin version
Anaconda/Miniconda	4.1.1/4.1.11	-
Anaconda Accelerate	2.3.0	4.1.0
Anaconda Enterprise Notebooks	4.0.0	4.1.1
Anaconda Mosaic	1.3.1	4.1.0
Anaconda Repository	2.19.7	4.1.1
Anaconda Scale (Dask/Distributed)	0.10.2/1.11.3	4.1.0
Anaconda Scale (Jupyter Notebook)	4.2.2	4.1.0

## Features

Added support for installations via proxy (HTTP and HTTPS).

### Bug fixes

Fixed issue with the creation of a custom home directory for the `anaconda` user.

### Download Adam

- Link: [https://anaconda.org/anaconda-adam/adam-installer/4.1.2/download/adam-installer-4.1.2-Linux-x86\\_64.sh](https://anaconda.org/anaconda-adam/adam-installer/4.1.2/download/adam-installer-4.1.2-Linux-x86_64.sh).
- MD5: 672611f7cdc5902fad40c36549b9e214.
- SHA256: db6b78338e126e017fcc6082add46f5d87a2bb48a21e5fd6191277ecb700031e.

### Anaconda Adam 4.1.1

Released: August 18, 2016

Platform component	Version	Plugin version
Anaconda/Miniconda	4.1.1/4.1.11	-
Anaconda Accelerate	2.3.0	4.1.0
Anaconda Enterprise Notebooks	4.0.0	4.1.0
Anaconda Mosaic	1.3.1	4.1.0
Anaconda Repository	2.19.7	4.1.0
Anaconda Scale (Dask/Distributed)	0.10.2/1.11.3	4.1.0
Anaconda Scale (Jupyter Notebook)	4.2.2	4.1.0

### Bug fixes

- Fixed issue with Salt API job responses.
- Fixed issue with `invoke_shell` buffer size.

### Download Adam

- Link: [https://anaconda.org/anaconda-adam/adam-installer/4.1.1/download/adam-installer-4.1.1-Linux-x86\\_64.sh](https://anaconda.org/anaconda-adam/adam-installer/4.1.1/download/adam-installer-4.1.1-Linux-x86_64.sh).
- MD5: 48a6fda5c16842ea2f138fe59723f425.
- SHA256: c4c6f14d3c4ed0d85d7eb8eaa1faa2d5959cecfbad87d0025cfcfa2f521ed7db.

### Anaconda Adam 4.1.0

Released: August 17, 2016

Platform component	Version	Plugin version
Anaconda/Miniconda	4.1.1/4.1.11	-
Anaconda Accelerate	2.3.0	4.1.0
Anaconda Enterprise Notebooks	4.0.0	4.1.0
Anaconda Mosaic	1.3.1	4.1.0
Anaconda Repository	2.19.7	4.1.0
Anaconda Scale (Dask/Distributed)	0.10.2/1.11.3	4.1.0
Anaconda Scale (Jupyter Notebook)	4.2.2	4.1.0

## Bug fixes

- Fixed issue when attempting to disable SELinux.
- Fixed licensing check when recreating an existing cluster.
- Fixed use of `host` during installation of Anaconda Enterprise Notebooks.

## Backend improvements

- Renamed `fqdn` to `host` in cluster profile.
- Changed default AEN Gateway port to 8089 in Anaconda Enterprise Notebooks.
- Changed default system account to `anaconda-server` for Anaconda Repository.
- Added diagnostic SSH checks to initial cluster provision.
- Implemented asynchronous Salt jobs for cluster-wide tasks.
- Added support for DSA and ECDSA SSH keys.
- Added optional `invoke_shell` mode for installations with restricted `sudo` functionality.
- Updated to Salt 2016.3.1.

## Platform component updates

- Updated to Miniconda 4.1.11 (conda 4.1.11).
- Updated to Anaconda Repository 2.19.7.
- Updated to Jupyter Notebook 4.2.2.
- Initial release of Anaconda Scale platform component (replaces Anaconda for cluster management).

## Download Adam

- Link: [https://anaconda.org/anaconda-adam/adam-installer/4.1.0/download/adam-installer-4.1.0-Linux-x86\\_64.sh](https://anaconda.org/anaconda-adam/adam-installer/4.1.0/download/adam-installer-4.1.0-Linux-x86_64.sh).
- MD5: 063b75a7352e711626dd6e4eabef5228.
- SHA256: 6dd4b344bec10ed6933a04d1d014260e94a6afb1b3acda4ca8093c60e80b6d3f.

## Anaconda Adam 4.0.1

Released: July 23, 2016

Platform component	Version	Plugin version
Anaconda/Miniconda	4.1.1/4.0.5	-
Anaconda Accelerate	2.3.0	4.0.0
Anaconda Enterprise Notebooks	4.0.0	4.0.1
Anaconda Mosaic	1.3.1	4.0.0
Anaconda Repository	2.19.2	4.0.0
Dask/Distributed	0.10.1/1.11.2	4.0.0
Jupyter Notebook	4.2.1	4.0.0

### Backend improvements

- Store Anaconda Adam API certificates and keys in isolated location.
- Disabled `requiretty` setting in `/etc/sudoers` when installing Anaconda Enterprise Notebooks.

### Download Adam

- Link: [https://anaconda.org/anaconda-adam/adam-installer/4.0.1/download/adam-installer-4.0.1-Linux-x86\\_64.sh](https://anaconda.org/anaconda-adam/adam-installer/4.0.1/download/adam-installer-4.0.1-Linux-x86_64.sh).
- MD5: 90027abca5f16917946df2c9018a443f.
- SHA256: df1e21a03745f60dba60ce99124275526deac64013f6a6d1c03b52c01eccb1b0.

## Anaconda Adam 4.0.0

Released: July 22, 2016

Platform component	Version	Plugin version
Anaconda/Miniconda	4.1.1/4.0.5	-
Anaconda Accelerate	2.3.0	4.0.0
Anaconda Enterprise Notebooks	4.0.0	4.0.0
Anaconda Mosaic	1.3.1	4.0.0
Anaconda Repository	2.19.2	4.0.0
Dask/Distributed	0.10.1/1.11.2	4.0.0
Jupyter Notebook	4.2.1	4.0.0

### Features

- Sync Anaconda Adam version with Anaconda Platform version.
- Fixed password setting for Jupyter Notebook.

## Download Adam

- Link: [https://anaconda.org/anaconda-adam/adam-installer/4.0.0/download/adam-installer-4.0.0-Linux-x86\\_64.sh](https://anaconda.org/anaconda-adam/adam-installer/4.0.0/download/adam-installer-4.0.0-Linux-x86_64.sh).
- MD5: 37662cf0d58955fc46205f2059372cd9.
- SHA256: 57781eabbae9269171f3360dfff56afd9e016480ce43cfd907d62151ef380c12.

## Anaconda Adam 1.6.2

Released: July 21, 2016

Platform component	Version	Plugin version
Anaconda/Miniconda	4.1.1/4.0.5	-
Anaconda Accelerate	2.3.0	1.6.0
Anaconda Enterprise Notebooks	4.0.0	1.6.0
Anaconda Mosaic	1.3.1	1.6.2
Anaconda Repository	2.19.2	1.6.0
Dask/Distributed	0.10.1/1.11.2	1.6.1
Jupyter Notebook	4.2.1	1.6.0

## Features

Added `conda channel_alias` setting for global Anaconda installation.

## Platform component updates

- Updated to Dask 0.10.0 and Distributed 1.11.0.
- Updated to Anaconda Mosaic 1.3.1.

## Download Adam

- Link: [https://anaconda.org/anaconda-adam/adam-installer/1.6.2/download/adam-installer-1.6.2-Linux-x86\\_64.sh](https://anaconda.org/anaconda-adam/adam-installer/1.6.2/download/adam-installer-1.6.2-Linux-x86_64.sh).
- MD5: 859d1b4b759cc0562866ee58a8ceeb35.
- SHA256: 5d378bc7cb681f80f0b80435467d1f889788dd5efc61b5be0f1a07c5993d131e.

## Anaconda Adam 1.6.0

Released: July 19, 2016

Platform component	Version	Plugin version
Anaconda/Miniconda	4.1.1/4.0.5	-
Anaconda Accelerate	2.3.0	1.6.0
Anaconda Enterprise Notebooks	4.0.0	1.6.0
Anaconda Mosaic	1.2.3	1.6.0
Anaconda Repository	2.19.2	1.6.0
Dask/Distributed	0.10.0/1.11.0	1.6.0
Jupyter Notebook	4.2.1	1.6.0

## Features

- Improvements to air gapped installation process for Adam core library.
- Added optional `sudo_su` mode for installations with restricted `sudo` functionality.
- A `licenses` directory is now created in the root of the `adam` installation location.

## Backend improvements

Improved checks for failed remote commands and `conda` commands.

## Bug fixes

Fixed hash key/value check for Anaconda/Miniconda installers.

## Download Adam

- Link: [https://anaconda.org/anaconda-adam/adam-installer/1.6.0/download/adam-installer-1.6.0-Linux-x86\\_64.sh](https://anaconda.org/anaconda-adam/adam-installer/1.6.0/download/adam-installer-1.6.0-Linux-x86_64.sh).
- MD5: `ae7a4614b8e1312812baa9402f462aac`.
- SHA256: `996e66e0ca956aaa05cc089cf66ebaf76bb1d8532d69900abb765f9246d5bf60`.

## Anaconda Adam 1.5.5

Released: July 14, 2016

Platform component	Version	Plugin version
Anaconda/Miniconda	4.1.1/4.0.5	-
Anaconda Accelerate	2.3.0	1.5.2
Anaconda Enterprise Notebooks	4.0.0	1.5.2
Anaconda Mosaic	1.2.3	1.5.2
Anaconda Repository	2.19.2	1.5.4
Dask/Distributed	0.10.0/1.11.0	1.5.1
Jupyter Notebook	4.2.1	1.5.2

## Bug fixes

Fixed password-based SSH commands used during provision/installation.

## Download Adam

- Link: [https://anaconda.org/anaconda-adam/adam-installer/1.5.5/download/adam-installer-1.5.5-Linux-x86\\_64.sh](https://anaconda.org/anaconda-adam/adam-installer/1.5.5/download/adam-installer-1.5.5-Linux-x86_64.sh).
- MD5: e28887409326f3539743eda9beeff0b6.
- SHA256: 9e6eb3854ed2bff57aab6573804478ec05f8586e8b4ecd8ee6d0cd5faa44d570.

## Anaconda Adam 1.5.4

Released: July 13, 2016

Platform component	Version	Plugin version
Anaconda/Miniconda	4.1.1/4.0.5	-
Anaconda Accelerate	2.3.0	1.5.2
Anaconda Enterprise Notebooks	4.0.0	1.5.2
Anaconda Mosaic	1.2.3	1.5.2
Anaconda Repository	2.19.2	1.5.4
Dask/Distributed	0.10.0/1.11.0	1.5.1
Jupyter Notebook	4.2.1	1.5.2

## Features

- Added `conda channels` setting for global Anaconda installation.
- Support for multiple conda channels in conda commands.
- Added explicit Anaconda and platform component installation steps to `adam provision`, `adam ec2`, and `adam up`.
- Added customizable platform component settings to cluster definition.
- Ability to configure security settings for IPTables and SELinux.
- Improved confirmation/details when destroying Amazon EC2 instances.

## Bug fixes

Fixed password-based SSH logins for cluster nodes.

## Platform component updates

- Updated to Anaconda 4.1.1 (conda 4.1.6).
- Updated to Anaconda Repository 2.19.2.

### Download Adam

- Link: [https://anaconda.org/anaconda-adam/adam-installer/1.5.4/download/adam-installer-1.5.4-Linux-x86\\_64.sh](https://anaconda.org/anaconda-adam/adam-installer/1.5.4/download/adam-installer-1.5.4-Linux-x86_64.sh).
- MD5: 348928b0816c93a9ccb20a32fa6a6b20.
- SHA256: a3f76295b61b02cda3d2f31c24dfd08fdb4739fb7aff3312753c5ba87ca3eaff.

### Anaconda Adam 1.5.3

Released: July 11, 2016

Platform component	Version	Plugin version
Anaconda/Miniconda	4.1.0/4.0.5	-
Anaconda Accelerate	2.3.0	1.5.1
Anaconda Enterprise Notebooks	4.0.0	1.5.1
Anaconda Mosaic	1.2.3	1.5.1
Anaconda Repository	2.19.1	1.5.2
Dask/Distributed	0.10.0/1.11.0	1.5.0
Jupyter Notebook	4.2.1	1.5.1

### Features

Changed default admin username and password for Anaconda Repository.

### Bug fixes

Added `setuptools` as dependency for Adam.

### Platform component updates

Updated to Anaconda 4.1.0 (conda 4.1.4).

### Download Adam

- Link: [https://anaconda.org/anaconda-adam/adam-installer/1.5.3/download/adam-installer-1.5.3-Linux-x86\\_64.sh](https://anaconda.org/anaconda-adam/adam-installer/1.5.3/download/adam-installer-1.5.3-Linux-x86_64.sh).
- MD5: 4e30813039ec5a7010324a3cf577c621.
- SHA256: 83b03a7704b448bda9eec05b1cf6aa0c7b384cb4c4401a820559e077c2c104d6.

### Anaconda Adam 1.5.1

Released: July 8, 2016



Platform component	Version	Plugin version
Anaconda/Miniconda	4.0.0/4.0.5	-
Anaconda Accelerate	2.3.0	1.5.1
Anaconda Enterprise Notebooks	4.0.0	1.5.1
Anaconda Mosaic	1.2.3	1.5.1
Anaconda Repository	2.19.1	1.5.1
Dask/Distributed	0.10.0/1.11.0	1.5.0
Jupyter Notebook	4.2.1	1.5.0

## Features

- Changed default AEN Gateway port to 8088 in Anaconda Enterprise Notebooks.
- Added profile settings for Anaconda Repository.

## Download Adam

- Link: [https://anaconda.org/anaconda-adam/adam-installer/1.5.1/download/adam-installer-1.5.1-Linux-x86\\_64.sh](https://anaconda.org/anaconda-adam/adam-installer/1.5.1/download/adam-installer-1.5.1-Linux-x86_64.sh).
- MD5: 8dfe05136a4f022c9611092b1cfc2373.
- SHA256: 89b500affce32c0fb2df78b553d2c96277f0d7852037553710838ed4e82df36f.

## Anaconda Adam 1.5.0

Released: July 7, 2016

Platform component	Version	Plugin version
Anaconda/Miniconda	4.0.0/4.0.5	-
Anaconda Accelerate	2.3.0	1.5.1
Anaconda Enterprise Notebooks	4.0.0	1.5.0
Anaconda Mosaic	1.2.3	1.5.1
Anaconda Repository	2.19.1	1.5.0
Dask/Distributed	0.10.0/1.11.0	1.5.0
Jupyter Notebook	4.2.1	1.5.0

## Backend improvements

Updated license checks to be compatible with new platform component names.

## Platform component updates

- Updated to Anaconda Repository 2.19.1.
- Updated to Anaconda Accelerate 2.3.0.
- Updated to Anaconda Mosaic 1.2.3.

## Download Adam

- Link: [https://anaconda.org/anaconda-adam/adam-installer/1.5.0/download/adam-installer-1.5.0-Linux-x86\\_64.sh](https://anaconda.org/anaconda-adam/adam-installer/1.5.0/download/adam-installer-1.5.0-Linux-x86_64.sh).
- MD5: b162d5425b0d41c96da6b65e45f841e7.
- SHA256: 00d23cae15fc55fea1c82645f79d10d34e085d05c105d4a556402138730d7ae4.

## Anaconda Adam 1.4.2

Released: July 6, 2016

Platform component	Version	Plugin version
Anaconda/Miniconda	4.0.0/4.0.5	-
Anaconda Accelerate	2.2.0	1.4.1
Anaconda Enterprise Notebooks	4.0.0	1.4.1
Anaconda Mosaic	1.2.2	1.4.1
Anaconda Repository	2.18.1	1.4.1
Dask/Distributed	0.10.0/1.11.0	1.4.2
Jupyter Notebook	4.2.1	1.4.2

## Features

Added `adam describe` command to get detailed information about clusters and profiles.

## Bug fixes

Fixed issue with compute node registration in Anaconda Enterprise Notebooks.

## Platform component updates

- Updated to Dask 0.10.0 and Distributed 1.11.0.
- Updated to Jupyter 1.4.2.

## Download Adam

- Link: [https://anaconda.org/anaconda-adam/adam-installer/1.4.2/download/adam-installer-1.4.2-Linux-x86\\_64.sh](https://anaconda.org/anaconda-adam/adam-installer/1.4.2/download/adam-installer-1.4.2-Linux-x86_64.sh).
- MD5: c8c906b1623bf109813c588a126d7407.
- SHA256: 0c17e670e13da18dc2d64e09980ce790bc0812754802f6937cc9ecc44efd0da0.

## Anaconda Adam 1.4.1

Released: June 28, 2016

Platform component	Version	Plugin version
Anaconda/Miniconda	4.0.0/4.0.5	-
Anaconda Accelerate	2.2.0	1.4.1
Anaconda Enterprise Notebooks	4.0.0	1.4.0
Anaconda Mosaic	1.2.2	1.4.1
Anaconda Repository	2.18.1	1.4.1
Dask/Distributed	0.9.0/1.10.2	1.4.1
Jupyter Notebook	-	1.4.1

## Features

Updated license checks in Dask and Notebook platform components.

## Bug fixes

Fixed issue with license check.

## Download Adam

- Link: [https://anaconda.org/anaconda-adam/adam-installer/1.4.1/download/adam-installer-1.4.1-Linux-x86\\_64.sh](https://anaconda.org/anaconda-adam/adam-installer/1.4.1/download/adam-installer-1.4.1-Linux-x86_64.sh).
- MD5: 5ec1faec73d8cf53c3fdb6742f86daf5.
- SHA256: 8f61c01029eaff31a1910bf56fbc3b33a0a4a845fcd86ddc12c673706dd1e06e.

## Anaconda Adam 1.4.0

Released: June 28, 2016

Platform component	Version	Plugin version
Anaconda/Miniconda	4.0.0/4.0.5	-
Anaconda Accelerate	2.2.0	1.4.1
Anaconda Enterprise Notebooks	4.0.0	1.4.0
Anaconda Mosaic	1.2.2	1.4.1
Anaconda Repository	2.18.1	1.4.1
Dask/Distributed	0.9.0/1.10.2	1.4.0
Jupyter Notebook	-	1.4.1

## Features

- Added `adam info` command with license information.
- Added `adam remove` command to remove cluster definition file.
- License files are now uploaded to nodes for each platform component.
- Improved handling of license issues.
- Installers are now automatically built and uploaded.

### Backend improvements

Updated Salt to 2016.3.0.

### Bug fixes

- Fixed Salt API timeout issue.
- Fixed issue with Salt master and minions starting up.

### Download Adam

- Link: [https://anaconda.org/anaconda-adam/adam-installer/1.4.0/download/adam-installer-1.4.0-Linux-x86\\_64.sh](https://anaconda.org/anaconda-adam/adam-installer/1.4.0/download/adam-installer-1.4.0-Linux-x86_64.sh).
- MD5: 7d9d2ebfb02e33977fb41d1dcf1240fc.
- SHA256: a2f9c98338d4ba4e224ea815bb338d45ee719cc002af0f5c7d18a8f593a33d54.

## 4.4.3 Anaconda for Cluster Management

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**Note:** This product is discontinued. This archived copy of the product documentation is provided for those customers who are still using it.

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NOTE: Anaconda for cluster management has been replaced by [Anaconda Scale](#). This documentation is made available for existing installations only.

To use Anaconda with a cluster, please use Anaconda Scale and refer to the [Anaconda Scale](#) documentation.

---

Anaconda for cluster management provides resource management tools to easily deploy Anaconda across a cluster. It helps you manage multiple conda environments and packages (including Python and R) on bare-metal or cloud-based clusters. Supported platforms include Amazon EC2, bare-metal clusters, or even a collection of virtual machines.

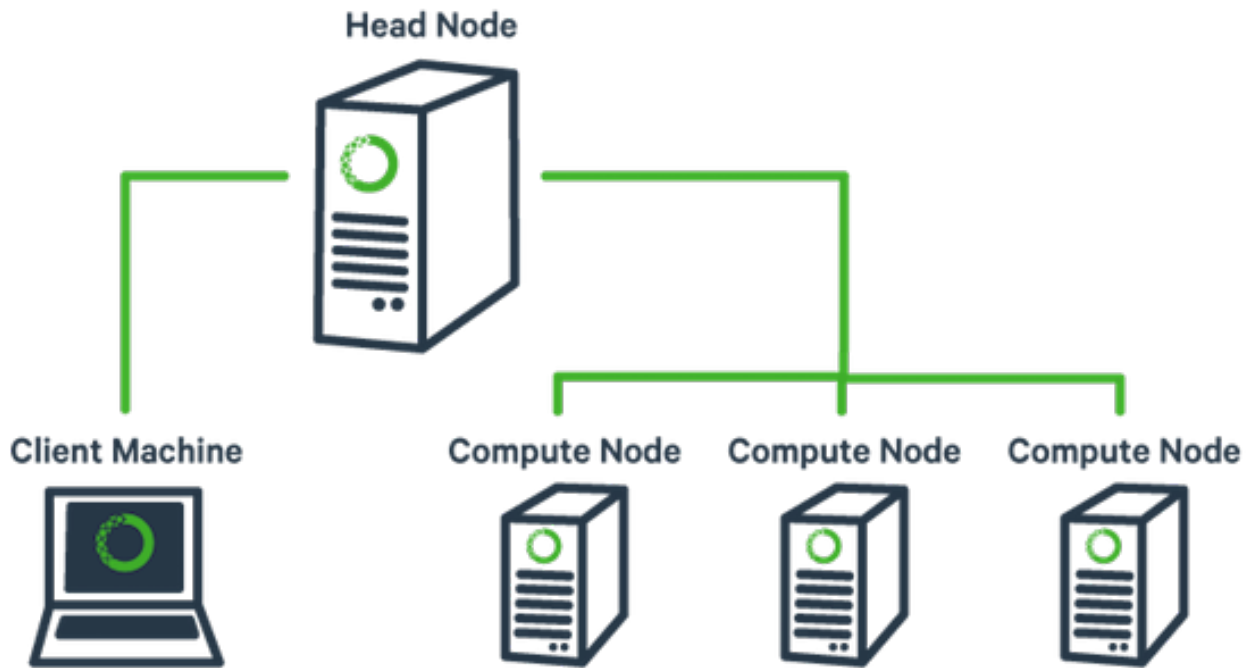
Anaconda for cluster management can be used with distributed computation frameworks such as Spark or Dask and works alongside enterprise Hadoop distributions such as Cloudera CDH or Hortonworks HDP.

Anaconda for cluster management is freely available via Anaconda Cloud for unlicensed, unsupported use with up to 4 cluster nodes. Anaconda Workgroup and Enterprise include licenses for 8 and 16 nodes, respectively. If you would like to use Anaconda for cluster management with additional nodes on a bare-metal, on-premises, or cloud-based cluster, please contact [sales@anaconda.com](mailto:sales@anaconda.com).

#### Features of Anaconda for cluster management:

- Easily install Python and R packages across multiple cluster nodes
- Manage multiple conda environments across a cluster
- Push local conda environments to all cluster nodes
- Manage both cloud-based and bare-metal clusters
- Remotely SSH and upload/download files to and from cluster nodes

#### Typical configuration of Anaconda for cluster management:



## Table of contents:

### Quickstart

This quickstart provides a walkthrough of Anaconda for cluster management using Amazon Web Services (AWS) Elastic Compute Cloud (EC2). The steps covered in this quickstart include defining and launching a cloud-based cluster on Amazon EC2, managing conda packages on the cluster nodes, and installing plugins.

### Installation

Install Anaconda for cluster management on your local machine following the instructions on the installation page.

### Create a provider

A sample providers file (shown below) is included with a new installation of Anaconda for cluster management and is located within the `~/ .acluster/providers.yaml` file.

```
aws_east:
  cloud_provider: ec2
  keyname: my-private-key
  location: us-east-1
  private_key: ~/.ssh/my-private-key.pem
  secret_id: AKIAXXXXXX
  secret_key: XXXXXXXXXX
```

Edit this file and replace the settings and credentials with your information.

Refer to the [Provider settings](#) page for more details about provider settings, including security groups.

You can list the providers with the command:

```
$ acluster list providers
```

### Create a profile

A sample profile is included with a new installation of Anaconda for cluster management and is located in the `~/ .acluster/profiles.d/` directory. The sample profile named `aws_profile_sample` is shown below:

```
name: aws_profile_sample
provider: aws_east
num_nodes: 4
node_id: ami-d05e75b8 # Ubuntu 14.04, us-east-1 region
node_type: m3.large
user: ubuntu
```

You can use this profile to create a 4-node cluster based on Ubuntu 14.04.

Refer to the [Profile settings](#) page for more details about profile settings.

You can list the profiles with the command:

```
$ acluster list profiles
```

### Create the cluster

After the provider and profile files are defined, you can create a cluster using the command:

```
$ acluster create demo_cluster --profile aws_profile_sample
```

This will create your new cluster on Amazon EC2 and provision the cluster nodes, which typically requires between 5 and 10 minutes. You will see updates as the tasks and initialization steps are completed.

### Install conda packages

Now that you have a cluster running, you can install conda packages using the `acluster conda` command. The `acluster` command can be prepended to most of the conda commands.

To install numpy, scipy, and pandas on all of the cluster nodes, use the following command:

```
$ acluster conda install numpy scipy pandas
```

**Note:** Refer to the [Conda management](#) page for a full list of remote conda commands.

## Install plugins

Anaconda for cluster management supports multiple plugins such as Apache Spark, Hadoop Distributed File System (HDFS), the Jupyter Notebook, and more. These plugins can be installed on the cluster by using the `acluster install` command.

For example, the following command can be used to install IPython Notebook on the cluster:

```
$ acluster install notebook
```

The notebook will be available on `http://{ HEAD_NODE_IP }:8888`. You can open the respective URLs for many of these applications in your browser using the `acluster open` command:

```
$ acluster open notebook
```

Run the `acluster open` command to view a complete list of supported applications.

## Destroy the cluster

When you are finished, the following command can be used to destroy the cluster and terminate all instances in it. It will prompt for confirmation before destroying the cluster.

```
$ acluster destroy demo_cluster
```

## Further information

Refer to the [Python with Spark How-tos](#) page for more example use cases for use-cases and example scripts.

## Creating a cluster

### Requirements

- **Client machine:**
  - Windows, Mac, or Linux, 64-bit
  - Anaconda for cluster management client library installed
- **Cluster Nodes:**
  - One or more 64-bit Linux machines with 8+ GB RAM, 8+ cores (recommended)
  - Access to ports 22, 4505, and 4506 from the client machine to the cluster nodes to provision the cluster via SSH and Salt

### Supported operating systems

For the cluster nodes, we support and test Anaconda for cluster management with the following Linux distributions:

- CentOS 6 and CentOS 7
- RHEL 6 and RHEL 7
- Ubuntu 12.04 and Ubuntu 14.04

### Cloud-based or bare-metal cluster creation

For more information about configuring and creating a cloud-based or bare-metal cluster, refer to the following documentation:

## Cloud-based Cluster Setup

Anaconda for cluster management can launch and bootstrap clusters on a variety of cloud services. We currently support [Amazon EC2](#). Other providers such as Microsoft Azure, Rackspace, Google Cloud Platform, and others are on our roadmap. If you are interested in using a cloud provider that is not listed here, please contact us at [sales@anaconda.com](mailto:sales@anaconda.com).

Cloud configuration involves the use of `profiles` and `providers`. Splitting configurations allows users to easily share and distribute specific cluster configurations (`profiles`), while retaining private authentication credentials (`providers`).

### 1. Provider Setup

Authentication and cloud definitions are managed in a single provider file on the client machine: `~/.acluster/providers.yaml`. A provider file can contain multiple providers with different settings and credentials.

A sample providers file is included with a new installation of Anaconda for cluster management and is located within the `~/.acluster/providers.yaml` file on the client machine. You can edit the contents of this file to reflect the settings and credentials for your cloud provider.

An example `~/.acluster/providers.yaml` file with a provider named `aws_east` that is configured for Amazon EC2 is shown below:

```
aws_east:
  cloud_provider: ec2
  keyname: my-private-key
  location: us-east-1
  private_key: ~/.ssh/my-private-key.pem
  secret_id: AKIAXXXXXX
  secret_key: XXXXXXXXXXXX
```

Note that you will need access to ports 22, 4505, and 4506 from the client machine to the cluster nodes to provision the cluster via SSH and Salt.

Refer to the [Provider settings](#) page for more details about provider settings, including security groups.

**Linux or Mac:** You should set the permissions of `providers.yaml` file to 0600.

### 2. Profile Setup

The settings for each cluster are managed in a profile file.

A sample profile is included with a new installation of Anaconda for cluster management and is located in the `~/.acluster/profiles.d/` directory on the client machine. You can edit the contents of this file to reflect the settings for your cluster.

An example profile located at `~/.acluster/profiles.d/profile_name.yaml` and named `profile_name` that is configured to use the `aws_east` provider is shown below:

```
name: profile_name
provider: aws_east
num_nodes: 4
node_id: ami-d05e75b8 # Ubuntu 14.04, us-east-1 region
node_type: m3.large
user: ubuntu
```



Anaconda for cluster management supports and is tested with the following Linux-based AMIs on Amazon EC2 (us-east-1 region), which can be set as the `node_id`:

OS	AMI	User
Ubuntu 12.04	ami-08faa660	ubuntu
Ubuntu 14.04	ami-d05e75b8	ubuntu
CentOS 6.6	ami-d89fb7b0	root

For more information on AMIs that are available in other Amazon EC2 regions, refer to the [Amazon EC2 documentation](#) or the [Ubuntu Amazon EC2 AMI Locator](#).

Refer to the [Profile settings](#) page for more details about profile settings.

### 3. Create Cluster

Use the following command to launch a cluster with the specified profile:

```
$ acluster create demo_cluster --profile profile_name
```

**Note:** Replace `demo_cluster` with the name of your cluster, and `profile_name` with the name of your profile.

After this command is executed, the cloud-based cluster will be created, and you will see updates as the tasks and initialization steps are completed.

A typical launch takes between 5 and 10 minutes, and has output similar to the following:

```
$ acluster create demo_cluster --profile profile_name
Creating cluster
Number of existing nodes: 0
Number of requested nodes: 4
Licensed nodes: 16
License is valid for the current number of nodes.
INFO: Creating new cluster "demo_cluster" with profile "profile_name"
INFO: Creating 4 instances
INFO: Instances configuration:
INFO:   Name: demo_cluster
INFO:   Security Group: ['all-open']
INFO:   Number of Nodes: 4
INFO:   Type: <NodeSize: id=m3.large, name=Large Instance, ram=7168
        disk=32000 bandwidth=None price=0.14 driver=Amazon EC2 ...>
INFO:   Location: us-east-1
INFO:   Additional Tags {'billingProject': 'anaconda-cluster'}
INFO: Successfully created instances
INFO: Cluster info: {'ips': ['54.81.228.35', '54.167.198.242',
        '54.145.107.208', '54.166.207.40'], 'user': 'ubuntu',
        'ids': ['i-29818d89', 'i-2c818d8c', 'i-2e818d8e', 'i-2f818d8f'],
        'name': u'demo_cluster'}
Saving cluster file
Cluster "demo_cluster": 4 nodes
Number of existing nodes: 4
Number of requested nodes: 0
Licensed nodes: 16
License is valid for the current number of nodes.
Checking ssh connection
INFO: Checking SSH connection
Checking sudo
```

(continues on next page)

(continued from previous page)

```
Bootstrapping conda
INFO: Installing miniconda
INFO: Anaconda URL: https://repo.anaconda.com/miniconda/Miniconda-latest-Linux-x86_64.
↪ sh
INFO: Checking conda installation
INFO: Checking conda installation
Bootstrapping salt
INFO: Setting up Salt master and Minions
INFO: Creating conda env for salt
INFO: Installing salt
INFO: Settings grains/roles
INFO: Head roles: []
INFO: Compute roles: []
Starting salt
INFO: Flushing iptables rules
INFO: Setting SELinux to permissive
INFO: Starting salt-master daemon
INFO: Starting salt-minion daemon
Checking salt connection
Uploading formulas
INFO: Uploading formulas to head
INFO: Uploading profile
Syncing formulas
Done
```

The cluster is now ready for use.

View the [Troubleshooting FAQ](#) if you encounter errors while creating a cluster.

## 4. Destroy Cluster

If you want to destroy a cluster, use the following command:

```
$ acluster destroy demo_cluster
```

**Note:** Replace the name `demo_cluster` above with the actual name of your cluster.

After issuing the above command, you will be prompted to confirm termination of the specified cluster.

## Bare-metal Cluster Setup

Anaconda for cluster management can be used to manage pre-existing clusters, such as bare-metal machines, collections of virtual machines (Vagrant, Docker, etc.), or previously instantiated cloud instances. These types of installations are collectively referred to as *bare-metal installations*.

### Additional bare-metal cluster requirements:

- **Client machine:**
  - Passwordless SSH access to all cluster nodes
- **Cluster Nodes:**
  - Matching user account/credentials on all nodes with passwordless sudo enabled

## Provisioning instructions

### 1. Provider Setup

A sample providers file is included with a new installation of Anaconda for cluster management and is located within the `~/.acluster/providers.yaml` file on the client machine. You can edit the contents of this file to reflect the settings for your bare metal provider.

An example `~/.acluster/providers.yaml` file with a provider named `bare_metal` is shown below:

```
bare_metal:
  cloud_provider: none
  private_key: ~/.ssh/my-private-key
```

Refer to the [Provider settings](#) page for more details about provider settings.

### 2. Profile Setup

Create a file on the client machine located at `~/.acluster/profiles.d/profile_name.yaml` that defines the following information:

```
name: profile_name
provider: bare_metal
node_id: bare_metal
node_type: bare_metal
user: ubuntu
num_nodes: 4
machines:
  head:
    - 192.168.1.1
  compute:
    - 192.168.1.2
    - 192.168.1.3
    - 192.168.1.4

# Optional for Anaconda Server
# (note that the ports might be different in your configuration)
anaconda_url: http://[your-anaconda-server-ip]:9000/Miniconda-latest-Linux-x86_64.sh
conda_channels:
  - http://[your-anaconda-server-ip]:8080/conda/anaconda-cluster
  - http://[your-anaconda-server-ip]:8080/conda/anaconda
  - defaults
```

The example profile shown above is named `profile_name` and is configured for a 4-node bare-metal cluster.

Refer to the [Profile settings](#) page for more details about profile settings.

### 3. Configure Cluster

Use the following command to configure a bare-metal cluster with the specified profile:

```
$ acluster create demo_cluster --profile profile_name
```

**Note:** Replace `demo_cluster` with the name of your cluster, and `profile_name` with the name of your profile.

After this command is executed, the bare-metal cluster will be configured, and you will see updates as the tasks and initialization steps are completed.

A typical bare-metal cluster configuration takes a few minutes, and has output similar to the following:

```
$ acluster create demo_cluster --profile profile_name
Creating cluster
Number of existing nodes: 0
Number of requested nodes: 4
Licensed nodes: 16
License is valid for the current number of nodes.
INFO: Creating new cluster "demo_cluster" with profile "profile_name"
INFO: Creating 4 instances
INFO: Successfully created instances
INFO: Cluster info: {'ips': ['54.84.227.194', '52.23.192.232',
    '54.84.184.193', '54.88.116.203'], 'user': 'ubuntu',
    'name': u'demo_cluster'}
Saving cluster file
Cluster "demo_cluster": 4 nodes
Number of existing nodes: 4
Number of requested nodes: 0
Licensed nodes: 16
License is valid for the current number of nodes.
Checking ssh connection
INFO: Checking SSH connection
Checking sudo
Bootstrapping conda
INFO: Installing miniconda
INFO: Anaconda URL: https://repo.anaconda.com/miniconda/Miniconda-latest-Linux-x86_64.
↪ sh
INFO: Checking conda installation
INFO: Checking conda installation
Bootstrapping salt
INFO: Setting up Salt master and Minions
INFO: Creating conda env for salt
INFO: Installing salt
Starting salt
INFO: Flushing iptables rules
INFO: Setting SELinux to permissive
INFO: Starting salt-master daemon
INFO: Starting salt-minion daemon
Checking salt connection
Uploading formulas
INFO: Uploading formulas to head
INFO: Uploading profile
Setting Roles
INFO: Settings grains/roles
Syncing formulas
Done
```

The cluster is now ready for use.

View the [Troubleshooting FAQ](#) if you encounter errors while creating a cluster.

## Configuration

After installing Anaconda for cluster management and running any `acluster` command, the `~/ .acluster` directory is created, along with a sample provider file located in `~/ .acluster/providers.yaml` and a sample

profile file located in `~/ .acluster/profiles.d/`.

An example of an `~/ .acluster` directory with multiple clusters and profiles is shown below:

```
/home/user/.acluster
├── clusters.d
│   ├── cluster1.yaml
│   ├── cluster2.yaml
│   └── cluster3.yaml
├── profiles.d
│   ├── profile1.yaml
│   └── profile2.yaml
└── providers.yaml
```

The `profiles.d` directory contains information about cluster setups, including the number and type of nodes, plugins, and other settings.

The `providers.yaml` file contains information about cloud providers.

The `clusters.d` directory contains information about clusters that are currently running.

For more information about profile and provider settings, refer to the following pages:

## Profile settings

The following profile settings can be used to define cluster configurations for cloud-based or bare-metal clusters. Each named profile file should contain information for a single cluster definition.

- *Profile settings*
  - *anaconda\_url (optional)*
  - *aws (optional)*
  - *conda\_channels (optional)*
  - *default\_channels (optional)*
  - *channel\_alias (optional)*
  - *name*
  - *node\_id*
  - *node\_type*
  - *num\_nodes*
  - *machines (optional)*
  - *plugins (optional)*
  - *provider*
  - *root\_size (optional)*
  - *security (optional)*
  - *user*
- *Sample cloud-based profile file*
- *Sample bare-metal profile file*

### Profile settings

#### **anaconda\_url** (optional)

Set a custom location to download Anaconda/Miniconda from (default: Miniconda with Python 2).

```
anaconda_url: http://localhost/miniconda/Miniconda-latest-Linux-x86_64.sh
```

#### **aws** (optional)

Set AWS options for all instances:

- `tags` are optional key/value metadata that are assigned to each instance.
- `termination_protection` prevents your instances from being accidentally terminated (default: `true`).
- `use_private_ip` uses the private IP addresses of the AWS nodes instead of the public IP addresses. This is useful if you are using a custom security group (default: `false`).

```
aws:  
  tags:  
    - billingProject: anaconda-cluster  
    - cluster_version: production  
    - ...  
  termination_protection: true  
  use_private_ip: true
```

#### **conda\_channels** (optional)

Set custom channels to download conda packages from on the cluster nodes. This setting will overwrite all of the configured conda channels, including the default channels. If you are using this setting, you will need to explicitly include the two default channels, `defaults` and `anaconda-cluster`, followed by your custom channels.

```
conda_channels:  
- defaults  
- anaconda-cluster  
- blaze  
- pypi  
- username  
- https://conda.anaconda.org/username/
```

#### **default\_channels** (optional)

Set `default_channels` to download the default conda packages from the URL defined. This setting will overwrite the default conda channels: <http://repo.anaconda.com>.

```
default_channels: http://localhost/conda/anaconda
```

### channel\_alias (optional)

Set `channel_alias` to instruct conda to look for channels in a local repository. This setting will overwrite the default: `http://conda.anaconda.org`.

```
channel_alias: http://localhost/conda/
```

### name

Name of the profile.

```
name: profile_name
```

### node\_id

Image to configure on each node. For bare-metal clusters, a dummy value such as `bare-metal` can be used.

```
node_id: ami-d05e75b8 # Ubuntu 14.04, us-east-1 region
```

### node\_type

The type of node to launch. For bare-metal clusters, a dummy value such as `bare-metal` can be used.

```
node_type: m3.large
```

### num\_nodes

Number of nodes to launch (cloud-based) or manage (bare-metal).

```
num_nodes: 4
```

### machines (optional)

IP addresses of head and compute nodes in the cluster. Note that only IP addresses should be used with this setting, not hostnames or FQDNs.

This is used along with the *Bare-metal Cluster Setup* and can refer to bare-metal nodes, cloud-based nodes that were manually launched outside of Anaconda for cluster management, or a collection of virtual machines. If SSH is running on a port other than 22, you can optionally include the SSH port number (e.g., `192.168.1.1:2222`).

```
machines:
  head:
    - 192.168.1.1
  compute:
    - 192.168.1.2
    - 192.168.1.3
    - 192.168.1.4
```

### plugins (optional)

Install plugins upon cluster creation or provisioning. Some plugins also have configurable settings. Refer to the *Plugin Settings* documentation for more information.

```
plugins:
- notebook
- dask
```

### provider

Name of the provider to use to launch instances for a cloud-based or bare-metal cluster. For more information, refer to the *Provider settings* documentation.

```
provider: aws_east
```

### root\_size (optional)

Size of the root volume (GB). Currently only used for Amazon EBS volumes.

```
root_size: 200
```

### security (optional)

Security settings to enable/disable SELinux or flush iptables rules (default: true).

```
security:
  disable_selinux: true
  flush_iptables: true
```

### user

User to SSH to the cluster nodes as. This user must have passwordless sudo access.

```
user: ubuntu
```

### Sample cloud-based profile file

Below is a sample cloud-based profile named `profile_name` located in the `~/.acluster/profiles/profile_name.yaml` file that is configured with all required and optional settings.

```
name: profile_name
node_id: ami-d05e75b8 # Ubuntu 14.04, us-east-1 region
node_type: m3.large
num_nodes: 4
provider: aws_east
root_size: 50
user: ubuntu
```

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```

anaconda_url: http://localhost/miniconda/Miniconda-latest-Linux-x86_64.sh

aws:
  tags:
    - billingProject: anaconda-cluster

plugins:
  - notebook
  - dask

default_channels: http://localhost/conda/anaconda

channel_alias: http://localhost/conda/

conda_channels:
  - defaults
  - anaconda-cluster
  - blaze
  - pypi
  - username
  - https://conda.anaconda.org/username/

security:
  disable_selinux: true
  flush_iptables: true

```

### Sample bare-metal profile file

Below is a sample bare-metal profile named `profile_name` located in the `~/.acluster/profiles/profile_name.yaml` file that is configured with all required and optional settings.

```

name: profile_name
node_id: bare_metal
node_type: bare_metal
num_nodes: 4
provider: bare_metal
user: ubuntu
anaconda_url: http://localhost/miniconda/Miniconda-latest-Linux-x86_64.sh

machines:
  head:
    - 192.168.1.1
  compute:
    - 192.168.1.2
    - 192.168.1.3
    - 192.168.1.4

plugins:
  - notebook
  - dask

default_channels: http://localhost/conda/anaconda

channel_alias: http://localhost/conda/

```

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```
conda_channels:
- defaults
- anaconda-cluster
- blaze
- pypi
- username
- https://conda.anaconda.org/username/

security:
  disable_selinux: false
  flush_iptables: false
```

## Provider settings

The following provider settings can be used to define settings for creating cloud-based or bare-metal clusters. The `providers.yaml` file can contain credentials and settings for multiple providers.

- *Provider settings*
  - *cloud\_provider*
  - *keyname (optional)*
  - *location (optional)*
  - *private\_key*
  - *secret\_id (optional)*
  - *secret\_key (optional)*
  - *security\_group (optional)*
- *Sample providers file*

## Provider settings

### cloud\_provider

Name of the cloud provider (`ec2`, `none`). Use `none` for bare-metal clusters.

```
cloud_provider: ec2
```

### keyname (optional)

Name of the key to authenticate with the cluster nodes. This setting is used with a cloud provider.

```
keyname: my-private-key
```

**location (optional)**

Region or location to use with a cloud provider.

```
location: us-east-1
```

**private\_key**

Path to the private SSH key on the client machine.

```
private_key: ~/.ssh/my-private-key.pem
```

**secret\_id (optional)**

Secret ID to authenticate with a cloud provider.

```
secret_id: AKIA*****
```

**secret\_key (optional)**

Secret key to authenticate with a cloud provider.

```
secret_key: RXE*****
```

**security\_group (optional)**

Security Group to use with a cloud provider. Note that this is the “Group Name” in the AWS Console, not the “Name” or “Group ID”. Note that you will need access to ports 22, 4505, and 4506 from the client machine to the cluster nodes to provision the cluster via SSH and Salt. If this parameter is not specified, then a default Security Group will be created for you, called `anaconda-cluster-default`, with all ports open.

```
security_group: my-security-group
```

**Sample providers file**

Below is a sample providers file located in the `~/.acluster/providers.yaml` file that is configured with all required and optional settings. The `providers.yaml` file can contain credentials and settings for multiple providers. The sample providers file shown below defines two providers named `aws_east` and `bare_metal` for cloud-based and bare-metal clusters, respectively.

```
aws_east:
  cloud_provider: ec2
  keyname: my-private-key
  location: us-east-1
  private_key: ~/.ssh/my-private-key.pem
  secret_id: AKIAXXXXXX
  secret_key: XXXXXXXXXX
  security_group: my-security-group
```

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```
bare_metal:  
  cloud_provider: none  
  private_key: ~/.ssh/my-private-key
```

## Plugins

- *List of available plugins*
- *Installing Plugins*
- *Plugin Settings*
  - *Conda*
  - *Dask*
  - *HDFS*
  - *Jupyter Notebook*
  - *Custom download settings for plugins*
- *Managing Plugins*
  - *Plugin Status*
  - *Open Plugin UIs*
  - *Restart Plugins*
  - *Stop Plugins*
- *Plugin Notes and Network Ports*
  - *HDFS*
  - *Jupyter Notebook*
  - *Miniconda*
  - *Salt*
  - *Spark*
  - *YARN*

## List of available plugins

Anaconda for cluster management can install and manage the following plugins on a cluster:

- Anaconda distribution
- Dask/Distributed
- Ganglia
- IPython Parallel
- Jupyter Notebook

- Salt

The following plugins are unsupported and should only be used for prototyping/experimental purposes:

- Elasticsearch
- HDFS
- Hive
- Impala
- Kibana
- Logstash
- Spark (standalone mode or YARN)
- Storm
- YARN
- ZooKeeper

If you're interested in using Anaconda with production Hadoop clusters, Anaconda for cluster management works with enterprise Hadoop distributions such as [Cloudera CDH](#) or [Hortonworks HDP](#).

On clusters with existing enterprise Hadoop installations, Anaconda for cluster management can manage packages (e.g., for PySpark, SparkR, or Dask) and can install and manage the Jupyter Notebook and Dask plugins.

## Installing Plugins

Plugins can be installed using two methods:

1. Using the `cluster_profile.yaml` file when creating or provisioning a cluster.
2. Using the `acluster install` command after the cluster is created.

### 1. Install plugins with the `profile.yaml` file

When creating or provisioning a cluster, create or edit the file `~/.acluster/profiles.d/profile_name.yaml` as shown in the example below:

```
name: profile_name
provider: aws
node_id: ami-d05e75b8 # Ubuntu 14.04, us-east-1 region
user: ubuntu
node_type: m3.large
num_nodes: 5
plugins:
  - notebook
  - dask
```

Optionally, you can configure some plugin settings from within your profile. For example, you can specify a password to protect a Jupyter Notebook using:

```
name: profile_name
provider: aws
node_id: ami-d05e75b8 # Ubuntu 14.04, us-east-1 region
user: ubuntu
node_type: m3.large
num_nodes: 5
```

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```
plugins:
- notebook:
  password: secret
```

Refer to the [Plugin Settings](#) section for more details on configuring plugin settings.

## 2. Install plugins using the `acluster install` command

After the cluster has been created, you can view a list of available plugins with the command `acluster install` as shown in the example below:

```
$ acluster install
Usage: acluster install [OPTIONS] COMMAND [ARGS]...

  Install plugins across the cluster

Options:
  -h, --help  Show this message and exit.

Commands:
  conda          Install (mini)conda
  dask           Install Dask/Distributed
  elasticsearch  Install Elasticsearch
  ganglia        Install Ganglia
  hdfs           Install HDFS
  hive           Install Hive
  impala         Install Impala
  ipython-parallel  Install IPython Parallel
  kibana         Install Kibana
  notebook      Install Jupyter Notebook
  logstash      Install Logstash
  salt          Install Salt
  spark-standalone  Install Spark (standalone)
  spark-yarn     Install Spark (YARN)
  storm         Install Storm
  yarn          Install YARN
  zookeeper     Install Zookeeper
```

All of the above subcommands can optionally receive a `--cluster/-x` option to specify a cluster. This option is not required if you only have one cluster running.

**Note:** Salt is the base for all plugins except Conda. Therefore, the Salt plugin needs to be installed before the other plugins can be installed. Salt is installed by default when you create or provision a cluster using the `acluster create` or `acluster provision` command.

## Plugin Settings

The following plugins support custom settings that can be defined within a profile.

### Conda

Configure conda packages and environments to be installed upon cluster creation or provisioning:

```
name: profile_name
plugins:
  - conda:
      environments:
        root:
          - numpy
        py27:
          - python=2.7
          - scipy
          - numba
        py34:
          - python=3.4
          - pandas
          - nltk
```

Configure the installation location of conda (default: `/opt/anaconda`):

```
name: profile_name
plugins:
  - conda:
      install_prefix: /opt/another_anaconda
```

Set `conda_sh` to `false` to disable the creation of `/etc/profile.d/conda.sh` on cluster nodes (default: `true`):

```
name: profile_name
plugins:
  - conda:
      conda_sh: false
```

Set `conda_group_name` to any valid unix group (default: `anaconda`):

```
name: profile_name
plugins:
  - conda:
      conda_group_name: anaconda
```

Set `conda_acl` to a list of users who will be given access for Anaconda Cluster admin capabilities. Note: When using this setting at least one user must have `sudo` access during the provisioning phase. Typically, this will include the user previously set above as `user`.

```
name: profile_name
plugins:
  - conda:
      conda_acl:
        - user1
        - user2
```

Set `ssl_verify` to a custom SSL path or to `False` to disable SSL verification for conda. Refer to the [conda documentation](#) for more information.

```
name: profile_name
plugins:
  - conda:
      ssl_verify: False
```

### Dask

You can optionally set the number of processes (`nprocs`) to use for the Dask/Distributed workers and the `host` to access the Dask/Distributed UI via a browser. Refer to the [Dask distributed scheduler documentation](#) for more information about these settings.

```
name: profile_name
plugins:
  - dask:
      nprocs: 8
      host: dask-ui.com
```

### HDFS

By default, the HDFS plugin is configured to use the following directories: `/data/dfs/nn` on the namenode and `/data/dfs/dn` on the datanodes. When multiple drives are available, the same directories are used on all non-root drives.

You can optionally set custom directories for the HDFS namenode and datanode. For example, the following settings can be used if you want to utilize a large root volume (e.g., using the `root_volume` profile setting with Amazon EC2):

```
name: profile_name
plugins:
  - hdfs:
      namenode_dirs:
        - /data/dfs/nn
      datanode_dirs:
        - /data/dfs/dn
```

### Jupyter Notebook

Set a custom password to protect a Jupyter Notebook (default: `acluster`):

```
name: profile_name
plugins:
  - notebook:
      password: acluster
```

Set a custom port for the Jupyter Notebook server (default: `8888`):

```
name: profile_name
plugins:
  - notebook:
      port: 8888
```

Set a custom directory for Jupyter Notebooks (default: `/opt/notebooks`):

```
name: profile_name
plugins:
  - notebook:
      directory: /opt/notebooks
```



## Custom download settings for plugins

Most plugins are installed from the standard package management repositories for your Linux distribution. Some plugins are downloaded directly from their source/project website. You can override the default download settings for the following plugins:

```
name: profile_name
plugins:
  - elasticsearch:
      download_url: https://download.elasticsearch.org/elasticsearch/release/org/
↳ elasticsearch/distribution/tar/elasticsearch/2.1.0/elasticsearch-2.1.0.tar.gz
      download_hash: sha1=b6d681b878e3a906fff8c067b3cfe855240bffb
      version: elasticsearch-2.1.0
  - logstash:
      download_url: https://download.elastic.co/logstash/logstash/logstash-2.1.1.tar.
↳ gz
      download_hash: sha1=d71a6e015509030ab6012adcf79291994ece0b39
      version: logstash-2.1.1
  - kibana:
      download_url: https://download.elastic.co/kibana/kibana/kibana-4.3.0-linux-x64.
↳ tar.gz
      download_hash: sha1=d64e1fc0ddeaaab85e168177de6c78ed82bb3a3b
      version: kibana-4.3.0-linux-x64
  - storm:
      source_url: http://apache.arvixe.com/storm/apache-storm-0.9.5/apache-storm-0.9.
↳ 5.tar.gz
      version_name: apache-storm-0.9.5
```

## Managing Plugins

The following commands can be used to manage your plugins:

### Plugin Status

Check the status of the plugins by using the `acluster status` command:

```
$ acluster status
Usage: acluster status [OPTIONS] COMMAND [ARGS]...

Options:
  -x, --cluster TEXT           Cluster name
  -l, --log-level [info|debug|error]
                                Library logging level
  -h, --help                   Show this message and exit.

Commands:
  conda           Check Conda status
  dask            Check Dask/Distributed status
  elasticsearch   Check Elasticsearch status
  ganglia         Check Ganglia status
  hdfs           Check HDFS status
  hive           Check Hive status
  impala         Check Impala status
  ipython-parallel Check IPython Parallel status
```

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kibana	Check Kibana status
notebook	Check IPython/Jupyter Notebook status
salt	Check Salt package status
salt-conda	Check Salt Conda module status
salt-key	Check salt-minion keys status
spark-standalone	Check Spark (standalone) status
ssh	Check SSH status
storm	Check Storm status
yarn	Check YARN status

**Example:**

```
$ acluster status conda
Checking status of conda on cluster: demo_cluster
54.81.187.22: True
54.91.219.252: True
54.163.26.229: True
54.145.10.211: True
Status all: True

$ acluster status salt
54.167.128.130: True
54.205.160.114: True
50.16.32.99: True
50.16.34.82: True
54.163.143.34: True
Status all: True

$ acluster status salt-key
ip-10-156-23-215.ec2.internal: True
ip-10-147-47-235.ec2.internal: True
ip-10-225-181-251.ec2.internal: True
ip-10-237-145-2.ec2.internal: True
ip-10-156-30-32.ec2.internal: True
Status all: True

$ acluster status salt-conda
ip-10-156-23-215.ec2.internal: True
ip-10-237-145-2.ec2.internal: True
ip-10-225-181-251.ec2.internal: True
ip-10-147-47-235.ec2.internal: True
ip-10-156-30-32.ec2.internal: True
Status all: True
```

The multiple salt status checks perform different checks. The `acluster status salt` command verifies that the salt package is installed, the `acluster status salt-key` command verifies that the salt minions are connected to the head node, and the `acluster status salt-conda` command verifies that the salt conda module is distributed across the cluster and is operational.

All of the above checks should return a successful status after executing `acluster install salt`.

## Open Plugin UIs

Some of the plugins provide a browser UI that can be displayed to the user. The `acluster open` command is a utility command that opens a browser window corresponding to each plugin. The command:

```
$ acluster open notebook
```

will open a browser window to the Jupyter Notebook (port 8888).

Use the `--no-browser` option to print the URL for the plugin interface without opening a browser window.

```
$ acluster open notebook --no-browser
notebook: http://54.172.82.53:8888
```

## Restart Plugins

If a plugin is not working correctly, restart the processes by using the `acluster restart` command.

## Stop Plugins

To stop a plugin, use the `acluster stop` command.

## Plugin Notes and Network Ports

### HDFS

Requires: `salt`

Distributed file system used by many of the distributed analytics engines such as Impala, Hive, and Spark.

Service	Location	Port
NameNode UI	Head node	50070
HDFS Master	Head node	9000
WebHDFS	Head node	14000

### Jupyter Notebook

Requires: `salt`

Web-based interactive computational environment for Python.

Service	Location	Port
Notebook	Head node	8888

Notebooks are saved in the directory `/opt/notebooks`. You can upload and download notebooks from the cluster by using the `put` and `get` commands, respectively.

```
$ acluster put mynotebook.ipynb /opt/notebooks/mynotebook.ipynb
$ acluster get /opt/notebooks/mynotebook.ipynb mynotebook.ipynb
```

## Miniconda

Python distribution from [Anaconda](#) – ships with Python libraries for large-scale data processing, predictive analytics, and scientific computing.

### Salt

Requires: `conda`

Configuration management system.

Service	Location	Port
Salt Master/Minion	All nodes	4505
Salt Master/Minion	All nodes	4506

### Spark

Computing framework and analytics engine written in Java/Scala with a Python interface (PySpark).

Service	Location	Port
Spark UI (standalone)	Head node	8080

### YARN

Resource manager in which all Hadoop and Hadoop-like jobs are run.

Service	Location	Port
Resource UI	Head node	9026
NodeManager	Compute node(s)	9035

### Cluster management

- *Overview*
- *SSH access*
- *Executing commands*
- *Upload/download files*
- *Command history*
- *Centralized logging*
- *Anaconda for cluster management client information*
- *Advanced: Running Salt modules*
- *Advanced: Syncing Salt formulas*

### Overview

Anaconda for cluster management provides functionality to easily interact with clusters, including:

- Secure shell (SSH) to cluster nodes

- Executing commands on cluster nodes
- Uploading (put) and downloading (get) files from cluster nodes
- Executing salt module commands: <http://docs.saltstack.com/en/latest/ref/modules/all/>

For a concise overview of all of the available commands, view the Anaconda for cluster management Cheat Sheet.

For the `acluster` commands shown below, you can optionally specify a `--cluster/-x` option to specify a target cluster to operate on. This option is not required if only one cluster is running.

## SSH access

The command `acluster ssh` can be used to SSH into any node within the cluster.

The first (optional) argument is a zero-indexed number that refers to a node, where 0 is the head node, 1 is the first compute node, and so on.

**Note:** This functionality requires SSH. **Windows users:** Install an SSH client such as [PuTTY](#).

## Executing commands

The `acluster cmd` command allows commands to be executed across multiple nodes on the cluster. This functionality is performed via salt (default) or fabric (using the `--ssh/-s` flag).

Salt provides faster execution times (especially in large clusters) of remote commands, assuming salt is installed and running on the cluster. Salt is installed by default on cloud providers and can be installed on bare-metal clusters using the command `acluster install salt`.

Fabric provides remote command execution based on SSH, which can be slow in big clusters but does not require salt to be installed on the cluster. Using fabric, you can also target specific nodes using the `--target/-t` option. The `--target/-t` option can receive the keywords 'head' and 'compute', a number (zero-indexed, where 0 is the head node and 1 is the first compute node), or two numbers separated by a comma to target a group of consecutive nodes.

Example:

```
$ acluster cmd 'date'
Executing command "date" target: "*" cluster: "demo_cluster"
4 nodes response: Thu May 14 19:21:48 UTC 2015
1 nodes response: Thu May 14 19:21:44 UTC 2015
1 nodes response: Thu May 14 19:21:47 UTC 2015

$ acluster cmd 'date' --ssh
54.196.149.0: Thu May 14 19:22:06 UTC 2015
54.159.15.86: Thu May 14 19:22:03 UTC 2015
107.21.159.226: Thu May 14 19:22:06 UTC 2015
107.20.60.246: Thu May 14 19:22:06 UTC 2015
54.237.177.104: Thu May 14 19:22:06 UTC 2015
54.227.91.24: Thu May 14 19:22:06 UTC 2015

$ acluster cmd 'date' --ssh -t head
107.21.159.226: Thu May 14 19:23:02 UTC 2015

$ acluster cmd 'date' --ssh -t 3,6
54.196.149.0: Thu May 14 19:23:29 UTC 2015
54.159.15.86: Thu May 14 19:23:26 UTC 2015
54.227.91.24: Thu May 14 19:23:29 UTC 2015
```

## Upload/download files

The commands `acluster put` and `acluster get` allow files to be uploaded to and downloaded from any node in the cluster. By default, the `put` and `get` commands target the head node.

Both of the `put` and `get` commands have the same `--target/-t` option, which has the same functionality as `cmd` with the `-ssh/-s` flag.

Example:

```
$ acluster put environment.yml /tmp/env.yml
Uploading file "environment.yml" to "/tmp/env.yml" - cluster: "demo_cluster" - hosts:
"['107.21.159.226']"

$ acluster put environment.yml /tmp/env.yml --all
Uploading file "environment.yml" to "/tmp/env.yml" - cluster: "demo_cluster" - hosts:
"['107.21.159.226', '107.20.60.246', '54.237.177.104', '54.159.15.86', '54.196.149.0',
'54.227.91.24']"

$ acluster put environment.yml /tmp/env.yml -t ,3
Uploading file "environment.yml" to "/tmp/env.yml" - cluster: "demo_cluster" - hosts:
"['107.21.159.226', '107.20.60.246', '54.237.177.104']"

$ acluster put environment.yml /tmp/env.yml -t compute
Uploading file "environment.yml" to "/tmp/env.yml" - cluster: "demo_cluster" - hosts:
"['107.20.60.246', '54.237.177.104', '54.159.15.86', '54.196.149.0', '54.227.91.24']"
```

The `get` command has similar behavior. Although the `-target/-t` option is also available, it might not make sense to download the same file repeatedly since it will get overwritten.

Example:

```
$ acluster get /tmp/env.yml env2.yml
Downloading file "/tmp/env.yml" to "env2.yml" - cluster: "demo_cluster" - hosts:
"['107.21.159.226']"

$ acluster get /tmp/env.yml env2.yml --all
Downloading file "/tmp/env.yml" to "env2.yml" - cluster: "demo_cluster" - hosts:
"['107.21.159.226', '107.20.60.246', '54.237.177.104', '54.159.15.86', '54.196.149.0',
'54.227.91.24']"
Warning: Local file /tmp/env2.yml already exists and is being overwritten.
Warning: Local file /tmp/env2.yml already exists and is being overwritten.
```

## Command history

The `acluster history` command displays commands that were previously executed using `acluster`. By default, the ten most recent commands are shown.

```
$ acluster history
2015-06-09 23:39:22,515: acluster create demo_cluster --profile profile_name
2015-06-10 00:00:46,151: acluster ssh
2015-06-10 00:01:35,304: acluster acluster conda install numpy scipy
2015-06-10 00:02:01,029: acluster open notebook
```

## Centralized logging

You can install the Elasticsearch, Logstash, and Kibana (ELK) plugins and use them to collect, search, and analyze data. When you install the ELK plugins, they come preconfigured for centralized logging of other Anaconda for cluster management plugins. For more information about plugins, refer to the [Plugins](#) documentation.

To install the ELK plugins, insert the following in your cluster profile before you create or provision a cluster:

```
plugins:
  - elasticsearch
  - logstash
  - kibana
```

or, use the following command to install the ELK plugins on an active cluster:

```
$ acluster install elasticsearch logstash kibana
```

After the ELK plugins are installed, they will begin collecting logs for various services, and the log data can be searched using Elasticsearch and visualized using Kibana. You can open the Kibana UI in your browser using the following command:

```
$ acluster open kibana
```

By default, the following index patterns are available in Kibana:

```
YYYY-MM-DD
salt
hdfs
yarn
spark_yarn
spark_standalone
zookeeper
impala
hive
hbase
hadoop-httpfs
mapreduce
syslog
```

Note that you can use the ELK plugins in a number of different workflows once they are installed on the cluster, including:

- Viewing and searching logs for all cluster-related plugins
- Viewing logs for Spark or YARN jobs for centralized job monitoring and troubleshooting
- Utilizing centralized logging capabilities from your application

## Anaconda for cluster management client information

The `acluster info` command displays version information related to the Anaconda for cluster management client installation.

```
$ acluster info
anaconda-cluster version: 1.0
Platform: Darwin-14.3.0-x86_64
Processor: i386
```

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```
Byte-ordering: little
Python version: 2.7.10 |Continuum Analytics, Inc.| (default, May 28 2015, 17:04:42)
[GCC 4.2.1 (Apple Inc. build 5577)]
apache-libcloud version: 0.16.0
yaml version: 3.11
```

## Advanced: Running Salt modules

By default, salt provides quite a bit of functionality in its default modules. All of this functionality is available by using the `acluster function` command.

For example, you can ping all of the cluster nodes to see that they are available:

```
$ acluster function test.ping
ip-10-153-156-45.ec2.internal:
  True
ip-10-169-57-125.ec2.internal:
  True
ip-10-181-18-153.ec2.internal:
  True
ip-10-144-199-24.ec2.internal:
  True
ip-10-113-145-230.ec2.internal:
  True
ip-10-136-78-206.ec2.internal:
  True
```

Advanced functions are also available, such as listing all of the IP address associated with a node:

```
$ acluster function network.ipaddr
ip-10-169-57-125.ec2.internal:
  - 10.169.57.125
ip-10-144-199-24.ec2.internal:
  - 10.144.199.24
ip-10-181-18-153.ec2.internal:
  - 10.181.18.153
ip-10-153-156-45.ec2.internal:
  - 10.153.156.45
ip-10-136-78-206.ec2.internal:
  - 10.136.78.206
ip-10-113-145-230.ec2.internal:
  - 10.113.145.230
```

Another common salt command can be used to install packages using the system package manager:

```
$ acluster function pkg.install httpd
ip-10-136-78-206.ec2.internal:
  ...
  httpd:
    -----
    new:
      2.2.15-39.el6.centos
    old:
  ...
```

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```
ip-10-144-199-24.ec2.internal:
...
  httpd:
    -----
    new:
      2.2.15-39.el6.centos
    old:
    ...
...

```

For more information on salt commands, see <http://docs.saltstack.com/en/latest/ref/modules/all/>

### Advanced: Syncing Salt formulas

The `acluster sync` command is an advanced feature that synchronizes the Salt formulas from the client to the head node and then across the cluster.

### Conda management

- *Overview*
- *Installing packages from channels*
- *List of remote conda commands*
- *Example remote conda commands*
  - *Install conda packages*
  - *List conda packages*
  - *Update conda packages*
  - *Remove conda packages*
  - *Create conda environments*
  - *Push conda environments*
  - *List conda environments*

### Overview

One of the primary features of Anaconda for cluster management is the remote deployment and management of Anaconda environments across a cluster.

Prepending `acluster` to core conda commands will execute those commands across all of the cluster nodes.

For example, to view the conda environments on all of the cluster nodes:

```
$ acluster conda info -e
All nodes (x3) response:
# conda environments:
```

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```
#
root          *   /opt/anaconda
```

To install numpy on all of the cluster nodes:

```
$ acluster conda install numpy
Installing (u'numpy',) on cluster "demo_cluster"
Node "ip-10-234-8-208.ec2.internal":
    Successful actions: 1/1
Node "ip-10-170-59-28.ec2.internal":
    Successful actions: 1/1
Node "ip-10-232-42-58.ec2.internal":
    Successful actions: 1/1
```

For a concise overview of all of the available commands, view the [Anaconda for cluster management Cheat Sheet](#).

## Installing packages from channels

You can install packages from [Anaconda Cloud](#) or from an Anaconda Repository installation by adding the `--channel/-c` option. For example, to install the `apache-libcloud` package from the `anaconda-cluster` channel:

```
$ acluster conda install -c https://conda.anaconda.org/anaconda-cluster apache-
↳ libcloud
Installing (u'apache-libcloud',) on cluster "demo_cluster"
Node "ip-10-136-80-92.ec2.internal":
    Successful actions: 1/1
Node "ip-10-63-173-62.ec2.internal":
    Successful actions: 1/1
$ acluster conda list | grep apache-libcloud
- 'apache-libcloud: 0.16.0 (py27_0)'
```

## List of remote conda commands

The following conda commands are available in Anaconda for cluster management:

- `acluster conda install` – Install package(s)
- `acluster conda update` – Update package(s)
- `acluster conda remove` – Remove package(s)
- `acluster conda list` – List package(s)
- `acluster conda create` – Create conda environment
- `acluster conda info` – Display information about current conda install
- `acluster conda push` – Push conda environment to cluster

For more information about conda, refer to the [conda documentation](#).

## Example remote conda commands

## Install conda packages

Any conda package can be installed on a cluster managed by Anaconda for cluster management:

```
$ acluster conda install numpy

Node "ip-10-136-80-92.ec2.internal":
    Successful actions: 1/1
Node "ip-10-63-173-62.ec2.internal":
    Successful actions: 1/1
```

Verify that the package was installed using the `list` command:

```
$ acluster conda list

All nodes (x2) response:
...
- 'numpy: 1.9.2 (py27_0)'
...
```

You may also install multiple conda packages with a single command:

```
$ acluster conda install scipy pandas scikit-learn
Node "ip-10-136-80-92.ec2.internal":
    Successful actions: 3/3
Node "ip-10-63-173-62.ec2.internal":
    Successful actions: 3/3

$ acluster conda list
All nodes (x2) response:
...
- 'pandas: 0.16.1 (np19py27_0)'
...
- 'scikit-learn: 0.16.1 (np19py27_0)'
- 'scipy: 0.15.1 (np19py27_0)'
...
```

**Note:** It is recommended that you install all of the packages you want at once. Installing one package at a time can result in dependency conflicts.

## List conda packages

A useful conda command to run on a cluster is to list the packages that are available on the nodes (by default all of the nodes should have the same packages):

```
$ acluster conda list

All nodes (x2) response:
- 'libsodium: 0.4.5 (0)'
- 'sqlite: 3.8.4.1 (1)'
- 'conda-env: 2.1.4 (py27_0)'
- 'python: 2.7.9 (3)'
...
```

## Update conda packages

You can also specify which versions of conda packages to install or update:

```
$ acluster conda install pandas==0.13
Installing (u'pandas==0.13',) on cluster "demo_cluster"
Node "ip-10-136-80-92.ec2.internal":
    Successful actions: 1/1
Node "ip-10-63-173-62.ec2.internal":
    Successful actions: 1/1
$ acluster conda list | grep pandas
- 'pandas: 0.13.0 (np18py27_0)'

$ acluster conda update pandas
Updating (u'pandas',) on cluster "demo_cluster"
Node "ip-10-136-80-92.ec2.internal":
    Successful actions: 1/1
Node "ip-10-63-173-62.ec2.internal":
    Successful actions: 1/1
$ acluster conda list | grep pandas
- 'pandas: 0.16.1 (np19py27_0)'
```

## Remove conda packages

You can remove conda packages across a cluster:

```
$ acluster conda remove pandas
Removing (u'pandas',) on cluster "demo_cluster"
Node "ip-10-136-80-92.ec2.internal":
    Successful actions: 1/1
Node "ip-10-63-173-62.ec2.internal":
    Successful actions: 1/1

$ acluster conda list | grep pandas
... NO OUTPUT ...
```

## Create conda environments

You can also manage conda environments across a cluster with Anaconda for cluster management.

To create a new conda environment that contains Python and numpy, use the command `conda create -n test_env numpy`.

On a cluster, use the same command and simply prepend `acluster` as shown:

```
$ acluster conda create -n test_env numpy
All nodes (x2) response:
Conda environment "test_env" created
```

Once the environment is created, refer to that named environment by adding the `-n` name option to conda commands:

```
$ acluster conda list -n test_env
All nodes (x2) response:
- 'sqlite: 3.8.4.1 (1)'
```

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```

- 'python: 2.7.9 (3)'
- 'zlib: 1.2.8 (0)'
- 'openssl: 1.0.1k (1)'
- 'system: 5.8 (2)'
- 'tk: 8.5.18 (0)'
- 'setuptools: 15.2 (py27_0)'
- 'pip: 6.1.1 (py27_0)'
- 'readline: 6.2 (2)'
- 'numpy: 1.9.2 (py27_0)'

$ acluster conda install -n test_env requests
Installing (u'requests',) on cluster "d" - target: "*"
Node "ip-10-136-80-92.ec2.internal":
    Successful actions: 1/1
Node "ip-10-63-173-62.ec2.internal":
    Successful actions: 1/1

$ acluster conda list -n test_env
All nodes (x2) response:
- 'sqlite: 3.8.4.1 (1)'
- 'python: 2.7.9 (3)'
- 'zlib: 1.2.8 (0)'
- 'openssl: 1.0.1k (1)'
- 'system: 5.8 (2)'
- 'tk: 8.5.18 (0)'
- 'setuptools: 15.2 (py27_0)'
- 'pip: 6.1.1 (py27_0)'
- 'readline: 6.2 (2)'
- 'numpy: 1.9.2 (py27_0)'
- 'requests: 2.7.0 (py27_0)'

```

## Push conda environments

You can also push conda environments from the client machine to the cluster by using a `conda environment.yml` file:

```

$ acluster conda push ./environment.yml
['ip-10-234-8-208.ec2.internal'] nodes response:
Conda environment with "/tmp/anaconda-cluster/environment.yml" created
...

```

## List conda environments

To verify that the environment has been pushed to all nodes, use the `info` command:

```

$ acluster conda info -e
All nodes (x3) response:
# conda environments:
#
stats                /opt/anaconda/envs/stats
root                 *  /opt/anaconda

```

## Python with Spark How-tos

These how-tos will show you how to run Python tasks on a Spark cluster using the PySpark module. These how-tos will also show you how to interact with data stored within HDFS on the cluster.

While these how-tos are not dependent on each other and can be accomplished in any order it is recommended that you begin with the *Overview of Spark, YARN and HDFS* first.

## Overview of Spark, YARN and HDFS

[Spark](#) is an analytics engine and framework that is capable of running queries 100 times faster than traditional MapReduce jobs written in Hadoop. In addition to the performance boost, developers can write Spark jobs in Scala, Python and Java if they so desire. Spark can load data directly from disk, memory and other data storage technologies such as Amazon S3, Hadoop Distributed File System (HDFS), HBase, Cassandra, etc.

You can install Spark using an enterprise Hadoop distribution such as [Cloudera CDH](#) or [Hortonworks HDP](#).

## Submitting Spark Jobs

Spark scripts are often developed interactively and can be written as a script file or as a Jupyter notebook file.

A Spark script can be submitted to a Spark cluster using various methods:

- Running the script directly on the head node.
- Using the [spark-submit](#) script in either Standalone mode or with the YARN resource manager
- Interactively in an IPython shell or Jupyter Notebook on the cluster

To run a script on the head node, simply execute `python example.py` on the cluster.

Note: that in order to launch Jupyter Notebook on the cluster, the plugin must already be installed. See the [Plugins](#) documentation for more information.

## Working with Data in HDFS

Moving data in and around HDFS can be difficult. If you need to move data from your local machine to HDFS, from Amazon S3 to HDFS, from Amazon S3 to Redshift, from HDFS to Hive and so on, we recommend using [odo](#), which is part of the [Blaze ecosystem](#). Odo efficiently migrates data from the source to the target through a network of conversions.

If you are unfamiliar with Spark and/or SQL, we recommend using [Blaze](#) to express selections, aggregations, group-bys, etc. in a dataframe-like style. Blaze provides Python users with a familiar interface to query data that exists in different data storage systems.

## How to Run a Spark Standalone Job

### Overview

This is a minimal Spark script that imports PySpark, initializes a SparkContext and performs a distributed calculation on a Spark cluster in standalone mode.

## Who is this for?

This how-to is for users of a Spark cluster that has been configured in standalone mode who wish to run Python code.

## Spark Standalone Summary

1. *Before you start*
2. *Modifying the script*
3. *Running the job*
4. *Troubleshooting*
5. *Further information*

### Before you start

To execute this example, download the `cluster-spark-basic.py` example script to the cluster node where you submit Spark jobs.

For this example, you'll need Spark running with the standalone scheduler. You can install Spark using an enterprise Hadoop distribution such as [Cloudera CDH](#) or [Hortonworks HDP](#). Some additional configuration might be necessary to use Spark in standalone mode.

### Modifying the script

After downloading the `cluster-spark-basic.py` example script open the file in a text editor on your cluster. Replace `HEAD_NODE_HOSTNAME` with the hostname of the head node of the Spark cluster.

```
# cluster-spark-basic.py
from pyspark import SparkConf
from pyspark import SparkContext

conf = SparkConf()
conf.setMaster('spark://HEAD_NODE_HOSTNAME:7077')
conf.setAppName('spark-basic')
sc = SparkContext(conf=conf)

def mod(x):
    import numpy as np
    return (x, np.mod(x, 2))

rdd = sc.parallelize(range(1000)).map(mod).take(10)
print rdd
```

Let's analyze the contents of the `spark-basic.rst` example script. The first code block contains imports from PySpark.

The second code block initializes the `SparkContext` and sets the application name.

The third code block contains the analysis code that calculates the modulus of a range of numbers up to 1000 using the NumPy package and returns/prints the first 10 results.

Note: you may have to install NumPy with `acluster conda install numpy`.

### Running the job

You can run this script by submitting it to your cluster for execution using `spark-submit` or by running this command

```
python cluster-spark-basic.py
```

The output from the above command shows the first ten values that were returned from the `cluster-spark-basic.py` script.

```
16/05/05 22:26:53 INFO spark.SparkContext: Running Spark version 1.6.0

[...]

16/05/05 22:27:03 INFO scheduler.TaskSetManager: Starting task 0.0 in stage 0.0 (TID_
↪0, localhost, partition 0,PROCESS_LOCAL, 3242 bytes)
16/05/05 22:27:04 INFO storage.BlockManagerInfo: Added broadcast_0_piece0 in memory_
↪on localhost:46587 (size: 2.6 KB, free: 530.3 MB)
16/05/05 22:27:04 INFO scheduler.TaskSetManager: Finished task 0.0 in stage 0.0 (TID_
↪0) in 652 ms on localhost (1/1)
16/05/05 22:27:04 INFO cluster.YarnScheduler: Removed TaskSet 0.0, whose tasks have_
↪all completed, from pool
16/05/05 22:27:04 INFO scheduler.DAGScheduler: ResultStage 0 (runJob at PythonRDD.
↪scala:393) finished in 4.558 s
16/05/05 22:27:04 INFO scheduler.DAGScheduler: Job 0 finished: runJob at PythonRDD.
↪scala:393, took 4.951328 s
[(0, 0), (1, 1), (2, 0), (3, 1), (4, 0), (5, 1), (6, 0), (7, 1), (8, 0), (9, 1)]
```

### Troubleshooting

If something goes wrong consult the [FAQ / Known issues](#) page.

### Further information

See the [Spark](#) and [PySpark](#) documentation pages for more information.

### How to Run with the YARN resource manager

#### Overview

This script runs on the Spark cluster with the YARN resource manager and returns the hostname of each node in the cluster.

#### Who is this for?

This how-to is for users of a Spark cluster who wish to run Python code using the YARN resource manager.

### Spark YARN Summary

1. *Before you start*



2. *Running the Job*
3. *Troubleshooting*
4. *Further information*

## Before you start

To execute this example, download the `cluster-spark-yarn.py` example script to your cluster.

For this example, you'll need Spark running with the YARN resource manager. You can install Spark and YARN using an enterprise Hadoop distribution such as [Cloudera CDH](#) or [Hortonworks HDP](#).

## Running the Job

Here is the complete script to run the Spark + YARN example in PySpark:

```
# cluster-spark-yarn.py
from pyspark import SparkConf
from pyspark import SparkContext

conf = SparkConf()
conf.setMaster('yarn-client')
conf.setAppName('spark-yarn')
sc = SparkContext(conf=conf)

def mod(x):
    import numpy as np
    return (x, np.mod(x, 2))

rdd = sc.parallelize(range(1000)).map(mod).take(10)
print rdd
```

Note: you may have to install NumPy with `cluster conda install numpy`.

Run the script on the Spark cluster with `spark-submit`. The output shows the first ten values that were returned from the `cluster-spark-basic.py` script.

```
16/05/05 22:26:53 INFO spark.SparkContext: Running Spark version 1.6.0

[...]

16/05/05 22:27:03 INFO scheduler.TaskSetManager: Starting task 0.0 in stage 0.0 (TID_
↳0, localhost, partition 0,PROCESS_LOCAL, 3242 bytes)
16/05/05 22:27:04 INFO storage.BlockManagerInfo: Added broadcast_0_piece0 in memory_
↳on localhost:46587 (size: 2.6 KB, free: 530.3 MB)
16/05/05 22:27:04 INFO scheduler.TaskSetManager: Finished task 0.0 in stage 0.0 (TID_
↳0) in 652 ms on localhost (1/1)
16/05/05 22:27:04 INFO cluster.YarnScheduler: Removed TaskSet 0.0, whose tasks have_
↳all completed, from pool
16/05/05 22:27:04 INFO scheduler.DAGScheduler: ResultStage 0 (runJob at PythonRDD.
↳scala:393) finished in 4.558 s
16/05/05 22:27:04 INFO scheduler.DAGScheduler: Job 0 finished: runJob at PythonRDD.
↳scala:393, took 4.951328 s
[(0, 0), (1, 1), (2, 0), (3, 1), (4, 0), (5, 1), (6, 0), (7, 1), (8, 0), (9, 1)]
```

### Troubleshooting

If something goes wrong consult the [FAQ / Known issues](#) page.

### Further information

See the [Spark](#) and [PySpark](#) documentation pages for more information.

## How to perform a word count on text data in HDFS

### Overview

This example counts the number of words in text files that are stored in HDFS.

### Who is this for?

This how-to is for users of a Spark cluster who wish to run Python code using the YARN resource manager that reads and processes files stored in HDFS.

### Spark Wordcount Summary

1. *Before you start*
2. *Load HDFS data*
3. *Running the Job*
4. *Troubleshooting*
5. *Further information*

### Before you start

To execute this example, download the `cluster-spark-wordcount.py` example script and the `cluster-download-wc-data.py` script.

For this example, you'll need Spark running with the YARN resource manager and the Hadoop Distributed File System (HDFS). You can install Spark, YARN, and HDFS using an enterprise Hadoop distribution such as [Cloudera CDH](#) or [Hortonworks HDP](#).

You will also need valid [Amazon Web Services](#) (AWS) credentials.

### Load HDFS data

First, we will load the sample text data into the HDFS data store. The following script will transfer sample text data (approximately 6.4 GB) from a public Amazon S3 bucket to the HDFS data store on the cluster.

Download the `cluster-download-wc-data.py` script to your cluster and Insert your Amazon AWS credentials in the `AWS_KEY` and `AWS_SECRET` variables.

```
import subprocess

AWS_KEY = ''
AWS_SECRET = ''

s3_path = 's3n://{0}:{1}@blaze-data/enron-email'.format(AWS_KEY, AWS_SECRET)
cmd = ['hadoop', 'distcp', s3_path, 'hdfs:///tmp/enron']
subprocess.call(cmd)
```

**Note:** The `hadoop distcp` command might cause HDFS to fail on smaller instance sizes due to memory limits.

Run the `cluster-download-wc-data.py` script on the Spark cluster.

```
python cluster-download-wc-data.py
```

After a few minutes, the text data will be in the HDFS data store on the cluster and ready for analysis.

## Running the Job

Download the `cluster-spark-wordcount.py` example script to your cluster. This script will read the text files downloaded in step 2 and count all of the words.

```
# cluster-spark-wordcount.py
from pyspark import SparkConf
from pyspark import SparkContext

HDFS_MASTER = 'HEAD_NODE_IP'

conf = SparkConf()
conf.setMaster('yarn-client')
conf.setAppName('spark-wordcount')
conf.set('spark.executor.instances', 10)
sc = SparkContext(conf=conf)

distFile = sc.textFile('hdfs://{0}:9000/tmp/enron/*/*.txt'.format(HDFS_MASTER))

nonempty_lines = distFile.filter(lambda x: len(x) > 0)
print 'Nonempty lines', nonempty_lines.count()

words = nonempty_lines.flatMap(lambda x: x.split(' '))

wordcounts = words.map(lambda x: (x, 1)) \
    .reduceByKey(lambda x, y: x+y) \
    .map(lambda x: (x[1], x[0])).sortByKey(False)

print 'Top 100 words:'
print wordcounts.take(100)
```

Replace the `HEAD_NODE_IP` text with the IP address of the head node.

Run the script on your Spark cluster using `spark-submit`. The output shows the top 100 words from the sample text data that were returned from the Spark script.

```
54.237.100.240: Using Spark's default log4j profile: org/apache/spark/log4j-defaults.
→properties
15/06/13 04:58:42 INFO SparkContext: Running Spark version 1.4.0
```

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```
[...]

15/06/26 04:32:03 INFO YarnScheduler: Removed TaskSet 7.0, whose tasks have all_
↳completed, from pool
15/06/26 04:32:03 INFO DAGScheduler: ResultStage 7 (runJob at PythonRDD.scala:366)_
↳finished in 0.210 s
15/06/26 04:32:03 INFO DAGScheduler: Job 3 finished: runJob at PythonRDD.scala:366,_
↳took 18.124243 s
[(288283320, ''), (22761900, '\t'), (19583689, 'the'), (13084511, '\t0'), (12330608,
↳'-'),
(11882910, 'to'), (11715692, 'of'), (10822018, '0'), (10251855, 'and'), (6682827, 'in
↳'),
(5463285, 'a'), (5226811, 'or'), (4353317, '/'), (3946632, 'for'), (3695870, 'is'),
(3497341, 'by'), (3481685, 'be'), (2714199, 'that'), (2650159, 'any'), (2444644,
↳'shall'),
(2414488, 'on'), (2325204, 'with'), (2308456, 'Gas'), (2268827, 'as'), (2265197, 'this
↳'),
(2180110, '$'), (1996779, '\t$0'), (1903157, '12:00:00'), (1823570, 'The'), (1727698,
↳'not'),
(1626044, 'such'), (1578335, 'at'), (1570484, 'will'), (1509361, 'has'), (1506064,
↳'Enron'),
(1460737, 'Inc.'), (1453005, 'under'), (1411595, 'are'), (1408357, 'from'), (1334359,
↳'Data'),
(1315444, 'have'), (1310093, 'Energy'), (1289975, 'Set'), (1281998, 'Technologies'),
(1280088, '*****'), (1238125, '\t-'), (1176380, 'all'), (1169961, 'other'),_
↳(1166151, 'its'),
(1132810, 'an'), (1127730, '&'), (1112331, '>'), (1111663, 'been'), (1098435, 'This'),
(1054291, '0\t0\t0\t0\t'), (1021797, 'States'), (971255, 'you'), (971180, 'which'),_
↳(961102, '.'),
(945348, 'I'), (941903, 'it'), (939439, 'provide'), (902312, 'North'), (867218,
↳'Subject:'),
(851401, 'Party'), (845111, 'America'), (840747, 'Agreement'), (810554, '#N/A\t'),_
↳(807259, 'may'),
(800753, 'please'), (798382, 'To'), (771784, '\t$-'), (753774, 'United'), (740472, 'if
↳'),
(739731, '\t0.00'), (723399, 'Power'), (699294, 'To:'), (697798, 'From:'), (672727,
↳'Date:'),
(661399, 'produced'), (652527, '2001'), (651164, 'format'), (650637, 'Email'),_
↳(646922, '3.0'),
(645078, 'licensed'), (644200, 'License'), (642700, 'PST'), (641426, 'cite'), (640441,
↳'Creative'),
(640089, 'Commons'), (640066, 'NSF'), (639960, 'EML'), (639949, 'Attribution'),
(639938, 'attribution'), (639936, 'ZL'), (639936, '(http://www.zlti.com)'),_
↳(639936, '"ZL'),
(639936, 'X-ZLID:'), (639936, '<http://creativecommons.org/licenses/by/3.0/us/>'),_
↳(639936, 'X-SDOC:')]

```

## Troubleshooting

If something goes wrong consult the [FAQ / Known issues](#) page.

## Further information

See the [Spark](#) and [PySpark](#) documentation pages for more information.

## How to do Natural Language Processing

### Overview

This example provides a simple PySpark job that utilizes the [NLTK library](#). NLTK is a popular Python package for natural language processing. This example will demonstrate the installation of Python libraries on the cluster, the usage of Spark with the YARN resource manager and execution of the Spark job.

### Who is this for?

This how-to is for users of a Spark cluster who wish to run Python code using the YARN resource manager. This how-to will show you how to integrate third-party Python libraries with Spark.

### Spark NLTK summary

1. *Before you start*
2. *Install NLTK*
3. *Running the Job*
4. *Troubleshooting*
5. *Further information*

### Before you start

To execute this example, download the: `cluster-spark-nltk.py` example script or `cluster-spark-nltk.ipynb` example notebook.

For this example you'll need Spark running with the YARN resource manager. You can install Spark and YARN using an enterprise Hadoop distribution such as [Cloudera CDH](#) or [Hortonworks HDP](#).

### Install NLTK

If you have permission to install packages with `acluster` you can install NLTK as a conda package.

```
acluster conda install nltk
```

You should see output similar to this from each node, which indicates that the package was successfully installed across the cluster:

```
Node "ip-10-140-235-89.ec2.internal":
  Successful actions: 1/1
Node "ip-10-154-10-144.ec2.internal":
  Successful actions: 1/1
Node "ip-10-31-96-152.ec2.internal":
  Successful actions: 1/1
```

In order to use the full NLTK library, you will need to download the data for the NLTK project. You can download the data on all cluster nodes by using the `acluster cmd` command.

```
acluster cmd 'sudo /opt/anaconda/bin/python -m nltk.downloader -d /usr/share/nltk_
↳data all'
```

After a few minutes you should see output similar to this.

```
Execute command "sudo /opt/anaconda/bin/python -m nltk.downloader -d /usr/share/nltk_
↳data all" target: "*" cluster: "d"
  All nodes (x3) response: [nltk_data] Downloading collection 'all'
[nltk_data] |
[nltk_data] | Downloading package abc to /usr/share/nltk_data...
[nltk_data] | Unzipping corpora/abc.zip.
[nltk_data] | Downloading package alpino to /usr/share/nltk_data...
[nltk_data] | Unzipping corpora/alpino.zip.
[nltk_data] | Downloading package biocreative_ppi to
[nltk_data] | /usr/share/nltk_data...
....
[nltk_data] | Unzipping models/bllip_wsj_no_aux.zip.
[nltk_data] | Downloading package word2vec_sample to
[nltk_data] | /usr/share/nltk_data...
[nltk_data] | Unzipping models/word2vec_sample.zip.
[nltk_data] |
[nltk_data] Done downloading collection all
```

## Running the Job

Here is the complete script to run the Spark + NLTK example in PySpark.

```
# cluster-spark-nltk.py
from pyspark import SparkConf
from pyspark import SparkContext

conf = SparkConf()
conf.setMaster('yarn-client')
conf.setAppName('spark-nltk')
sc = SparkContext(conf=conf)

data = sc.textFile('file:///usr/share/nltk_data/corpora/state_union/1972-Nixon.txt')

def word_tokenize(x):
    import nltk
    return nltk.word_tokenize(x)

def pos_tag(x):
```

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```
import nltk
return nltk.pos_tag([x])

words = data.flatMap(word_tokenize)
print words.take(10)

pos_word = words.map(pos_tag)
print pos_word.take(5)
```

Let's walk through the above code example. First, we will create a `SparkContext`. Note that Anaconda for cluster management will not create a `SparkContext` by default. In this example, we use the YARN resource manager.

```
from pyspark import SparkConf
from pyspark import SparkContext

conf = SparkConf()
conf.setMaster('yarn-client')
conf.setAppName('spark-nltk')
sc = SparkContext(conf=conf)
```

After a `SparkContext` is created, we can load some data into Spark. In this case, the data file is from one of the example documents provided by NLTK.

```
data = sc.textFile('file:///usr/share/nltk_data/corpora/state_union/1972-Nixon.txt')
```

Next, we write a function that imports `nltk` and calls `nltk.word_tokenize`. The function is mapped to the text file that was read in the previous step.

```
def word_tokenize(x):
    import nltk
    return nltk.word_tokenize(x)

words = data.flatMap(word_tokenize)
```

We can confirm that the `flatMap` operation worked by returning some of the words in the dataset.

```
print words.take(10)
```

Finally, NTLK's [POS-tagger](#) can be used to find the part of speech for each word.

```
def pos_tag(x):
    import nltk
    return nltk.pos_tag([x])

pos_word = words.map(pos_tag)
print pos_word.take(5)
```

Run the script on the Spark cluster using the `spark-submit` script. The output shows the words that were returned from the Spark script, including the results from the `flatMap` operation and the POS-tagger.

```
Using Spark's default log4j profile: org/apache/spark/log4j-defaults.properties
15/06/13 05:14:29 INFO SparkContext: Running Spark version 1.4.0

[...]

['Address',
```

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```
'on',
'the',
'State',
'of',
'the',
'Union',
'Delivered',
'Before',
'a']

[...]

[('Address', 'NN')],
[('on', 'IN')],
[('the', 'DT')],
[('State', 'NNP')],
[('of', 'IN')]]
```

## Troubleshooting

If something goes wrong consult the *FAQ / Known issues* page.

## Further information

See the [Spark](#) and [PySpark](#) documentation pages for more information.

For more information on NLTK see the *NLTK book* <<http://www.nltk.org/book/>>.

## How to do Image Processing with GPUs

### Overview

To demonstrate the capability of running a distributed job in PySpark using a GPU, this example uses [NumbaPro](#) and the CUDA platform for image analysis. This example executes 2-dimensional FFT convolution on images in grayscale and compares the execution time of CPU-based and GPU-based calculations.

### Who is this for?

This how-to is for users of a Spark cluster who wish to run Python code using the YARN resource manager. This how-to will show you how to integrate third-party Python libraries with Spark.

### Image processing summary

1. *Before you start*
2. *Install dependencies*
3. *Load data into HDFS*
4. *Running the Job*



- 5. *Troubleshooting*
- 6. *Further information*

## Before you start

For this example, you'll need Spark running with the YARN resource manager. You can install Spark and YARN using an enterprise Hadoop distribution such as [Cloudera CDH](#) or [Hortonworks HDP](#).

You will also need valid [Amazon Web Services \(AWS\)](#) credentials in order to download the example data.

For this example, we recommend the use of the GPU-enabled AWS instance type `g2.2xlarge` and the AMI `ami-12fd8178` (us-east-1 region), which has CUDA 7.0 and the NVIDIA drivers pre-installed. An example profile (to be placed in `~/.acluster/profiles.d/gpu_profile.yaml`) is shown below:

```
name: gpu_profile
node_id: ami-12fd8178 # Ubuntu 14.04, Cuda 7.0, us-east-1 region
node_type: g2.2xlarge
num_nodes: 4
provider: aws_east
user: ubuntu
```

To execute this example, download the: `spark-numbapro.py` example script or `spark-numbapro.ipynb` example notebook.

If you wish to use the `spark-numbapro.ipynb` example notebook the Jupyter Notebook plugin can be installed on the cluster using the following command:

```
acluster install notebook
```

Once the Jupyter Notebook plugin is installed, you can view Jupyter Notebook in your browser using the following command:

```
acluster open notebook
```

## Install dependencies

If you have permission to install packages with `acluster` you can install the required packages on all nodes using the following command.

```
acluster conda install scipy matplotlib numbapro PIL
```

## Load data into HDFS

First, we will load the sample text data into the HDFS data store. The following script will transfer sample image data (approximately 1.1 GB) from a public Amazon S3 bucket to the HDFS data store on the cluster.

Download the `cluster-download-data.py` script to your cluster and insert your Amazon AWS credentials in the `AWS_KEY` and `AWS_SECRET` variables.

```
import subprocess

AWS_KEY = 'YOUR_AWS_KEY'
AWS_SECRET = 'YOUR_AWS_SECRET'
```

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```
s3_path = 's3n://{0}:{1}@blaze-data/dogs-cats-img/images'.format(AWS_KEY, AWS_SECRET)
cmd = ['hadoop', 'distcp', s3_path, 'hdfs:///tmp/dogs-cats']
subprocess.call(cmd)
```

**Note:** The `hadoop distcp` command might cause HDFS to fail on smaller instance sizes due to memory limits.

Run the `cluster-download-data.py` script on the cluster.

```
python cluster-download-data.py
```

After a few minutes, the image data will be in the HDFS data store on the cluster and ready for analysis.

## Running the Job

Run the `spark-numbapro.py` script on the Spark cluster using `spark-submit`. The output shows the image processing execution times for the CPU-based vs. GPU-based calculations.

```
54.164.123.31: Using Spark's default log4j profile: org/apache/spark/log4j-defaults.
→properties
15/11/09 02:33:21 INFO SparkContext: Running Spark version 1.5.1

[...]

15/11/09 02:33:45 INFO TaskSetManager: Finished task 6.0 in stage 1.0 (TID 13)
in 106 ms on ip-172-31-9-24.ec2.internal (7/7)
15/11/09 02:33:45 INFO YarnScheduler: Removed TaskSet 1.0, whose tasks have
all completed, from pool
15/11/09 02:33:45 INFO DAGScheduler: ResultStage 1
(collect at /tmp/anaconda-cluster/spark-numbapro.py:106) finished in 4.844 s
15/11/09 02:33:45 INFO DAGScheduler: Job 1 finished:
collect at /tmp/anaconda-cluster/spark-numbapro.py:106, took 4.854970 s

10 images
CPU: 6.91735601425
GPU: 4.88133311272

[...]

15/11/09 02:34:27 INFO TaskSetManager: Finished task 255.0 in stage 3.0 (TID 525)
in 139 ms on ip-172-31-9-24.ec2.internal (256/256)
15/11/09 02:34:27 INFO YarnScheduler: Removed TaskSet 3.0, whose tasks have
all completed, from pool
15/11/09 02:34:27 INFO DAGScheduler: ResultStage 3
(collect at /tmp/anaconda-cluster/spark-numbapro.py:126) finished in 19.340 s
15/11/09 02:34:27 INFO DAGScheduler: Job 3 finished:
collect at /tmp/anaconda-cluster/spark-numbapro.py:126, took 19.400670 s

500 images
CPU: 22.1282501221
GPU: 19.8209779263
```

## Troubleshooting

If something goes wrong consult the [FAQ / Known issues](#) page.

## Further information

See the [Spark](#) and [PySpark](#) documentation pages for more information.

For more information on NumbaPro see the [NumbaPro documentation](#).

## Using Anaconda with Cloudera CDH

NOTE: This page is superseded, please see <https://docs.continuum.io/anaconda-scale/cloudera-cdh>

There are two methods of using Anaconda on an existing cluster with [Cloudera CDH](#), Cloudera's Distribution Including Apache Hadoop: 1) the [Anaconda parcel for Cloudera CDH](#), and 2) Anaconda for cluster management. The instructions below describe how to uninstall the Anaconda parcel on a CDH cluster and transition to Anaconda for cluster management.

## Uninstalling the Anaconda parcel

If the Anaconda parcel is installed on the CDH cluster, use the following steps to uninstall the parcel. Otherwise, you can skip to the next section.

1. From the Cloudera Manager Admin Console, click the Parcels indicator in the top navigation bar.
2. Click the `Deactivate` button to the right of the Anaconda parcel listing.
3. Click `OK` on the Deactivate prompt to deactivate the Anaconda parcel and restart Spark and related services.
4. Click the arrow to the right of the Anaconda parcel listing and choose `Remove From Hosts`, which will prompt with a confirmation dialog.
5. The Anaconda parcel has been removed from the cluster nodes.

For more information about managing Cloudera parcels, refer to the [Cloudera documentation](#).

## Using Anaconda for cluster management

Anaconda for cluster management provides additional functionality, including the ability to manage multiple conda environments and packages (including Python and R) alongside an existing CDH cluster.

1. Configure the nodes with Anaconda for cluster management using the [Bare-metal Cluster Setup instructions](#).
2. During this process, you will create a profile and provider that describes the cluster.
3. Provision the cluster using the following command, replacing `cluster-cdh` with the name of your cluster and `profile-cdh` with the name of your profile:

```
$ acluster create cluster-cdh -p profile-cdh
```

4. You can submit Spark jobs along with the `PYSPARK_PYTHON` environment variable that refers to the location of Anaconda, for example:

```
$ PYSPARK_PYTHON=/opt/anaconda/bin/python spark-submit pyspark_script.py
```

### Support

#### Priority support

Support is included with the purchase of an Anaconda subscription. Please contact Anaconda for cluster management support at [ac\\_support@anaconda.com](mailto:ac_support@anaconda.com).

#### Report a bug

If you think you may have encountered a bug, please contact Anaconda for cluster management support at [ac\\_support@anaconda.com](mailto:ac_support@anaconda.com).

#### Additional nodes

With the unlicensed, unsupported version of Anaconda for cluster management, you can create and manage up to four cluster nodes. To request a license to manage more cluster nodes, please contact your account representative or [sales@anaconda.com](mailto:sales@anaconda.com).

#### Training and consulting

Training and consulting is available for Anaconda for cluster management and all Anaconda products. For more information, please contact your account representative or [sales@anaconda.com](mailto:sales@anaconda.com).

#### FAQ / Known issues

- *[Product FAQ](#)*
- *[Technical FAQ](#)*
- *[Troubleshooting FAQ](#)*
- *[Known Issues](#)*

#### Product FAQ

##### **Does Anaconda for cluster management work with a cluster that already has a managed Spark/Hadoop stack?**

Yes, Anaconda for cluster management can be installed alongside enterprise Hadoop distributions such as Cloudera CDH or Hortonworks HDP and can be used to manage Python and R conda packages and environments across a cluster.

##### **Does Anaconda for cluster management offer integration with Anaconda Repository or Anaconda Cloud?**

Yes, conda packages can be installed from Anaconda Repository or [Anaconda Cloud](#) by using channel specifications. Refer to the documentation regarding *[Installing packages from channels](#)* for more details.

##### **Which cloud providers does Anaconda for cluster management support?**

Currently Anaconda for cluster management offers full support for Amazon Elastic Compute Cloud (EC2). Other providers such as Microsoft Azure, Google Cloud Platform, Rackspace, and others are on our roadmap. If you are interested in a cloud provider that is not listed here, please contact us at [sales@anaconda.com](mailto:sales@anaconda.com).

**Can I use Anaconda for cluster management with a different cloud provider?**

Yes, you can manually create instances on another cloud provider, then provision the nodes as if you were using a bare-metal cluster. Refer to the [Bare-metal Cluster Setup](#) documentation for more information.

**Does Anaconda for cluster management support Amazon EMR?**

Anaconda for cluster management does not support Amazon Elastic MapReduce (EMR), which provides a managed Hadoop framework in the cloud. Anaconda for cluster management can be used to manage conda packages and environments across a cluster. Anaconda for cluster management does support Amazon EC2.

**Technical FAQ****Which versions of Python does Anaconda for cluster management support?**

Some of the plugins have dependencies that require the use of Python 2. Therefore, by default, Anaconda for cluster management installs Miniconda with Python 2 into the root conda environment.

However, you can easily create a new conda environment on the cluster with Python 3, or you can specify a different root version of Anaconda/Miniconda in the profile.

**Which network ports need to be accessible from the client machine and cluster nodes?**

From the client machine to the cluster nodes, you will need access to ports 22, 4505, and 4506 to provision the cluster via SSH and Salt. For communication between the cluster nodes, Salt uses ports 4505 and 4506.

**Can I use Anaconda for cluster management with iptables and SELinux?**

Yes, you can customize the security behavior of Anaconda for cluster management when creating or provisioning a cluster using the Security settings in the profile. Refer to the [Profile settings](#) documentation for more information.

**Troubleshooting FAQ****Errors when creating or provisioning a cluster**

Verify the following:

- The contents of your SSH private key are correct (and set to 600 permissions on Mac/Linux)
- The user name in your profile (e.g., `user: ubuntu`) is defined correctly
- Profile settings are defined correctly in `~/.acluster/profiles.d/<profile_name>.yaml`
- Provider settings are defined correctly in `~/.acluster/providers.yaml`

**Known Issues****No matching SLS error (Salt)**

When installing a plugin during cluster creation/provisioning or using the `acluster install` command, you might receive an error similar to:

```
===== Standard output =====
ip-10-144-206-102.ec2.internal:
- No matching sls found for 'cdh5.hdfs' in env 'base'
=====
```

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```
Fatal error: One or more hosts failed while executing task 'parallel_sudo'

Aborting.
One or more hosts failed while executing task 'parallel_sudo'
```

This is a known issue with Salt that periodically occurs. You can reprovision or reinstall the plugin that failed, and the installation should succeed.

### Theading error when creating a cluster

When creating/provisioning a cluster, you might receive an error similar to:

```
Uploading formulas
INFO: Uploading formulas to head
Syncing formulas
INFO: Syncing formulas across the cluster
Done
Exception in thread Thread-6 (most likely raised during interpreter shutdown):
Exception in thread Thread-8 (most likely raised during interpreter shutdown):
```

This is a known issue with Paramiko/Fabric. You can safely disregard this message. This issue was resolved in Anaconda for cluster management 1.3.1.

## Release notes

Below is a summary of features, bug fixes, and improvements for each Anaconda for cluster management release.

### Anaconda for cluster management 1.4.4

Note: This is the last feature release of Anaconda for cluster management. Anaconda for cluster management has been replaced by [Anaconda Scale](#).

Backend improvements:

- Use full paths for system commands

### Anaconda for cluster management 1.4.3

Backend improvements:

- Fix license check and support information

### Anaconda for cluster management 1.4.2

Features:

- Updates to examples in documentation

Backend improvements:

- Improved group configuration/detection on RHEL/CentOS
- Enabled configuration of `anaconda` group name

### Anaconda for cluster management 1.4.1

Features:

- Renamed `distributed` plugin to `dask`
- Enabled `notebook` and `dask` plugins to be installed alongside existing Hadoop installations

- Added `conda` profile plugin setting for `ssl_verify`

### **Anaconda for cluster management 1.4.0**

#### Features:

- Added setting for `channel_alias` for improved integration with Anaconda Repository

#### Bug Fixes:

- Fixed provisioning on Windows client machines
- Fixed issue with profile setting for `conda` access control lists
- Fixed issue with certain plugin status checks
- Fixed issue with Storm plugin installation

#### Backend improvements:

- Improved management and configurability of `distributed` plugin
- Updated version of Apache Libcloud dependency (0.20.1)
- Updated to accept new license format (backwards compatible with existing licenses)
- Removed deprecated `acluster submit` command due to inconsistencies with environments
- Removed `acluster defaultenv` and `acluster setenv` commands due to inconsistencies with environments
- Consolidated sample profile to a single profile

### **Anaconda for cluster management 1.3.3**

#### Bug Fixes:

- Fixed SSH private key permissions check

#### Backend improvements:

- Implemented Salt ACL functionality
- Implemented Salt PAM authentication
- Removed sudo requirement after install

### **Anaconda for cluster management 1.3.2**

#### Bug Fixes:

- Fixed installation prefix and default channel documentation and tests

#### Backend improvements:

- Improved detection of plugin installations and plugin status messages

### **Anaconda for cluster management 1.3.1**

#### Features:

- Updated plugin: Spark 1.6
- Added option to disable creation of `/etc/profile.d/conda.sh` on cluster nodes

#### Bug Fixes:

- Fixed R path for Jupyter Notebook
- Fixed issue with Amazon EC2 block device mapping

- Fixed issue with configuration of default conda channels
- Improved warnings for misconfigured SSH keys
- Improved error message when AWS Key Pair is missing

Backend improvements:

- Added configurable download URLs for plugins (used for airgap installations): Elasticsearch, Logstash, Kibana, Storm
- Added deprecated warning for `acluster submit` command due to inconsistencies with environments
- Added detection for enterprise Hadoop installations and warns before installing conflicting services
- Configured HDFS for short-circuit reads by default
- Pinned versions of dependencies in conda recipe

### Anaconda for cluster management 1.3.0

Features:

- Simplified bare-metal cluster setup using profile/provider instead of clusters.d
- Added ability to specify conda packages and environments in profile plugin settings
- Switched to system-wide `.condarc` file for users on cluster nodes
- Added centralized logging via Elasticsearch, Logstash, and Kibana plugins
- Added `--no-browser` option for `acluster open` command
- Added license information to `acluster info`
- Removed optional `security_group` setting from `providers.yaml` template and documentation
- Added `vpc_id` setting for Amazon EC2 to use with default security group
- Improved documentation for bare-metal and cloud-based cluster creation
- Added more information about requirements, FAQs, and known issues to documentation

Bug Fixes:

- Improved error messages for cloud providers, security groups, and when no clusters are defined
- Fixed error when command output contained Unicode characters
- Fixed repeated prompts when installing multiple plugins

Backend improvements:

- Added test for SSH connectivity during bare-metal cluster creation
- Added detection/removal of orphaned clusters upon `acluster destroy`
- Added detection/installation of missing `sudo/bzip2` packages upon cluster creation

### Anaconda for cluster management 1.2.2

Features:

- Moved bare metal cluster setup to profile and provider files
- Ability to specify private IPs for VPC clusters on Amazon EC2

### Anaconda for cluster management 1.2.1

Features:



- Updated plugin: Spark 1.5.1
- Consistent output when listing clusters and profiles
- New blog post and updated documentation

Bug Fixes:

- Removed duplicate error messages
- Fixed notebook plugin formulas

**Anaconda for cluster management 1.2.0**

Features:

- Dedicated salt/supervisor environments
- New cluster profile (no nesting)
- Documentation updates
- Improvements to CLI output

Bug Fixes:

- Storm plugin
- Notebook plugin
- Logstash plugin
- Kibana plugin
- Elasticsearch plugin
- Windows Fixes: push/submit

Backend improvements:

- Refactor status/stop/restart and plugin loading
- Refactor connection object
- Multiple backends (initial work)

**Anaconda for cluster management 1.1.0**

- Improved Jenkins testing
- Added Storm plugin
- Added Elasticsearch/Logstash/Kibana plugins (ELK stack)
- Added Dask plugin
- Fixes for single-node installations
- Profile updates
- Add setting for AWS Tags
- Added security options (SELinux/iptables)
- Added setting for notebook password

**Anaconda for cluster management 1.0.0**

- CLI rewrite
- Aggregated and improved CLI messaging

- Backend library refactoring
- Salt-packaging refactoring
- Easier bare-metal installation
- Added option for streaming output
- Fixed issue with Ganglia on Ubuntu
- Windows/libcloud Compatibility
- Added licensing with new CLI
- Conda remote fixes
- Install Anaconda/Miniconda from custom url

## Glossary

**Anaconda** A downloadable free, open source, high performance, optimized Python and R distribution with 100+ packages plus access to easily installing an additional 620+ popular open source packages for data science including advanced and scientific analytics. It also includes `conda`, an open source package, dependency and environment manager. Thousands more open source packages can be installed with the `conda` command. Available for Windows, OS X and Linux, all versions are supported by the community.

**Bare-metal cluster** On-site or in-house machines, collections of virtual machines (Vagrant, Docker, etc.), or previously instantiated cloud nodes.

**Cloud-based cluster** A cluster that consists of machines in a cloud provider such as Amazon EC2.

**Cluster** A group of computers that work in parallel to perform a single task. Also called “parallel computing” since the compute nodes can perform their operations in parallel.

**Client machine** The laptop or workstation that contains Anaconda for cluster management and manages the cluster nodes.

**Cluster file** The file that defines the configuration including the location of the head node, compute nodes, and authentication/configuration information.

**Compute node** The machines managed by the head node that all work together to complete a single task.

**Conda** Conda is an open source package management system and environment management system for installing multiple versions of software packages and their dependencies and switching easily between them. It works on Windows, Mac, and Linux. It was created for Python packages, but is able to package and distribute any software. Conda is included in all versions of Anaconda, Anaconda Server, and Miniconda.

**Head node** A system configured to act as the intermediary between the cluster and the outside network. Can also be referred to as the master or edge node.

**Miniconda** A minimal or “bootstrap” version of Anaconda. Installs only what you need to get conda running, including Python, conda, and its dependencies.

**PEM key** Privacy enhanced electronic mail file, originally for email and now a general file format for cryptographic keys. In Anaconda for cluster management, this is used for cloud-based clusters and can be obtained from the cloud provider.

**Plugin** In Anaconda for cluster management, plugins are analytics engines and management services that can be installed on a cluster.

**Profile** A configuration file that defines how a cluster should be configured. It contains information about the number and types of cluster nodes, plugins, and other settings.

**Provider** Configuration file that defines settings for cloud or bare metal providers. A provider is referenced by a profile and used to provision resources.

#### 4.4.4 Anaconda Launcher

---

**Note:** This product is discontinued. This archived copy of the product documentation is provided for those customers who are still using it.

---

##### Anaconda Launcher is now deprecated

As of Anaconda 4.0, Anaconda Launcher has been replaced by *Anaconda Navigator*. This section has been left in place as a reference for users of earlier versions of Anaconda. Some users who have upgraded from an earlier version may have both Navigator and Launcher installed, which is harmless.

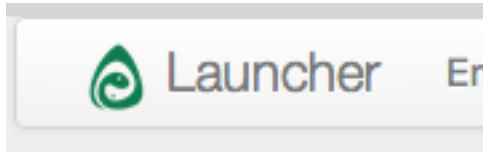
Launcher can be uninstalled with a single command:

```
conda remove launcher
```

##### Anaconda Launcher commands

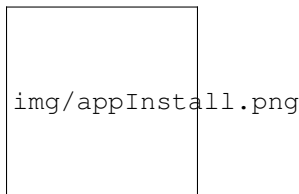
###### Refresh Application List

Click on **Launcher** to refresh the apps display.



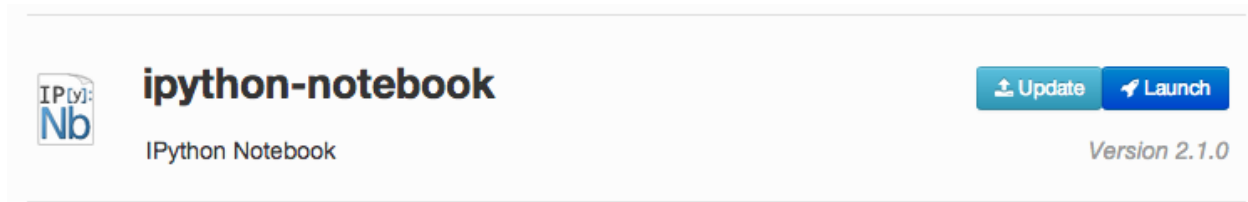
###### Install Listed Application

Click on the green **Install** button to install the desired app.



###### Launch Application

Click on the **Launch** button to launch the application.

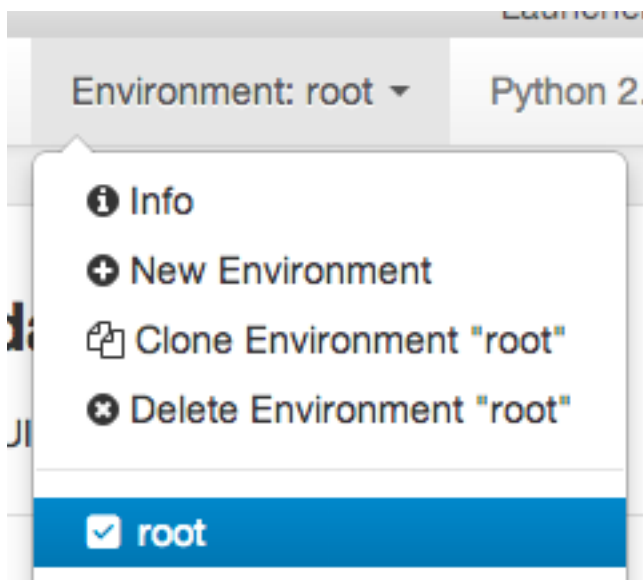


## Update Application

Click on the **Update** button to update the application.

## Change Environments

To change the current Environment, click on the **Environment:** pull down menu item and select the desired environment to make it active.



## Environment Information

To get a summary of the current environment, click on the **Environment:** menu item and select info.

You can also get a summary of the environment by click on the **Python version** menu item.



### Create New Environment

To create a new environment, click on the **Environment:** menu item and select **New Environment**.

When the **Create New Environment** dialog appears, enter the name of the new environment, select the desired **Python Version**, and click **Submit**.



### Clone Environment

To clone an environment, click on the **Environment:** menu item and select **Clone Environment**.

When the **Clone Environment** dialog appears, enter the name of the new environment and click **Submit**.

## Clone Environment root X

New Environment Name

Cancel Submit

### Delete Environment

To delete an environment, click on the **Environment:** menu item and select **Delete Environment**.

When the **Confirm Delete Environment** dialog appears, click **Yes** to delete the environment.

## Confirm Delete Environment

Are you sure you want to delete environment alpug?

Cancel Yes

### Manage Channels

To manage your current package channels, click on the **Manage Channels** menu item.

## Manage Conda Channels x

Enter a Binstar username or a URL. Conda will search these channels for packages. If the channel `defaults` is not present, Conda will not search the default channels.

[Online configuration help](#)

Add Channel

defaults
x

tpowell
x

Cancel
Submit

### Add Channel

Enter your channel into the text field to the left of the **Add Channel** button.

Click on the **Add Channel** to add your channel to your `.condarc` file.

### Remove Channel

Click on the **x** button to the right of the channel name you would like to remove.

Click **Cancel** to removed the changes to your channels.

Click **Submit** to save the channel updates.

### Anaconda Launcher Info

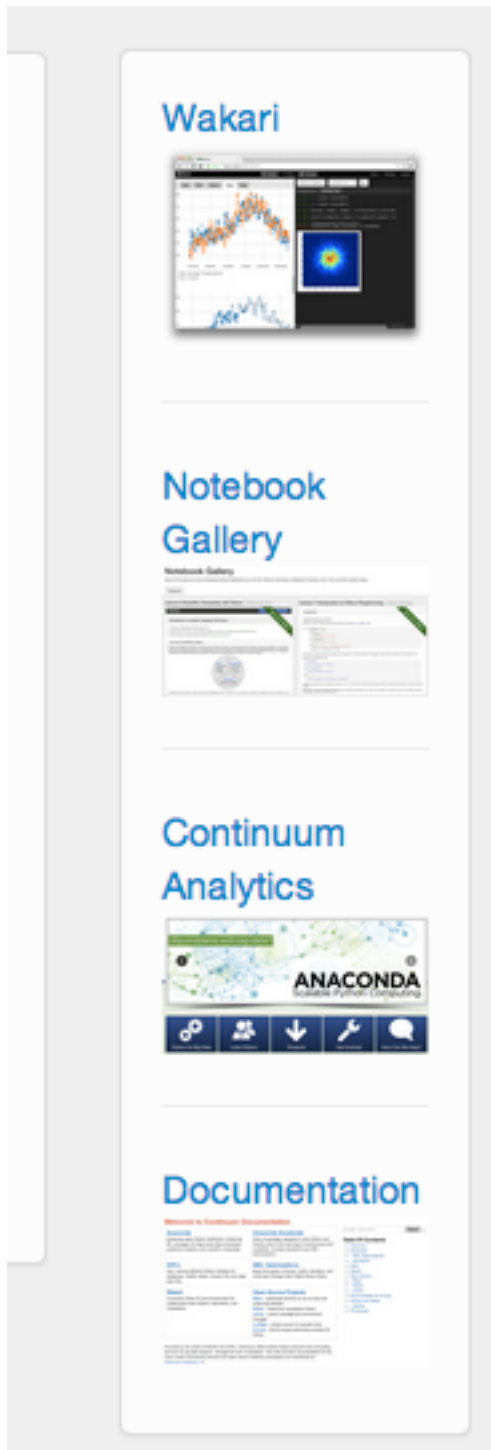
For Anaconda Launcher details, click on the version number in the upper right hand corner of the Anaconda Launcher Window.



img/launcherInfo.png

### Other Helpful Links

Along the right side of the launcher are some helpful links to additional documentation and various Anaconda and Anaconda Sponsored websites.





## 4.4.5 Anaconda Scale

### *Distributed Computing*

---

**Note:** This product is discontinued. This archived copy of the product documentation is provided for those customers who are still using it.

---

Anaconda Scale provides functionality to easily deploy Anaconda® packages and a distributed computation framework across a cluster. It helps you manage multiple conda environments and packages—including Python and R—on cluster nodes.

Anaconda Scale provides different options for deploying Anaconda on a cluster, including:

- Centrally managed installation of Anaconda, including multiple environments such as Python and R
- Anaconda parcel for Cloudera CDH, including custom-generated parcels
- Deployment of conda packages and environments with Spark jobs

### Features

- Easily install Anaconda—including [Anaconda Accelerate](#)—across multiple cluster nodes
- Provision distributed compute services with Dask
- Perform interactive, distributed computations with single-user Jupyter Notebook
- Easily launch and configure a cloud-based cluster on Amazon EC2

### Compatibility

Anaconda Scale can be used with distributed computation frameworks such as Spark or Dask and works alongside enterprise Hadoop distributions such as Cloudera CDH or Hortonworks HDP. Anaconda Scale has been tested with the following Hadoop distributions and Spark versions:

- Cloudera CDH 5.3.x through 5.11.x
- Hortonworks HDP 2.2.x through 2.6.x (with Apache Ambari 2.2.x and 2.4.x)
- Spark 1.3.x through 2.0.x

### License

Anaconda Scale is available with [Anaconda Enterprise](#). If you would like to use Anaconda Scale with a cluster on a bare-metal, on-premises, or cloud-based cluster, please [contact us](#).

### Using Scale

#### Installation

Anaconda Scale is installed and managed using the Anaconda platform installer, Anaconda Adam. For more information on installation, security, account, network and other Anaconda Scale requirements, see the [system requirements for Anaconda Adam](#). For more information about the installation process, see [the Anaconda Adam installation instructions](#).

After installing Anaconda Adam and provisioning a cluster, you can install a centrally managed version of Anaconda—including [Anaconda Accelerate](#)—on all of the cluster nodes using:

```
$ adam scale -n <cluster-name> cluster install
```

To install Dask and Distributed and then start Distributed workers on all of the cluster nodes, use:

```
$ adam scale -n <cluster-name> dask install
```

To install a single-user Jupyter Notebook server on the head node of the cluster, use:

```
$ adam scale -n <cluster-name> notebook install
```

## User guide

Using Anaconda Scale with Anaconda Adam, you can create and manage conda packages, including Python and R, in multiple conda environments across your nodes. You can prepend `adam scale` to a subset of familiar conda commands to install and manage conda packages and environments across a cluster.

```
$ adam scale -n cluster conda --help
Usage: adam conda [OPTIONS] COMMAND [ARGS]...

Options:
  -h, --help            Show this message and exit.

Commands:
  create  Create conda environment
  info    Get information about conda installation
  install Install package(s)
  list    List conda packages
  remove  Remove package(s)
  update  Update package(s)
```

By default, the root conda environment is installed in `/opt/continuum/anaconda` on all of the cluster nodes, which can be configured for a different location. You can manage multiple conda environments across the same cluster, such as Python 2, Python 3 and R, without affecting the framework installation of Python on the cluster nodes.

## Getting started

You can get started with Anaconda Scale by using Anaconda Adam, the Anaconda platform installer. See the [Anaconda Adam documentation](#) for more information.

With Anaconda Adam, you can install Anaconda Scale on a bare-metal cluster or existing cloud-based cluster. You can also use Anaconda Scale to easily launch and provision a cloud-based cluster with Anaconda. See the [Anaconda Adam installation instructions](#) for more information.

## Tasks

- [General functions](#)
- [Using Anaconda with Cloudera CDH](#)
- [Configuring Anaconda with Spark](#)

## Cheatsheet

Download the `Scale cheat sheet` (48 KB PDF) for a quick guide to using Anaconda Scale.

## General functions

### Installing conda packages

Install conda packages on the cluster nodes using `adam scale conda install`.

EXAMPLE: To install NumPy and pandas and their dependencies into the root conda environment on a cluster named `cluster`:

```
$ adam scale -n cluster conda install numpy pandas
All nodes (x4) response:
{
  "actions": {
    "LINK": [
      "mkl-11.3.3-0 /opt/continuum/anaconda/pkgs 1",
      "openssl-1.0.2h-1 /opt/continuum/anaconda/pkgs 1",
      "sqlite-3.13.0-0 /opt/continuum/anaconda/pkgs 1",
      "zlib-1.2.8-3 /opt/continuum/anaconda/pkgs 1",
      "python-2.7.11-5 /opt/continuum/anaconda/pkgs 1",
      "conda-env-2.5.1-py27_0 /opt/continuum/anaconda/pkgs 1",
      "numpy-1.11.0-py27_2 /opt/continuum/anaconda/pkgs 1",
      "pycosat-0.6.1-py27_1 /opt/continuum/anaconda/pkgs 1",
      "pytz-2016.4-py27_0 /opt/continuum/anaconda/pkgs 1",
      "pyyaml-3.11-py27_4 /opt/continuum/anaconda/pkgs 1",
      "requests-2.10.0-py27_0 /opt/continuum/anaconda/pkgs 1",
      "ruamel_yaml-0.11.7-py27_0 /opt/continuum/anaconda/pkgs 1",
      "setuptools-23.0.0-py27_0 /opt/continuum/anaconda/pkgs 1",
      "six-1.10.0-py27_0 /opt/continuum/anaconda/pkgs 1",
      "wheel-0.29.0-py27_0 /opt/continuum/anaconda/pkgs 1",
      "conda-4.1.4-py27_0 /opt/continuum/anaconda/pkgs 1",
      "pip-8.1.2-py27_0 /opt/continuum/anaconda/pkgs 1",
      "python-dateutil-2.5.3-py27_0 /opt/continuum/anaconda/pkgs 1",
      "pandas-0.18.1-np111py27_0 /opt/continuum/anaconda/pkgs 1"
    ],
    "PREFIX": "/opt/continuum/anaconda",
  },
  "success": true
}
```

### Creating conda environments

Create multiple conda environments on the cluster nodes using `adam scale conda create`.

EXAMPLE: To create a conda environment called `py3` with Python 3 on a cluster named `cluster`:

```
$ adam scale -n cluster conda create -n py3 python=3
All nodes (x4) response:
{
  "actions": {
    "LINK": [
```

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```

        "openssl-1.0.2h-1 1 None",
        "readline-6.2-2 1 None",
        "sqlite-3.13.0-0 1 None",
        "tk-8.5.18-0 1 None",
        "xz-5.2.2-0 1 None",
        "zlib-1.2.8-3 1 None",
        "python-3.5.1-5 1 None",
        "setuptools-23.0.0-py35_0 1 None",
        "wheel-0.29.0-py35_0 1 None",
        "pip-8.1.2-py35_0 1 None"
    ],
    "PREFIX": "/opt/continuum/anaconda/envs/py3",
    "SYMLINK_CONDA": [
        "/opt/continuum/anaconda"
    ],
},
"success": true
}

```

## Updating conda packages

Update conda packages on the cluster nodes using `adam scale conda update`.

**EXAMPLE:** To update pandas and its dependencies in the root conda environment on a cluster named `cluster`:

```

$ adam scale -n cluster conda update pandas
All nodes (x4) response:
{
  "actions": {
    "LINK": [
      "pandas-0.18.1-np111py27_0 1 None"
    ],
    "PREFIX": "/opt/continuum/anaconda",
    "SYMLINK_CONDA": [
      "/opt/continuum/anaconda"
    ],
    "UNLINK": [
      "pandas-0.18.0-np111py27_0"
    ],
  },
  "success": true
}

```

## Removing conda packages or environments

Remove conda packages on the cluster nodes using `adam scale conda remove`.

**EXAMPLE:** To remove pandas from the root conda environment on a cluster named `cluster`:

```

$ adam scale -n cluster conda remove pandas
All nodes (x4) response:
{
  "actions": {
    "PREFIX": "/opt/continuum/anaconda",

```

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```

    "UNLINK": [
        "pandas-0.18.1-np111py27_0"
    ],
},
"success": true
}

```

Remove conda environments on the cluster nodes using `adam scale conda remove`.

EXAMPLE: To remove an environment called `py3` on a cluster named `cluster`:

```

$ adam scale -n cluster conda remove -n py3 --all
All nodes (x4) response:
{
  "actions": {
    "PREFIX": "/opt/continuum/anaconda/envs/py3",
    "UNLINK": [
      "openssl-1.0.2j-0",
      "pip-8.1.2-py35_0",
      "python-3.5.2-0",
      "readline-6.2-2",
      "setuptools-27.2.0-py35_0",
      "sqlite-3.13.0-0",
      "tk-8.5.18-0",
      "wheel-0.29.0-py35_0",
      "xz-5.2.2-0",
      "zlib-1.2.8-3"
    ]
  },
  "success": true
}

```

## Listing conda packages

List conda packages on the cluster nodes using `adam scale conda list`.

EXAMPLE: To list conda packages in the root conda environment on a cluster named `cluster`:

```

$ adam scale -n cluster conda list
All nodes (x4) response:
+-----+-----+-----+
| Package      | Version | Build  |
+-----+-----+-----+
| numpy         | 1.11.0  | py27_2 |
| conda-env     | 2.5.1   | py27_0 |
| tk            | 8.5.18  | 0      |
| pip           | 8.1.2   | py27_0 |
| readline      | 6.2     | 2      |
| setuptools    | 23.0.0  | py27_0 |
| openssl       | 1.0.2h  | 1      |
| pycosat       | 0.6.1   | py27_1 |
| python-dateutil | 2.5.3   | py27_0 |
| sqlite        | 3.13.0  | 0      |
| pytz          | 2016.4  | py27_0 |
| mkl           | 11.3.3  | 0      |

```

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yaml	0.1.6	0	
ruamel_yaml	0.11.7	py27_0	
zlib	1.2.8	3	
pyyaml	3.11	py27_4	
requests	2.10.0	py27_0	
wheel	0.29.0	py27_0	
python	2.7.11	5	
conda	4.1.4	py27_0	
pycrypto	2.6.1	py27_0	
six	1.10.0	py27_0	
+-----+-----+-----+			

## Getting conda information

View information about the conda installation on the cluster nodes using `adam scale conda info`.

**EXAMPLE:** To view information about the root conda environment on a cluster named `cluster`:

```
$ adam scale -n cluster conda info
All nodes (x4) response:
Current conda install:

    platform : linux-64
    conda version : 4.1.4
    conda-env version : 2.5.1
    conda-build version : not installed
    python version : 2.7.11.final.0
    requests version : 2.10.0
    root environment : /opt/continuum/anaconda (writable)
    default environment : /opt/continuum/anaconda
    envs directories : /opt/continuum/anaconda/envs
    package cache : /opt/continuum/anaconda/pkgs
    channel URLs : https://repo.anaconda.com/pkgs/free/linux-64/
                  https://repo.anaconda.com/pkgs/free/noarch/
                  https://repo.anaconda.com/pkgs/pro/linux-64/
                  https://repo.anaconda.com/pkgs/pro/noarch/
    config file : None
    offline mode : False
    is foreign system : False
```

Or to view a list of conda environments on the cluster nodes:

```
$ adam scale -n cluster conda info -e
All nodes (x4) response:
# conda environments:
#
py27                /opt/continuum/anaconda/envs/py27
py35                /opt/continuum/anaconda/envs/py35
r                   /opt/continuum/anaconda/envs/r
root                * /opt/continuum/anaconda
```

## Managing conda with environment definition files

Manage conda environments on the cluster nodes using `adam scale env`:

```
$ adam scale -n cluster env
Usage: adam scale env [OPTIONS] COMMAND [ARGS]...
```

## Options:

```
-h, --help Show this message and exit.
```

## Commands:

```
create Create conda environment
list List conda environments
remove Remove conda environment
update Update conda environment
```

This functionality uses `conda-env` and conda environment environment definition–YAML–files.

EXAMPLE: The following `environment.yml` file describes a conda environment named `my-env` with Python 2.7 and additional packages:

```
name: my-env
channels:
- defaults
dependencies:
- python=2.7.*
- bokeh
- dask
- distributed
- pandas
```

Use `adam scale env create` to create a conda environment based on the above conda environment definition file `environment.yml`:

```
$ adam scale -n cluster env create -f environment.yml
All nodes (x4) response:
```

```
{
  "actions": {
    "EXTRACT": [
      "msgpack-python-0.4.8-py27_0",
      "numpy-1.11.2-py27_0",
      "psutil-5.0.0-py27_0",
      "pytz-2016.7-py27_0",
      "tblib-1.3.0-py27_0",
      "python-dateutil-2.6.0-py27_0",
      "zict-0.1.0-py27_0",
      "pandas-0.19.1-np111py27_0",
      "tornado-4.4.2-py27_0",
      "bokeh-0.12.3-py27_0",
      "dask-0.12.0-py27_0",
      "distributed-1.14.1-py27_0"
    ],
    "FETCH": [
      "msgpack-python-0.4.8-py27_0",
      "numpy-1.11.2-py27_0",
      "psutil-5.0.0-py27_0",
      "pytz-2016.7-py27_0",
      "tblib-1.3.0-py27_0",
      "python-dateutil-2.6.0-py27_0",
      "zict-0.1.0-py27_0",
      "pandas-0.19.1-np111py27_0",
```

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```

    "tornado-4.4.2-py27_0",
    "bokeh-0.12.3-py27_0",
    "dask-0.12.0-py27_0",
    "distributed-1.14.1-py27_0"
],
"LINK": [
    "mkl-11.3.3-0 1",
    "openssl-1.0.2j-0 1",
    "readline-6.2-2 1",
    "sqlite-3.13.0-0 1",
    "tk-8.5.18-0 1",
    "yaml-0.1.6-0 1",
    "zlib-1.2.8-3 1",
    "python-2.7.12-1 1",
    "backports-1.0-py27_0 1",
    "backports_abc-0.4-py27_0 1",
    "click-6.6-py27_0 1",
    "cloudpickle-0.2.1-py27_0 1",
    "futures-3.0.5-py27_0 1",
    "heapdict-1.0.0-py27_1 1",
    "loket-0.2.0-py27_1 1",
    "markupsafe-0.23-py27_2 1",
    "msgpack-python-0.4.8-py27_0 1",
    "numpy-1.11.2-py27_0 1",
    "psutil-5.0.0-py27_0 1",
    "pytz-2016.7-py27_0 1",
    "pyyaml-3.12-py27_0 1",
    "requests-2.11.1-py27_0 1",
    "setuptools-27.2.0-py27_0 1",
    "six-1.10.0-py27_0 1",
    "tblib-1.3.0-py27_0 1",
    "toolz-0.8.0-py27_0 1",
    "wheel-0.29.0-py27_0 1",
    "chest-0.2.3-py27_0 1",
    "jinja2-2.8-py27_1 1",
    "partd-0.3.6-py27_0 1",
    "pip-9.0.1-py27_0 1",
    "python-dateutil-2.6.0-py27_0 1",
    "singledispatch-3.4.0.3-py27_0 1",
    "ssl_match_hostname-3.4.0.2-py27_1 1",
    "zict-0.1.0-py27_0 1",
    "pandas-0.19.1-np111py27_0 1",
    "tornado-4.4.2-py27_0 1",
    "bokeh-0.12.3-py27_0 1",
    "dask-0.12.0-py27_0 1",
    "distributed-1.14.1-py27_0 1"
],
"PREFIX": "/opt/continuum/anaconda/envs/my-env",
"SYMLINK_CONDA": [
    "/opt/continuum/anaconda"
],
"op_order": [
    "RM_FETCHED",
    "FETCH",
    "RM_EXTRACTED",
    "EXTRACT",
    "UNLINK",

```

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```

        "LINK",
        "SYMLINK_CONDA"
    ],
    "success": true
}

```

**NOTE:** The command `adam scale env create` is compatible only with conda dependencies and ignores any pip or other non-conda dependencies that are specified in the conda environment definition file.

Use `adam scale env list` to list conda environments on the cluster:

```

$ adam scale -n cluster env list
All nodes (x4) response:
# conda environments:
#
my-env          /opt/continuum/anaconda/envs/my-env
root            * /opt/continuum/anaconda

```

Use `adam scale env update` to update packages in an existing conda environment based on a conda environment definition file:

```

$ adam scale -n cluster env update -f environment.yml
All nodes (x4) response:
{
  "message": "All requested packages already installed.",
  "success": true
}

```

Use `adam scale env remove` to remove a conda environment from the cluster:

```

$ adam scale -n cluster env remove -n my-env
All nodes (x4) response:
{
  "actions": {
    "PREFIX": "/opt/continuum/anaconda/envs/my-env",
    "UNLINK": [
      "mkl-11.3.3-0",
      "numpy-1.11.2-py27_0",
      "openssl-1.0.2j-0",
      "pandas-0.18.0-np111py27_0",
      "pip-9.0.1-py27_0",
      "python-2.7.12-1",
      "python-dateutil-2.6.0-py27_0",
      "pytz-2016.7-py27_0",
      "readline-6.2-2",
      "setuptools-27.2.0-py27_0",
      "six-1.10.0-py27_0",
      "sqlite-3.13.0-0",
      "tk-8.5.18-0",
      "wheel-0.29.0-py27_0",
      "zlib-1.2.8-3"
    ]
  },
  "success": true
}

```

### Using Anaconda with Cloudera CDH

There are different methods of using Anaconda Scale on a cluster with [Cloudera CDH](#):

- The freely available Anaconda parcel for Cloudera CDH.
- Custom [Anaconda parcels for Cloudera CDH](#)
- A dynamic, managed version of Anaconda on all of the nodes using Anaconda Scale

The freely available Anaconda parcel is based on Python 2.7 and includes the default conda packages that are available in the free Anaconda distribution.

Anaconda Enterprise users can also leverage Anaconda Repository to *create and distribute their own custom Anaconda parcels for Cloudera Manager*.

If you need more dynamic functionality than the Anaconda parcels offer, Anaconda Scale lets you dynamically install and manage multiple conda environments—such as Python 2, Python 3, and R environments—and packages across a cluster.

### Using the Anaconda parcel

For more information about installing the Anaconda parcel on a CDH cluster using Cloudera Manager, see the [Anaconda parcel documentation](#).

### Transitioning to the dynamic, managed version of Anaconda Scale

To transition from the Anaconda parcel for CDH to the dynamic, managed version of Anaconda Scale, follow the instructions below to uninstall the Anaconda parcel on a CDH cluster and then transition to a centrally managed version of Anaconda.

### Uninstalling the Anaconda parcel

If the Anaconda parcel is installed on the CDH cluster, uninstall the parcel:

1. From the Cloudera Manager Admin Console, in the top navigation bar, click the Parcels indicator.
2. To the right of the Anaconda parcel listing, click the Deactivate button.
3. When prompted, click OK to deactivate the Anaconda parcel and restart Spark and related services.
4. Click the arrow to the right of the Anaconda parcel listing and select Remove From Hosts.
5. In the confirmation dialog box, confirm removal of the Anaconda parcel from the cluster nodes.

For more information about managing Cloudera parcels, see the [Cloudera documentation](#).

### Transitioning to a centrally managed Anaconda installation

Once you've uninstalled the Anaconda parcel, see the [Anaconda Scale installation instructions](#) for more information about installing a centrally managed version of Anaconda.

## Using Anaconda with Spark

[Apache Spark](#) is an analytics engine and parallel computation framework with Scala, Python and R interfaces. Spark can load data directly from disk, memory and other data storage technologies such as Amazon S3, Hadoop Distributed File System (HDFS), HBase, Cassandra and others.

Anaconda Scale can be used with a cluster that already has a managed Spark/Hadoop stack. Anaconda Scale can be installed alongside existing enterprise Hadoop distributions such as [Cloudera CDH](#) or [Hortonworks HDP](#) and can be used to manage Python and R conda packages and environments across a cluster.

To run a script on the head node, simply execute `python example.py` on the cluster. Alternatively, you can install Jupyter Notebook on the cluster using Anaconda Scale. See the [Installation](#) documentation for more information.

## Different ways to use Spark with Anaconda

You can develop Spark scripts interactively, and you can write them as Python scripts or in a Jupyter Notebook.

You can submit a PySpark script to a Spark cluster using various methods:

- Run the script directly on the head node by executing `python example.py` on the cluster.
- Use the `spark-submit` command either in Standalone mode or with the YARN resource manager.
- Submit the script interactively in an IPython shell or Jupyter Notebook on the cluster. For information on using Anaconda Scale to install Jupyter Notebook on the cluster, see [Installation](#).

You can also use Anaconda Scale with enterprise Hadoop distributions such as Cloudera CDH or Hortonworks HDP.

## Using Anaconda Scale with Spark

The topics listed below describe how to:

- Use Anaconda and Anaconda Scale with Apache Spark and PySpark
- Interact with data stored within the Hadoop Distributed File System (HDFS) on the cluster

While these tasks are independent and can be performed in any order, we recommend that you begin with [Configuring Anaconda with Spark](#).

## Configuring Anaconda with Spark

You can configure Anaconda to work with Spark jobs in three ways: *with the “`spark-submit`” command*, or *with Jupyter Notebooks and Cloudera CDH*, or *with Jupyter Notebooks and Hortonworks HDP*.

After you configure Anaconda with one of those three methods, then you can *create and initialize a SparkContext*.

## Configuring Anaconda with the `spark-submit` command

You can submit Spark jobs using the `PYSPARK_PYTHON` environment variable that refers to the location of the Python executable in Anaconda.

EXAMPLE:

```
PYSPARK_PYTHON=/opt/continuum/anaconda/bin/python spark-submit pyspark_script.py
```

## Configuring Anaconda with Jupyter Notebooks and Cloudera CDH

Configure Jupyter Notebooks to use Anaconda Scale with Cloudera CDH using the following Python code at the top of your notebook:

```
import os
import sys
os.environ["PYSPARK_PYTHON"] = "/opt/continuum/anaconda/bin/python"
os.environ["JAVA_HOME"] = "/usr/java/jdk1.7.0_67-cloudera/jre"
os.environ["SPARK_HOME"] = "/opt/cloudera/parcels/CDH/lib/spark"
os.environ["PYLIB"] = os.environ["SPARK_HOME"] + "/python/lib"
sys.path.insert(0, os.environ["PYLIB"] + "/py4j-0.9-src.zip")
sys.path.insert(0, os.environ["PYLIB"] + "/pyspark.zip")
```

The above configuration was tested with Cloudera CDH 5.11 and Spark 1.6. Depending on the version of Cloudera CDH that you have installed, you might need to customize these paths according to the location of Java, Spark and Anaconda on your cluster.

If you've installed a custom Anaconda parcel, the path for PYSPARK\_PYTHON will be /opt/cloudera/parcels/PARCEL\_NAME/bin/python, where PARCEL\_NAME is the name of the custom parcel you created.

## Configuring Anaconda with Jupyter Notebooks and Hortonworks HDP

Configure Jupyter Notebooks to use Anaconda Scale with Hortonworks HDP using the following Python code at the top of your notebook:

```
import os
import sys
os.environ["PYSPARK_PYTHON"] = "/opt/continuum/anaconda/bin/python"
os.environ["SPARK_HOME"] = "/usr/hdp/current/spark-client"
os.environ["PYLIB"] = os.environ["SPARK_HOME"] + "/python/lib"
sys.path.insert(0, os.environ["PYLIB"] + "/py4j-0.9-src.zip")
sys.path.insert(0, os.environ["PYLIB"] + "/pyspark.zip")
```

The above configuration was tested with Hortonworks HDP 2.6, Apache Ambari 2.4 and Spark 1.6. Depending on the version of Hortonworks HDP that you have installed, you might need to customize these paths according to the location of Spark and Anaconda on your cluster.

If you've installed a custom Anaconda management pack, the path for PYSPARK\_PYTHON will be /opt/continuum/PARCEL\_NAME/bin/python, where PARCEL\_NAME is the name of the custom parcel you created.

## Creating a SparkContext

Once you have configured the appropriate environment variables, you can initialize a SparkContext—in yarn-client client mode in this example—using:

```
from pyspark import SparkConf
from pyspark import SparkContext
conf = SparkConf()
conf.setMaster('yarn-client')
conf.setAppName('anaconda-pyspark')
sc = SparkContext(conf=conf)
```

For more information about configuring Spark settings, see the [PySpark documentation](#).

Once you've initialized a `SparkContext`, you can start using Anaconda with Spark jobs. For examples of Spark jobs that use libraries from Anaconda, see *Using Anaconda with Spark*.

## Running PySpark as a Spark standalone job

This example runs a minimal Spark script that imports PySpark, initializes a `SparkContext` and performs a distributed calculation on a Spark cluster in standalone mode.

### Who is this for?

This example is for users of a Spark cluster that has been configured in standalone mode who wish to run a PySpark job.

### Before you start

Download the `spark-basic.py` example script to the cluster node where you submit Spark jobs.

You need Spark running with the standalone scheduler. You can install Spark using an enterprise Hadoop distribution such as [Cloudera CDH](#) or [Hortonworks HDP](#). Some additional configuration might be necessary to use Spark in standalone mode.

### Modifying the script

After downloading the `spark-basic.py` example script, open the file in a text editor on your cluster. Replace `HEAD_NODE_HOSTNAME` with the hostname or IP address of the Spark master as defined in your Hadoop configuration.

```
# spark-basic.py
from pyspark import SparkConf
from pyspark import SparkContext

conf = SparkConf()
conf.setMaster('spark://HEAD_NODE_HOSTNAME:7077')
conf.setAppName('spark-basic')
sc = SparkContext(conf=conf)

def mod(x):
    import numpy as np
    return (x, np.mod(x, 2))

rdd = sc.parallelize(range(1000)).map(mod).take(10)
print rdd
```

Examine the contents of the `spark-basic.py` example script.

The first code block contains imports from PySpark.

The second code block initializes the `SparkContext` and sets the application name.

The third code block contains the analysis code that uses the NumPy package to calculate the modulus of a range of numbers up to 1000, then returns and prints the first 10 results.

The fourth code block runs the calculation on the Spark cluster and prints the results. The code uses the NumPy library from Anaconda on each Spark worker.

NOTE: You may need to install NumPy on the cluster nodes using `adam scale -n cluster conda install numpy`.

### Running the job

Run the script by submitting it to your cluster for execution using `spark-submit` or by running this command:

```
$ python spark-basic.py
```

The output from the above command shows the first 10 values returned from the `spark-basic.py` script:

```
16/05/05 22:26:53 INFO spark.SparkContext: Running Spark version 1.6.0

[...]

16/05/05 22:27:03 INFO scheduler.TaskSetManager: Starting task 0.0 in stage 0.0 (TID_
↪0, localhost, partition 0,PROCESS_LOCAL, 3242 bytes)
16/05/05 22:27:04 INFO storage.BlockManagerInfo: Added broadcast_0_piece0 in memory_
↪on localhost:46587 (size: 2.6 KB, free: 530.3 MB)
16/05/05 22:27:04 INFO scheduler.TaskSetManager: Finished task 0.0 in stage 0.0 (TID_
↪0) in 652 ms on localhost (1/1)
16/05/05 22:27:04 INFO cluster.YarnScheduler: Removed TaskSet 0.0, whose tasks have_
↪all completed, from pool
16/05/05 22:27:04 INFO scheduler.DAGScheduler: ResultStage 0 (runJob at PythonRDD.
↪scala:393) finished in 4.558 s
16/05/05 22:27:04 INFO scheduler.DAGScheduler: Job 0 finished: runJob at PythonRDD.
↪scala:393, took 4.951328 s
[(0, 0), (1, 1), (2, 0), (3, 1), (4, 0), (5, 1), (6, 0), (7, 1), (8, 0), (9, 1)]
```

### Troubleshooting

If something goes wrong, see [Help and support](#).

### Further information

See the [Spark](#) and [PySpark](#) documentation:

### Running PySpark with the YARN resource manager

This example runs a script on the Spark cluster with the YARN resource manager and returns the hostname of each node in the cluster.

### Who is this for?

This example is for users of a Spark cluster who wish to run a PySpark job using the YARN resource manager.

### Before you start

Download the `spark-yarn.py` example script to your cluster.

You need Spark running with the YARN resource manager. You can install Spark and YARN using an enterprise Hadoop distribution such as [Cloudera CDH](#) or [Hortonworks HDP](#).

## Running the job

This code is almost the same as the code on the page [Running PySpark as a Spark standalone job](#), which describes the code in more detail.

Here is the complete script to run the Spark + YARN example in PySpark:

```
# spark-yarn.py
from pyspark import SparkConf
from pyspark import SparkContext

conf = SparkConf()
conf.setMaster('yarn-client')
conf.setAppName('spark-yarn')
sc = SparkContext(conf=conf)

def mod(x):
    import numpy as np
    return (x, np.mod(x, 2))

rdd = sc.parallelize(range(1000)).map(mod).take(10)
print rdd
```

NOTE: You may need to install NumPy on the cluster nodes using `adam scale -n cluster conda install numpy`.

Run the script on the Spark cluster with `spark-submit`. The output shows the first 10 values that were returned from the `spark-basic.py` script.

```
16/05/05 22:26:53 INFO spark.SparkContext: Running Spark version 1.6.0

[...]

16/05/05 22:27:03 INFO scheduler.TaskSetManager: Starting task 0.0 in stage 0.0 (TID_
↳0, localhost, partition 0,PROCESS_LOCAL, 3242 bytes)
16/05/05 22:27:04 INFO storage.BlockManagerInfo: Added broadcast_0_piece0 in memory_
↳on localhost:46587 (size: 2.6 KB, free: 530.3 MB)
16/05/05 22:27:04 INFO scheduler.TaskSetManager: Finished task 0.0 in stage 0.0 (TID_
↳0) in 652 ms on localhost (1/1)
16/05/05 22:27:04 INFO cluster.YarnScheduler: Removed TaskSet 0.0, whose tasks have_
↳all completed, from pool
16/05/05 22:27:04 INFO scheduler.DAGScheduler: ResultStage 0 (runJob at PythonRDD.
↳scala:393) finished in 4.558 s
16/05/05 22:27:04 INFO scheduler.DAGScheduler: Job 0 finished: runJob at PythonRDD.
↳scala:393, took 4.951328 s
[(0, 0), (1, 1), (2, 0), (3, 1), (4, 0), (5, 1), (6, 0), (7, 1), (8, 0), (9, 1)]
```

## Troubleshooting

If something goes wrong, see [Help and support](#).

### Further information

See the [Spark](#) and [PySpark](#) documentation pages for more information.

### Performing a word count on text data in HDFS

This example counts the number of words in text files that are stored in HDFS.

### Who is this for?

This example is for users of a Spark cluster who wish to run a PySpark job—with the YARN resource manager—that reads and processes text files stored in HDFS.

### Before you start

Download the `spark-wordcount.py` example script and the `download-data.py` script.

You need Spark running with the YARN resource manager and the Hadoop Distributed File System (HDFS). You can install Spark, YARN and HDFS using an enterprise Hadoop distribution such as [Cloudera CDH](#) or [Hortonworks HDP](#).

You also need valid [Amazon Web Services \(AWS\)](#) credentials.

### Load HDFS data

Load the sample text data into HDFS. The following script transfers sample text data (approximately 6.4 GB) from a public Amazon S3 bucket to the HDFS data store on the cluster.

Download the `download-data.py` script to your cluster and insert your Amazon AWS credentials in the `AWS_KEY` and `AWS_SECRET` variables.

```
import subprocess

AWS_KEY = ''
AWS_SECRET = ''

s3_path = 's3n://{0}:{1}@blaze-data/enron-email'.format(AWS_KEY, AWS_SECRET)
cmd = ['hadoop', 'distcp', s3_path, 'hdfs:///tmp/enron']
subprocess.call(cmd)
```

**NOTE:** The `hadoop distcp` command might fail to run on smaller Amazon EC2 instance sizes due to memory limits.

Run the `download-data.py` script on the Spark cluster:

```
$ python download-data.py
```

After a few minutes, the text data is loaded into HDFS and ready for analysis.



## Running the job

The following script reads the text files downloaded in the previous step and counts all of the words. Download the `spark-wordcount.py` example script to your cluster, and then replace `HEAD_NODE_IP` with the IP address of the head node.

```
# spark-wordcount.py
from pyspark import SparkConf
from pyspark import SparkContext

HDFS_MASTER = 'HEAD_NODE_IP'

conf = SparkConf()
conf.setMaster('yarn-client')
conf.setAppName('spark-wordcount')
conf.set('spark.executor.instances', 10)
sc = SparkContext(conf=conf)

distFile = sc.textFile('hdfs://{0}:9000/tmp/enron/*/*.txt'.format(HDFS_MASTER))

nonempty_lines = distFile.filter(lambda x: len(x) > 0)
print 'Nonempty lines', nonempty_lines.count()

words = nonempty_lines.flatMap(lambda x: x.split(' '))

wordcounts = words.map(lambda x: (x, 1)) \
    .reduceByKey(lambda x, y: x+y) \
    .map(lambda x: (x[1], x[0])).sortByKey(False)

print 'Top 100 words:'
print wordcounts.take(100)
```

Run the script on your Spark cluster using `spark-submit`. The output shows the 100 most frequently occurring words from the sample text data:

```
54.237.100.240: Using Spark's default log4j profile: org/apache/spark/log4j-defaults.
↳properties
15/06/13 04:58:42 INFO SparkContext: Running Spark version 1.4.0

[...]

15/06/26 04:32:03 INFO YarnScheduler: Removed TaskSet 7.0, whose tasks have all_
↳completed, from pool
15/06/26 04:32:03 INFO DAGScheduler: ResultStage 7 (runJob at PythonRDD.scala:366)_
↳finished in 0.210 s
15/06/26 04:32:03 INFO DAGScheduler: Job 3 finished: runJob at PythonRDD.scala:366,_
↳took 18.124243 s
[(288283320, ''), (22761900, '\t'), (19583689, 'the'), (13084511, '\t0'), (12330608,
↳'-'),
(11882910, 'to'), (11715692, 'of'), (10822018, '0'), (10251855, 'and'), (6682827, 'in
↳'),
(5463285, 'a'), (5226811, 'or'), (4353317, '/'), (3946632, 'for'), (3695870, 'is'),
(3497341, 'by'), (3481685, 'be'), (2714199, 'that'), (2650159, 'any'), (2444644,
↳'shall'),
(2414488, 'on'), (2325204, 'with'), (2308456, 'Gas'), (2268827, 'as'), (2265197, 'this
↳'),
(2180110, '$'), (1996779, '\t$0'), (1903157, '12:00:00'), (1823570, 'The'), (1727698,
↳'not'),
```

(continues on next page)

(continued from previous page)

```
(1626044, 'such'), (1578335, 'at'), (1570484, 'will'), (1509361, 'has'), (1506064,
↪ 'Enron'),
(1460737, 'Inc.'), (1453005, 'under'), (1411595, 'are'), (1408357, 'from'), (1334359,
↪ 'Data'),
(1315444, 'have'), (1310093, 'Energy'), (1289975, 'Set'), (1281998, 'Technologies'),
(1280088, '*****'), (1238125, '\t-'), (1176380, 'all'), (1169961, 'other'), ↪
↪ (1166151, 'its'),
(1132810, 'an'), (1127730, '&'), (1112331, '>'), (1111663, 'been'), (1098435, 'This'),
(1054291, '0\t0\t0\t0\t'), (1021797, 'States'), (971255, 'you'), (971180, 'which'), ↪
↪ (961102, '.'),
(945348, 'I'), (941903, 'it'), (939439, 'provide'), (902312, 'North'), (867218,
↪ 'Subject:'),
(851401, 'Party'), (845111, 'America'), (840747, 'Agreement'), (810554, '#N/A\t'), ↪
↪ (807259, 'may'),
(800753, 'please'), (798382, 'To'), (771784, '\t$-'), (753774, 'United'), (740472, 'if
↪ '),
(739731, '\t0.00'), (723399, 'Power'), (699294, 'To:'), (697798, 'From:'), (672727,
↪ 'Date:'),
(661399, 'produced'), (652527, '2001'), (651164, 'format'), (650637, 'Email'), ↪
↪ (646922, '3.0'),
(645078, 'licensed'), (644200, 'License'), (642700, 'PST'), (641426, 'cite'), (640441,
↪ 'Creative'),
(640089, 'Commons'), (640066, 'NSF'), (639960, 'EML'), (639949, 'Attribution'),
(639938, 'attribution'), (639936, 'ZL'), (639936, '(http://www.zlti.com)."), ↪
↪ (639936, '"ZL'),
(639936, 'X-ZLID:'), (639936, '<http://creativecommons.org/licenses/by/3.0/us/>'), ↪
↪ (639936, 'X-SDOC:')] ]
```

## Troubleshooting

If something goes wrong, see [Help and support](#).

## Further information

See the [Spark](#) and [PySpark](#) documentation:

## Distributed natural language processing

This example provides a simple PySpark job that utilizes the [NLTK library](#). NLTK is a popular Python package for natural language processing. This example shows you how to integrate third-party Python libraries with Spark. This example demonstrates the installation of Python libraries on the cluster, the usage of Spark with the YARN resource manager and execution of the PySpark job.

## Who is this for?

This example is for users of a Spark cluster who wish to run a PySpark job with the YARN resource manager.

## Before you start

Download the `spark-nltk.py` example script or `spark-nltk.ipynb` example notebook.

You need Spark running with the YARN resource manager. You can install Spark and YARN using an enterprise Hadoop distribution such as [Cloudera CDH](#) or [Hortonworks HDP](#).

## Install NLTK

Install NLTK on all of the cluster nodes using the `adam scale` command:

```
$ adam scale -n cluster conda install nltk
```

You should see output similar to this from each node, which indicates that the package was successfully installed across the cluster:

```
All nodes (x4) response:
{
  "actions": {
    "EXTRACT": [
      "conda-env-2.5.2-py27_0",
      "conda-4.1.11-py27_0"
    ],
    "FETCH": [
      "conda-env-2.5.2-py27_0",
      "conda-4.1.11-py27_0"
    ],
    "LINK": [
      "conda-env-2.5.2-py27_0 1 None",
      "conda-4.1.11-py27_0 1 None"
    ],
    "PREFIX": "/opt/continuum/anaconda",
    "SYMLINK_CONDA": [
      "/opt/continuum/anaconda"
    ],
    "UNLINK": [
      "conda-4.1.6-py27_0",
      "conda-env-2.5.1-py27_0"
    ],
    "op_order": [
      "RM_FETCHED",
      "FETCH",
      "RM_EXTRACTED",
      "EXTRACT",
      "UNLINK",
      "LINK",
      "SYMLINK_CONDA"
    ]
  },
  "success": true
}
```

For this example, you need to download the NLTK sample data. Download the data on all cluster nodes by using the `adam cmd` command:

```
$ adam cmd 'sudo /opt/continuum/anaconda/bin/python -m nltk.downloader -d /usr/share/
↪nltk_data all'
```

The sample data is downloaded over a few minutes. After the download completes, you should see output similar to:

```
All nodes (x4) response: [nltk_data] Downloading collection 'all'
[nltk_data] |
[nltk_data] | Downloading package abc to /usr/share/nltk_data...
[nltk_data] | Unzipping corpora/abc.zip.
[nltk_data] | Downloading package alpino to /usr/share/nltk_data...
[nltk_data] | Unzipping corpora/alpino.zip.
[nltk_data] | Downloading package biocreative_ppi to
[nltk_data] | /usr/share/nltk_data...
....
[nltk_data] | Unzipping models/bllip_wsj_no_aux.zip.
[nltk_data] | Downloading package word2vec_sample to
[nltk_data] | /usr/share/nltk_data...
[nltk_data] | Unzipping models/word2vec_sample.zip.
[nltk_data] |
[nltk_data] Done downloading collection all
```

## Running the job

Here is the complete script to run the Spark + NLTK example in PySpark:

```
# spark-nltk.py
from pyspark import SparkConf
from pyspark import SparkContext

conf = SparkConf()
conf.setMaster('yarn-client')
conf.setAppName('spark-nltk')
sc = SparkContext(conf=conf)

data = sc.textFile('file:///usr/share/nltk_data/corpora/state_union/1972-Nixon.txt')

def word_tokenize(x):
    import nltk
    return nltk.word_tokenize(x)

def pos_tag(x):
    import nltk
    return nltk.pos_tag([x])

words = data.flatMap(word_tokenize)
print words.take(10)

pos_word = words.map(pos_tag)
print pos_word.take(5)
```

Examine the above code example. First, it imports PySpark and creates a SparkContext:

```
from pyspark import SparkConf
from pyspark import SparkContext

conf = SparkConf()
conf.setMaster('yarn-client')
conf.setAppName('spark-nltk')
sc = SparkContext(conf=conf)
```

After a `SparkContext` is created, we can load some data into Spark. In this case, the data file is from one of the example documents provided by NLTK.

NOTE: You could also copy the data to HDFS and load it from Spark.

```
data = sc.textFile('file:///usr/share/nltk_data/corpora/state_union/1972-Nixon.txt')
```

Next is a function called `word_tokenize` that imports `nltk` on the Spark worker nodes and calls `nltk.word_tokenize`. The function is mapped to the text file that was read in the previous step:

```
def word_tokenize(x):
    import nltk
    return nltk.word_tokenize(x)

words = data.flatMap(word_tokenize)
```

You can confirm that the `flatMap` operation worked by returning some of the words in the dataset:

```
print words.take(10)
```

Finally, you can use NLTK's [part-of-speech tagger](#) to attach the part of speech to each word in the data set:

```
def pos_tag(x):
    import nltk
    return nltk.pos_tag([x])

pos_word = words.map(pos_tag)
print pos_word.take(5)
```

Run the script on the Spark cluster using the `spark-submit` script. The output shows the words that were returned from the Spark script, including the results from the `flatMap` operation and the POS-tagger:

```
Using Spark's default log4j profile: org/apache/spark/log4j-defaults.properties
15/06/13 05:14:29 INFO SparkContext: Running Spark version 1.4.0

[...]
```

```
[ 'Address',
  'on',
  'the',
  'State',
  'of',
  'the',
  'Union',
  'Delivered',
  'Before',
  'a' ]

[...]
```

```
[ ('Address', 'NN') ],
[ ('on', 'IN') ],
[ ('the', 'DT') ],
[ ('State', 'NNP') ],
[ ('of', 'IN') ]
```

### Troubleshooting

If something goes wrong, consult [Help and support](#).

### Further information

See the [Spark](#) and [PySpark](#) documentation:

For more information on NLTK, see the [NLTK book](#).

### Help and support

Support is included with the purchase of an Anaconda subscription. Visit the [support section of our website](#) for documentation and contact information for priority support.

### Training and consulting

Training and consulting is available for Anaconda Scale. For more information, please [contact us](#).

## 4.4.6 NumbaPro

---

**Note:** This product is discontinued. This archived copy of the product documentation is provided for those customers who are still using it.

---

NumbaPro has been deprecated, and its code generation features have been moved into open-source [Numba](#). The CUDA library functions have been moved into [Accelerate](#), along with some Intel MKL functionality. High-level functions and access to additional native library implementations will be added in future releases of [Accelerate](#), and there will be no further updates to NumbaPro.

A NumbaPro compatibility layer (listed as release 0.22.0 of NumbaPro) provides access to the new [Accelerate](#) packages through the old NumbaPro package names. This avoids the need to change any existing code immediately for use with [Accelerate](#). A warning will be generated upon import of the compatibility layer, to highlight the deprecation of the NumbaPro package.

[Archived NumbaPro documentation](#) is still available.

### NumbaPro

[Get started with the NumbaPro Quick Start \[pdf\]](#)

*NumbaPro* is an enhanced version of [Numba](#) which adds premium features and functionality that allow developers to rapidly create optimized code that integrates well with [NumPy](#).

With NumbaPro, Python developers can define NumPy [ufuncs](#) and [generalized ufuncs](#) (gufuncs) in Python, which are compiled to machine code dynamically and loaded on the fly. Additionally, NumbaPro offers developers the ability to target multicore and GPU architectures with Python code for both [ufuncs](#) and general-purpose code.

For targeting the GPU, NumbaPro can either do the work automatically, doing its best to optimize the code for the GPU architecture. Alternatively, CUDA-based API is provided for writing [CUDA](#) code specifically in Python for ultimate control of the hardware (with thread and block identities).

## Getting Started

Let's start with a simple function to add together all the pairwise values in two NumPy arrays. Asking NumbaPro to compile this Python function to vectorized machine code for execution on the CPU is as simple as adding a single line of code (invoked via a decorator on the function):

Similarly, one can instead target the GPU for execution of the same Python function by modifying a single line in the above example:

```
@vectorize(['float32(float32, float32)'], target='gpu')
```

Targeting the GPU for execution introduces the potential for numerous GPU-specific optimizations so as a starting point for more complex scenarios, one can also target the GPU with NumbaPro via its *Just-In-Time* (JIT) compiler:

## Features

Here's a list of highlighted features:

- Portable data-parallel programming through ufuncs and gufuncs for single core CPU, multicore CPU and GPU
- Bindings to CUDA libraries: cuRAND, cuBLAS, cuFFT
- Python CUDA programming for maximum control of hardware resources

## User Guide

New users should first read the installation manual:

## Installation

NumbaPro is part of the *Anaconda Accelerate* product. Please refer to the [Anaconda Accelerate Documentation](#) for instructions on downloading and installation.

## Purchasing a License

Accelerate is included with [Anaconda Workgroup](#) and [Anaconda Enterprise](#) subscriptions.

To start a 30-day free trial just download and install the Anaconda Accelerate package.

If you already have [Anaconda](#) (free Python distribution) installed:

```
conda update conda
conda install accelerate
```

If you do not have Anaconda installed, you can download it [here](#).

Anaconda Accelerate can also be installed into your own (non-Anaconda) Python environment. For more information about Accelerate please contact [sales@anaconda.com](mailto:sales@anaconda.com).

### Update Instructions

With Anaconda Accelerate already installed, first update the `conda` package management tool to the latest version, then use `conda` to update the NumbaPro module. In the terminal:

```
$ conda update conda
$ conda update numbapro
```

### CUDA GPUs Setup

#### CUDA Driver

NumbaPro does not ship the CUDA driver. It is users responsibility to ensure their systems are using the **latest driver**. Currently, users should use the driver shipped with [CUDA 5.5 SDK](#).

#### CUDA Support & Detection

NumbaPro GPU support currently requires [NVIDIA CUDA GPUs](#) with **compute-capability 2.0 or above**. Users should check their hardware with the following:

```
import numbapro
numbapro.check_cuda()
```

A sample output looks like:

```
-----libraries detection-----
Finding cublas
  located at /Users/.../lib/libcublas.dylib
Finding cusparse
  located at /Users/.../lib/libcusparse.dylib
Finding cufft
  located at /Users/.../lib/libcufft.dylib
Finding curand
  located at /Users/.../lib/libcurand.dylib
Finding nvvm
  located at /Users/.../lib/libnvvm.dylib
In /Users/.../lib
  finding libdevice.compute_20.bc      ok
  finding libdevice.compute_30.bc      ok
  finding libdevice.compute_35.bc      ok
-----hardware detection-----
Found 1 CUDA devices
id 0      GeForce GT 650M                [SUPPORTED]
        compute capability: 3.0
        pci device id: 0
        pci bus id: 1
Summary:
  1/1 devices are supported
```

This performs CUDA library and GPU detection. Discovered GPUs are listed with information for compute capability and whether it is supported by NumbaPro.

The message “cuda disabled by user” means that either the environment variable `NUMBA_DISABLE_CUDA` is set to 1 and must be set to 0, or the system is 32-bit. CUDA does not support 32-bit systems.



Basics:

## Quick Start

Numba/NumbaPro uses decorators extensively to annotate function for compilation. This document explains the major decorators: `jit`, `autojit`, `vectorize` and `guvectorize`.

## Types

Numba/NumbaPro decorators specializes generic python function to typed native function. All decorators except `autojit` requires type information to be supplied. Here is a table of common Numba type objects:

Kind	Numba Types
signed integer	<code>int8</code> , <code>int16</code> , <code>int32</code> , <code>int64</code>
unsigned integer	<code>uint8</code> , <code>uint16</code> , <code>uint32</code> , <code>uint64</code>
float-points	<code>float32</code> , <code>float64</code>
complex numbers	<code>complex64</code> , <code>complex128</code>
boolean	<code>bool_</code>
others	<code>void</code>

## Compiler Target `target="..."`

All decorators, `jit`, `autojit`, `vectorize` and `guvectorize`, have a `target` keyword argument to select the code generation target. User provides a string to name the target. Numba supports only the `"cpu"` target. NumbaPro adds `"parallel"` and `"gpu"`. The `"parallel"` target is only available for `vectorize`, which will distributes the work across CPU threads. The `"gpu"` offloads the computation to a Nvidia CUDA GPU.

High-level APIs for CPU/GPU:

## Universal Functions

With NumbaPro, [universal functions](#) (ufuncs) can be created by applying the `vectorize` decorator on to simple scalar functions. A ufunc can operates on scalars or NumPy arrays. When used on arrays, the ufunc apply the core scalar function to every group of elements from each arguments in an element-wise fashion. NumPy [Broadcasting](#) is applied to every argument with mismatching dimensions.

## Example: Basic

Here is a simple example to perform element-wise addition:

The ufunc is compiled to operate on `float32` and `float64` arrays. It is used to compute element-wise addition of array *a* and *b* which are arrays of `numpy.float64` with 10 elements. The output

## Usage

A generalization of the usage of the `vectorize` decorator is described in this section.

**`vectorize`** (*type\_signatures*`[, target='cpu']`)

Returns a vectorizer object to be applied to python functions.

**Parameters**

- **type\_signatures** – an iterable of type signatures, which are either function type object or a string describing the function type.
- **target** – a string for hardware target; e.g. “cpu”, “parallel”, “gpu”.

**Returns** a vectorizers object.

To use multithreaded version, change the target to “parallel”:

For CUDA target, use “gpu” for target: 

```
from numba import vectorize
```

**Performance Guideline**

A general guideline is to choose different targets for different data sizes and algorithms. The “cpu” target works well for small data sizes (approx. less than 1KB) and low compute intensity algorithms. It has the least amount of overhead. The “parallel” target works well for medium data sizes (approx. less than 1MB). Threading adds a small delay. The “gpu” target works well for big data sizes (approx. greater than 1MB) and high compute intensity algorithms. Transferring memory to and from the GPU adds significant overhead.

**Universal Function Targets**

There are several vectorizer versions available. The different options are listed below:

Target	Description
cpu	Single-threaded CPU
parallel	Multi-core CPU
stream	Optimize for CPU cache
	<b>Note:</b> Experimental. Computation speeds may vary.
gpu	CUDA GPU
	<b>Note:</b> This creates an <i>ufunc-like</i> object. See <a href="#">documentation for CUDA ufunc</a> for detail.

**Generalized Ufuncs****GPU Reduction**

Python CUDA Programming

## CUDA Programming Introduction

NumbaPro provides multiple entry points for programmers of different levels of expertise on CUDA. For expert CUDA-C programmers, NumbaPro provides a Python dialect [<CUJit.html>](#) for low-level programming on the CUDA hardware. It provides full control over the hardware for fine tuning the performance of CUDA kernels. For new CUDA programmers, the high-level API such as the [universal functions \(ufunc\)](#) and [generalized ufuncs \(gufunc\)](#) are the easiest way to write array operations for the GPU.

## A Very Brief Introduction to CUDA

A [CUDA GPU](#) contains one or more *streaming multiprocessors* (SMs). Each SM is a manycore processor that is optimized for high throughput. The *manycore* architecture is very different from the common multicore CPU architecture. Instead of having a large cache and complex logic for instruction level optimization, a manycore processor achieves high throughput by executing many threads in parallel on many simpler cores. It overcomes latency due to cache miss or long operations by using zero-cost context switching. It is common to launch a CUDA kernel with hundreds or thousands of threads to keep the GPU busy.

The CUDA programming model is similar to the SIMD vector model in modern CPUs. A CUDA SM schedules the same instruction from a *warp* of 32-threads at each issuing cycle. The advantage of CUDA is that the programmer does not need to handle the divergence of execution path in a warp, whereas a SIMD programmer would be required to properly mask and shuffle the vectors. The CUDA model decouples the data structure from the program logic.

To know more about CUDA, please refer to [NVIDIA CUDA-C Programming Guide](#).

## CUDA Ufuncs and Generalized Ufuncs

This page describes the CUDA ufunc-like object.

To support the programming pattern of CUDA programs, CUDA Vectorize and GUVectorize cannot produce a conventional ufunc. Instead, a ufunc-like object is returned. This object is a close analog but not fully compatible with a regular NumPy ufunc. The CUDA ufunc adds support for passing intra-device arrays (already on the GPU device) to reduce traffic over the PCI-express bus. It also accepts a *stream* keyword for launching in asynchronous mode.

## Example: Calling Device Functions

All CUDA ufunc kernels have the ability to call other CUDA device functions:

```
from numbapro import vectorize, cuda

# define a device function
@cuda.jit('float32(float32, float32, float32)', device=True, inline=True)
def cu_device_fn(x, y, z):
    return x ** y / z

# define a ufunc that calls our device function
@vectorize(['float32(float32, float32, float32)'], target='gpu')
def cu_ufunc(x, y, z):
    return cu_device_fn(x, y, z)
```

### Generalized CUDA ufuncs

Generalized ufuncs may be executed on the GPU using CUDA, analogous to the CUDA ufunc functionality. This may be accomplished as follows:

```
from numbaipro import guvectorize

@guvectorize(['void(float32[:, :], float32[:, :], float32[:, :])'],
             '(m,n), (n,p)->(m,p)', target='gpu')
def matmulcore(A, B, C):
    ...
```

There are times when the gufunc kernel uses too many of a GPU's resources, which can cause the kernel launch to fail. The user can explicitly control the maximum size of the thread block by setting the `max_blocksize` attribute on the compiled gufunc object.

```
from numbaipro import guvectorize

@guvectorize(..., target='gpu')
def very_complex_kernel(A, B, C):
    ...

very_complex_kernel.max_blocksize = 32  # limits to 32 threads per block
```

### Writing CUDA-Python

#### CUDA Libraries Host API

#### CUDA Device Management

#### CUDA Support

---

**Note:** Platforms supported: Linux, Windows and Mac OSX 32/64-bit. Only support CUDA devices with **compute capability 2.0 and above**. Please see [CUDA GPUs](#) for a list of CUDA GPUs and their compute capability.

---

---

**Note:** As of version 0.12.2, [Anaconda](#) is distributing a subset of CUDA toolkit 5.5 libraries. The following information is no longer necessary for most users.

---

NumbaPro searches in the system shared library path for the CUDA drivers and CUDA libraries (e.g. cuRAND, cuBLAS). Users can set environment variable **LD\_LIBRARY\_PATH** to the directory of the CUDA drivers to ensure that NumbaPro can find them. The instruction to do so is printed at the end of the CUDA SDK installation.

User can override the search path with the following environment variables:

- **NUMBAPRO\_CUDA\_DRIVER** path to CUDA driver shared library file
- **NUMBAPRO\_NVVM** path to CUDA libNVVM shared library file
- **NUMBAPRO\_LIBDEVICE** path to CUDA libNVVM libdevice directory which contains .bc files.

## CUDA Python Specification (v0.2)

(This documents reflects the implementation of CUDA Python in NumbaPro 0.12. In time, we may refine the specification.)

As usage of Python on CUDA GPUs is becoming more mature, it has become necessary to define a formal specification for a dialect and its mapping to the [PTX ISA](#). There are places where the semantic of this dialect differs from the Python semantic. The change in semantic is necessary for us to generate high-performance code that is otherwise hard to achieve.

### No-Python Mode (NPM)

CUDA Python is a superset of the *No-Python mode* (NPM). NPM is a statically typed subset of the Python language. It does not use the Python runtime; thus, it only supports lower level types; such as booleans, ints, floats, complex numbers and arrays. It does not support Python objects. Since we drop the support for objects entirely, many basic language constructs must be handled differently. For instance, a simple for-loop is:

```
for i in range(10):
    ...
```

where range returns an iterable. NPM restricts the language so that only `range` or `xrange` can be used.

For array support, NPM models the NumPy ndarray. An array is a structure with a pointer to the data, an array of shape and an array of strides. Valid attributes are `shape`, `strides`, `size` and `ndim`. Arrays cannot be unpacked. The only way to access array elements is through the `__getitem__` and `__setitem__` operators (e.g. `ary[i, j]`). Slicing is not supported. When indexing into an array, a N-dimension array must be provided with N indices.

Tuples are minimally supported for unpacking array `shape` and `strides` attributes and some return value of calls.

In time, we aim to enhance NPM to expand the supported subset and recognize more idiomatic Python patterns.

#### Summary:

- no object;
- no exception;
- for-loop only works on `range` or `xrange`;
- supported types: ints, floats, complex numbers, and arrays.

### Type Inference

The type inference algorithm for CUDA Python differs from Numba as we recognize that its users require stronger typing to better predict code performance. This is a summary of the type inference rules:

- Implicit coercion for all ints and floats only.
- Variable type is assigned at definition but a variable can be redefined; thus its type can be modified at the next assignment.
- Inside a loop, the variable type remains unchanged even at redefinition. The type assigned at the preloop block (the dominator of the basic-block) is assumed. This greatly differs from Python semantic.

User can force the type of any value by using the type object defined in `numbapro` namespace:

```
from numbapro import cuda, int16, float32

@cuda.autojit
def a_cuda_kernel(arg):
    must_be_int16 = int16(123)
    must_be_float32 = float32(321)
```

## Basic Arithmetic Operations

For binary operators `+` `-` `*`, the operands are coerced to the most generic type of the two before the computation. The result type is the coerced type.

**For `floordiv //`, the coercion rule on operands for basic binary operators** applies. But, the result type is always coerced to an integer of the same bitwidth and at least has 32-bits.

For `truediv /`, the operands are promoted to a floating point representation with bitwidth equals to the maximum of the two operands before the computation and at least has 32-bits. The result type is the coerced type.

For binary bitwise `&` `|` `^` `>>` `<<`, the operands must be of integer types and they are coerced to the most generic type of the two before the computation. The result type is the coerced type.

For complex numbers, only `+` `-` `*` are defined.

Please refer to the [CUDA-C Programming Guide: Arithmetic Instructions](#) for the precision each operation.

## Intp

`intp` is used to represent the integer whose width equals the address width.

## Array Operations

Array attributes are read-only:

- `shape` contains the number of elements for each dimension. It can be indexed or unpacked like a tuple. It is a tuple of `intp`.
- `strides` contains the number of bytes skip to move forward to the next element for a given dimension. It can be indexed or unpacked like a tuple. It is a tuple of `intp`.
- `size` contains the number of elements in the array but may not be correspond to the actual size of the data buffer since strides can be zero or negative. It is an `intp`.
- `ndim` contains the number of dimension in the array. It is an `intp`.

`__getitem__` returns the element at the given index. Slicing or fancy indexing are not supported. The result type is always the same as the element type of the array.

`__setitem__` stores a value into the array at an index. The value is coerced if necessary.

## CUDA Intrinsics

All intrinsics are defined under the `numbapro.cuda` namespace.

Thread ID intrinsics:

- `cuda.threadIdx.x`, `cuda.threadIdx.y`, `cuda.threadIdx.z` are the X, Y and Z IDs of the thread.

- `cuda.blockIdx.x`, `cuda.blockIdx.y` are the X and Y ID of the block.
- `cuda.blockDim.x`, `cuda.blockDim.y`, `cuda.blockDim.z` are the X, Y and Z width of the thread block.
- `cuda.gridDim.x`, `cuda.gridDim.y` are the X and Y width of the grid.

Barrier intrinsics:

- `cuda.syncthreads()` equivalent to `__syncthreads()` in CUDA-C. It is a thread block level barrier.

Shared memory intrinsics

- `cuda.shared.array(shape, dtype)` constructs a statically allocated array in the shared memory of kernel. `dtype` argument must be a type object defined in the `NumbaPro` namespace. It must be declared in the entry block of the kernel.

## Math

Python Dialect for CUDA translates math functions defined in the `math` module of the Python standard library. All the functions use the semantic of the CUDA-C definition. Please refer to the [CUDA-C Programming Guide: Math Function](#).

Supported functions:

```
math.acos
math.asin
math.atan
math.arctan
math.acosh
math.asinh
math.atanh
math.cos
math.sin
math.tan
math.cosh
math.sinh
math.tanh
math.atan2
math.exp
math.expm1           # not available in Python 2.6
math.fabs
math.log
math.log10
math.log1p
math.sqrt
math.pow
math.ceil
math.floor
math.copysign
math.fmod
math.isnan
math.isinf
```

## Fast Math

*coming soon in the next release...*

### Learn by Examples

The developer team maintains a public [GitHub repository of examples](#). Many examples are designed to show off the potential performance gain by using GPUs.

### Requirements

Base:

- Python 2.6, 2.7, 3.3, 3.4
- LLVM 3.3

For CUDA GPU features:

- Latest NVIDIA CUDA driver
- CUDA Toolkit 5.5 or above
- At least one CUDA GPU with compute capability 2.0 or above

Python modules:

- llvmpy 0.12.7 or above
- numba 0.14.0 or above

### Release Notes

#### Version (0.21.0)

NumbaPro will be deprecated with most code generation features moved into the opensource Numba and the CUDA bindings moved into a new commercial package called “Accelerate”. The new package will feature more high-level API functions from the CUDA libraries as well as MKL.

The next release of NumbaPro will provide aliases to the features that are moved to Numba and Accelerate. There will not be any new feature added to NumbaPro. In the future, there may be bug fix releases for maintaining the aliases to the moved features.

Changes:

- Depends on numba 0.21.0
- Fix auto thread-per-block tuning support for CUDA CC 3.7 devices
- `Blas.dotu` is deprecated. A warning is generated when it is used. `Blas.dot` is an alias to it and is preferred.

#### Version (0.20.0)

This release depends on numba 0.20, which has upgraded to CUDA 7 for GPU support. CUDA 7 has deprecated the support for all 32-bit platforms. The oldest supported Windows version is Windows 7.0. This does not affect CPU features.



**Version (0.19.0)**

- Depends on numba 0.19
- Fixes issue with GPU ufunc broadcasting
- Improves GPU ufunc implementation

**Version (0.18.0)**

- Depends on numba 0.18.1
- **Improve CUDA gufunc implementation**
  - Simplified code generation
  - Smarter blocksize selection

**Version (0.17.1)**

- Depends on numba 0.17.0
- Warns about incompatible numba version at import time
- Fixes some CUDA library APIs on windows

**Version (0.17.0)**

- Depends on numba 0.16.0
- Replaces llvmpy with llvmlite, which also upgrades to llvm3.5
- Update occupancy autotuner for CC 5.0 and CC 5.2 devices
- Fix handling of empty array in GPU reduction
- Fix occupancy autotuner that may pick invalid blocksize

**Version (0.16.0)**

- Add *numbapro.cuda.reduce* for autogeneration of CUDA reduce kernels and driver.
- Fix device to host auto transfer logic in some ufunc function.
- Upgrades to Numba 0.15

**Version (0.15.0)**

- **Add *numbapro.cudalib.sorting*:**
  - Added GPU radixsort and radixselect using implementation from <http://nvlabs.github.io/cub>
  - Added GPU segmented sort from <http://nvlabs.github.io/moderngpu>
- Fix GPU *print()* when there are multiple arguments

### Version (0.14.3)

- CUDA driver is initialized lazily
- Improved stability of CUDA ufunc machinery
- Improved stability of parallel ufunc

### Version (0.14.2)

- Unify numba.cuda and numbapro.cuda backend
- Enable Python 3 support
- Fixes workqueue module import for embedded python usecase

### Version (0.14.1)

Fixes:

- UnboundReferenceError due to mishandling of incompatible driver (pre CUDA5.5 driver). The fix relaxes the driver requirement by allowing some features to fail on use.
- numbapro.cuda.\* symbols are still exported when CUDA is not available. They would raise exception on use.

### Version (0.14.0)

Features:

- Add cuSparse API
- Improve CUDA driver and resource management
- Some of CUDA-python language feature is now opensourced as numba.cuda

Fixes:

- New CUDA driver system prevents freezing OSX on kernel launch error

### Version (0.13.2)

- Fix problem with numpy 18 array scalar contiguousness
- Fix CUDA target auto initialization on *import numbapro*
- Fix an access violation error on Windows 8 due to mishandling by LLVM.
- Add non-public API for profiler control.

### Version (0.13.1)

- Guard error due to mishandling of interleaved memory buffer (#60)
- Update to use Numba 0.12.1
- Fix powi bug

**Version (0.13)**

- Add print statement for strings and scalar numeric types for debugging on GPU
- Add constant and local memory array allocation on GPU
- Add debug mode for GPU
- Allow raising exception classes on GPU
- Update CUDA toolkit libraries
- Fix boolean mapping

**Version (0.12.7)**

- Fix major bug that mistreats py2 division as inplace floor-division for real numbers.
- Fix using of array as argument of a CUDA device function.
- Delay initialization the CUDA subsystem upon first import of the cuda package.
- Add docstrings.

**Version (0.12.6)**

- Fix major bug that mistreats py2 division as floor-division for real numbers.

**Version (0.12.5)**

- Update to Numba 0.10.2
- Update to LLVM 3.3
- Various bug fixes

**Version (0.12.4)**

- Update to Numba 0.10.0
- Minor bug fixes

**Version (0.12.3)**

- Accept older driver by deferring driver error to first use of specific API
- Report incompatible GPU at context creation
- Improve device information reporting
- Autotuning base on compiler info and occupancy calculator
- Add basic support for ravel and reshape

### Version (0.12.2)

- Distribute CUDA toolkit in Anaconda
- Better error message
- Fix gufunc signature parsing to accept trailing comma.
- Fix CUDA driver log info bug
- Support JIT linking

### Version (0.12.1)

- Fix libNVVM search path (now accept directory path)
- Fix sign-extension error in forloop precondition
- Fix support for true-division

### Version (0.12.0)

- Use CUDA 5.5rc
- Expand math support through CUDA NVVM libdevice
- Rewritten nopython mode for CUDA-Python
- Removed experimental CU API
- Removed minivectorize

### Version (0.11.0)

- Add cuBlas binding
- Improve CUDA ndarray and memory management
- Add CUDA mapped host memory
- Add CUDA event

### Version (0.10.1)

- Fix CU memory leak
- Fix CU hanging on some GPU
- Improve error message for unsupported GPU devices
- Add cuFFT

### Version (0.10)

- Added Compute Unit (CU) API
- Added cuRAND binding
- Added CUDA device array
- Various improvements to CUDA support

### Version (0.9)

- Improve CUDA driver discovery.

### Version 0.8

- Update for SSA types inference in Numba
- Allow user to select CUDA device
- Add support for pinned and mapped CUDA memory
- Improvement on small memory allocation in CUDA
- Default to use libNVVM from Anaconda
- Bug fixes

### Version 0.7

- Prange: parallel for-range
- Array slicing
- Refactor CUDA dispatch mechanisms
- Migrate to NVVM instead of PTX for CUDA codegen

### Version 0.6 and earlier

- Array expressions
- Fast ufuncs and generalized-ufunc (gufunc) with single-core, multi-core and CUDA
- CUDA JIT.

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### Third Party Dependencies

The following sections enumerate NumbaPro thirdparty dependencies and their license information.

#### CUDA Toolkit Redistributable Libraries

The `cuda-toolkit` conda package contains redistributable binaries from the CUDA toolkit. See CUDA toolkit EULA at <http://docs.nvidia.com/cuda/eula/index.html>

#### CUB

The `nbpro_radixsort.so` library (shipped in `numbapro_cudalib` conda package) uses CUB (<http://nvlabs.github.io/cub>) which has the following license:

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```



## ModernGPU

The `nbpro_segsort.so` library (shipped in `numbapro_cudalib` conda package) uses ModernGPU (<http://nvlabs.github.io/moderngpu>) which has the following license:

```
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### 4.4.7 MKL Optimizations

Developed specifically for science, engineering, and financial computations, Intel™ Math Kernel Library (MKL) is a set of threaded and vectorized math routines that work to accelerate various math functions and applications. Anaconda has packaged MKL-powered binary versions of some of the most popular numerical/scientific Python libraries into MKL Optimizations for improved performance.

#### MKL Optimizations includes:

- Speed-boosted NumPy, SciPy, scikit-learn, and NumExpr
- The packaging of MKL with redistributable binaries in Anaconda for easy access to the MKL runtime library.
- Python bindings to the low level MKL service functions, which allow for the modification of the number of threads being used during runtime.

#### Included Packages

##### Packages upgraded to use MKL

- NumPy
- NumExpr
- SciPy
- Scikit-Learn

### mkl-service

This package exposes a few functions which are declared in `mkl_service.h`. The main purpose of the package is to allow the user to change the number of CPU's MKL is using at runtime.

#### Example:

In this small example, we first query how many CPU are being used, and then change this number.

```
>>> import mkl
>>> mkl.get_max_threads()
2
>>> mkl.set_num_threads(1)
>>> mkl.get_max_threads()
1
```

### Reference

#### mkl service functions:

**mkl.get\_cpu\_clocks()** -> int Return the CPU clocks as an integer.

**mkl.get\_cpu\_frequency()** -> float Return CPU frequency in GHz as a float.

**mkl.get\_max\_threads()** -> int Return the number of threads Intel MKL is targeting for parallelism.

**mkl.get\_version\_string()** -> str Return the MKL library version information as a string.

**mkl.mem\_stat(n)** -> int Returns an amount of memory, allocated by the MKL Memory Allocator.

**mkl.set\_num\_threads(n)** Set the number of threads MKL should use. This is only a hint, and no guaranteed is made this number of threads will actually be used. This function takes precedence over the environment variable `MKL_NUM_THREADS`.

### Installation

In Anaconda versions 2.5 and later, MKL is [freely available by default in Anaconda](#).

If you already have the free [Anaconda](#) Python distribution installed, get MKL by upgrading to the latest version:

```
conda update conda
conda update anaconda
```

If you do not have Anaconda installed, you can download it [here](#).

Existing MKL licenses can be viewed and removed with the graphical Anaconda Navigator license manager or manually with your operating system.

### Configuration

Anaconda now also includes a small utility package called `mkl-service` which provides a Python interface to some useful MKL functions that are declared in `mkl_service.h`, such as setting the number of threads to use.

## Uninstalling MKL

MKL takes roughly 100MB and some use cases do not need it, so users can opt out of MKL and instead use [OpenBLAS](#) for Linux or the native Accelerate Framework for MacOSX. To opt out, run `conda install nomkl` and then use `conda install` to install packages that would normally include MKL or depend on packages that include MKL, such as `scipy`, `numpy`, and `pandas`. Conda will install the non-MKL versions of these packages together with their dependencies. If you are using OS X or Linux, have already installed these packages or already installed all of Anaconda, and wish to switch away from MKL, use the command `conda install nomkl numpy scipy scikit-learn numexpr` followed by `conda remove mkl mkl-service`.

## Updating

If you already have the free Anaconda Python distribution installed and wish to update MKL:

```
conda update conda
conda update mkl
```

## Dismissing MKL Trial warnings

Because past versions of Anaconda did not include MKL linked binaries by default, some users who have used `conda update --all` may see an MKL Trial warning or a license expiration error, even though MKL linked packages are now free and installed by default. A license expiration error message may read, “You cannot run MKL without a license any longer.”

To resolve this, set your installation to use the mkl-linked libraries that do not require a license:

```
conda remove mkl-rt
conda install -f mkl
```

Then run `conda install` with the specific packages you choose:

```
conda install numpy scipy scikit-learn numexpr
```

or with all of Anaconda:

```
conda install anaconda
```

## Resolving MKL shared library “permission denied” errors

On Linux platforms that have SELinux enabled, you may encounter security errors like the following:

```
error while loading shared libraries: <libmkl_intel.so>: cannot restore segment prot_
↪after reloc: Permission denied
```

This is because MKL requires text relocation permissions, which SELinux denies by default. This prevents MKL from being loaded by Numpy, preventing Numpy from being imported.

There are two known solutions to this issue:

1. Does not require root privileges. Replace MKL with OpenBLAS by issuing the command:

```
conda install nomkl numpy scipy scikit-learn numexpr
```

You may revert back to the MKL default versions at any time by using:

```
conda remove nomkl
conda install mkl
```

2. Requires root privileges. Temporarily disable SELinux enforcement. From a root-privileged terminal enter:

```
/usr/sbin/setenforce 0
```

NOTE: If you prefer to make this change permanent, in the file `/etc/selinux/config` change “enforcing” to “disabled” and then reboot.

## License Agreement

The MKL Optimizations are included in the free Anaconda python distribution, and have been made available by the terms of the *End User License Agreement - Anaconda® Individual Edition*.

Past versions of MKL Optimizations were not freely available in Anaconda, and have been made available separately by the terms of the *MKL Optimizations End User License Agreement*.

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### 4.4.8 IOPro

IOPro loads NumPy arrays (and Pandas DataFrames) directly from files, SQL databases, and NoSQL stores—including ones with millions of rows—without creating millions of temporary, intermediate Python objects, or requiring expensive array resizing operations.

IOPro provides a drop-in replacement for the NumPy functions `loadtxt()` and `genfromtxt()`, but dramatically improves performance and reduces memory overhead.

The current (and final) version of IOPro 1.9.1 was released on March 1, 2017.

## The open source successors to IOPro

All of the code in IOPro was released in 2017 under a BSD open source license. As part of that release, the code was refactored into its several component libraries, and version numbers of each were set to 2.0.0 to indicate they supersede the code under the IOPro name.

The several libraries are available on GitHub at:

- [TextAdapter](#) (CSV, JSON, etc)
- [DBAdapter](#) (SQL derivatives)
- [PostgresAdapter](#) (PostgreSQL)
- [AccumuloAdapter](#) (Apache Accumulo)
- [MongoAdapter](#) (MongoDB)

These various packages may be available as conda packages (using lowercase versions of their names) in the conda-forge channel. Maintenance, improvements, and packaging will be a community-led project.

## How to get IOPro

To get IOPro just download and install the IOPro package.

If you already have [Anaconda](#) (free Python platform) or [Miniconda](#) installed:

```
conda update conda
conda install -c pkgs/pro iopro=1.9.1
```

If you do not have Anaconda installed, you can [download it](#).

### Requirements

- Python 2.7 or 3.4+
- NumPy 1.10+

Optional Python modules:

- Boto (for S3 support)
- Pandas (to use DataFrames)

### What's new in version 1.9?

The documentation has been substantially updated for version 1.9.0. Numba has been removed and the code has been cleaned up, but no other features were added or removed. Some refactoring was done that didn't change functionality. We recommend that users not use older versions. See [Release notes](#) for additional detail.

### Getting started

Some of the basic usage patterns look like these. Create TextAdapter object for data source:

```
>>> import iopro
>>> adapter = iopro.text_adapter('data.csv', parser='csv')
```

Define field dtypes (example: set field 0 to unsigned int and field 4 to float):

```
>>> adapter.set_field_types({0: 'u4', 4: 'f4'})
```

Parse text and store records in NumPy array using slicing notation:

```
>>> # read all records
>>> array = adapter[:]

>>> # read first ten records
>>> array = adapter[0:10]

>>> # read last record
>>> array = adapter[-1]

>>> # read every other record
>>> array = adapter[::2]
```

### User guide

#### Installation

If you do not already have Anaconda installed, please download it via the [downloads page](#) and install it.



IOPro is included with [Anaconda Workgroup](#) and [Anaconda Enterprise](#) subscriptions.

To start a 30-day free trial just download and install the IOPro package.

If you already have [Anaconda](#) (free Python platform) or [Miniconda](#) <<http://conda.io/miniconda.html>> installed:

```
conda update conda
conda install iopro
```

If you do not have Anaconda installed, you can [download it](#).

For more information about IOPro please contact [sales@anaconda.com](mailto:sales@anaconda.com).

## IOPro Update Instructions

If you have Anaconda (free Python platform) installed, first update the conda package management tool to the latest version, then use conda to update the IOPro product installation:

```
conda update conda
conda update iopro
```

## Uninstall

To uninstall using conda:

```
conda remove iopro
```

## Installing license

The IOPro license can be installed with the graphical Anaconda Navigator license manager or manually with your operating system. In your organization this may be handled by your site administrator or IT department.

## TextAdapter First Steps

### Basic Usage

IOPro works by attaching to a data source, such as a local CSV file. Before we get started, let's create a sample CSV file to work with:

```
from random import random, randint, shuffle
import string

NUMROWS = 10
with open('data/table.csv', 'w') as data:
    # Header
    for n in range(1, 5):
        print("f%d" % n, end=", ", file=data)
    print("comment", file=data)

    # Body
    letters = list(string.ascii_letters)
    for n in range(NUMROWS):
```

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```

shuffle(letters)
s = "".join(letters[:randint(5,20)])
vals = (n, randint(1000,2000), random(), random()*100, s)
print("%d,%d,%f,%f,%s" % vals, file=data)

```

Let's read in the local CSV file created here. Because this small file easily fits in memory it would work to use the csv or pandas modules, but we will demonstrate the interfaces and capabilities that will apply to much larger data.

```

>>> import iopro
>>> adapter = iopro.text_adapter('data/table.csv', parser='csv')
>>> adapter.get_field_names()
['f1', 'f2', 'f3', 'f4', 'comment']

```

We can specify the data types for values in the columns of the CSV file being read; but first we look at the ability of IOPro's TextAdapter to auto-discover the data types used.

We can ask IOPro's TextAdapter to parse text and return records in NumPy arrays from selected portions of the CSV file using slicing notation:

```

>>> # the inferred datatypes
>>> array = adapter[:]
>>> array.dtype
dtype([('f1', '<u8'), ('f2', '<u8'), ('f3', '<f8'), ('f4', '<f8'),
      ('comment', 'O')])

```

Let's define field dtypes (example: set field 0 to a 16-bit unsigned int and field 3 to a 32-bit float).

Massage the datatypes:

```

>>> adapter.set_field_types({0: 'u2', 3: 'f4'})
>>> array = adapter[:]
>>> array.dtype
dtype([('f1', '<u2'), ('f2', '<u8'), ('f3', '<f8'), ('f4', '<f4'),
      ('comment', 'O')])

```

The first five records:

```

>>> array = adapter[0:5]
>>> print(array)
[(0, 1222, 0.926116, 84.44437408447266, 'MlzvBRyquns')
 (1, 1350, 0.553585, 81.03726959228516, 'ikgEauJeTZvd')
 (2, 1932, 0.710919, 31.59865951538086, 'uUQmHJFZhniRecAvx')
 (3, 1494, 0.622391, 57.90607452392578, 'iWQBAZodkfHODtI')
 (4, 1981, 0.820246, 40.848018646240234, 'igxeXdBpqE')]

```

Read last five records:

```

>>> array = adapter[-5:]
>>> print(array)
[(5, 1267, 0.694631, 6.999039173126221, 'bRSrwitHeY')
 (6, 1166, 0.37465, 38.7022705078125, 'qzbMgVThXtHpFDNrd')
 (7, 1229, 0.390566, 55.338134765625, 'hyarmvWi')
 (8, 1816, 0.201106, 59.74718475341797, 'DcHymelRusO')
 (9, 1416, 0.725697, 42.50992965698242, 'QMUGRAWe')]

```

Read every other record:

```
>>> array = adapter[:,2]
>>> print(array)
[(0, 1222, 0.926116, 84.44437408447266, 'MlzvBRyquns'),
 (2, 1932, 0.710919, 31.59865951538086, 'uUQmHJFZhnirecAvx'),
 (4, 1981, 0.820246, 40.848018646240234, 'igxeXdBpqE'),
 (6, 1166, 0.37465, 38.7022705078125, 'qzbMgVThXtHpFDNrd'),
 (8, 1816, 0.201106, 59.74718475341797, 'DcHymelRusO')]
```

Read first and second, third fields only:

```
>>> array = adapter[[0,1,2]][:,]
>>> list(array)
[(0, 1222, 0.926116),
 (1, 1350, 0.553585),
 (2, 1932, 0.710919),
 (3, 1494, 0.622391),
 (4, 1981, 0.820246),
 (5, 1267, 0.694631),
 (6, 1166, 0.37465),
 (7, 1229, 0.390566),
 (8, 1816, 0.201106),
 (9, 1416, 0.725697)]
```

Read fields named 'f2' and 'comment' only:

```
>>> array = adapter[['f2', 'comment']][:]
>>> list(array)
[(1222, 'MlzvBRyquns'),
 (1350, 'ikgEauJeTZvd'),
 (1932, 'uUQmHJFZhnirecAvx'),
 (1494, 'iWQBAZodkfHODtI'),
 (1981, 'igxeXdBpqE'),
 (1267, 'bRSrwitHeY'),
 (1166, 'qzbMgVThXtHpFDNrd'),
 (1229, 'hyarmvWi'),
 (1816, 'DcHymelRusO'),
 (1416, 'QMUGRAwe')]
```

## JSON Support

Text data in JSON format can be parsed by specifying 'json' for the parser argument:

Content of file data/one.json:

```
{"id":123, "name":"xxx"}
```

Single JSON object:

```
>>> adapter = iopro.text_adapter('data/one.json', parser='json')
>>> adapter[:]
array([(123, 'xxx')],
      dtype=[('id', '<u8'), ('name', 'O')])
```

Currently, each JSON object at the root level is interpreted as a single NumPy record. Each JSON object can be part of an array, or separated by a newline. Examples of valid JSON documents that can be parsed by IOPro, with the NumPy array result:

Content of file data/two.json:

```
[{"id":123, "name":"xxx"}, {"id":456, "name":"yyy"}]
```

Array of two JSON objects:

```
>>> iopro.text_adapter('data/two.json', parser='json')[:]
array([(123, 'xxx'), (456, 'yyy')],
      dtype=[('id', '<u8'), ('name', 'O')])
```

Content of file data/three.json:

```
{"id":123, "name":"xxx"}
{"id":456, "name":"yyy"}
```

Two JSON objects separated by newline:

```
>>> iopro.text_adapter('data/three.json', parser='json')[:]
array([(123, 'xxx'), (456, 'yyy')],
      dtype=[('id', '<u8'), ('name', 'O')])
```

## Massaging data in the adapter

A custom function can be used to modify values as they are read.

```
>>> import iopro, io, math
>>> stream = io.StringIO('3,abc,3.3\n7,xxx,9.9\n4,,')
>>> adapter = iopro.text_adapter(stream, parser='csv', field_names=False)
```

Override default converter for first field:

```
>>> adapter.set_converter(0, lambda x: math.factorial(int(x)))
>>> adapter[:]
array([(6, 'abc', 3.3), (5040, 'xxx', 9.9), (24, '', nan)],
      dtype=[('f0', '<u8'), ('f1', 'O'), ('f2', '<f8')])
```

We can also force data types and set fill values for missing data.

Apply data types to columns:

```
>>> stream = io.StringIO('3,abc,3.3\n7,xxx,9.9\n4,,')
>>> adapter = iopro.text_adapter(stream, parser='csv', field_names=False)
>>> adapter.set_field_types({1:'S3', 2:'f4'})
>>> adapter[:]
array([(3, b'abc', 3.299999952316284), (7, b'xxx', 9.899999618530273),
      (4, b'', nan)],
      dtype=[('f0', '<u8'), ('f1', 'S3'), ('f2', '<f4')])
```

Set fill value for missing values in each field:

```
>>> adapter.set_fill_values({1:'ZZZ', 2:999.999})
>>> adapter[:]
array([(3, b'abc', 3.299999952316284), (7, b'xxx', 9.899999618530273),
      (4, b'ZZZ', 999.9990234375)],
      dtype=[('f0', '<u8'), ('f1', 'S3'), ('f2', '<f4')])
```

## Combining regular expressions and typecasting

A later section discusses regular expressions in more detail. This example is a quick peek into using them with IOPro.

Content of the file `data/transactions.csv`:

```
$2.56, 50%, September 20 1978
$1.23, 23%, April 5 1981
```

Combining features:

```
>>> import iopro
>>> regex_string = '\$(\d)\.(\d{2}),\s*([0-9])\%,\s*([A-Za-z]+) '
>>> adapter = iopro.text_adapter('data/transactions.csv',
...                             parser='regex',
...                             regex_string=regex_string,
...                             field_names=False,
...                             infer_types=False)
```

Set dtype of fields and their names:

```
>>> adapter.set_field_types({0:'i2', 1:'u2', 2:'f4', 3:'S10'})
>>> adapter.set_field_names(['dollars', 'cents', 'percentage', 'month'])
>>> adapter[:]
array([(2, 56, 50.0, b'September'), (1, 23, 23.0, b'April')],
      dtype=[('dollars', '<i2'), ('cents', '<u2'),
              ('percentage', '<f4'), ('month', 'S10')])
```

## Advanced TextAdapter

### `iopro.loadtxt()` versus `iopro.genfromtxt()`

Within IOPro there are two closely related functions. `loadtxt()`, which we have been looking at, makes a more optimistic assumption that your data is well-formatted. `genfromtxt()` has a number of arguments for handling messier data, and special behaviors for dealing with missing data.

`loadtxt()` is already highly configurable for dealing with data under many CSV and other delimited formats. `genfromtxt()` contains a superset of these arguments.

## Gzip Support

IOPro can decompress gzip'd data on the fly, simply by indicating a `compression` keyword argument.

```
>>> adapter = iopro.text_adapter('data.gz', parser='csv', compression='gzip')
>>> array = adapter[:]
```

As well as being able to store and work with your compressed data without having to decompress it first, you also do not need to sacrifice any performance in doing so. For example, with one test 419 MB CSV file of numerical data, and a 105 MB file of the same data compressed with gzip, the following are run times on a test machine for loading the entire contents of each file into a NumPy array. Exact performance will vary between machines, especially between machines with HDD and SSD architecture.:

```
- uncompressed: 13.38 sec
- gzip compressed: 14.54 sec
```

In the test, the compressed file takes slightly longer, but consider having to uncompress the file to disk before loading with IOPro:

- uncompressed: 13.38 sec
- gzip compressed: 14.54 sec
- gzip compressed (decompress to disk, then load): 21.56 sec

## Indexing CSV Data

One of the most useful features of IOPro is the ability to index data to allow for fast random lookup.

For example, to retrieve the last record of the compressed 109 MB dataset we used above:

```
>>> adapter = iopro.text_adapter('data.gz', parser='csv', compression='gzip')
>>> array = adapter[-1]
```

Retrieving the last record into a NumPy array takes 14.82 sec. This is about the same as the time to read the entire array, because the entire dataset has to be parsed to get to the last record.

To make seeking faster, we can build an index:

```
>>> adapter.create_index('index_file')
```

The above method creates an index in memory and saves it to disk, taking 9.48 sec. Now when seeking to and reading the last record again, it takes a mere 0.02 sec.

Reloading the index only takes 0.18 sec. If you build an index once, you get near instant random access to your data forever (assuming the data remains static):

```
>>> adapter = iopro.text_adapter('data.gz', parser='csv',
...                               compression='gzip',
...                               index_name='index_file')
```

Let's try it with a moderate sized example. You can download this data from the [Exoplanets Data Explorer](#) site.

```
>>> adapter = iopro.text_adapter('data/exoplanets.csv.gz',
...                               parser='csv', compression='gzip')
>>> print(len(adapter[:]), "rows")
>>> print(', '.join(adapter.field_names[:3]),
...       '...%d more...\n' % (adapter.field_count-6),
...       ', '.join(adapter.field_names[-3:]))
2042 rows
name, mass, mass_error_min ...73 more...
    star_teff, star_detected_disc, star_magnetic_field
```

```
>>> adapter.field_types
{0: dtype('O'),
 1: dtype('float64'),
 2: dtype('float64'),
 3: dtype('O'),
 4: dtype('float64'),
 5: dtype('float64'),
 6: dtype('float64'),
 7: dtype('float64'),
 8: dtype('O'),
 9: dtype('float64'),
```

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```
[... more fields ...]
69: dtype('float64'),
70: dtype('float64'),
71: dtype('float64'),
72: dtype('float64'),
73: dtype('float64'),
74: dtype('O'),
75: dtype('float64'),
76: dtype('float64'),
77: dtype('O'),
78: dtype('uint64')}
```

Do some timing (using an IPython magic):

```
>>> %time row = adapter[-1]
CPU times: user 35 ms, sys: 471 µs, total: 35.5 ms
Wall time: 35.5 ms
```

```
>>> %time adapter.create_index('data/exoplanets.index')
CPU times: user 15.7 ms, sys: 3.35 ms, total: 19.1 ms
Wall time: 18.6 ms
```

```
>>> %time row = adapter[-1]
CPU times: user 18.3 ms, sys: 1.96 ms, total: 20.3 ms
Wall time: 20.1 ms
```

```
>>> new_adapter = iopro.text_adapter('data/exoplanets.csv.gz', parser='csv',
...                                 compression='gzip',
...                                 index_name='data/exoplanets.index')
```

```
>>> %time row = new_adapter[-1]
CPU times: user 17.3 ms, sys: 2.12 ms, total: 19.4 ms
Wall time: 19.4 ms
```

## Regular Expressions

Some people, when confronted with a problem, think “I know, I’ll use regular expressions.” Now they have two problems. —Jamie Zawinski

IOPro supports using regular expressions to help parse messy data. Take for example the following snippet of actual NASDAQ stock data found on the Internet:

The content of the file `data/stocks.csv`:

```
Name,Symbol,Exchange,Range
Apple,AAPL,NasdaqNM,363.32 - 705.07
Google,GOOG,NasdaqNM,523.20 - 774.38
Microsoft,MSFT,NasdaqNM,24.30 - 32.95
```

The first three fields are easy enough: name, symbol, and exchange. The fourth field presents a bit of a problem. Let’s try IOPro’s regular expression based parser:

```
>>> regex_string = '([A-Za-z]+),([A-Z]{1,4}),([A-Za-z]+),'\
...               '(\d+\.\d{2})\s*\-\s*(\d+\.\d{2})'\
>>> adapter = iopro.text_adapter('data/stocks.csv', parser='regex',
...                               regex_string=regex_string)
```

```
>>> # Notice that header does not now match the regex
>>> print(adapter.field_names)
['Name', 'Symbol', 'Exchange', 'Range', ' ', ' ', ' ', ' ']
```

```
>>> # We can massage the headers to reflect our match pattern
>>> info = adapter.field_names[0].split(',')[3]
>>> adapter.field_names = info + ["Low", "High"]
>>> adapter[:]
array([('Apple', 'AAPL', 'NasdaqNM', 363.32, 705.07),
      ('Google', 'GOOG', 'NasdaqNM', 523.2, 774.38),
      ('Microsoft', 'MSFT', 'NasdaqNM', 24.3, 32.95)],
      dtype=[('Name', 'O'), ('Symbol', 'O'),
            ('Exchange', 'O'), ('Low', '<f8'), ('High', '<f8')])
```

Regular expressions are compact and often difficult to read, but they are also very powerful. By using the above regular expression with the grouping operators ‘(’ and ‘)’, we can define exactly how each record should be parsed into fields. Let’s break it down into individual fields:

- ([A-Za-z]+) defines the first field (stock name) in our output array
- ([A-Z]{1-4}) defines the second (stock symbol)
- ([A-Za-z]+) defines the third (exchange name)
- (\d+\.\d{2}) defines the fourth field (low price)
- \s\*\-\s\* is skipped because it is not part of a group
- (\d+\.\d{2}) defines the fifth field (high price)

The output array contains five fields: three string fields and two float fields. Exactly what we want.

### S3 Support

IOPro can parse CSV data stored in Amazon’s S3 cloud storage service. In order to access S3 files, you need to specify some credentials along with the resource you are accessing.

The first two parameters are your AWS access key and secret key, followed by the S3 bucket name and key name. The S3 CSV data is downloaded in 128K chunks and parsed directly from memory, bypassing the need to save the entire S3 data set to local disk.

Let’s take a look at what we have stored from the Health Insurance Marketplace data. There’s a little bit of code with BeautifulSoup just to prettify the raw XML query results.

```
>>> import urllib.request
>>> url = 'http://s3.amazonaws.com/product-training/'
>>> xml = urllib.request.urlopen(url).read()
```

```
>>> import bs4, re
>>> r = re.compile(r'^(\s*)', re.MULTILINE)
>>> def display(bs, encoding=None, formatter="minimal", indent=4):
...     print(r.sub(r'\1' * indent, bs.prettify(encoding, formatter)))
```

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```
>>> display(bs4.BeautifulSoup(xml, "xml"))
<?xml version="1.0" encoding="utf-8"?>
<ListBucketResult xmlns="http://s3.amazonaws.com/doc/2006-03-01/">
  <Name>
    product-training
  </Name>
  <Prefix/>
  <Marker/>
  <MaxKeys>
    1000
  </MaxKeys>
  <IsTruncated>
    false
  </IsTruncated>
  <Contents>
    <Key>
      BusinessRules.csv
    </Key>
    <LastModified>
      2016-06-25T00:03:20.000Z
    </LastModified>
    <ETag>
      "a565ebede6a7e6e060cd4526a7ae4345"
    </ETag>
    <Size>
      8262590
    </Size>
    <StorageClass>
      STANDARD
    </StorageClass>
  </Contents>
  <Contents>
    [... more files ...]
  </Contents>
</ListBucketResult>
```

In simple form, we see details about some S3 resources. Let's access one of them. Note that you will need to fill in your actual AWS access key and secret key.

```
>>> user_name = "class1"
>>> aws_access_key = "ABCD"
>>> aws_secret_key = "EFGH/IJK"
>>> bucket = 'product-training'
>>> key_name = 'BusinessRules.csv' # 21k lines, 8MB
>>> # key_name = 'PlanAttributes.csv' # 77k lines, 95MB
>>> # key_name = 'Rate.csv.gz' # 13M lines, 2GB raw, 110MB compressed
>>> adapter = iopro.s3_text_adapter(aws_access_key, aws_secret_key,
...                                bucket, key_name)
>>> # Don't try with the really large datasets, works with the default one
>>> df = adapter.to_dataframe()
>>> df.iloc[:6,:6]
```

IOPro can also build an index for S3 data just as with disk based CSV data, and use the index for fast random access lookup. If an index file is created with IOPro and stored with the S3 dataset in the cloud, IOPro can use this remote index to download and parse just the subset of records requested. This allows you to generate an index file once and share it on the cloud along with the data set, and does not require others to download the entire index file to use it.

## iopro.pyodbc First Steps

iopro.pyodbc extends pyodbc with methods that allow data to be fetched directly into numpy containers. These functions are faster than regular fetch calls in pyodbc, providing also the convenience of being returned in a container appropriate to fast analysis.

This notebook is intended to be a tutorial on iopro.pyodbc. Most of the material is applicable to pyodbc (and based on pyodbc tutorials). There will be some examples specific to iopro.pyodbc. When that's the case, it will be noted.

## Concepts

In pyodbc there are two main classes to understand:

- connection
- cursor

A connection is, as its name says, a connection to a datasource. A datasource is your database. It may be a database handled by a DBMS or just a plain file. A cursor allows you to interface with statements. Interaction with queries and other commands is performed through a cursor. A cursor is associated to a connection and commands over a cursor are performed over that connection to the datasource. In order to use iopro.pyodbc you must import it:

```
>>> import iopro.pyodbc as pyodbc
```

## Connection to a datasource

In order to operate with pyodbc you need to connect to a datasource. Typically this will be a database. This is done by creating a connection object. To create a connection object you need a connection string. This string describes the datasource to use as well as some extra parameters. You can learn more about connection strings here.:

```
>>> connection_string = '''DSN=SQLServerTest;DATABASE=Test'''
>>> connection = pyodbc.connect(connection_string)
```

pyodbc.connect supports a keyword parameter autocommit. This controls the way the connection is handle. The default value (False) means that the commands that modify the database statements need to be committed explicitly. All commands between commits will form a single transaction. If autocommit is enabled every command will be issued and committed. It is also possible to change autocommit status after the connection is established.:

```
>>> connection.autocommit = True #enable autocommit
>>> connection.autocommit = False # disable autocommit
```

When not in autocommit mode, you can end a transaction by either committing it or rolling it back.:

```
In[6]: connection.commit() # commit the transaction
In[7]: connection.rollback() # rollback the transaction
```

Note that commit/rollback is always performed at the connection level. pyodbc provides a commit/rollback method in the cursor objects, but they will act on the associated connection.

## Working with cursors

Command execution in pyodbc is handled through cursors. You can create a cursor from a connection using the cursor() method. The first step is creating a cursor:

```
In[8]: cursor = connection.cursor()
```

With a cursor created, we can start issuing SQL commands using the execute method.

### Creating a sample table

First, create a sample table in the database. The following code will create a sample table with three columns of different types.:

```
>>> def create_test_table(cursor):
...     try:
...         cursor.execute('drop table test_table')
...     except:
...         pass
...     cursor.execute('''create table test_table (
...                         name varchar(10),
...                         fval float(24),
...                         ival int)''')
...     cursor.commit()
>>> create_test_table(cursor)
```

### Filling the sample table with sample data

After creating the table, rows can be inserted by executing insert into the table. Note you can pass parameters by placing a ? into the SQL statement. The parameters will be taken in order for the sequence appears in the next parameter.:

```
>>> cursor.execute('insert into test_table values (?, ?, ?)', ('foo', 3.0, 2))
>>> cursor.rowcount
1
```

Using executemany a sequence of parameters to the SQL statement can be passed and the statement will be executed many times, each time with a different parameter set. This allows us to easily insert several rows into the database so that we have a small test set:

```
>>> cursor.executemany('insert into test_table values (?, ?, ?)', [
...     ('several', 2.1, 3),
...     ('tuples', -1.0, 2),
...     ('can', 3.0, 1),
...     ('be', 12.0, -3),
...     ('inserted', 0.0, -2),
...     ('at', 33.0, 0),
...     ('once', 0.0, 0)
... ])
```

Remember that if autocommit is turned off the changes won't be visible to any other connection unless we commit.:

```
>>> cursor.commit() # remember this is a shortcut to connection.commit() method
```

### Querying the sample data from the sample table

Having populated our sample database, we can retrieve the inserted data by executing select statements.:

```
>>> cursor.execute('''select * from test_table''')
<pyodbc.Cursor at 0x6803510>
```

After calling `execute` with the `select` statement we need to retrieve the data. This can be achieved by calling `fetch` methods in the cursor. `fetchone` fetches the next row in the cursor, returning it in a tuple:

```
>>> cursor.fetchone()
('foo', 3.0, 2)
```

`fetchmany` retrieves several rows at a time in a list of tuples:

```
>>> cursor.fetchmany(3)
[('several', 2.09999999046325684, 3), ('tuples', -1.0, 2), ('can', 3.0, 1)]
```

`fetchall` retrieves all the remaining rows in a list of tuples:

```
>>> cursor.fetchall()
[('be', 12.0, -3), ('inserted', 0.0, -2), ('at', 33.0, 0), ('once', 0.0, 0)]
```

All the calls to any kind of `fetch` advances the cursor, so the next `fetch` starts in the row after the last row fetched. `execute` returns the cursor object. This is handy to retrieve the full query by chaining `fetchall`. This results in a one-liner::

```
>>> cursor.execute('''select * from test_table''').fetchall()
[('foo', 3.0, 2),
 ('several', 2.09999999046325684, 3),
 ('tuples', -1.0, 2),
 ('can', 3.0, 1),
 ('be', 12.0, -3),
 ('inserted', 0.0, -2),
 ('at', 33.0, 0),
 ('once', 0.0, 0)]
```

## **iopro.pyodbc extensions**

When using `iopro.pyodbc` it is possible to retrieve the results from queries directly into `numpy` containers. This is accomplished by using the new cursor methods `fetchdictarray` and `fetchsarray`.

### **fetchdictarray**

`fetchdictarray` fetches the results of a query in a dictionary. By default `fetchdictarray` fetches all remaining rows in the cursor::

```
>>> cursor.execute('''select * from test_table''')
>>> dictarray = cursor.fetchdictarray()
>>> type(dictarray)
dict
```

The keys in the dictionary are the column names::

```
>>> dictarray.keys()
['ival', 'name', 'fval']
```

Each column name is mapped to a `numpy` array (`ndarray`) as its value::

```
>>> ', '.join([type(dictarray[i]).__name__ for i in dictarray.keys()])
'ndarray, ndarray, ndarray'
```

The types of the numpy arrays are inferred from the database column information. So for our columns we get an appropriate numpy type. Note that in the case of name the type is a string of 11 characters even if in test\_table is defined as varchar(10). The extra parameter is there to null-terminate the string::

```
>>> ', '.join([repr(dictarray[i].dtype) for i in dictarray.keys()])
"dtype('int32'), dtype('|S11'), dtype('float32')"
```

The numpy arrays will have a shape containing a single dimension with the number of rows fetched::

```
>>> ', '.join([repr(dictarray[i].shape) for i in dictarray.keys()])
'(8L,), (8L,), (8L,)'
```

The values in the different column arrays are index coherent. So in order to get the values associated to a given row it suffices to access each column using the appropriate index. The following snippet shows this correspondence::

```
>>> print '\n'.join(
...     [' ', '.join(
...         [repr(dictarray[i][j]) for i in dictarray.keys()])
...         for j in range(dictarray['name'].shape[0])])
2, 'foo', 3.0
3, 'several', 2.0999999
2, 'tuples', -1.0
1, 'can', 3.0
-3, 'be', 12.0
-2, 'inserted', 0.0
0, 'at', 33.0
0, 'once', 0.0
```

Having the results in numpy containers makes it easy to use numpy to analyze the data::

```
>>> import numpy as np
>>> np.mean(dictarray['fval'])
6.5124998092651367
```

fetchdictarray accepts an optional parameter that places an upper bound to the number of rows to fetch. If there are not enough elements left to be fetched in the cursor the arrays resulting will be sized accordingly. This way it is possible to work with big tables in chunks of rows::

```
>>> cursor.execute('select * from test_table')
>>> dictarray = cursor.fetchdictarray(6)
>>> print dictarray['name'].shape
(6L,)
>>> dictarray = cursor.fetchdictarray(6)
>>> print dictarray['name'].shape
(2L,)
```

## fetchsarray

fetchsarray fetches the result of a query in a numpy structured array::

```
>>> cursor.execute('select * from test_table')
>>> sarray = cursor.fetchsarray()
```

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```
>>> print sarray
[('foo', 3.0, 2) ('several', 2.09999999046325684, 3) ('tuples', -1.0, 2)
 ('can', 3.0, 1) ('be', 12.0, -3) ('inserted', 0.0, -2) ('at', 33.0, 0)
 ('once', 0.0, 0)]
```

The type of the result is a numpy array (ndarray)::

```
>>> type(sarray)
numpy.ndarray
```

The dtype of the numpy array contains the description of the columns and their types::

```
>>> sarray.dtype
dtype([('name', '<S11'), ('fval', '<f4'), ('ival', '<i4')])
```

The shape of the array will be one-dimensional, with cardinality equal to the number of rows fetched::

```
>>> sarray.shape
(8L,)
```

It is also possible to get the shape of a column. In this way it will look similar to the code needed when using dictarrays:

```
>>> sarray['name'].shape
(8L,)
```

In a structured array it is as easy to access data by row or by column::

```
>>> sarray['name']
array(['foo', 'several', 'tuples', 'can', 'be', 'inserted', 'at', 'once'],
      dtype='<S11')

>>> sarray[0]
('foo', 3.0, 2)
```

It is also very easy and efficient to feed data into numpy functions::

```
>>> np.mean(sarray['fval'])
6.5124998092651367
```

## fetchdictarray vs fetchsarray

Both methods provide ways to input data from a database into a numpy-friendly container. The structured array version provides more flexibility extracting rows in an easier way. The main difference is in the memory layout of the resulting object. An in-depth analysis of this is beyond the scope of this notebook. Suffice it to say that you can view the dictarray laid out in memory as a structure of arrays (in fact, a dictionary or arrays), while the structured array would be laid out in memory like an array of structures. This can make a lot of difference performance-wise when working with large chunks of data.

## iopro.pyodbc Enhanced Capabilities

### Demo code showing the enhanced capabilities of iopro.pyodbc submodule

This demo shows the basic capabilities for the iopro.pyodbc module. It first will connect with the database of your choice by ODBC, create and fill a new table (market) and then retrieve data with different methods (fetchall(), fetchdictarray() and fetchsarray()).

Author: Francesc Altet, Anaconda

```
>>> import iopro.pyodbc as pyodbc
>>> # Open the database (use the most appropriate for you)
>>> connect_string = 'DSN=odbcsqlite;DATABASE=market.sqlite' # SQLite
>>> #connect_string = 'Driver={SQL Server};SERVER=MyWinBox;DATABASE=Test;USER=Devel;
↳PWD=XXX' # SQL Server
>>> #connect_string = 'DSN=myodbc3;UID=devel;PWD=XXX;DATABASE=test' # MySQL
>>> #connect_string = 'DSN=PSQL;UID=devel;PWD=XXX;DATABASE=test' # PostgreSQL
>>> connection = pyodbc.connect(connect_string)
>>> cursor = connection.cursor()
```

### Create the test table (optional if already done)

```
>>> try:
...     cursor.execute('drop table market')
... except:
...     pass
>>> cursor.execute('create table market (symbol_ varchar(5), open_ float, low_ float,
↳high_ float, close_ float, volume_ int)')
```

### Fill the test table (optional if already done)

```
>>> from time import time
>>> t0 = time()
>>> N = 1000*1000
>>> for i in xrange(N):
...     cursor.execute(
...         "insert into market(symbol_, open_, low_, high_, close_, volume_)"
...         " values (?, ?, ?, ?, ?, ?)",
...         (str(i), float(i), float(2*i), None, float(4*i), i))
>>> cursor.execute("commit") # not supported by SQLite
>>> t1 = time() - t0
>>> print "Stored %d rows in %.3fs" % (N, t1)
```

### Do the query in the traditional way

```
>>> # Query of the full table using the traditional fetchall
>>> query = "select * from market"
>>> cursor.execute(query)
>>> %time all = cursor.fetchall()
CPU times: user 5.23 s, sys: 0.56 s, total: 5.79 s
Wall time: 7.09 s
```

## Do the query and get a dictionary of NumPy arrays

```
>>> # Query of the full table using the fetchdictarray (retrieve a dictionary of
↳ arrays)
>>> cursor.execute(query)
>>> %time dictarray = cursor.fetchdictarray()
CPU times: user 0.92 s, sys: 0.10 s, total: 1.02 s
Wall time: 1.44 s
```

## Peek into the retrieved data

```
>>> dictarray.keys()
['high_', 'close_', 'open_', 'low_', 'volume_', 'symbol_']
>>> dictarray['high_']
array([ nan,  nan,  nan, ...,  nan,  nan,  nan])
>>> dictarray['symbol_']
array(['0', '1', '2', ..., '99999', '99999', '99999'], dtype='<S6')
```

## Do the query and get a NumPy structured array

```
>>> # Query of the full table using the fetchsarray (retrieve a structured array)
>>> cursor.execute(query)
>>> %time sarray = cursor.fetchsarray()
CPU times: user 1.08 s, sys: 0.11 s, total: 1.20 s
Wall time: 1.99 s
```

## Peek into retrieved data

```
>>> sarray.dtype
dtype([('symbol_', 'S6'), ('open_', '<f8'), ('low_', '<f8'), ('high_', '<f8
↳ '), ('close_', '<f8'), ('volume_', '<i4')])
>>> sarray[0:10]
array([('0', 0.0, 0.0, nan, 0.0, 0), ('1', 1.0, 2.0, nan, 4.0, 1),
      ('2', 2.0, 4.0, nan, 8.0, 2), ('3', 3.0, 6.0, nan, 12.0, 3),
      ('4', 4.0, 8.0, nan, 16.0, 4), ('5', 5.0, 10.0, nan, 20.0, 5),
      ('6', 6.0, 12.0, nan, 24.0, 6), ('7', 7.0, 14.0, nan, 28.0, 7),
      ('8', 8.0, 16.0, nan, 32.0, 8), ('9', 9.0, 18.0, nan, 36.0, 9)],
      dtype=[('symbol_', 'S6'), ('open_', '<f8'), ('low_', '<f8'), ('high_', '<
↳ f8'), ('close_', '<f8'), ('volume_', '<i4')])
>>> sarray['symbol_']
array(['0', '1', '2', ..., '99999', '99999', '99999'], dtype='<S6')
```

## ioopro.pyodbc Cancelling Queries

Starting with version 1.5, the pyodbc submodule of IOPro makes it possible to cancel operations. This is done by exposing the SQLCancel ODBC function as a cancel method in the Cursor object.



## A Simple Example

A very simple example would be:

```
conn = iopro.pyodbc.connect(conn_str)
cursor = conn.cursor()
cursor.execute('SELECT something FROM sample_table')
result = cursor.fetchone()
cursor.cancel()
```

This is not very interesting, and it doesn't add much to the functionality of pyodbc.

What makes the cancel method more interesting is that it is possible to cancel running statements that are blocking another thread.

## A Sample With Threading

Having access to the cancel method it is possible to stop running queries following different criteria. For example, it would be possible to execute queries with a time-out. If the time runs out, the query gets cancelled.

```
import iopro.pyodbc
import time
import threading

def query_with_time_out(conn, query, timeout):
    def watchdog(cursor, time_out):
        time.sleep(wait_time)
        cursor.cancel()

    cursor = conn.cursor()

    t = threading.Thread(target=watchdog, args=(cursor, timeout))
    t.start()
    try:
        cursor.execute(query)

        result = cursor.fetchall()
    except iopro.pyodbc.Error:
        result = 'timed out'

    return result
```

This is just one possibility. As cursor exposes directly the SQLCancel, many opportunities open in implementing policies to cancel running queries.

## Finishing notes

In order for this to work, the underlying ODBC driver must support SQLCancel.

The pyodbc submodule of IOPro releases the Python GIL when it calls ODBC, so while queries are being executed other Python threads continue to execute while the thread that performed the query is blocked. This allows for cancel to be called by another thread. Coupled with threading, the cancel method is a very useful primitive.

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### IOPro Release Notes

#### 2016-07-30: 1.9.0

- Remove warnings and documentation for unsupported Numba use
- Rewrite most documentation for clarity and accuracy
- Improve unit tests

#### 2016-04-05: 1.8.0:

- Add PostgresAdapter for reading data from PostgreSQL databases

- Add AccumuloAdapter for reading data from Accumulo databases

**2015-10-09: 1.7.2:**

- Fix an issue with pyodbc where result NumPy arrays could return uninitialized data after the actual data null character. Now it pads the results with nulls.

**2015-05-04: 1.7.1**

- Properly cache output string objects for better performance

**2015-03-02: 1.7.0**

- Add Python 3 support
- Add support for parsing utf8 text files
- Add ability to set/get field types in MongoAdapter

**2015-02-02: 1.6.11**

- Fix issue with escape char not being parsed correctly inside quoted strings

**2014-12-17: 1.6.10**

- Fix issue with using field filters with json parser

**2014-12-02: 1.6.9**

- Fix issue with json field names getting mixed up

**2014-11-20: 1.6.8**

- Fix issue with return nulls returning wrong “null” for large queries (more than 10000 rows) in some circumstances.
- Fix issue with reading slices of json data
- Change json parser so that strings fields of numbers do not get converted to number type by default
- Allow json field names to be specified with field\_names constructor argument
- If user does not specify json field names, use json attribute names as field names in array result

**2014-07-03: 1.6.7**

- Fix issue when reading more than 10000 rows containing unicode strings in platform where ODBC uses UTF-16/UCS2 encoding (notably Windows and unixODBC). The resulting data could be corrupt.

**2014-06-16: 1.6.6**

- Fix possible segfault when dealing with unicode strings in platforms where ODBC uses UTF-16/UCS2 encoding (notably Windows and unixODBC)
- Add `iopro_set_text_limit` function to `iopro`. It globally limits the size of text fields read by `fetchdictarray` and `fetchsarray`. By default it is set to 1024 characters.
- Fix possible segfault in `fetchdictarray` and `fetchsarray` when failing to allocate some NumPy array. This could notably happen in the presence of “TEXT” fields. Now it will raise an `OutOfMemory` error.
- Add lazy loading of submodules in `IOPro`. This reduces upfront import time of `IOPro`. Features are imported as they are used for the first time.

**2014-05-07: 1.6.5**

- Fix crash when building textadapter index

**2014-04-29: 1.6.4**

- Fix default value for null strings in `IOPro/pyodbc` changed to be an empty string instead of ‘NA’. NA was not appropriate as it can collide with valid data (Namibia country code is ‘NA’, for example), and it failed with single character columns.
- Ignore `SQLRowCount` when performing queries with `fetchsarray` and `fetchdictarray`, since `SQLRowCount` sometimes returns incorrect number of rows.

**2014-03-25: 1.6.3**

- Fix SQL `TINYINT` is now returned as an unsigned 8 bit integer in `fetchdictarray`/`fetchsarray`. This is to match the range specified in SQL (0..255). It was being returned as a signed 8 bit integer before (range -128..127)
- Add Preliminary unicode string support in `fetchdictarray`/`fetchsarray`.

**2014-02-12: 1.6.2**

- Disable Numba support for version 0.12 due to lack of string support.

**2014-01-30: 1.6.1**

- Fix a regression that made possible some garbage in string fields when using `fetchdictarray`/`fetchsarray`.
- Fix a problem where heap corruption could happen in `IOPro.pyodbc` `fetchdictarray`/`fetchsarray` related to nullable string fields.
- Fix the allocation guard debugging code: `iopro.pyodbc.enable_mem_guards(True|False)` should no longer crash.
- Merge Vertica fix for cancelling queries

**2013-10-30: 1.6.0**

- Add JSON support
- Misc bug fixes
- Fix crash in IOPro.pyodbc when dealing with nullable datetimes in `fetch_dictarray` and `fetch_sarray`.

**2013-06-12: 1.5.5**

- Fix issue parsing negative ints with leading whitespace in csv data.

**2013-06-10: 1.5.4**

- Allow delimiter to be set to None for csv files with single field.
- Fill in missing csv fields with fill values.
- Fill in blank csv lines with fill values for pandas dataframe output.
- Allow list of field names for TextAdapter `field_names` parameter.
- Change default missing fill value to empty string for string fields.

**2013-06-05: 1.5.3**

- Temporary fix for IndexError exception in TextAdapter.`__read_slice` method.

**2013-05-28: 1.5.2**

- Add ability to specify escape character in csv data

**2013-05-23: 1.5.1**

- fixed coredump when using datetime with numpy < 1.7

**2013-05-22: 1.5.0**

- Added a cancel method to the Cursor object in `iopro.pyodbc`. This method wraps ODBC `SQLCancel`.
- DECIMAL and NUMERIC types are now working on `iopro.pyodbc` on regular fetch functions. They are still unsupported in `fetchsarray` and `fetchdict` and `fetchsarray`
- Add ftp support
- Performance improvements to S3 support
- Misc bug fixes

### 2013-04-05: 1.4.3

- Update loadtxt and genfromtxt to reflect numpy versions' behavior for dealing with whitespace (default to any whitespace as delimiter, and treat multiple whitespace as one delimiter)
- Add read/write field\_names property
- Add support for pandas dataframes as output
- Misc bug fixes

## Reference guide

### TextAdapter

#### Contents

- *TextAdapter*
  - *Methods*
  - *Basic Usage*
  - *Advanced Usage*

The TextAdapter module reads CSV data and produces a NumPy array containing the parsed data. The following features are currently implemented:

- The TextAdapter engine is written in C to ensure text is parsed as fast as data can be read from the source. Text is read and parsed in small chunks instead of reading entire data into memory at once, which enables very large files to be read and parsed without running out of memory.
- Python slicing notation can be used to specify a subset of records to be read from the data source, as well as a subset of fields.
- Fields can be specified in any one of three ways: by a delimiter character, using fixed field widths, or by a regular expression. This enables a larger variety of CSV-like and other types of text files to be parsed.
- A gzipped file can be parsed without having to uncompress it first. Parsing speed is about the same as an uncompressed version of same file.
- An index of record offsets in a file can be built to allow fast random access to records. This index can be saved to disk and loaded again later.
- Converter functions can be specified for converting parsed text to proper dtype for storing in NumPy array.
- The TextAdapter engine has automatic type inference so the user does not have to specify dtypes of the output array. The user can still specify dtypes manually if desired.
- Remote data stored in Amazon S3 can be read. An index can be built and stored with S3 data. Index can be read remotely, allowing for random access to S3 data.

## Methods

The TextAdapter module contains the following factory methods for creating TextAdapter objects:

**text\_adapter** (source, parser='csv', compression=None, comment='#',



```
quote='\"', num_records=0, header=0, field_names=True, indexing=False, index_name=None,
encoding='utf-8')
```

Create a text adapter for reading CSV, JSON, or fixed width text files, or a text file defined by regular expressions.

source - filename, file object, StringIO object, BytesIO object, S3 key, http url, or python generator  
 parser - Type of parser for parsing text. Valid parser types are 'csv', 'fixed width', 'regex', and 'json'.  
 encoding - type of character encoding (current ascii and utf8 are supported)  
 compression - type of data compression (currently only gzip is supported)  
 comment - character used to indicate comment line  
 quote - character used to quote fields  
 num\_records - limits parsing to specified number of records; defaults to all records  
 header - number of lines in file header; these lines are skipped when parsing  
 footer - number of lines in file footer; these lines are skipped when parsing  
 indexing - create record index on the fly as characters are read  
 index\_name - name of file to write index to  
 output - type of output object (numpy array or pandas dataframe)

**If parser is set to 'csv', additional parameters include:**

delimiter - Delimiter character used to define fields in data source. Default is ','.

**If parser is set to 'fixed\_width', additional parameters include:**

field\_widths - List of field widths

**If parser is set to 'regex', additional parameters include:**

regex - Regular expression used to define records and fields in data source. See the regular expression example in the Advanced Usage section.

**s3\_text\_adapter (access\_key, secret\_key, bucket\_name, key\_name, remote\_s3\_index=False)**

```
parser='csv', compression=None, comment='#', quote='\"', num_records=0, header=0,
field_names=True, indexing=False, index_name=None, encoding='utf-8')
```

Create a text adapter for reading a text file from S3. Text file can be CSV, JSON, fixed width, or defined by regular expressions

In addition to the arguments described for the text\_adapter function above, the s3\_text\_adapter function also has the following parameters:

access\_key - AWS access key  
 secret\_key - AWS secret key  
 bucket\_name - name of S3 bucket  
 key\_name - name of key in S3 bucket  
 remote\_s3\_index - use remote S3 index (index name must be key name + '.idx' extension)

The TextAdapter object returned by the text\_adapter factory method contains the following methods:

### **set\_converter (field, converter)**

Set converter function for field

field - field to apply converter function

converter - python function object

### **set\_missing\_values (missing\_values)**

Set strings for each field that represents a missing value

missing\_values - dict of field name or number, and list of missing value strings

Default missing values: 'NA', 'NaN', 'inf', '-inf', 'None', 'none', ''

### **set\_fill\_values (fill\_values, loose=False)**

Set fill values for each field

fill\_values - dict of field name or number, and fill value

loose - If value cannot be converted, and value does not match any of the missing values, replace with fill value anyway.

Default fill values for each data type: | int - 0 | float - numpy.nan | char - 0 | bool - False | object - numpy.nan | string - numpy.nan

### **create\_index (index\_name=None, density=1)**

Create an index of record offsets in file

index\_name - Name of file on disk used to store index. If None, index will be created in memory but not saved.

density - density of index. Value of 1 will index every record, value of 2 will index every other record, etc.

### **to\_array ()**

Parses entire data source and returns data as NumPy array object

### **to\_dataframe ()**

Parses entire data source and returns data as Pandas DataFrame object

The TextAdapter object contains the following properties:

#### **size (readonly)**

Number of records in data source. This value is only set if entire data source has been read or indexed, or number of records was specified in text\_adapter factory method when creating object.

#### **field\_count (readonly)**

Number of fields in each record

#### **field\_names**

Field names to use when creating output NumPy array. Field names can be set here before reading data or in `text_adapter` function with `field_names` parameter.

### **field\_types**

NumPy dtypes for each field, specified as a dict of fields and associated dtype. (Example: `{0:'u4', 1:'f8', 2:'S10'}`)

### **field\_filter**

Fields in data source to parse, specified as a list of field numbers or names (Examples: `[0, 1, 2]` or `['f1', 'f3', 'f5']`). This filter stays in effect until it is reset to empty list, or is overridden with array slicing (Example: `adapter[[0, 1, 3, 4]][:]`).

**See the NumPy data types documentation for more details:** <http://docs.continuum.io/anaconda/numpy/reference/arrays.dtypes.html>

The TextAdapter object supports array slicing:

Read all records: `adapter[:]`

Read first 100 records: `adapter[0:100]`

Read last record (only if data has been indexed or entire dataset has been read once before): `adapter[-1]`

Read first field in all records by specifying field number: `adapter[0][:]`

Read first field in all records by specifying field name: `adapter['f0'][:]`

Read first and third fields in all records: `adapter[[0, 2]][:]`

## **Basic Usage**

Create TextAdapter object for data source:

```
>>> import iopro
>>> adapter = iopro.text_adapter('data.csv', parser='csv')
```

Parse text and store records in NumPy array using slicing notation:

```
>>> # read all records
>>> array = adapter[:]

>>> # read first ten records
>>> array = adapter[0:10]

>>> # read last record
>>> array = adapter[-1]

>>> # read every other record
>>> array = adapter[::2]
```

## Advanced Usage

user defined converter function for field 0:

```
>>> import iopro
>>> import io

>>> data = '1, abc, 3.3\n2, xxx, 9.9'
>>> adapter = iopro.text_adapter(io.StringIO(data), parser='csv', field_names=False)

>>> # Override default converter for first field
>>> adapter.set_converter(0, lambda x: int(x)*2)
>>> adapter[:]
array([(2L, ' abc', 3.3), (4L, ' xxx', 9.9)],
      dtype=[('f0', '<u8'), ('f1', 'S4'), ('f2', '<f8')])
```

overriding default missing and fill values:

```
>>> import iopro
>>> import io

>>> data = '1,abc,inf\n2,NA,9.9'
>>> adapter = iopro.text_adapter(io.StringIO(data), parser='csv', field_names=False)

>>> # Define field dtypes (example: set field 1 to string object and field 2 to float)
>>> adapter.field_types = {1:'O', 2:'f4'}

>>> # Define list of strings for each field that represent missing values
>>> adapter.set_missing_values({1:['NA'], 2:['inf']})

>>> # Set fill value for missing values in each field
>>> adapter.set_fill_values({1:'xxx', 2:999.999})
>>> adapter[:]
array([(' abc', 999.9990234375), ('xxx', 9.8999999618530273)],
      dtype=[('f0', 'O'), ('f1', '<f4')])
```

creating and saving tuple of index arrays for gzip file, and reloading indices:

```
>>> import iopro
>>> adapter = iopro.text_adapter('data.gz', parser='csv', compression='gzip')

>>> # Build index of records and save index to disk.
>>> adapter.create_index(index_name='index_file')

>>> # Create new adapter object and load index from disk.
>>> adapter = iopro.text_adapter('data.gz', parser='csv', compression='gzip',
↳ indexing=True, index_name='index_file')

>>> # Read last record
>>> adapter[-1]
array([(100, 101, 102)], dtype=[('f0', '<u4'), ('f1', '<u4'), ('f2', '<u4')])
```

Use regular expression for finer control of extracting data:

```
>>> import iopro
>>> import io
```

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```

>>> # Define regular expression to extract dollar amount, percentage, and month.
>>> # Each set of parentheses defines a field.
>>> data = '$2.56, 50%, September 20 1978\n$1.23, 23%, April 5 1981'
>>> regex_string = '([0-9]\.[0-9][0-9]+)\,\s ([0-9]+)\%\,\s ([A-Za-z]+) '
>>> adapter = iopro.text_adapter(io.StringIO(data), parser='regex', regex_
↳ string=regex_string, field_names=False, infer_types=False)

>>> # set dtype of field to float
>>> adapter.field_types = {0:'f4', 1:'u4', 2:'S10'}
>>> adapter[:]
array([(2.56, 50L, 'September'), (1.23, 23L, 'April')],
      dtype=[('f0', '<f8'), ('f1', '<u8'), ('f2', 'S9')])

```

## iopro.pyodbc

This project is an enhancement of the Python database module for ODBC that implements the Python DB API 2.0 specification. You can see the original project here:

**homepage** <http://code.google.com/p/pyodbc>

**source** <http://github.com/mkleehammer/pyodbc>

**source** <http://code.google.com/p/pyodbc/source/list>

The enhancements are documented in this file. For general info about the pyodbc package, please refer to the original project documentation.

This module enhancement requires:

- Python 2.4 or greater
- ODBC 3.0 or greater
- NumPy 1.5 or greater (1.7 is required for datetime64 support)

The enhancements in this module consist mainly in the addition of some new methods for fetching the data after a query and put it in a variety of NumPy containers.

Using NumPy as data containers instead of the classical list of tuples has a couple of advantages:

- 1) The NumPy container is much more compact, and hence, it requires much less memory, than the original approach.
- 2) As a NumPy container can hold arbitrarily large arrays, it requires much less object creation than the original approach (one Python object per datum retrieved).

This means that this enhancements will allow to fetch data out of relational databases in a much faster way, while consuming significantly less resources.

## API additions

### Variables

- *pyodbc.npversion* The version for the NumPy additions

## Methods

### **Cursor.fetchdictarray** (size=cursor.arraysize)

This is similar to the original *Cursor.fetchmany(size)*, but the data is returned in a dictionary where the keys are the names of the columns and the values are NumPy containers.

For example, if a SELECT is returning 3 columns with names 'a', 'b' and 'c' and types *varchar(10)*, *integer* and *timestamp*, the returned object will be something similar to:

```
{ 'a': array(..., dtype='S11'),  
  'b': array(..., dtype=int32),  
  'c': array(..., dtype=datetime64[us]) }
```

Note that the *varchar(10)* type is translated automatically to a string type of 11 elements ('S11'). This is because the ODBC driver needs one additional space to put the trailing '0' in strings, and NumPy needs to provide the room for this.

Also, it is important to stress that all the *timestamp* types are translated into a NumPy *datetime64* type with a resolution of microseconds by default.

### **Cursor.fetchsarray** (size=cursor.arraysize)

This is similar to the original *Cursor.fetchmany(size)*, but the data is returned in a NumPy structured array, where the name and type of the fields matches to those resulting from the SELECT.

Here it is an example of the output for the SELECT above:

```
array([(...),  
      (...)],  
      dtype=[('a', '<S11'), ('b', '<i4'), ('c', '<M8[us]', {})])
```

Note that, due to efficiency considerations, this method is calling the *fetchdictarray()* behind the scenes, and then doing a conversion to get an structured array. So, in general, this is a bit slower than its *fetchdictarray()* counterpart.

## Data types supported

The new methods listed above have support for a subset of the standard ODBC. In particular:

- String support (SQL\_VARCHAR) is supported.
- Numerical types, be them integers or floats (single and double precision) are fully supported. Here it is the complete list: SQL\_INTEGER, SQL\_TINYINT, SQL\_SMALLINT, SQL\_FLOAT and SQL\_DOUBLE.
- Dates, times, and timestamps are mapped to the *datetime64* and *timedelta* NumPy types. The list of supported data types are: SQL\_DATE, SQL\_TIME and SQL\_TIMESTAMP,
- Binary data is not supported yet.
- Unicode strings are not supported yet.

## NULL values

As there is not (yet) a definitive support for missing values (NA) in NumPy, this module represents NA data as particular values depending on the data type. Here it is the current table of the particular values:

```

int8: -128 (-2**7)
uint8: 255 (2**8-1)
int16: -32768 (-2**15)
uint16: 65535 (2**16-1)
int32: -2147483648 (-2**31)
uint32: 4294967295 (2**32-1)
int64: -9223372036854775808 (-2**63)
uint64: 18446744073709551615 (2**64-1)
float32: NaN
float64: NaN
datetime64: NaT
timedelta64: NaT (or -2**63)
string: 'NA'

```

## Improvements for 1.1 release

- The rowcount is not trusted anymore for the *fetchdict()* and *fetchsarray()* methods. Now the NumPy containers are built incrementally, using realloc for a better use of resources.
- The Python interpreter does not exit anymore when fetching an exotic datatype not supported by NumPy.
- The docsstrings for *fetchdict()* and *fetchsarray()* have been improved.

## MongoAdapter

### Contents

- *MongoAdapter*
  - *Methods*
  - *Basic Usage*

The MongoAdapter module reads data from a Mongo database collection and produces a NumPy array containing the loaded. The following features are currently implemented:

- The MongoAdapter engine is written in C to ensure data is loaded fast with minimal memory usage.
- Python slicing notation can be used to specify the subset of records to be read from the data source.
- The MongoAdapter engine has automatic type inference so the user does not have to specify dtypes of the output array.

## Methods

The MongoAdapter module contains the following constructor for creating MongoAdapter objects:

### MongoAdapter (host, port, database, collection)

MongoAdapter constructor

host - Host name where Mongo database is running.

port - Port number where Mongo database is running.

database - Mongo database to connect to

collection - Mongo database collection

### **set\_field\_names (names)**

Set field names to read when creating output NumPy array.

### **get\_field\_names ()**

Returns names of fields that will be read when reading data from Mongo database.

### **set\_field\_types (types=None)**

Set NumPy dtypes for each field, specified as a dict of field names/indices and associated dtype. (Example: {0:'u4', 1:'f8', 2:'S10'})

### **get\_field\_types ()**

Returns dict of field names/indices and associated NumPy dtype.

The MongoAdapter object contains the following properties:

### **size (readonly)**

Number of documents in the Mongo database + collection specified in constructor.

## Basic Usage

1. Create MongoAdapter object for data source

```
>>> import iopro
>>> adapter = iopro.MongoAdapter('localhost', 27017, 'database_name', 'collection_
↳name')
```

2. Load Mongo collection documents into NumPy array using slicing notation

```
>>> # read all records for 'field0' field
>>> array = adapter['field0'][:]
```

```
>>> # read first ten records for 'field0' and 'field1' fields
>>> array = adapter[['field0', 'field1']][0:10]
```

```
>>> # read last record
>>> array = adapter['field0'][-1]
```

```
>>> # read every other record
>>> array = adapter['field0'][:,2]
```

## Accumulo Adapter

### Contents

- *Accumulo Adapter*



- *Adapter Methods*
- *Adapter Properties*
- *Basic Usage*

The AccumuloAdapter module reads data from Accumulo key/value stores and produces a NumPy array containing the parsed values.

- The AccumuloAdapter engine is written in C to ensure returned data is parsed as fast as data can be read from the source. Data is read and parsed in small chunks instead of reading entire data into memory at once.
- Python slicing notation can be used to specify a subset of records to be read from the data source.

## Adapter Methods

Accumulo Adapter Constructor:

**AccumuloAdapter** (server='localhost', port=42424, username='', password='', table=None, field\_type='f8', start\_key=None, stop\_key=None, start\_key\_inclusive=True, stop\_key\_inclusive=False, missing\_values=None, fill\_value=None):

Create an adaptor for connecting to an Accumulo key/value store.

server: Accumulo server address

port: Accumulo port

username: Accumulo user name

password: Accumulo user password

table: Accumulo table to read data from

field\_type: str, NumPy dtype to interpret table values as

start\_key: str, key of record where scanning will start from

stop\_key: str, key of record where scanning will stop at

start\_key\_inclusive: If True, start\_key is inclusive (default is True)

stop\_key\_inclusive: If True, stop\_key is inclusive (default is False)

missing\_values: list, missing value strings. Any values in table equal to one of these strings will be replaced with fill\_value.

fill\_value: fill value used to replace missing value when scanning

**close ()**

Close connection to the database.

The AccumuloAdapter object supports array slicing:

Read all records: adapter[:]

Read first ten records: adapter[0:10]

Read last record: adapter[-1]

Read every other record: adapter[::2]

## Adapter Properties

### field\_type (readonly)

Get dtype of output NumPy array

### start\_key

Get/set key of record where reading/scanning will start.

The start\_key\_inclusive property specifies whether this key is inclusive (default is inclusive).

### stop\_key

Get/set key of record where reading/scanning will stop.

The stop\_key\_inclusive property specifies whether this key is inclusive (default is exclusive).

### start\_key\_inclusive

Toggle whether start key is inclusive. Default is true.

### stop\_key\_inclusive

Toggle whether stop key is inclusive. Default is False.

### missing\_values

Get/Set missing value strings. Any values in Accumulo table matching one of these strings will be replaced with fill\_value.

### fill\_value

Fill value used to replace missing\_values. Fill value type should match specified output type.

## Basic Usage

Create AccumuloAdapter object for data source:

```
>>> import iopro
>>> adapter = iopro.AccumuloAdapter(server='172.17.0.1',
                                   port=42424,
                                   username='root',
                                   password='password',
                                   field_type='f4',
                                   table='iopro_tutorial_data')
```

IOPro adapters use slicing to retrieve data. To retrieve records from the table or query, the standard NumPy slicing notation can be used:

```
>>> # read all records
>>> array = adapter[:]
array([ 0.5,  1.5,  2.5,  3.5,  4.5], dtype=float32)
```

```
>>> # read first three records
>>> array = adapter[0:3]
array([ 0.5,  1.5,  2.5], dtype=float32)
```

```
>>> # read every other record from the first four records
>>> array = adapter[:4:2]
array([ 0.5,  2.5], dtype=float32)
```

The Accumulo adapter does not support seeking from the last record.

The `field_types` property can be used to see what type the output NumPy array will have:

```
>>> adapter.field_type
'f4'
```

Since Accumulo is essentially a key/value store, results can be filtered based on key. For example, a start key using the `start_key` property. This will retrieve all values with a key equal to or greater than the start key.

```
>>> adapter.start_key = 'row02'
>>> adapter[:]
array([ 1.5,  2.5,  3.5,  4.5], dtype=float32)
```

Likewise, a stop key. This will retrieve all values with a key less than the stop key but equal to or greater than the start key.

```
>>> adapter.stop_key = 'row04'
>>> adapter[:]
array([ 1.5,  2.5], dtype=float32)
```

By default, the start key is inclusive. This can be changed by setting the `start_key_inclusive` property to `False`.

```
>>> adapter.start_key_inclusive = False
>>> adapter[:]
array([ 2.5], dtype=float32)
```

By default, the stop key is exclusive. This can be changed by setting the `stop_key_inclusive` property to `True`.

```
>>> adapter.stop_key_inclusive = True
>>> adapter[:]
array([ 2.5,  3.5], dtype=float32)
```

The Accumulo adapter can handle missing values. If it is known that the strings 'NA' and 'nan' signify missing float values, the `missing_values` property can be used to tell the adapter to treat these strings as missing values: Also, the `fill_value` property can be used to specify what value to replace missing values with.

```
>>> adapter = iopro.AccumuloAdapter('172.17.0.1', 42424, 'root', 'password', 'iopro_
↳tutorial_missing_data', field_type='S10')
>>> adapter[:]
array([b'NA', b'nan'], dtype='<S10')
```

```
>>> adapter = iopro.AccumuloAdapter('172.17.0.1', 42424, 'root', 'secret', 'iopro_
↳tutorial_missing_data', field_type='f8')
>>> adapter.missing_values = ['NA', 'nan']
>>> adapter.fill_value = np.nan
>>> adapter[:]
array([ nan,  nan])
```

**Close database connection:**

```
>>> adapter.close()
```

## PostgresAdapter, PostGIS, and GreenPlum

### Contents

- *PostgresAdapter, PostGIS, and GreenPlum*
  - *Adapter Methods*
  - *Adapter Properties*
  - *Basic Usage*

The PostgresAdapter module reads data from PostgreSQL based databases and produces a NumPy array or a Pandas Dataframe containing the parsed data. The PostgresAdapter can be used to access data from PostgreSQL and GreenPlum, and has enhancements to support PostGIS points, lines, multilines, polygons, and multipolygons. The following features are currently implemented:

- The PostgresAdapter engine is written in C to ensure returned data is parsed as fast as data can be read from the source. Data is read and parsed in small chunks instead of reading entire data into memory at once.
- Python slicing notation can be used to specify a subset of records to be read from the data source.
- A subset of columns can be specified to be returned instead of returning all columns for the records.

### Adapter Methods

PostgreSQL Adapter Constructor:

**PostgresAdapter** (connection\_uri, table=None, query=None, field\_filter=None, dataframe=False, field\_names=None, field\_types=None, field\_shapes=None):

Create an adaptor for connecting to a PostgreSQL based database.

connection\_uri: string URI describing how to connect to database

table: string, name of table to read records from. Only table parameter or query parameter can be set, but not both.

query: string, custom query to use for reading records. Only query parameter or table parameter can be set, but not both. field\_filter parameter cannot be set when query parameter is set (since it is trivial to specify fields in query string).

field\_filter: names of fields include in query (only valid when table parameter is specified)

dataframe: bool, return results as dataframe instead of array

field\_names: list, names of fields in output array or dataframe. Defaults to database table column names.

field\_types: list, NumPy dtype for each field in output array or dataframe. Defaults to database table column types.

field\_shapes: list, shape of each field value for geometry field types with variable length data. For example, for a 'path' database column with 2d points, the points of the path will be stored in a list object by default. If a field shape of '10' is specified, the points will be stored in a 2x10 float subarray (2 floats per point\* 10 points max). A field shape of the form (x,y) should be specified for types like multipolygon where x is the max number of polygons and y is the max length of each polygon (the size of the point is inferred).

close ()

Close connection to the database.

The PostgresAdapter object supports array slicing:

Read all records: `adapter[:]`

Read first 100 records: `adapter[0:100]`

Read last record: `adapter[-1]`

Read every other record: `adapter[::2]`

## Adapter Properties

### **num\_records (readonly)**

Get number of records that will be returned from table or custom query.

### **num\_fields (readonly)**

Get number of fields in records that will be returned from table or custom query

### **field\_names**

Get/set names of fields in final array or dataframe. Field names can be set by specifying a list of names, or dict mapping of field number to field name. If names is a list, the length of list must match the number of fields in data set. If names is a dict, the field name from the database will be used if no name in dict is specified for that field.

### **field\_types**

Get/set field types in final array or dataframe. Field types can be set by specifying a list of NumPy dtypes, or a dict mapping of field number or name to field type. If types is a list, the length of list must match the number of fields in data set. If types is a dict, the field type from the database will be used if type is not specified in dict.

### **field\_shapes**

Get/set field shapes for variable length fields. Field shapes can be set by specifying a list of shape tuples (or a single integer if shape has one dimension), or a dict mapping of field number or name to field shape. If shapes is a list, the length of the list must match the number of fields in data set. A value of None or zero for a field, or an unspecified shape, means that an infinite length value will be allowed for field, and value will be stored in Python list object if field is PostgreSQL geometry type, or as Well Known Text string objects if field is PostGIS type.

## Basic Usage

Create PostgresAdapter object for data source:

```
>>> import iopro
>>> adapter = iopro.PostgresAdapter('host=localhost dbname=db_name user=user_
↳table=table_name')
```

IOPro adapters use slicing to retrieve data. To retrieve records from the table or query, the standard NumPy slicing notation can be used:

```
>>> # read all records
>>> array = adapter[:]
```

```
>>> # read first ten records
>>> array = adapter[0:10]
```

```
>>> # read last record
>>> array = adapter[-1]
```

```
>>> # read every other record
>>> array = adapter[::2]
```

The PostgreSQL adapter has a few properties that we can use to find out more about our data. To get the number of records in our dataset:

```
>>> adapter.num_records
5
```

or the number of fields:

```
>>> adapter.num_fields
5
```

To find the names of each field:

```
>>> adapter.field_names
['field1', 'real', 'name', 'point2d', 'multipoint3d']
```

These names come from the names of the columns in the database and are used by default for the field names in the NumPy array result. These names can be changed by setting the field names property using a list of field names:

```
>>> adapter.field_names = ['field1', 'field2', 'field3', 'field4', 'field5']
>>> adapter[:].dtype
dtype([('field1', '<i4'), ('field2', '<f4'), ('field3', '<U10'), ('field4', '<f8', (2,
↪)), ('field5', 'O'))]
```

Individual fields can also be set by using a dict, where the key is the field number and the value is the field name we want:

```
>>> adapter.field_names = {1: 'AAA'}
>>> adapter[:].dtype
dtype([('integer', '<i4'), ('AAA', '<f4'), ('string', '<U10'), ('point2d', '<f8', (2,
↪)), ('multipoint3d', 'O')])
```

To find out the NumPy dtype of each field:

```
>>> adapter.field_types
['i4', 'f4', 'U10', 'f8', 'O']
```

Similar to the field names property, the types property can be set using a list or dict to force a field to be cast to a specific type:

```
>>> adapter.field_types = {0: 'f4', 1: 'i4', 2: 'U3', 4: 'O'}
```

To filter the fields returned by passing a list of field names to the constructor:

```
>>> adapter = iopro.PostgresAdapter('host=localhost dbname=db_name user=user',
                                     table='data',
                                     field_filter=['field1', 'field2'])
```

For fields like path or multipoint3d with a variable length, the adapter will return values as a list of tuples containing the float components of each point (if a PostgreSQL geometric type) or as string objects in Well Known Text format (if a PostGIS type). For improved performance, a field shape can be specified which will set the max dimensions of the field values. For example, a multipoint3d field can be set to have a maximum of two points so that each set of 3d points will be stored in a 2x3 subarray of floats:

```
>>> adapter = iopro.PostgresAdapter('host=localhost dbname=db_name user=user'
                                     table='data',
                                     field_filter=['multipoint3d'],
                                     field_shapes={'multipoint3d': 2})

>>> adapter[:]
array([([[0.0, 1.0, 2.0], [3.0, 4.0, 5.0]]),
       ([[6.0, 7.0, 8.0], [9.0, 10.0, 11.0]]),
       ([[12.0, 13.0, 14.0], [15.0, 16.0, 17.0]]),
       ([[18.0, 19.0, 20.0], [21.0, 22.0, 23.0]]),
       ([[24.0, 25.0, 26.0], [27.0, 28.0, 29.0]])],
      dtype=[('multipoint3d', '<f8', (2, 3))])
```

For more advanced queries, a custom select query can be passed to the constructor. Either a table name or a custom query can be passed to the constructor, but not both.

```
>>> adapter = iopro.PostgresAdapter('host=localhost dbname=db_name user=user',
                                     query='select integer, string from data where_
↳ data.integer > 2')
>>> adapter[:]
```

Data can also be returned as a pandas dataframe using the adapter constructor's dataframe' argument:

```
>>> adapter = iopro.PostgresAdapter('host=localhost dbname=iopro_tutorial user=jayvius
↳ ',
                                     table='data',
                                     dataframe=True)
```

To retrieve some PostGIS data that falls within a given bounding box:

```
>>> adapter = iopro.PostgresAdapter('host=localhost dbname=db_name user=user',
                                     query='select integer, point2d from data '
↳ 'where data.point2d @ ST_MakeEnvelope(0, 0,
↳ 4, 4) ')
```

**Close database connection:**

```
>>> adapter.close()
```

## iopro.loadtxt

Load data from a text file.

Each row in the text file must have the same number of values.

## Parameters

**fname** [file or str] File, filename, or generator to read. If the filename extension is `.gz` or `.bz2`, the file is first decompressed. Note that generators should return byte strings for Python 3k.

**dtype** [data-type, optional] Data-type of the resulting array; default: `float`. If this is a record data-type, the resulting array will be 1-dimensional, and each row will be interpreted as an element of the array. In this case, the number of columns used must match the number of fields in the data-type.

**comments** [str, optional] The character used to indicate the start of a comment; default: `'#'`.

**delimiter** [str, optional] The string used to separate values. By default, this is any whitespace.

**converters** [dict, optional] A dictionary mapping column number to a function that will convert that column to a float. E.g., if column 0 is a date string: `converters = {0: datestr2num}`. Converters can also be used to provide a default value for missing data (but see also `iopro.genfromtxt`): `converters = {3: lambda s: float(s.strip() or 0)}`. Default: `None`.

**skiprows** [int, optional] Skip the first *skiprows* lines; default: 0.

**usecols** [sequence, optional] Which columns to read, with 0 being the first. For example, `usecols = (1, 4, 5)` will extract the 2nd, 5th and 6th columns. The default, `None`, results in all columns being read.

**unpack** [bool, optional] If `True`, the returned array is transposed, so that arguments may be unpacked using `x, y, z = iopro.loadtxt(...)`. When used with a record data-type, arrays are returned for each field. Default is `False`.

**ndmin** [int, optional] The returned array will have at least *ndmin* dimensions. Otherwise mono-dimensional axes will be squeezed. Legal values: 0 (default), 1 or 2. .. versionadded:: 1.6.0

## Returns

**out** [ndarray] Data read from the text file.

## See Also

`iopro.genfromtxt` : Load data with missing values handled as specified.

## Examples

### simple parse of StringIO object data

```
>>> import iopro
>>> from io import StringIO # StringIO behaves like a file object
>>> c = StringIO("0 1\n2 3")
>>> iopro.loadtxt(c)
>>> array([[ 0.,  1.],
          [ 2.,  3.]])
```

### set dtype of output array

```
>>> d = StringIO("M 21 72\nF 35 58")
>>> iopro.loadtxt(d, dtype={'names': ('gender', 'age', 'weight'),
...                          'formats': ('S1', 'i4', 'f4')})
>>> array([('M', 21, 72.0), ('F', 35, 58.0)],
          dtype=[('gender', '<|S1'), ('age', '<i4'), ('weight', '<f4')])
```



**set delimiter and columns to parse**

```

>>> c = StringIO("1,0,2\\n3,0,4")
>>> x, y = iopro.loadtxt(c, delimiter=',', usecols=(0, 2), unpack=True)
>>> x
array([ 1.,  3.])
>>> y
array([ 2.,  4.])

```

**iopro.genfromtxt**

Load data from a text file, with missing values handled as specified.

Each line past the first *skip\_header* lines is split at the *delimiter* character, and characters following the *comments* character are discarded.

**Parameters**

**fname** [file or str] File, filename, or generator to read. If the filename extension is *.gz* or *.bz2*, the file is first decompressed. Note that generators must return byte strings in Python 3k.

**dtype** [dtype, optional] Data type of the resulting array. If *None*, the dtypes will be determined by the contents of each column, individually.

**comments** [str, optional] The character used to indicate the start of a comment. All the characters occurring on a line after a comment are discarded

**delimiter** [str, int, or sequence, optional] The string used to separate values. By default, any consecutive whitespaces act as delimiter. An integer or sequence of integers can also be provided as width(s) of each field.

**skip\_header** [int, optional] The numbers of lines to skip at the beginning of the file.

**skip\_footer** [int, optional] The numbers of lines to skip at the end of the file

**converters** [variable, optional] The set of functions that convert the data of a column to a value. The converters can also be used to provide a default value for missing data: `converters = {3: lambda s: float(s or 0)}`.

**missing\_values** [variable, optional] The set of strings corresponding to missing data.

**filling\_values** [variable, optional] The set of values to be used as default when the data are missing.

**usecols** [sequence, optional] Which columns to read, with 0 being the first. For example, `usecols = (1, 4, 5)` will extract the 2nd, 5th and 6th columns.

**names** [{None, True, str, sequence}, optional] If *names* is *True*, the field names are read from the first valid line after the first *skip\_header* lines. If *names* is a sequence or a single-string of comma-separated names, the names will be used to define the field names in a structured dtype. If *names* is *None*, the names of the dtype fields will be used, if any.

**excludelist** [sequence, optional] A list of names to exclude. This list is appended to the default list ['return', 'file', 'print']. Excluded names are appended an underscore: for example, *file* would become *file\_*.

**deletechars** [str, optional] A string combining invalid characters that must be deleted from the names.

**defaultfmt** [str, optional] A format used to define default field names, such as "*f%i*" or "*f\_%02i*".

**autostrip** [bool, optional] Whether to automatically strip white spaces from the variables.

**replace\_space** [char, optional] Character(s) used in replacement of white spaces in the variables names. By default, use a `'_'`.

**case\_sensitive** [{True, False, 'upper', 'lower'}, optional] If True, field names are case sensitive. If False or 'upper', field names are converted to upper case. If 'lower', field names are converted to lower case.

**unpack** [bool, optional] If True, the returned array is transposed, so that arguments may be unpacked using `x, y, z = loadtxt(...)`

**usemask** [bool, optional] If True, return a masked array. If False, return a regular array.

**invalid\_raise** [bool, optional] If True, an exception is raised if an inconsistency is detected in the number of columns. If False, a warning is emitted and the offending lines are skipped.

## Returns

**out** [ndarray] Data read from the text file. If *usemask* is True, this is a masked array.

## See Also

`iopro.loadtxt` : equivalent function when no data is missing.

## Notes

- When spaces are used as delimiters, or when no delimiter has been given as input, there should not be any missing data between two fields.
- When the variables are named (either by a flexible dtype or with *names*, there must not be any header in the file (else a `ValueError` exception is raised).
- Individual values are not stripped of spaces by default. When using a custom converter, make sure the function does remove spaces.

## Examples

```
>>> import iopro
>>> from io import StringIO
```

Comma delimited file with mixed dtype

```
>>> s = StringIO("1,1.3,abcde")
>>> data = iopro.genfromtxt(s, dtype=[('myint', 'i8'), ('myfloat', 'f8'),
... ('mystring', 'S5')], delimiter=",")
>>> data
array((1, 1.3, 'abcde'),
      dtype=[('myint', '<i8'), ('myfloat', '<f8'), ('mystring', '|S5')])
```

Using `dtype = None`

```
>>> s.seek(0) # needed for StringIO example only
>>> data = iopro.genfromtxt(s, dtype=None,
... names = ['myint', 'myfloat', 'mystring'], delimiter=",")
>>> data
```

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```
array((1, 1.3, 'abcde'),
      dtype=[('myint', '<i8'), ('myfloat', '<f8'), ('mystring', '|S5')])
```

### Specifying dtype and names

```
>>> s.seek(0)
>>> data = iopro.genfromtxt(s, dtype="i8,f8,S5",
... names=['myint', 'myfloat', 'mystring'], delimiter=",")
>>> data
array((1, 1.3, 'abcde'),
      dtype=[('myint', '<i8'), ('myfloat', '<f8'), ('mystring', '|S5')])
```

### An example with fixed-width columns

```
>>> s = StringIO("11.3abcde")
>>> data = iopro.genfromtxt(s, dtype=None, names=['intvar', 'fltvar', 'strvar'],
... delimiter=[1,3,5])
>>> data
array((1, 1.3, 'abcde'),
      dtype=[('intvar', '<i8'), ('fltvar', '<f8'), ('strvar', '|S5')])
```

## Previous Versions

This documentation is provided for the use of our customers who have not yet upgraded to the current version.

NOTE: We recommend that users not use older versions of IOPro.

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