

Introduction to Conda



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- Conda is an open source package and environment management system.
- It runs on Windows, Mac OS and Linux.
- Conda can quickly install, run, and update packages and dependencies.
- Conda can create, save, load, and switch between project specific software environments on your local computer.
- Conda was created for Python programs, but it can package and distribute software for any language.
- **Do not require superuser privileges**

Person #1

Computer environment

R	(v3.5)
Python	(v2.7)
Rtsne	(v1.0)
Seurat	(v3.0)
Stats	(v2.0)

Run Sauron

Results!



CONDA environment

R	(v3.5)
Python	(v2.7)
Rtsne	(v1.0)
Seurat	(v3.0)

Run Sauron

Results!



Person #2

Computer environment

R	(v2.9)
Python	(v3.6)
Rtsne	-
Seurat	(v1.0)
Stats	(v1.0)

Run Sauron

ERROR ! ❌

Rtsne missing!
Seurat not v3.0!
You need R v3.2!

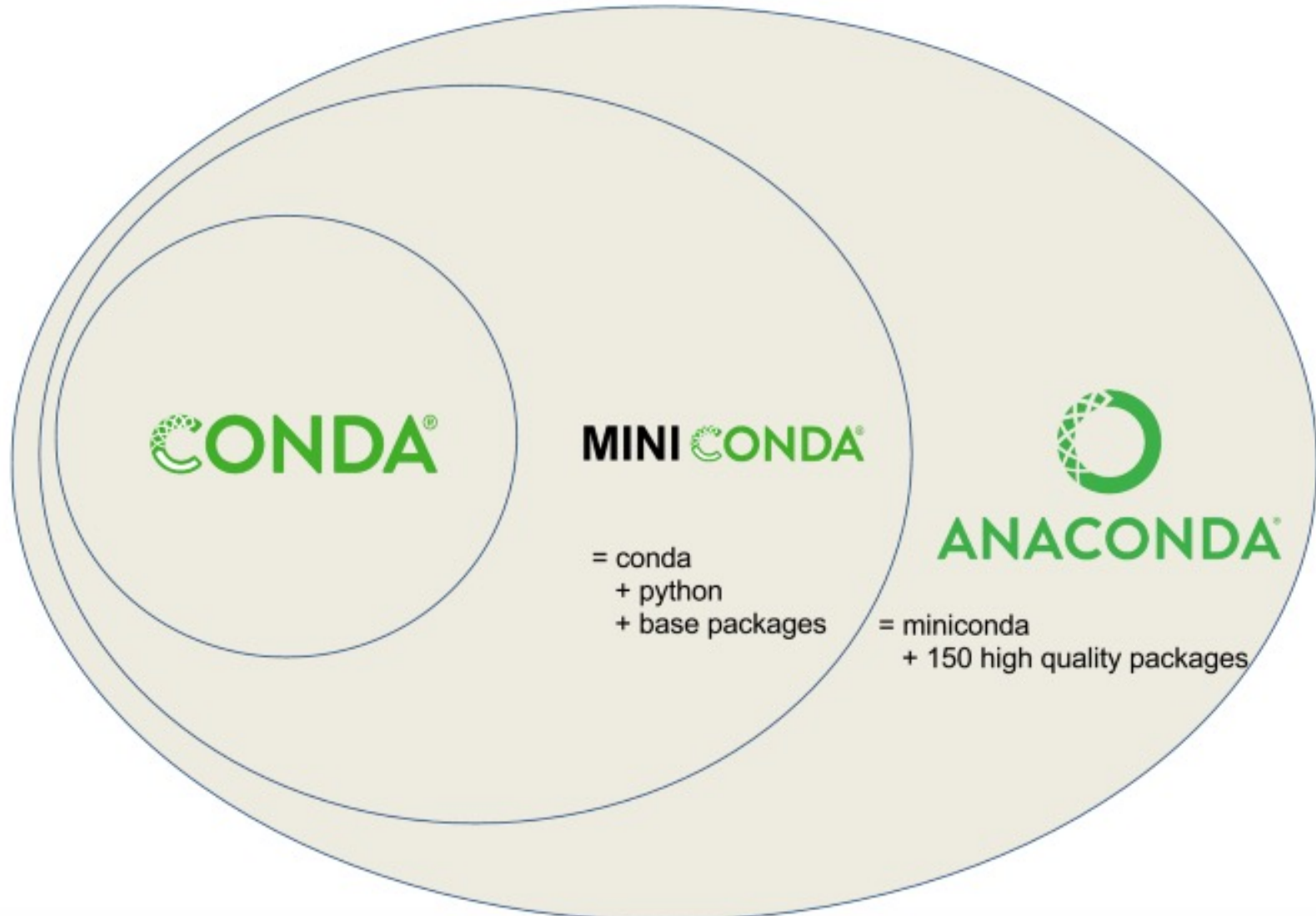
Results!



CONDA environment

R	(v3.5)
Python	(v2.7)
Rtsne	(v1.0)
Seurat	(v3.0)

Run Sauron



The screenshot displays the Anaconda Navigator desktop application. At the top, the title bar reads "Anaconda Navigator". The main header area shows the "ANACONDA NAVIGATOR" logo on the left, the text "Connected to Nucleus, Team Edition" in the center, and a "Connect" button on the right. A left-hand sidebar contains navigation options: "Home", "Environments", "Learning", and "Community". Below these is a "Join Now" button for "ANACONDA NUCLEUS" and links to "Documentation" and "Anaconda Blog".

The main content area is titled "Applications on miniconda3" and features a grid of application cards. Each card includes an icon, the application name, version number, a brief description, and a button to either "Launch" or "Install" the application. The applications shown are:

- Datalore** (version 1.0.0): Online Data Analysis Tool with smart coding assistance by JetBrains. Edit and run your Python notebooks in the cloud and share them with your team. (Launch button)
- IBM Watson Studio Cloud** (version 1.0.0): IBM Watson Studio Cloud provides you the tools to analyze and visualize data, to cleanse and shape data, to create and train machine learning models. Prepare data and build models, using open source data science tools or visual modeling. (Launch button)
- Glueviz** (version 1.0.0): Multidimensional data visualization across files. Explore relationships within and among related datasets. (Install button)
- JupyterLab** (version 3.0.14): An extensible environment for interactive and reproducible computing, based on the Jupyter Notebook and Architecture. (Install button)
- Jupyter Notebook** (version 6.4.3): Web-based, interactive computing notebook environment. Edit and run human-readable docs while describing the data analysis. (Install button)
- Orange 3** (version 3.26.0): Component based data mining framework. Data visualization and data analysis for novice and expert. Interactive workflows with a large toolbox. (Install button)
- PyCharm Professional** (version 5.1.0): A full-fledged IDE by JetBrains for both Scientific and Web Python development. Supports HTML, JS, and SQL. (Install button)
- Qt Console** (version 5.1.0): PyQt GUI that supports inline figures, proper multiline editing with syntax highlighting, graphical calltips, and more. (Install button)
- RStudio** (version 1.1.456): A set of integrated tools designed to help you be more productive with R. Includes R essentials and notebooks. (Install button)
- Spyder** (version 5.0.5): Scientific Python Development Environment. Powerful Python IDE with advanced editing, interactive testing, debugging and introspection features. (Install button)

<https://docs.conda.io/en/latest/miniconda.html#linux-installers>

Conda
latest

Search docs

Conda
Conda-build

Miniconda

- System requirements
- Latest Miniconda Installer Links
- Windows installers
- MacOSX installers
- Linux installers**
- Installing
- Other resources

Help and support
Contributing
Conda license

Linux installers

Linux

Python version	Name	Size	SHA256 hash
Python 3.9	Miniconda3 Linux 64-bit	63.6 MiB	<code>1ea2f885b4dbc3098662845560bc64271eb17085387a70c2ba3f29fff6f8d52f</code>
	Miniconda3 Linux-aarch64 64-bit	62.6 MiB	<code>4879820a10718743f945d88ef142c3a4b30dfc8e448d1ca08e019586374b773f</code>
	Miniconda3 Linux-ppc64le 64-bit	60.6 MiB	<code>fa92ee4773611f58ed9333f977d32bbb64769292f605d518732183be1f3321fa</code>
Python 3.8	Miniconda3 Linux-s390x 64-bit	57.1 MiB	<code>1faed9abecf4a4ddd4e0d8891fc2cdaa3394c51e877af14ad6b9d4aad4e90d8</code>
	Miniconda3 Linux 64-bit	98.8 MiB	<code>935d72deb16e42739d69644977290395561b7a6db059b316958d97939e9bdf3d</code>
	Miniconda3 Linux-aarch64 64-bit	94.8 MiB	<code>19584b4fb5c0656e0cf9de72aaa0b0a7991fbd6f1254d12e2119048c9a47e5cc</code>
Python 3.7	Miniconda3 Linux-ppc64le 64-bit	93.3 MiB	<code>c1ac79540cb77b2e0ca5b9f78b3bc367567d810118500a167dea4a0bcab5d063</code>
	Miniconda3 Linux-s390x 64-bit	89.0 MiB	<code>55f514110a50e98549a68912cbb03e43a36193940a1889e1c8beb30009b4da19</code>
	Miniconda3 Linux 64-bit	84.9 MiB	<code>a1a7285dea0edc430b2bc7951d89bb30a2a1b32026d2a7b02aacaaa95cf69c7c</code>
Python 3.6	Miniconda3 Linux-aarch64 64-bit	89.2 MiB	<code>65f400a906e3132ddbba35a38d619478be77d32210a2acab05133d92ba08f111</code>
	Miniconda3 Linux-ppc64le 64-bit	88.1 MiB	<code>e4f8b4a5eb8da1badf0b0c91fd7ee25e39120d4d77443e7a1ef3661fd439a997</code>
	Miniconda3 Linux-s390x 64-bit	84.1 MiB	<code>7ab9f813dd84cb0951a2d755cd84708263ce4e03c656e65e2fa79ed0f024f0f7</code>

```
-bash-4.2$ mkdir -p ~/softwares/miniconda3
```

```
-bash-4.2$ cd ~/softwares/miniconda3
```

```
-bash-4.2$ wget https://repo.anaconda.com/miniconda/Miniconda3-  
py38_4.10.3-Linux-x86_64.sh
```

```
-bash-4.2$ chmod 775 Miniconda3-py38_4.10.3-Linux-x86_64.sh
```



```
-bash-4.2$ ./Miniconda3-latest-Linux-x86_64.sh -b -p  
~/softwares/miniconda3 -f
```

- b** run install in batch mode (without manual intervention), it is expected the license terms are agreed upon
- f** no error if install prefix already exists
- h** print this help message and exit
- p** PREFIX install prefix, defaults to /root/miniconda3, must not contain spaces.
- s** skip running pre/post-link/install scripts
- u** update an existing installation
- t** run package tests after installation (may install conda-build)

```
-bash-4.2$ source ~/softwares/miniconda3/bin/activate
```

```
(base) -bash-4.2$ conda init bash
```

```
(base) -bash-4.2$ rm Miniconda3-latest-Linux-x86_64.sh
```

```
(base) -bash-4.2$ conda config --add channels defaults  
(base) -bash-4.2$ conda config --add channels conda-forge  
(base) -bash-4.2$ conda config --add channels anaconda  
(base) -bash-4.2$ conda config --add channels bioconda  
(base) -bash-4.2$ conda config --add channels biobuilds  
(base) -bash-4.2$ conda config --add channels R  
(base) -bash-4.2$ conda config --add channels intel  
(base) -bash-4.2$ conda config --add channels trent  
(base) -bash-4.2$ conda config --add channels plotly
```

List channels

```
(base) -bash-4.2$ conda config --get channels
```

Removing channels

```
(base) -bash-4.2$ conda config --remove channels trent
```

Bioinformatics 1

```
(base) -bash-4.2$ conda create --yes --name bioinfo1 python=3.8
```

or

```
(base) -bash-4.2$ conda create -y -n bioinfo1 python=3.8
```

Bioinformatics 2

```
(base) -bash-4.2$ conda create -y -n bioinfo2 python=2.7
```

Deep learning

```
(base) -bash-4.2$ conda create -y -n dl python=3.9
```

R 3.6

```
(base) -bash-4.2$ conda create -y -n r3.6 -c conda-forge r-base=3.6.3 r-essentials=3.6.0 python=3.8
```

R 4.1

```
(base) -bash-4.2$ conda create -y -n r4.1 -c conda-forge r-base=4.1.0 r-essentials=4.1 python=3.8
```

R 4.1 (choose one library)

https://conda-forge.org/docs/maintainer/knowledge_base.html?highlight

```
(base) -bash-4.2$ install -y -n r4.1 "libblas=*=*mkl"
```

```
(base) -bash-4.2$ install -y -n r4.1 "libblas=*=*openblas"
```

```
(base) -bash-4.2$ install -y -n r4.1 "libblas=*=*blis"
```

```
(base) -bash-4.2$ install -y -n r4.1 "libblas=*=*netlib"
```

```
(base) -bash-4.2$ conda env list
```

```
-bash-4.2$ conda env list
# conda environments:
#
base * /mnt/home/pelicion/software/conda3
Renv3.6 /mnt/home/pelicion/software/conda3/envs/Renv3.6
Renv4.0 /mnt/home/pelicion/software/conda3/envs/Renv4.0
gatk3 /mnt/home/pelicion/software/conda3/envs/gatk3
imputeme /mnt/home/pelicion/software/conda3/envs/imputeme
ivdp /mnt/home/pelicion/software/conda3/envs/ivdp
ivdp2 /mnt/home/pelicion/software/conda3/envs/ivdp2
r-env4.0 /mnt/home/pelicion/software/conda3/envs/r-env4.0
sra /mnt/home/pelicion/software/conda3/envs/sra
```

Bioinformatics 1

```
(base) -bash-4.2$ conda install -y -n bioinfo1 -c bioconda gatk4
```

or

```
(base) -bash-4.2$ conda install -y -n bioinfo1 -c bioconda  
gatk4=4.2.3.0
```

Bioinformatics 2

```
(base) -bash-4.2$ conda install -y -n bioinfo2 -c bioconda  
platypus-variant
```




🔍 platypus variant caller + conda





bioconda / packages / platypus-variant 0.8.1



0

A Haplotype-Based Variant Caller For Next Generation Sequence Data

Conda

Files

Labels

Badges

License: **GPLv3**

19731 total downloads

Last upload: 7 months and 7 days ago

Installers

Info: This package contains files in non-standard **labels**.

conda install ?

linux-64 v0.8.11

osx-64 v0.8.11

To install this package with conda run one of the following:

```
conda install -c bioconda platypus-variant
```

```
conda install -c bioconda/label/cf201901 platypus-variant
```

Description



🔍 platypus variant caller + conda + recipe



BIOCONDA®

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Quick search

recipe platypus-variant

A Haplotype-Based Variant Caller For Next Generation Sequence Data

Homepage: <http://www.well.ox.ac.uk/platypus>

License: GPLv3

Recipe: </platypus-variant/meta.yaml>

package platypus-variant

downloads **20k** container **none**

Versions: 0.8.1.2-2, 0.8.1.2-1, 0.8.1.2-0, 0.8.1.1-3, 0.8.1.1-2, 0.8.1.1-1, 0.8.1.1-0, 0.8.1-1, 0.8.1-0

Depends: [htslib](#) ^o >=1.12, <1.13.0a0, [libgcc-ng](#) ^x >=9.3.0,

[python](#) ^x >=2.7, <2.8.0a0, [python_abi](#) ^x 2.7.* *_cp27mu

Required By: • [xyalign](#) ^o

Installation

With an activated Bioconda channel (see [2. Set up channels](#)), install with:

```
conda install platypus-variant
```

```
(base) -bash-4.2$ conda search r-base
```

```
r-base 4.0.3 ha43b4e8_3 conda-forge
r-base 4.0.3 hd23ff56_4 conda-forge
r-base 4.0.3 hd23ff56_5 conda-forge
r-base 4.0.3 hd23ff56_6 conda-forge
r-base 4.0.5 h8cab1ac_0 conda-forge
r-base 4.0.5 h9e01966_1 conda-forge
r-base 4.0.5 hb67fd72_2 conda-forge
r-base 4.0.5 hb93adac_3 conda-forge
r-base 4.1.0 h9e01966_0 conda-forge
r-base 4.1.0 h9e01966_1 conda-forge
r-base 4.1.0 hb67fd72_2 conda-forge
r-base 4.1.1 hb67fd72_0 conda-forge
r-base 4.1.1 hb93adac_1 conda-forge
```

Activate

```
(base) -bash-4.2$ conda activate bioinfo1  
(bioinfo1) -bash-4.2$
```

Deactivate

```
(bioinfo1) -bash-4.2$ conda deactivate  
(base) -bash-4.2$
```

Activate and stack

```
(base) -bash-4.2$ conda activate bioinfo1  
(bioinfo1) -bash-4.2$ conda activate --stack r4.1  
(r4.1) -bash-4.2$
```

Removing an environment

```
(base) -bash-4.2$ conda remove --n bioinfo2 --all
```

Updating a package

```
(base) -bash-4.2$ conda update -n bioinfo1 gatk4
```

Removing a package

```
(base) -bash-4.2$ conda remove -n bioinfo1 gatk4
```

or

```
(bioinfo1) -bash-4.2$ conda remove gatk4
```

Sharing an environment

```
(base) -bash-4.2$ conda env export -n bioinfo1 > bioinfo1.yml
```

Sharing an environment across Mac OS, Windows, and Linux

```
(base) -bash-4.2$ conda env export -n bioinfo1 --from-history >  
bioinfo1_fh.yml
```

Creating an environment from an .yml file

```
(base) -bash-4.2$ conda env create -f bioinfo1.yml
```




<https://github.com/rodrigopsav/conda>



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