

« Easy » bioinformatics with (ana/mini) CONDA



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<https://tinyurl.com/yy4d8vyb>

The FAIR data principles

Findable



Accessible



Interoperable



Reusable



- Last Thomas Denecker's presentation :

A problem of reproducibility in Biology

70 %

analyses in Experimental Biology **are not reproducible**

(Monya Baker, *Nature*, 2016)

Because material and methods are (were ?) not FAIR

Gene expression data processing and normalization. The publicly available data sets with CRC tumor samples from the Gene Expression Omnibus (Supplementary Table 3) were normalized using the robust multi-array average (RMA) method as implemented in the 'affy' package³⁹. Over 100 samples in GSE14333 and GSE17536 were excluded from GSEA for network analysis and training a consensus subtype classifier. All public Affymetrix data sets were renormalized using the single-sample frozen RMA method³³ as implemented in the 'frma' package for R/Bioconductor.

Colon and rectal tumor sets were analyzed on full genome Agilent microarrays (Agilent SurePrint G3 8x60K). Samples were hybridized against a common CRC reference pool, and full genome data was normalized using loess and local background subtraction ('limma' package). Details about sample processing and microarray analysis can be found in ref. 3.

Level 3 TCGA RNA-seq data for colon and rectal was downloaded from the TCGA data portal (January 2014). RSEM-normalized data⁴⁰ was further log-transformed, and non-expressed genes were removed. Principal component analysis (PCA) revealed that the first two principal components were highly correlated (data not shown), and samples were clustered by tumor type without a significant difference. A strong separation between genome analyzer (GA) and HiSeq samples and was batch-corrected using the ComBat method³².

Versions?
Parameters?

Versions?
Parameters?

$\log_2(n)$?,
 $\log_{10}(n)$?, $\log(n+1)$?,
etc.

Versions?
Parameters?

Could you redo the analysis ?

And even if you have a detailed protocol (workflow)

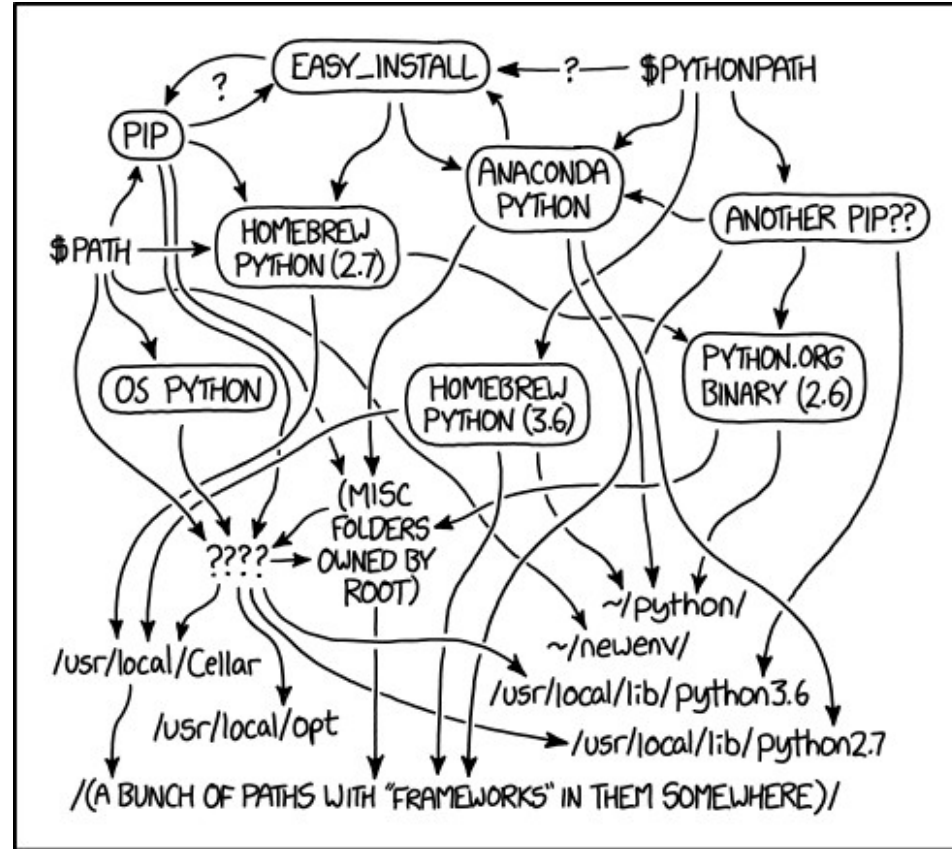
Problems still too frequent

- **Impossibility to install tools**
 - OS not compatible
 - Dependency no longer available
- **Update of the tool rendering the codes unusable**
 - Python 2 and Python 3 !
 - Changing the arguments of the functions used (R)
- **Impossibility to reproduce the results of the computational analysis**
 - IDE : stable version of the language different according to the OS (Rstudio)
 - Package versions

Credits : T .Denecker

Most of the time we don't have skills to solve these problems

And if you think you have skills, your configuration can look like this



MY PYTHON ENVIRONMENT HAS BECOME SO DEGRADED
THAT MY LAPTOP HAS BEEN DECLARED A SUPERFUND SITE.

Not really FAIR

Credits : xkcd

For a given biological question addressed with bioinformatics.

You need the right :

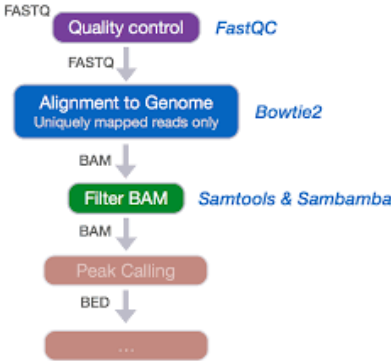
ressources



tools

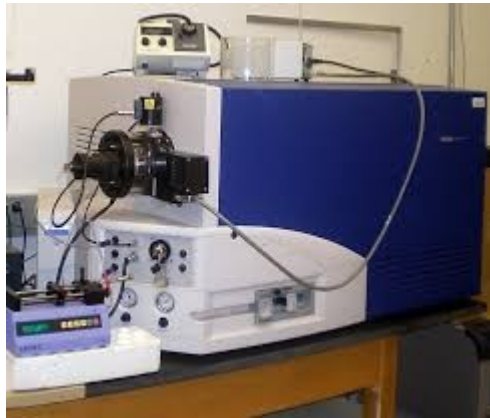
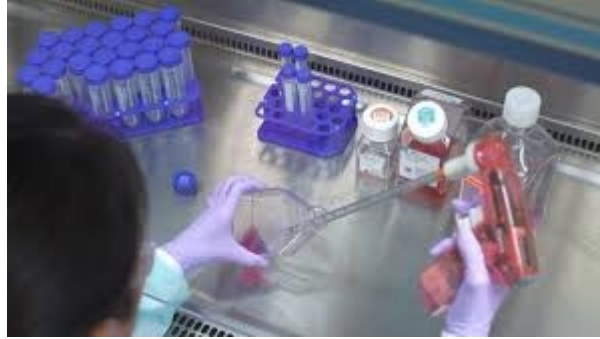


methods



Each choice has consequences

Same problems in wet biology



Many choices and solutions to set up your working environment



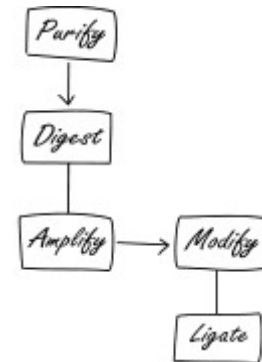
??



Life
Roche
Agilent
Qiagen
Applied
...



Power supply
Waste
Gaz
Fluids
Etc...



How to fit the FAIR data principles in bioinformatics ?

the FAIR data principles

Findable



Accessible



Interoperable



Reusable



CONDA



SNAKEMAKE





Conda (package manager)

From Wikipedia, the free encyclopedia

Conda is an open-source,^[1] cross-platform,^[2] language-agnostic package manager and environment management system. It was originally developed to solve difficult package management challenges faced by Python data scientists, and today is a popular Python/R package manager.^{[3][4]} It is released under the Berkeley Software Distribution License by Anaconda Inc.^{[1][5][6][7][8][9]}



- To install / desinstall programs
- To manage software environments
- To deal with dependancies (and OS)
- To manage program versions
- To get and distribute software environments
- To keep a « clean » machine
-

CONDA

Learn



Try & developp

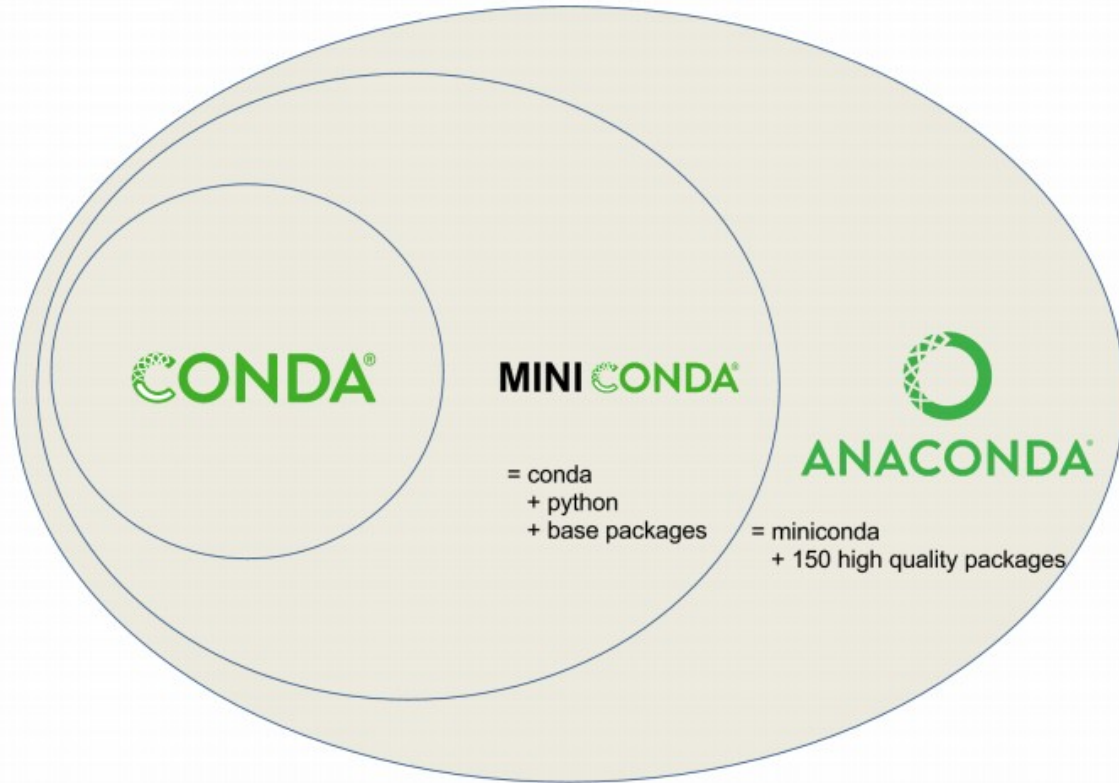


Keep tools accessible

Easy Uninstall

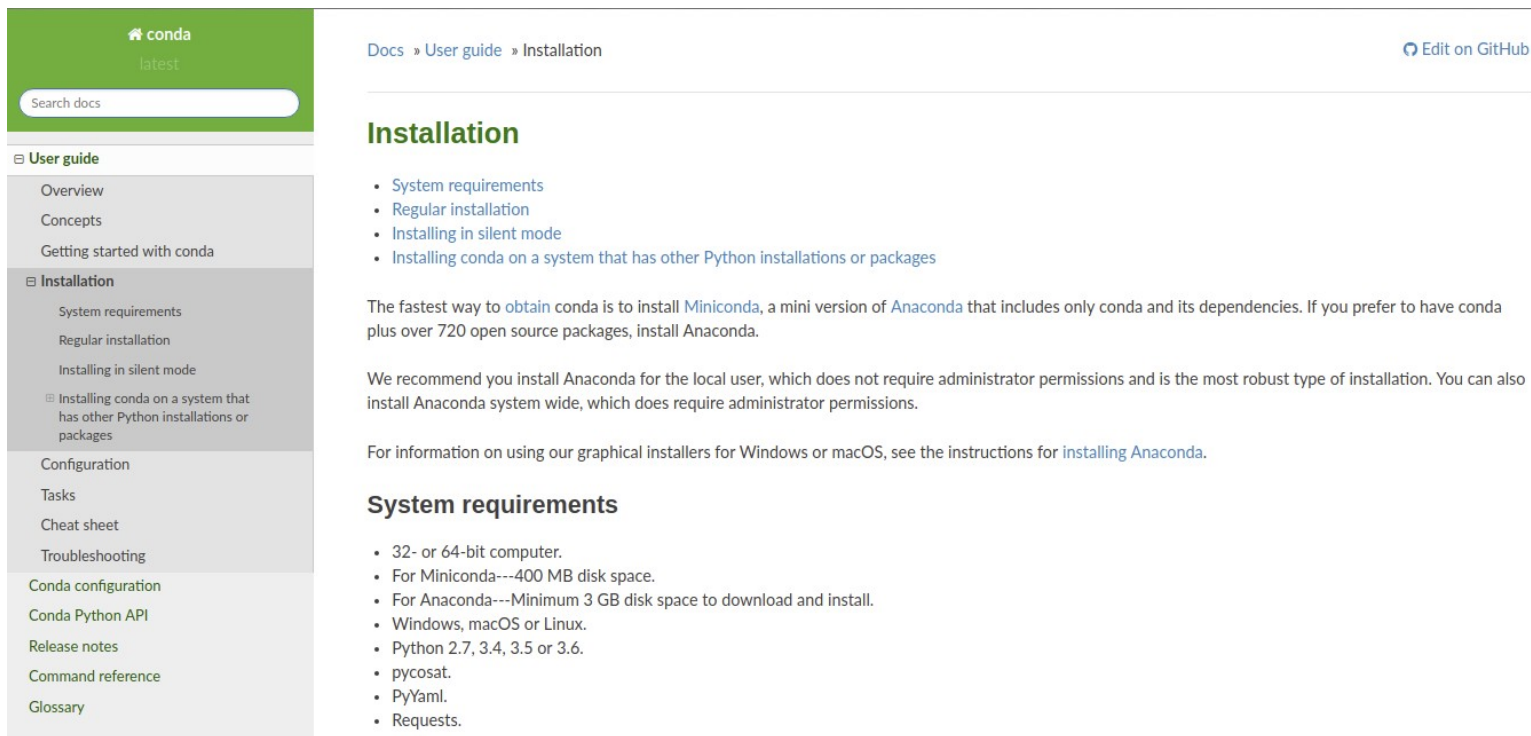
Which CONDA do we need?

Conda : package and environment manager for any language



Miniconda installation

Follow instructions <https://conda.io/projects/conda/en/latest/user-guide/install/index.html>



The screenshot shows the 'Installation' page of the conda.io documentation. The page has a green header with the 'conda' logo and 'latest' version indicator. A search bar is present below the header. The left sidebar contains a navigation menu with categories like 'User guide', 'Installation', 'Configuration', 'Tasks', 'Cheat sheet', and 'Troubleshooting'. The main content area is titled 'Installation' and includes a list of links to system requirements, regular installation, and silent mode. A paragraph explains that Miniconda is a mini version of Anaconda. Another paragraph recommends installing Anaconda for local use. A final paragraph provides information on graphical installers for Windows and macOS. The page also includes a 'System requirements' section with a list of hardware and software prerequisites.

conda
latest

Search docs

Docs » User guide » Installation [Edit on GitHub](#)

Installation

- [System requirements](#)
- [Regular installation](#)
- [Installing in silent mode](#)
- [Installing conda on a system that has other Python installations or packages](#)

The fastest way to [obtain](#) conda is to install [Miniconda](#), a mini version of [Anaconda](#) that includes only conda and its dependencies. If you prefer to have conda plus over 720 open source packages, install [Anaconda](#).

We recommend you install [Anaconda](#) for the local user, which does not require administrator permissions and is the most robust type of installation. You can also install [Anaconda](#) system wide, which does require administrator permissions.

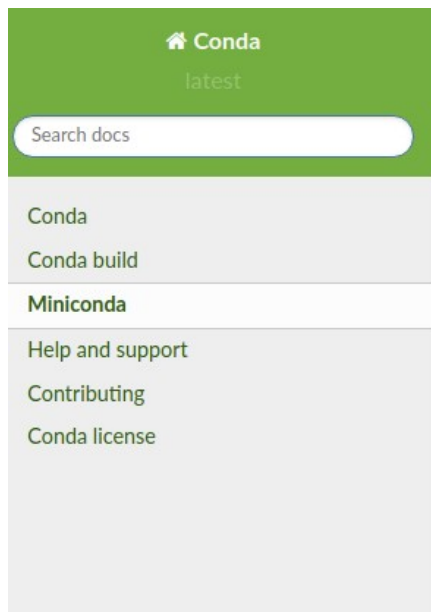
For information on using our graphical installers for Windows or macOS, see the instructions for [installing Anaconda](#).

System requirements

- 32- or 64-bit computer.
- For Miniconda---400 MB disk space.
- For Anaconda---Minimum 3 GB disk space to download and install.
- Windows, macOS or Linux.
- Python 2.7, 3.4, 3.5 or 3.6.
- pycosat.
- PyYaml.
- Requests.

Miniconda installation

Go to <https://docs.conda.io/en/latest/miniconda.html> and download installer file



The sidebar shows the Conda documentation navigation menu. It includes a search bar, a home icon, and a list of menu items: Conda, Conda build, Miniconda, Help and support, Contributing, and Conda license. The 'Miniconda' item is highlighted in green.

Docs » Miniconda

[Edit on GitHub](#)

Miniconda

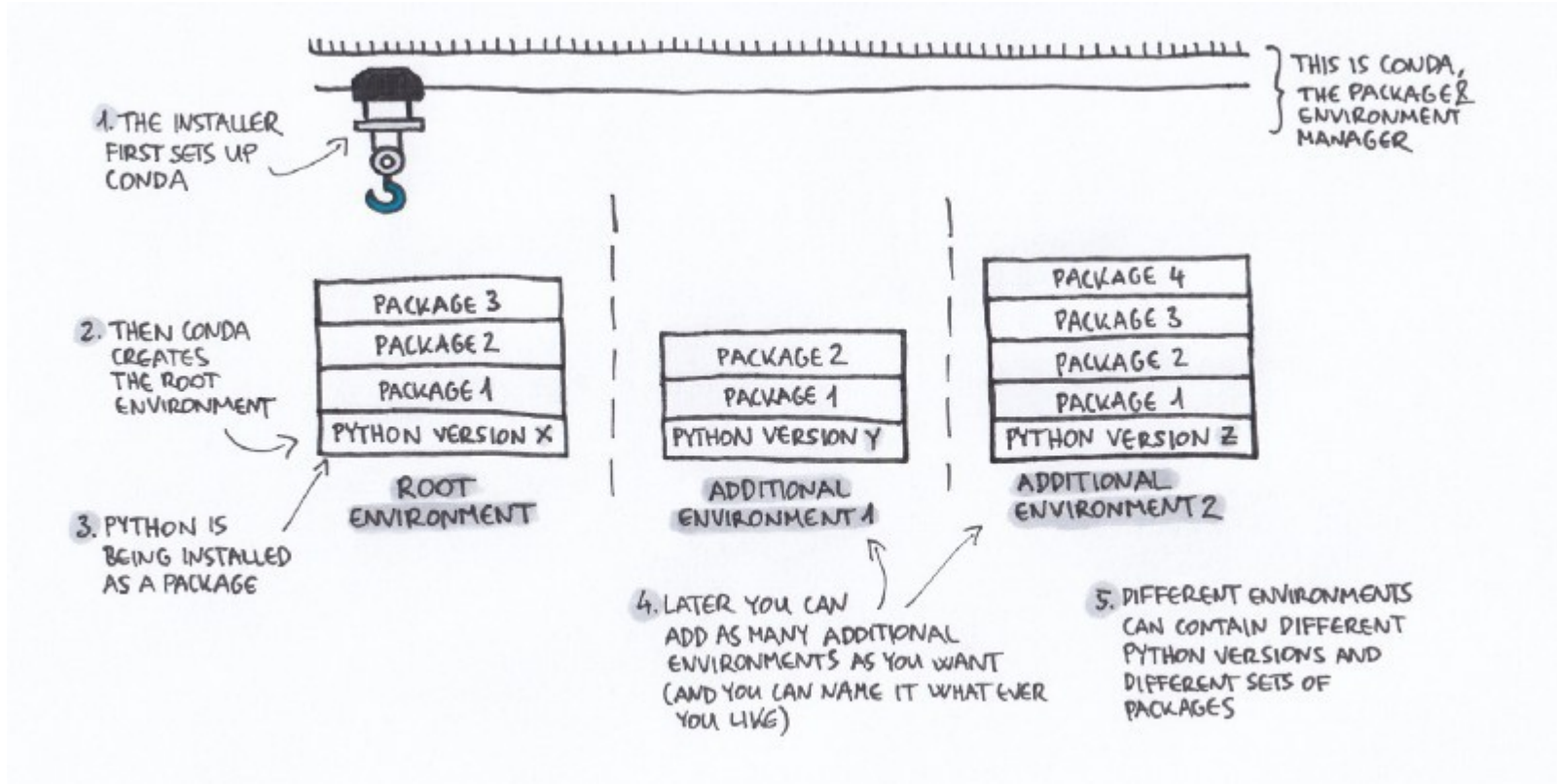
	Windows	Mac OS X	Linux
Python 3.7	64-bit (exe installer)	64-bit (bash installer)	64-bit (bash installer)
	32-bit (exe installer)	64-bit (.pkg installer)	32-bit (bash installer)
Python 2.7	64-bit (exe installer)	64-bit (bash installer)	64-bit (bash installer)
	32-bit (exe installer)	64-bit (.pkg installer)	32-bit (bash installer)

[Installation instructions](#)

HOW

CONDA

WORKS ?



Hands-on

- We will use a Docker container which run linux and contains the required files
 - Pros :
 - What is done in docker stays in docker !
 - Everybody share the same environment
 - Cons :
 - You need to install Docker !

Launch Docker

- PC : click on Docker-desktop icon
- MAC : click on Docker-desktop icon
- Linux : wait



Open a terminal

- PC : type « cmd » or « powershell » in search bar
- MAC : Control + Option + Shift + T
- Linux : Ctrl + Alt + t

Check docker images

docker images

Windows PowerShell

PS C:\Users\olivi> docker images

REPOSITORY	TAG	IMAGE ID	CREATED	SIZE
okirsh/tpconda	latest	e7ee4154dce4	26 hours ago	182MB
okirsh/miniconda	latest	2bd3a56e8ff1	2 weeks ago	431MB

PS C:\Users\olivi>

It should be like me If you read the mail and did your homework !

Start a linux container

```
docker run -it okirsh/tpconda
```

Your machine env

```
Windows PowerShell
Copyright (C) Microsoft Corporation. Tous droits réservés.

Testez le nouveau système multiplateforme PowerShell https://aka.ms/pscore6

PS C:\Users\olivi> docker images
REPOSITORY          TAG                 IMAGE ID            CREATED             SIZE
okirsh/tpconda      latest              e7ee4154dce4       7 days ago         182MB
okirsh/miniconda    latest              2bd3a56e8ff1       3 weeks ago        431MB
PS C:\Users\olivi> docker run -it okirsh/tpconda
root@535c2857d260:/#
```

Inside docker container

Install miniconda

```
cd /tpconda
```

```
ls -l
```

```
root@65593ada410e: /tpconda
```

```
root@65593ada410e:/tpconda# ls -l
total 73500
-rw-r--r-- 1 root root 75257002 Jul 29 14:25 Miniconda3-latest-Linux-x86_64.sh
-rwxr-xr-x 1 root root      241 Sep 11 07:20 bedtools.yml
root@65593ada410e:/tpconda#
```

Install miniconda

```
bash Miniconda3-latest-Linux-x86_64.sh
```

Tip : use tab completion !! no need to type everything

And press ENTER

```
root@65593ada410e: /tpconda
root@65593ada410e:/tpconda# ls -l
total 73500
-rw-r--r-- 1 root root 75257002 Jul 29 14:25 Miniconda3-latest-Linux-x86_64.sh
-rwxr-xr-x 1 root root      241 Sep 11 07:20 bedtools.yml
root@65593ada410e:/tpconda# bash Miniconda3-latest-Linux-x86_64.sh

Welcome to Miniconda3 4.7.10

In order to continue the installation process, please review the license
agreement.
Please, press ENTER to continue
>>>
```

Install miniconda

Read the license terms ...

yes

```
root@65593ada410e: /tpconda
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.

Do you accept the license terms? [yes|no]
[no] >>>
Please answer 'yes' or 'no':'
```


Install miniconda

Press ENTER

```
root@65593ada410e: /tpconda
```

```
Please answer 'yes' or 'no':
```

```
>>> yes
```

```
Miniconda3 will now be installed into this location:
```

```
/root/miniconda3
```

- Press ENTER to confirm the location
- Press CTRL-C to abort the installation
- Or specify a different location below

```
[/root/miniconda3] >>>
```

Install miniconda

yes

```
root@65593ada410e: /tpconda
```

```
wheel          pkgs/main/linux-64::wheel-0.33.4-py37_0
xz             pkgs/main/linux-64::xz-5.2.4-h14c3975_4
yaml          pkgs/main/linux-64::yaml-0.1.7-had09818_2
zlib          pkgs/main/linux-64::zlib-1.2.11-h7b6447c_3
zstd          pkgs/main/linux-64::zstd-1.3.7-h0b5b093_0
```

```
Preparing transaction: done
```

```
Executing transaction: - WARNING conda.core.envs_manager:register_env(46): Unable to create environment. Path not writable or missing.
```

```
  environment location: /root/miniconda3
```

```
  registry file: /root/.conda/environments.txt
```

```
done
```

```
installation finished.
```

```
Do you wish the installer to initialize Miniconda3
```

```
by running conda init? [yes|no]
```

```
[no] >>> _
```

Install miniconda

```
root@65593ada410e: /tpconda
```

```
registry file: /root/.conda/environments.txt
done
installation finished.
Do you wish the installer to initialize Miniconda3
by running conda init? [yes|no]
[no] >>> yes
no change      /root/miniconda3/condabin/conda
no change      /root/miniconda3/bin/conda
no change      /root/miniconda3/bin/conda-env
no change      /root/miniconda3/bin/activate
no change      /root/miniconda3/bin/deactivate
no change      /root/miniconda3/etc/profile.d/conda.sh
no change      /root/miniconda3/etc/fish/conf.d/conda.fish
no change      /root/miniconda3/shell/condabin/Conda.psm1
no change      /root/miniconda3/shell/condabin/conda-hook.ps1
no change      /root/miniconda3/lib/python3.7/site-packages/xontrib/conda.xsh
no change      /root/miniconda3/etc/profile.d/conda.csh
modified       /root/.bashrc
```

==> For changes to take effect, close and re-open your current shell. <==

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
```

Thank you for installing Miniconda3!

Install miniconda

```
source /root/.bashrc
```

```
root@65593ada410e: /tpconda
```

```
root@65593ada410e:/tpconda# source /root/.bashrc  
(base) root@65593ada410e:/tpconda#
```

Et voilà !! miniconda is installed, added in your \$PATH and loaded

(Mini) conda exploration

Type :

conda

Or

conda --help

```
olivier@dellolinux:~$ conda
usage: conda [-h] [-V] command ...

conda is a tool for managing and deploying applications, environments and packages.

Options:

positional arguments:
  command
  clean                Remove unused packages and caches.
  config              Modify configuration values in .condarc. This is modeled
                    after the git config command. Writes to the user .condarc
                    file (/home/olivier/.condarc) by default.
  create              Create a new conda environment from a list of specified
                    packages.
  help                Displays a list of available conda commands and their help
                    strings.
  info                Display information about current conda install.
  init                Initialize conda for shell interaction. [Experimental]
  install             Installs a list of packages into a specified conda
                    environment.
  list                List linked packages in a conda environment.
  package             Low-level conda package utility. (EXPERIMENTAL)
  remove              Remove a list of packages from a specified conda environment.
  uninstall           Alias for conda remove.
  run                 Run an executable in a conda environment. [Experimental]
  search              Search for packages and display associated information. The
                    input is a MatchSpec, a query language for conda packages.
                    See examples below.
  update              Updates conda packages to the latest compatible version.
  upgrade             Alias for conda update.

optional arguments:
  -h, --help          Show this help message and exit.
  -V, --version       Show the conda version number and exit.

conda commands available from other packages:
  env
```

(Mini) conda exploration

Type :

`conda env --help`

```
(base) root@65593ada410e:/tpconda# conda env
usage: conda-env [-h] {create,export,list,remove,update} ...

positional arguments:
  {create,export,list,remove,update}
    create                Create an environment based on an environment file
    export                Export a given environment
    list                  List the Conda environments
    remove                Remove an environment
    update                Update the current environment based on environment
                        file

optional arguments:
  -h, --help            Show this help message and exit.

conda commands available from other packages:
  env
(base) root@65593ada410e:/tpconda#
```

(Mini) conda basic command

conda info

conda info -e

conda env list

conda list

conda deactivate

which python

conda activate

which python

conda list

```
olivier@dellolinux:~$ conda
usage: conda [-h] [-V] command ...

conda is a tool for managing and deploying applications, environments and packages.

Options:

positional arguments:
  command
  clean                Remove unused packages and caches.
  config              Modify configuration values in .condarc. This is modeled
                    after the git config command. Writes to the user .condarc
                    file (/home/olivier/.condarc) by default.
  create              Create a new conda environment from a list of specified
                    packages.
  help                Displays a list of available conda commands and their help
                    strings.
  info                Display information about current conda install.
  init                Initialize conda for shell interaction. [Experimental]
  install             Installs a list of packages into a specified conda
                    environment.
  list                List linked packages in a conda environment.
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  remove              Remove a list of packages from a specified conda environment.
  uninstall           Alias for conda remove.
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  update              Updates conda packages to the latest compatible version.
  upgrade             Alias for conda update.

optional arguments:
  -h, --help          Show this help message and exit.
  -V, --version       Show the conda version number and exit.

conda commands available from other packages:
  env
```

Create an environment

Conda is environment management system :

You can create insulated software envs (like different rooms in the lab)

The command is like `conda create -n envname toolname`

Or like `conda install -n envname toolname` (if the env already exists)

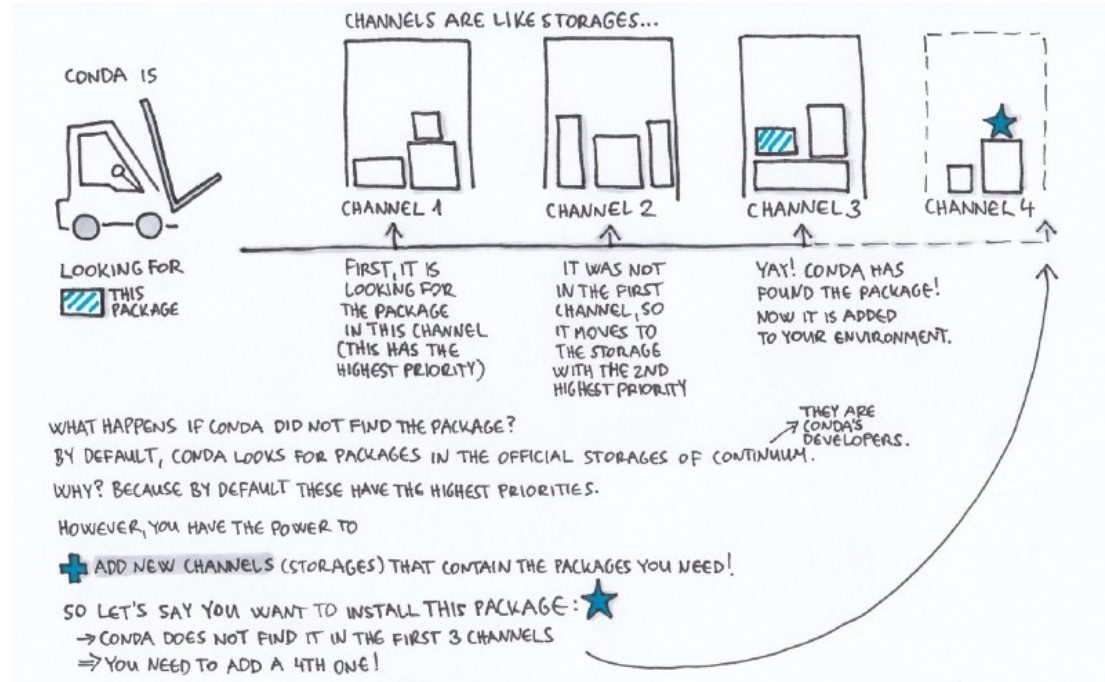
Important notice : the « base » env shouldn't be used (or modified).
Always create a new or modify an existing env if you want to try something

How does it work ?

Conda is package manager system :

You can any program from dedicated repositories (channels)

Conda will find the required dependencies for your packages



Usefull channel / repository

BIOCONDA

Navigation

[User Docs](#)

[Contributing to Bioconda](#)

[Developer Docs](#)

[Bioconda @ Github](#)

[Recipe Index](#)

[chat on gitter](#)

Quick search

BIOCONDA[®]

Bioconda is a channel for the [conda](#) package manager specializing in bioinformatics software. Bioconda consists of:

- a [repository of recipes](#) hosted on GitHub
- a [build system](#) turning these recipes into conda packages
- a [repository of packages](#) containing over 6000 bioinformatics packages ready to use with `conda install`
- over 600 contributors and 500 members who add, modify, update and maintain the recipes

The conda package manager makes installing software a vastly more streamlined process. Conda is a combination of other package managers you may have encountered, such as pip, CPAN, CRAN, Bioconductor, apt-get, and homebrew. Conda is both language- and OS-agnostic, and can be used to install C/C++, Fortran, Go, R, Python, Java etc programs on Linux, Mac OSX, and Windows.

Conda allows separation of packages into repositories, or [channels](#). The main [defaults](#) channel has a large number of common packages. Users can add additional channels from which to install software packages not available in the defaults channel. Bioconda is one such channel specializing in bioinformatics software.

Repository of packages



Profile

bioconda













Organization created on Sep 11, 2015

Bioconda is a distribution of bioinformatics software realized as a channel for the versatile Conda package manager.

🔍 Packages

[View all \(7074\)](#)

-  [irida-uploader](#) 3 hours and 13 minutes ago
-  [circexplorer2](#) 3 hours and 15 minutes ago
-  [blksheep](#) 5 hours and 4 minutes ago
-  [r-bcbiornaseq](#) 8 hours and 16 minutes ago
-  [r-bcbiosinglecell](#) 9 hours and 4 minutes ago
-  [r-deseqanalysis](#) 9 hours and 8 minutes ago
-  [vsearch](#) 9 hours and 34 minutes ago
-  [phipack](#) 10 hours and 32 minutes ago
-  [r-acidplots](#) 10 hours and 32 minutes ago
-  [gridss](#) 11 hours and 35 minutes ago

Install bedtools

Search in anaconda-cloud
And click the link



ANACONDA CLOUD Search Anaconda Cloud

Gallery About Anaconda Help Download Anaconda Sign In

bioconda / packages / bedtools 2.29.0

A powerful toolset for genome arithmetic

Conda Files Labels Badges

License: GPL v2
Home: <http://bedtools.readthedocs.org/>
264808 total downloads
Last upload: 10 hours and 27 minutes ago

Installers

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

conda install ?

linux-64 v2.29.0
osx-64 v2.29.0

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

```
conda install -c bioconda bedtools  
conda install -c bioconda/label/cf201901 bedtools
```

Install bedtools in a new environment

```
conda create -n bedtools229 -c bioconda bedtools
```

Open & check your new environment

```
conda activate bedtools229
```

Check

```
conda list
```

```
bedtools --version
```

```
bedtools
```

```
(base) root@05b7772c32d1:/tpconda# conda create -n bedtools229 -c bioconda bedto
Collecting package metadata (current_repodata.json): done
Solving environment: done

==> WARNING: A newer version of conda exists. <==
  current version: 4.7.10
  latest version: 4.7.11

Please update conda by running

  $ conda update -n base -c defaults conda

## Package Plan ##

environment location: /root/miniconda3/envs/bedtools229

added / updated specs:
- bedtools

The following packages will be downloaded:

-----|-----|-----|-----|
package|          build|          |          |
-----|-----|-----|-----|
bedtools-2.29.0|          h6ed99ea_1|    13.8 MB| bioconda
bzip2-1.0.8|          h7b6447c_0|         78 KB|
-----|-----|-----|-----|
Total:|          |    13.9 MB|

The following NEW packages will be INSTALLED:

 _libgcc_mutex| pkgs/main/linux-64::libgcc_mutex-0.1-main
 bedtools| bioconda/linux-64::bedtools-2.29.0-h6ed99ea_1
 bzip2| pkgs/main/linux-64::bzip2-1.0.8-h7b6447c_0
 libgcc-ng| pkgs/main/linux-64::libgcc-ng-9.1.0-hdf63c60_0
 libstdcxx-ng| pkgs/main/linux-64::libstdcxx-ng-9.1.0-hdf63c60_0
 xz| pkgs/main/linux-64::xz-5.2.4-h14c3975_4
 zlib| pkgs/main/linux-64::zlib-1.2.11-h7b6447c_3

Proceed ([y]/n)?
```

Install an older version of bedtools and add bwa

Check available versions

```
conda search -c bioconda bedtools
```

```
(base) root@05b7772c32d1:/tpconda# conda search -c bioconda bedtools
Loading channels: done
# Name          Version          Build          Channel
bedtools        2.16.2           0              bioconda
bedtools        2.17.0           0              bioconda
bedtools        2.19.1           0              bioconda
bedtools        2.19.1           he860b03_2    bioconda
bedtools        2.19.1           he941832_1    bioconda
bedtools        2.20.1           0              bioconda
bedtools        2.20.1           he860b03_2    bioconda
bedtools        2.20.1           he941832_1    bioconda
bedtools        2.22             0              bioconda
bedtools        2.22             hdbcaa40_3    bioconda
```

You can create a new env or clone your env and downgrade software version

```
conda create --clone bedtools229 -n bedtools222
```

```
conda install -c bioconda -n bedtools222 bedtools=2.22 bwa
```

Export and share your envs

Check your env list

```
conda env list
```

Which env is « activated » ?

```
conda activate
```

Export environment configuration

```
conda env export -n bedtools222
```

```
conda env export --no-build -n bedtools222
```

Save it in a yml file

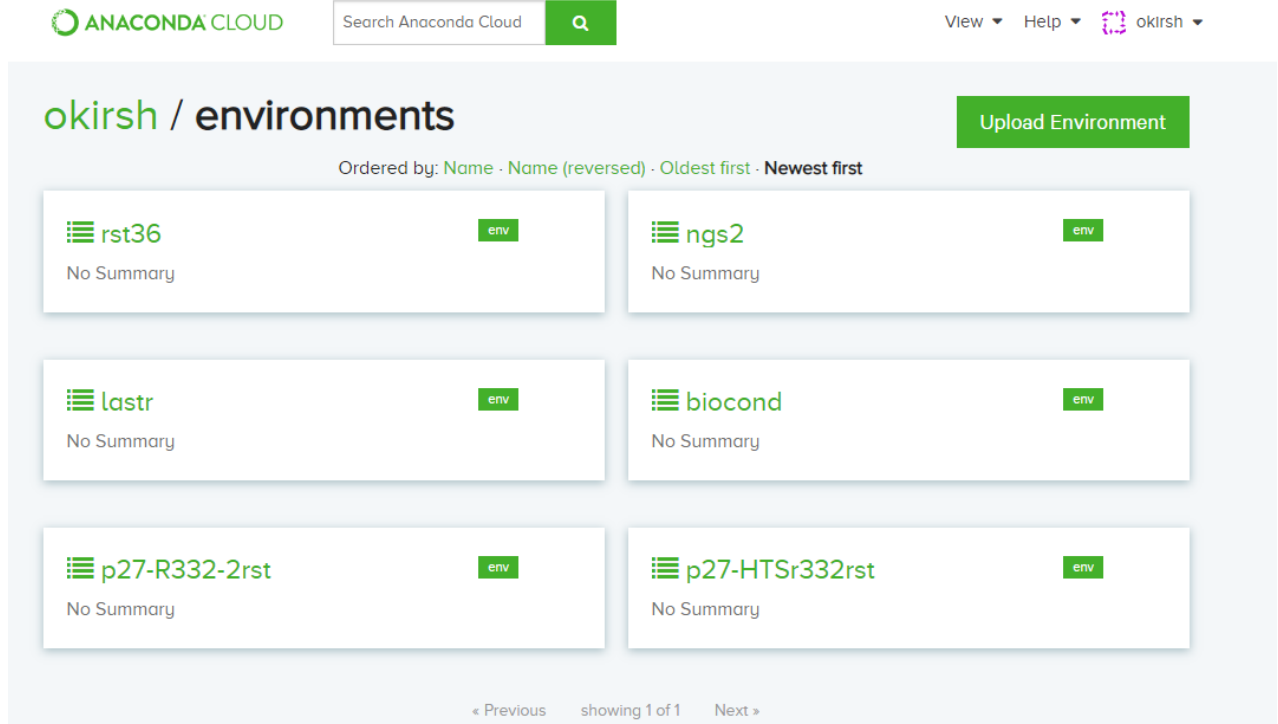
```
conda env export --no-build -n bedtools222 > bedtools222.yml
```

```
(bedtools229) root@05b7772c32d1:/tpconda# conda env list
# conda environments:
#
base                /root/miniconda3
bedtools222         /root/miniconda3/envs/bedtools222
bedtools229         * /root/miniconda3/envs/bedtools229
```

Export and share your envs

Send yml file by email

Share them on anaconda cloud









The screenshot displays the Anaconda Cloud user interface for a user named 'okirsh'. At the top, there is a search bar and navigation links for 'View', 'Help', and the user profile. The main heading is 'okirsh / environments', with a green 'Upload Environment' button on the right. Below the heading, the environments are sorted by 'Name (reversed) - Oldest first - Newest first'. The list contains six environment cards, each with a name, a 'No Summary' status, and a green 'env' button. The environments are: rst36, ngs2, lastr, biocond, p27-R332-2rst, and p27-HTSr332rst. At the bottom, there are navigation links: « Previous, showing 1 of 1, Next ».

ANACONDA CLOUD Search Anaconda Cloud View Help okirsh

okirsh / environments Upload Environment

Ordered by: Name · Name (reversed) · Oldest first · Newest first

 rst36 No Summary	env	 ngs2 No Summary	env
 lastr No Summary	env	 biocond No Summary	env
 p27-R332-2rst No Summary	env	 p27-HTSr332rst No Summary	env

« Previous showing 1 of 1 Next »

Managing envs

> Creating an env from a yml

```
(base) [okirsh@clust-slurm-client ~]$ conda env list
# conda environments:
#
base                * /shared/mfs/data/software/miniconda
bcftools-1.9        /shared/mfs/data/software/miniconda/envs/bcftools-1.9
bedtools-2.26.0     /shared/mfs/data/software/miniconda/envs/bedtools-2.26.0
bedtools-2.27.1     /shared/mfs/data/software/miniconda/envs/bedtools-2.27.1
biokevlar-0.6.1     /shared/mfs/data/software/miniconda/envs/biokevlar-0.6.1
blast-2.7.1         /shared/mfs/data/software/miniconda/envs/blast-2.7.1
bowtie-1.2.2        /shared/mfs/data/software/miniconda/envs/bowtie-1.2.2
bowtie2-2.3.4.3     /shared/mfs/data/software/miniconda/envs/bowtie2-2.3.4.3
bwa-0.7.17          /shared/mfs/data/software/miniconda/envs/bwa-0.7.17
ceas-1.0.2          /shared/mfs/data/software/miniconda/envs/ceas-1.0.2
clustalo-1.2.4      /shared/mfs/data/software/miniconda/envs/clustalo-1.2.4
coreutils-8.25      /shared/mfs/data/software/miniconda/envs/coreutils-8.25
csvkit-1.0.3        /shared/mfs/data/software/miniconda/envs/csvkit-1.0.3
cutadapt-1.10       /shared/mfs/data/software/miniconda/envs/cutadapt-1.10
cutadapt-1.8.3      /shared/mfs/data/software/miniconda/envs/cutadapt-1.8.3
cytoscape-3.7.1     /shared/mfs/data/software/miniconda/envs/cytoscape-3.7.1
deeptools-3.1.2     /shared/mfs/data/software/miniconda/envs/deeptools-3.1.2
deeptools-3.2.0     /shared/mfs/data/software/miniconda/envs/deeptools-3.2.0
delly-0.7.9         /shared/mfs/data/software/miniconda/envs/delly-0.7.9
```

View of available
conda env on nncr
(IFB cluster)

Managing envs

> Creating an env from a yml

Type :

```
ls -l
```

```
cat bedtools.yml
```

```
root@76a9d2488003:/tpconda# ll
total 73508
drwxr-xr-x 2 root root    4096 Sep 11 07:23 ./
drwxr-xr-x 1 root root    4096 Sep 12 09:20 ../
-rw-r--r-- 1 root root 75257002 Jul 29 14:25 Miniconda3-latest-Linux-x86_64.sh
-rwxr-xr-x 1 root root    241 Sep 11 07:20 bedtools.yml*
```

```
conda env create -n bedtoolsifb -f bedtools.yml
```

Managing envs

Remove an env :Simply delete the folder, or

```
conda env list
```

```
conda env remove -n bedtools229
```

Set up « Channels »

- <https://bioconda.github.io/user/install.html#set-up-channels>

2. Set up channels

After installing conda you will need to add the bioconda channel as well as the other channels bioconda depends on. **It is important to add them in this order** so that the priority is set correctly (that is, conda-forge is highest priority).

The conda-forge channel contains many general-purpose packages not already found in the `defaults` channel.

```
conda config --add channels defaults
conda config --add channels bioconda
conda config --add channels conda-forge
```

* order matters

First check your channel config with : `conda config --get channels`

This step is not mandatory but it's always good to « control » your machine

Is conda really FAIR ?

The FAIR data principles

Findable



Accessible



Interoperable



Reusable



a bedto

```
## Package Plan ##
```

```
environment location: /root/miniconda3/envs/bedtools229
```

```
added / updated specs:
```



PARIS7 BIOINFO CLUB

Bioinformatics Club – IJM, Epigenetics, BFA

<https://paris7bioinfo.wordpress.com/>

Thursday September 26, 10am: Presentation of eLabFTW (Nicolas Carpi, Institut Curie). eLabFTW is a free and open source electronic lab notebook designed for researchers. Note that we are not sure whether it is possible to implement it at IJM. In any case, this presentation should give you an overview of what you can do with electronic lab notebooks.

Thursday October 3rd, 10am: Do-it-yourself Extraction of differentially-expressed genes from an RNAseq experiment (Flora Borne, IJM) *Please bring your own laptop!*