



Retrieving, compiling and running own programs

CSC Training, 2019-12



CSC – Finnish expertise in ICT for research, education and public administration

Installing Qiime2

- QIIME2 installation instructions are at docs.qiime2.org

```
$ python -V  
$ python3 -V
```

```
$ wget https://repo.anaconda.com/miniconda/Miniconda2-latest-Linux-x86_64.sh  
$ bash Miniconda2-latest-Linux-x86_64.sh  
$ exit
```

```
$ conda update conda  
$ conda install wget
```

```
$ wget https://data.qiime2.org/distro/core/qiime2-2019.10-py36-linux-conda.yml  
$ conda env create -n qiime2-2019.10 --file qiime2-2019.10-py36-linux-conda.yml
```

```
$ conda activate qiime2-2019.10
```


Why Conda?

- Conda is an open source *package management system* and *environment management system* that runs on Windows, macOS and Linux.
 - Conda quickly installs, runs and updates packages and their dependencies.
 - You can set up totally separate environments to run different versions of software, while continuing to run your usual commands in your normal environment.
 - Miniconda is “mini” because by default, it does not include as many Python packages as Anaconda does. A minimum number of default packages uses less space on hard drives.
- Miniconda is not installed by default on Linux.

Conda basics

- To create/remove a new environment and install/remove software into it:

```
$ conda create -n env_name software [ software ... ]  
$ conda remove env_name
```

- To use installed software in its environment:

```
$ conda activate env_name
```

- To stop using software:

```
(env_name) $ conda deactivate
```

- Enable/disable Conda base at startup:

```
$ conda config --set auto_activate_base true|false
```

Bioconda

- Bioconda is a channel for the conda package manager specializing in bioinformatics software, see [Bioconda web page](#) for more information.

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

```
$ conda create -n aligners bwa bowtie
```

```
$ conda activate aligners  
$ conda deactivate
```

Compiling from source code

- If you are absolutely sure a ready-made executable does not exist, you need to compile the software yourself.

```
$ wget https://ftp.gnu.org/gnu/hello/hello-2.10.tar.gz
$ tar xzf hello-2.10.tar.gz
$ cd hello-2.10
$ ./configure --prefix=${HOME}/hello
$ make
$ make install
$ make clean
```

- Development libraries required for compiling might be missing from default install. If that's the case those need to be installed first.

```
$ sudo apt install libc-dev
```