

# Linux Software Installation – Exercises 1

## Part 1. Setup Conda

### 1.1 Login to the BioHPC machine and download the installer

Login (ssh) to the machine that you are assigned for this workshop (assigned machines: <https://biohpc.cornell.edu/ww/machines.aspx?i=117>). Prepare the working directory, and download the latest version of Miniconda/python3 installer into the working directory. Replace “xxxxx” in the commands with your BioHPC User ID. The link below is the latest version as of 3/9/2019. You can get the URL of the current version from the web site <https://docs.conda.io/en/latest/miniconda.html>

```
mkdir /workdir/xxxxx  
cd /workdir/xxxxx  
wget https://repo.anaconda.com/miniconda/Miniconda3-latest-Linux-x86\_64.sh
```

- wget is a Linux tool used to download a file from internet.

### 1.2 Run the installer

```
chmod u+x Miniconda3-latest-Linux-x86_64.sh  
. ./Miniconda3-latest-Linux-x86_64.sh
```

- The “chmod u+x” command makes the file executable.
- During the installation, you will be asked for multiple questions:
  - 1) “Please, press ENTER to continue”: press “ENTER” key;
  - 2) “More”: keep pressing “SPACE” key until you reach next question;
  - 3) “Do you accept the license terms?”: enter “yes”
  - 4) “Miniconda3 will now be installed into this location ... ”: press “ENTER” key and accept the default “/home/xxxxx/miniconda3”.
  - 5) “Do you wish the installer to prepend the miniconda3 install location to PATH in your /home/xxxxx/.bashrc” : Press ENTER to accept the default “no”;

### 1.3 Miniconda is ready.

## Part 2. Install and run a simple software in Conda

### 2.1 Install bwa in Conda

```
export PATH=/home/xxxxx/miniconda3/bin:$PATH  
conda install -c bioconda bwa
```

## 2.2

### 2.3 Run bwa in Conda

Next time you login, to run bwa that you installed:

```
export PATH=/home/xxxxx/miniconda3/bin:$PATH  
bwa
```

- While you are at this step, you might want to use “which” command to check which copy of “bwa” you are running. You can run this command before and after last step, you will find you are using different “bwa”.

```
which bwa
```

## Part 3. Work with Conda environment

### 3.1 Create a virtual environment and give it a name “pysam”, install pysam the virtual environment

```
conda create -c bioconda -n pysam pysam
```

- The command “conda create -n aligners” would create an environment called “pysam” (you can use any names), and install the pysam package into it.

### 3.2 Start the pysam environment, and run python

```
source activate pysam  
which python  
python -V  
which pip
```

- “which python” “which pip” would tell you which python and pip you are using .

### 3.3 Install other python modules in this environment

```
pip install numpy
```

The “pip” command would install numpy in the environment.

### 3.4 End the environment

```
conda deactivate
```

3.5. Now you installed pysam and numpy in miniconda3 in the home directory. Next time you need to use it in a new session, run these commands

```
export PATH=/home/xxxx/miniconda3/bin:$PATH  
source activate pysam  
## after the work is done  
conda deactivate
```

## Part 4. Create a Python2.7 environment in Miniconda3

```
conda create -n myNewPipeline python=2.7  
source activate myNewPipeline  
which python  
python -V  
conda deactivate
```

Note in the first command there is no package name. This step would create an empty python2.7 environment, within which you can use pip to install other python modules.