

# Linux Software Installation – Exercises

## 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://cbsu.tc.cornell.edu/ww/machines.aspx?i=104> ). Prepare the working directory, and download the latest version of Anaconda installer into the working directory. Replace “xxxxx” in the commands with your BioHPC User ID. The link below is the latest version as of 10/25/2018. You can get the URL of the current version from the web site <https://www.anaconda.com/download/#linux>

```
mkdir /workdir/xxxxx
cd /workdir/xxxxx
wget https://repo.anaconda.com/archive/Anaconda2-5.3.0-Linux-x86\_64.sh
```

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

### 1.2 Run the installer

```
chmod u+x Anaconda2-5.3.0-Linux-x86_64.sh
./Anaconda2-5.3.0-Linux-x86_64.sh
```

- The “chmod u+x” command makes the file as an executable file.
- During the installation, you will be asked for multiple questions:
  - 1) “Please, press ENTER to continue”: press “ENTER” key;
  - 2) “More”: keep press “SPACE” key until you reach next question;
  - 3) “Do you accept the license terms?”: enter “yes”
  - 4) “Anaconda2 will now be installed into this location ... ”: press “ENTER” key and accept the default “/home/xxxxx/anaconda2”.
  - 5) “Do you wish the installer to prepend the Anaconda2 install location to PATH in your /home/xxxxx/.bashrc” : Press ENTER to accept the default “no”;
  - 6) “Do you wish to proceed with the installation of Microsoft VSCode?”: Enter “no”

### 1.3 Anaconda is ready.

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

## 2.1 Install bwa in Conda

```
export PATH=/home/xxxxx/anaconda2/bin:$PATH
conda install -c bioconda bwa
```

## 2.2 Run bwa in Conda

```
export PATH=/home/xxxxx/anaconda2/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 virtual environment

## 3.1 Create a virtual environment and give it a name, install a new copy of bwa in the virtual environment

```
conda create -c bioconda -n aligners bwa
```

- The command “conda create -n aligners” would create an environment called “aligners” (you can use any names).
- As you provide a valid conda package name “bwa” at the end of the command, “conda” would install bwa package into the new environment.

## 3.2 Start the environment, and run bwa

```
source activate aligners
bwa
```

- You can run “which bwa” to check which “bwa” you are using at this step.

### 3.3 End the environment

```
source deactivate
```