CSC 314, Software Installation

<u>Overview</u>

In this class we will use Python and Biopython to write bioinformatics programs. In particular, we will work with the following:

1. *Python* (https://www.python.org/), a general purpose programming language
2. *Jupyter Notebook*s (https://jupyter.org/), a web-based platform for creating, explaining, and sharing code.
3. *Biopython (https://biopython.org/)*, a set of tools for biological computation in Python.

<u>Installing Python and Jupyter Notebook through the Anaconda Distribution</u>

Install the Anaconda Distribution for your system by following the directions at the following link: https://www.anaconda.com/distribution/

You will need to scroll down towards the bottom to where it says Anaconda Installers and select the installer appropriate for your system.

The Anaconda Distribution comes with Python and Jupyter Notebook.

Running Jupyter Notebook

Open Anaconda Navigator, and then click Launch under the Jupyter Notebook app.

For more information, see https://jupyter.readthedocs.io/en/latest/install.html
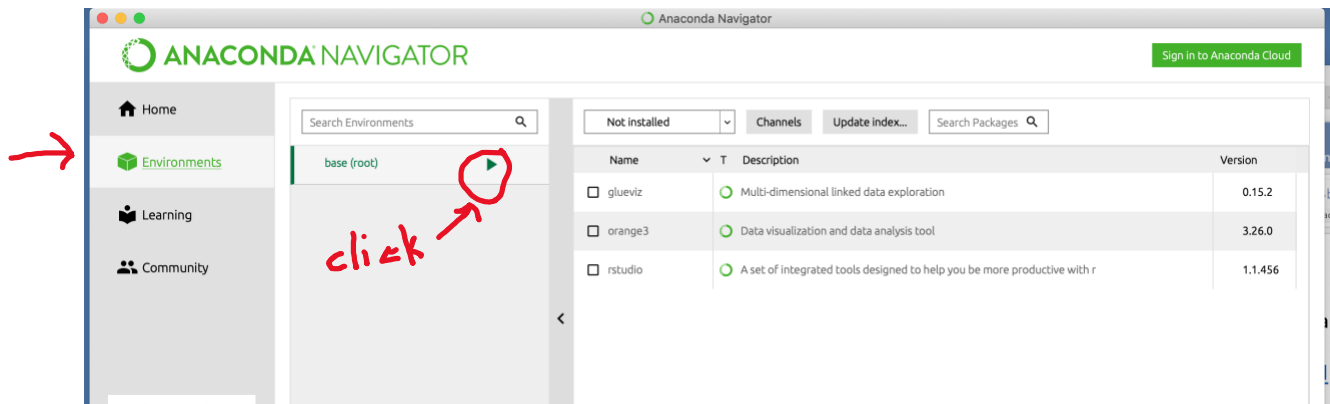
Installing Biopython

Open Anaconda Navigator, then click on Environments on the left hand side, and click on the arrow next to where it says base (root), and select Open Terminal. A screenshot of this is on the next page.

From the terminal, type the following and press enter:

```
conda install -c conda-forge biopython
```

If you are asked to update any packages, type 'y' (without the quotes) and enter to proceed.

After the packages are installed you can exit the terminal.

In order to test whether BioPython has been installed successfully, you can create a code cell in Jupyter Notebook containing the statements below. If you can run the cell without any errors, then BioPython has been installed successfully.

```
from Bio.Seq import Seq
s = Seq('ATGA')
s
```