Initial setup for installing bioinformatics tools on the CRC for Introduction to Biocomputing

- 1. Use ssh to log into the CRC ssh netID@crcfe01.crc.nd.edu
- 2. cd to Private
- 3. mkdir Biocomputing2022
- 4. Inside of Biocomputing2022, mkdir downloads and mkdir tools

Steps for installing Muscle on the CRC for Introduction to Biocomputing

- Go to https://www.drive5.com/muscle/ and click on the MUSCLE v3 link in the lower left
- 2. Right click on the "Linux Intel i86" 64 bit link (second down from top) and "Copy Link Address"
- In a terminal window that is connected to the CRC, make sure you're working directory is ~/Private/Biocomputing2022/downloads
- 4. Run wget <paste the copied url from Muscle> to download the tar.gz file for Muscle
- 5. Unpack the Muscle tar.gz using:
 - a. gzip -d muscle3.8.31 i86linux64.tar.gz
 - b. tar -xf muscle3.8.31 i86linux64.tar
- 6. Move the unpacked binary file to your tools directory:

mv muscle3.8.31_i86linux64 ../tools/muscle

Steps for installing hmmer on the CRC for Introduction to Biocomputing

- 1. Go to http://hmmer.org/download.html
- 2. Right click on the link at the top "[hmmer-3.3.2.tar.gz]" and "Copy Link Address"
- 3. In a terminal window that is connected to the CRC, make sure you're working directory is ~/Private/Biocomputing2022/downloads
- 4. Run wget <paste the copied url from HMMer> to download the tar.gz file for HMMer
- 5. Unpack the HMMer tar.gz using:
 - a. gzip -d hmmer-3.3.2.tar.gz
 - b. tar -xf hmmer-3.3.2.tar
- 6. There should now be a hmmer-3.3.2 directory in downloads. cd into that
- 7. Now that you are in the hmmer-3.3.2 directory, run the following commands:
 - a. ./configure --prefix ~/Private/Biocomputing2022/tools
 - b. make
 - c. make install
- 8. There should now be a bin and share directory in tools, cd to the tools/bin directory
- 9. Move two tools we need from bin to tools
 - a. mv hmmbuild ..
 - b. my hmmsearch ..