Weekly Update

Cappy Pugliese

10/15 – 10/25

Last Week

10/15

- was able to generate the html with fastQC (just needed more memory to run)
- unable to open the html on the cluster
  - tried first to open on a linked local host
    * did not work —> had to trouble shoot
    * was unable to get it to work
- needed to figure out how to send files over to my laptop

10/16

- tried sending file over with filezilla
  - filezilla was being a buttface and not connecting to the transfer node
- tried to use SSHFS software to mirror share files to my laptop
  - was able to get it to work, and am able to move files over to my laptop as well

10/17

- attempted to spend a little bit of time doing some lab work, but got distracted and ended up reorganizing my laptop's directories before I even made it onto the cluster

10/18

- took the day off to catch up on cleaning my apartment and running errands

This Week

10/22

- started to plan out my mock preproposal topic for class

10/23

- was able to access shared lab directory on the cluster
  - tried to create a user directory for myself, but I didn't have permission to do so
  - went back to my own directory
- continued following along with the WNS reanalysis doc
- trimmed sequence with bbduk
- ran the trimmed sequences through fastqc
- looked at the fastqc reports
- attempted to download reference genome
  - ran into problems with prefetching the proper name
  - used url to help with download
  - unsure if I properly downloaded it or not, but it did download something

10/24

- looks like reference genome was downloaded properly
- started to map the sequences
- loaded in a bunch of modules to get the code to work
  - had a bit of trouble at first (loaded in the wrong bwa-mem module)
  - added the modules into .bashrc file and reorganized the file itself
- was able to run the bwa-mem code and got out a bam file
- loaded in the picard module, but did not run the code yet