

Assignment 1

- Download *Hydrozoa.fst* found in this directory
- Take the last 40 nucleotide sequences from this file and put them into a new file using command line tools
- Make the file you just created that contains the 40 sequences read only
- Align the 40 sequences using *clustal* and *muscle* both of which are installed on your virtual machines
- All of the commands you use to generate or modify files should be placed into a script (.sh file with `#!/bin/bash` header)

Questions to answer:

What file format is *Hydrozoa.fst*?

Are the two alignments the same or different? If they are different describe in a sentences how they differ?

Submit your work to me via email, as a tar archive using *tar cvzf* to create a *tar.gz* file (see command line reference on the github page).

Submit all files you generated and a text file (you can generate the text file with nano) with your answers to the questions. Please put all the code you used to generate files and make file modification into a script file (.sh).