Assignment 1

- Download the 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 both *clustal* and *muscle* both of which are installed on your virtual machines

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