

## Assignment 1

- Download *Barcodes.fst* using *wget* from the followin address:  
  
[https://raw.githubusercontent.com/bastodian/2021\\_Bioinformatics/main/Assignment\\_1/Barcodes.fst](https://raw.githubusercontent.com/bastodian/2021_Bioinformatics/main/Assignment_1/Barcodes.fst)
- Take the last 40 nucleotide sequences from this file and put them into a new file using command line tools
- Use *chmod* to make the file you just created read only (ie, remove write permission)
- Align the 40 sequences using *clustalw* and *muscle* both of which we 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 Barcodes.fst?**

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

Submit your script and answers to me via email by Wed, Sep 15, 2021.