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Introduction to Computational Biology

Work Documentation One

Week of January 16, 2024- January 18, 2024
(January 18.)(Unix Tutorial) I started the Unix Tutorial worksheet and found out and learned some very interesting concepts and ideas. I had first become confused when I tried to figure out how to make a directory in the student directories and ran the code wrong many times. I had placed the file in the wrong folder and accidentally added a space after "triana_sanmiguel" so when I tried to "cd triana_sanmiguel" it would never work and gave me the error "this directory does not exist". I then made an alias to my own personal directory by using the "% alias cd triana_sanmiguel='cd /stor/work/Bio321G_RY_Spring2023/StudentDirectories/triana_sanmiguel". After this I completed half of the Unix tutorial worksheet. This was done outside of class with the tips I had learned from the mentors.

Week of January 23, 2024- January 25, 2024
(January 22, 2024)(Unix Video) After last week's class I realized that I was still confused on a couple topics from edupod and Unix itself. Therefore, I watched the Unix Tutorial for beginners youtube videos and learned many tips from it. For example, I learned how to be able to find the number of sequences in a certain file and also how many lines it contained. (January 23, 2024)(Central Dogma Activity) I completed this activity right before the beginning of class to learn more about the concepts of the Central Dogma and what players and processes are important to Intermolecular Biology. I reinstated my previous knowledge about the flow of genetic information from DNA to RNA or from RNA directly to the protein itself.

Week of January 30, 2024-February 1, 2024
(January 30 2024) After going to class and getting shown tips and tricks on how to be more comfortable with Public Speaking I decided to look up some videos to continue my journey with trouble with speaking in front of others. I watched [7 Public Speaking Tips for Beginners - YouTubewww.youtube.com](https://www.youtube.com) which made me feel a lot better about Public Speaking by giving me tips such as always make good eye contact, keep your head up high, and if you make a mistake its okay as long as you move past it. (February 1, 2024)(Evolution) I knew that we would be going over Evolution in class so I knew I would have to do some research to prepare for it. I went to the extra resources for Evolution and went to the website where I studied Evolution 101, Understanding homology and convergent evolution, and the Tree room, where I got a deep dive on Evolution and how animals and plants are connected.

Week of February 5, 2024-February 8, 2024

(February 5)(R for the Intimidated) I was very confused about the concept of R even after class so I decided to watch some of the videos provided such as "Basic Functions","Naming Structures", and "Vectors Lesson One". The Basic Function one was pretty simple with tips on how to import data sets, what each of the folders meant, and how to run code itself. However the naming structures and vectors lesson one video really did confuse me so I decided to ask about it in mentor meetings. (Febuary 8)(TidyVerse). I struggled with the installation of tidyverse and rmarkdown on my computer so I decided to look up articles that could come to my aid. From the https://cran.r-project.org/web/packages/tidyverse/index.html website I was able to learn more about tidyverse and how this package can aid in my overall coding experience

Week of February 12, 2024-February 16, 2024

(February 12)(Problem Set 1) This problem set was very tricky. I struggled to fix the permissions of the fasta file because my terminal keep on copying my data files from my statistics class to this FRI class. To fix this problem I had to perform all my code on R Studio. There I figured out how to utilize nano and bash scripting in order to code for the amount of sequences in the file. I also used bash to code for the amount of times that my name appeared in the fasta file.

```
#!/bin/bash
cp /stor/work/Bio321G_RY_Spring2024/Genes_IndividualProject/SticklebackSequences_Assigned.fasta .
mv SticklebackSequences_Assigned.fasta DNA4.fasta
grep -c ">" DNA4.fasta
grep -A1 Triana_San_Miguel DNA4.fasta | grep -v Triana_San_Miguel > TrianaSequence.txt
wc -l TrianaSequence.txt
```

This code aided me in realizing both question 3 and 4. I then went to the ensemble to find out the code process for the Stickleback fish gene and how the ensemble itself worked.