**Lecture 1:**

1. Set up your computer. Done
2. Follow the installation instructions. Done
3. How can you tell that you were successful?  I can tell I was successful by running doctor.py. If it generates a similar output in the book and confirms that all the tools I installed are functioning correctly, then I know everything was set up properly.
4. Can you run the **samtools** program?
5. What version is your **samtools** program?

samtools 1.20

1. Share the link to your GitHub repository that you have set up.

https://github.com/Ewura-Esi/BMMB-852\_Project

**Lecture 2:**

1. Describe a Unix command not discussed in the class or the book. Try to find something that might be useful. When would you use that command?

Chmod. I would use the chmod command when I need to change the permissions of a file or directory. For instance, if I want to give a colleague access to edit a file we are collaborating on, or if I need to restrict access to my personal work in a group folder, I can modify the permissions accordingly using chmod.

1. Describe a customization for the command you chose above (describe the effect of a flag/parameter).

A customization for the chmod command is the use of numeric codes to specify the exact permissions. For example, using **chmod 755 filename** sets the permissions so that the owner can read, write, and execute the file (7), while others can only read and execute (5).

1. What flags will make the **ls** command write out the files sizes in “human-friendly” mode?

-h

1. What flag will make the **rm** command ask for permission when removing a file?

-i

1. Create a nested directory structure. Create files in various directories.

**Nested Directory Structure**

**`mkdir -p assignment1/section1/setA assignment1/section1/setB assignment1/section2/setC assignment1/section2/setD`**

Assuming I would like to create files in the setA,setB,setC and setD directories, I will use the following command

touch assignment1/section1/setA/file1.txt assignment1/section1/setB/file2.txt assignment1/section2/setC/file3.txt assignment1/section2/setD/file4.txt

List the absolute and relative path to a file.

Absolute path: /home/biouser/assignment1/section1/setA/file1.txt

Assuming my current directory is assignment1, then the relative path to file1 will be: section1/setA/file1.txt

1. Demonstrate path shortcuts using the **home directory**, **current directory**, and **parent directory**.

Home directory -I can navigate from anywhere in the system to my home directory using the command `cd ~`

Current directory – To demonstrate path shortcuts using the current directory, I can use the `.` symbol, which represents the directory you are currently in. For example, I can list all files and directories in the current directory using `ls .`

Parent directory. I can use this shortcut to navigate to the parent directory `cd ..` For example, If I am in /assignment1/section1/setA and want to go up one level (i.e to the parent directory (i.e. to the parent directory section1) to /assignment1/section1, I can type `cd ..`