**1. How many sequences are in lab2\_nucleotide.fasta? How many sequences are in lab2\_protein.fasta? Give the command and the number of sequences for each fasta file.**

**There are 4 Sequences in the lab2\_nucleotide.fasta**

The command i used to get this is grep -c ”>” lab2\_nucleotide.fasta

**2. Give the sed command to replace “lab 2” with your name in lab2file1.txt.**

gsed -i 's/lab 2/Chloe/g' lab2file1.txt

(MAC)

**3. Give the sed command to delete lines containing the word “this” in lab2file1.txt.**

gsed '/this/d' lab2file1.txt

**4. Give the sed command to convert lab2\_nucleotide.fasta to lowercase.**

gsed 's/[A-Z]/\l&/g' lab2\_nucleotide.fasta

**5. Give the sed command to convert lab2file1.txt to uppercase.**

gsed 's/[a-z]/\U&/g' lab2\_nucleotide.fasta

**6. Give the grep command that counts all AT and GC in lab2\_nucleotide.fasta. How many are there?**

egrep -o "AT|GC" lab2\_nucleotide.fasta| wc -l

98

**7. Give the sed command that deletes lines with the last word being “text” in lab2file1.txt**

gsed '/text$/'d lab2file1.txt

**8. Give the grep command to count the number of lines in lab2\_protein.fasta that start with “M”. How many are there?**

grep -o "^M" lab2\_protein.fasta |wc -l

There are 7

**9. Give the grep command to print the lines and line numbers in lab2\_protein.fasta that DO NOT start with “M”.**

egrep -nv "^M" lab2\_protein.fasta

**10. Give the grep command to print out lines in lab2\_protein.fasta that contain “T\_\_A”, where the empty spaces can be any single character.**

grep --color "T..A" lab2\_protein.fasta

**BONUS 1 (2 pts): Give an awk command to display Sequence 4 through 6 (including headers) in lab2\_protein.fasta.**

**BONUS 2 (2 pts): Give an awk command to find the longest line in lab2\_protein.fasta. What is the length?**

**Bonus 3 (1 pt): Do any question in any other language (Python, Java, C, C++, C#, Rust, etc.) (please no Perl or Ruby). Please specify the question you are doing.**