1. grep -c "^>" lab2\_nucleotide.fasta : # of sequences=4

grep -c "^>" lab2\_protein.fasta

2. sed -i 's/lab 2/Max/g' lab2file

3. sed -i '/this/d' lab2file1.txt

4. sed -I ‘s/[A-Z]/\L&/g’ lab2\_nucleotide.fasta

5. sed -i 's/[a-z]/\U&/g' lab2\_file1.txt

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

Amount: 98

7. sed -i '/text$/d' lab2file1.txt

8. grep “^M”

9. grep [^M] lab2\_nucleotide.fasta

10. grep -eo "T[A-z]|[A-z]A" lab2\_protein.fasta