**Task 1: Biocomputing using Bash**

1. To print my name

echo Akinjide

2. To create a folder titled my name

mkdir Akinjide

3. To create another new directory titled ‘biocomputing’ and change to that directory with one line of command

mkdir biocomputing && cd biocomputing

4. To download the files

wget https://raw.githubusercontent.com/josoga2/dataset-repos/main/wildtype.fna /

https://raw.githubusercontent.com/josoga2/dataset-repos/main/wildtype.gbk /

https://raw.githubusercontent.com/josoga2/dataset-repos/main/wildtype.gbk

5. To move the ‘.fna’ file to the folder titled my name

mv \*.fna ../Akinjide

6. To delete the duplicate ‘gbk’ file

rm \*.gbk.\*

7. To confirm if the ‘.fna’ file is mutant ot wildtype

grep -q 'TATATATA' wildtype.fna && echo "Mutant" || echo "Wild type"

8. To count the number of lines excluding header in the ‘.gbk’ file

lines\_with\_header=$(wc -l wildtype.gbk | awk '{print $1}')

lines=$((lines\_with\_header - 1))

echo 'There are' $lines 'lines in the gbk file'

9. To print the sequence length of the ‘.gbk’ file using the LOCUS tag in the first line

echo "Sequence length:" $(awk '/^LOCUS/ {print $3}' wildtype.gbk)

10. To print the source organism  
echo "Source organism:" $(grep '^SOURCE' wildtype.gbk | awk '{print $2, $3}')

11. To list all the gene names of the source organism

echo "all the genes for our source organism are" $(grep '/gene=' wildtype.gbk | sed 's/\/gene\=/ /')

12a. To clear the terminal space

ctrl + l

12b. To print all commands used

history

13. To list the files in the two folders

ls Akinjide/ biocomputing/

**Task 2: Installing Bioinformatics software on the terminal**

1. Activate base conda enironment

conda activate

2. Create a conda environment named ‘funtools’

conda create --name 'funtools'

3. Activate the ‘funtool’ environment

conda activate funtools

4. Install figlet using apt-get

sudo apt-get update && sudo apt-get install figlet

5. Run ‘figlet (Akinjide)’

figlet Akinjide

6. Install softwares through bioconda channel

conda install -c bioconda bwa blast samtools bedtools spades bcftools fastp multiqc