**#Coding: Linux & BASh Fundamentals**

#Project 1

#Print your name

echo “Oluwaseyi\_Ashaka”

#Create a folder titled your name

mkdir Oluwaseyi\_Ashaka

#Create another new directory titled biocomputing and change to that directory with one line of command

mkdir biocomputing && cd biocomputing

#Download these 3 files:

#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

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

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

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

#Move the .fna file to the folder titled your name

mv \*.fna ~/Oluwaseyi\_Ashaka/

#Delete the duplicate gbk file

rm \*gbk.1

#Confirm if the .fna file is mutant or wild type (tatatata vs tata)

grep tatatata wildtype.fna

grep tata wildtype.fna

#If mutant, print all matching lines into a new file

grep tatatata wildtype.fna > mutant\_1.txt

#Count number of lines (excluding header) in the .gbk file

grep -v LOCUS wildtype.gbk |wc -l

#Print the sequence length of the .gbk file. (Use the LOCUS tag in the first line)

grep LOCUS wildtype.gbk

#Print the source organism of the .gbk file. (Use the SOURCE tag in the first line)

grep SOURCE wildtype.gbk

#List all the gene names of the .gbk file. Hint {grep '/gene='}

grep '/gene=' wildtype.gbk

#Clear your terminal space and print all commands used today

clear

history

ls biocomputing/ Oluwaseyi\_Ashaka/

#Project 2

#Activate your base conda environment

conda activate

#create a conda environment named funtools

conda create -n funtools python=3.10

#Activate the funtools environment

conda activate funtools

#Install Figlet using conda or apt-get

conda config --add channels conda-forge

conda config --set channel\_priority strict

conda install pyfiglet

sudo apt-get install figlet

#Run figlet <your name>

figlet Oluwaseyi Ashaka

#Install bwa through the bioconda channel

conda install bwa

#Install blast through the bioconda channel

conda install blast

#Install samtools through the bioconda channel

conda install samtools

#Install bedtools through the bioconda channel

conda install bedtools

#Install spades.py through the bioconda channel

conda create -n spades\_env spades

conda install spades

#Install bcftools through the bioconda channel

conda install bcftools

#Install fastp through the bioconda channel

conda install fastp

#Install multiqc through the bioconda channel

conda config --add channels bioconda

conda config --add channels conda-forge

conda config --set channel\_priority strict

conda create --name myenv python=3.11

conda activate myenv

conda install multiqc