1. echo AGENYI\_GODWIN

# to print name

1. mkdir AGENYI\_GODWIN

# to create folder titled name

1. mkdir biocomputing

# to create new folder ‘biocomputing’

cd biocomputing

# to change to the new folder with a single command

1. 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>

# to download files

1. mv wildtype.fna AGENYI\_GODWIN

# to move file to folder

1. rm wildtype.gbk

# to remove duplicate file

1. grep ‘tatatata’ wildtype.fna

# to scan file to confirm if mutant

1. grep ‘tatatata’ wildtype.fna > mutant\_file.txt

# to print all matching line into a new file

1. tail –n +2 wildtype.gbk.1 | wc -l

# to count number of lines excluding header in .gbk file

1. awk ‘/LOCUS/ {print $3}’ wildtype.gbk

# to print the sequence length of the .gbk file

1. grep ‘^SOURCE’ wildtype.gbk | head –l

# to print source organism of .gbk file

1. grep ‘/gene=’ wildtype.gbk

# to list gene names of .gbk file

1. clear

# to clear terminal space

history # to print all command used

1. ls

cd ../

ls

# to list files in folders

Project 2

1. wget <https://repo.anaconda.com/miniconda/Miniconda3-latest-Linux-x86_64.sh>

bash Miniconda3-latest-Linux-x86\_64.sh

# to activate base conda environment

conda config --add channels defaults

conda config --add channels bioconda

conda config --add channels conda-forge

# to configure channels for bioinformatics

1. conda create -n funtools python=3.10

# to create conda environment

1. conda activate funtools

# to activate funtools environment

1. sudo apt install figlet

# to install figlet

1. figlet ‘AGENYI\_GODWIN’

#to run figlet

1. conda deactivate

#to deactivate funtools

1. conda install bwa

# to install bwa through biconda channel

1. conda install blast

# to install blast through biconda channel

1. conda install samtools

# to install samtools through biconda channel

1. conda install bedtools

# to install bedtools through biconda channel

1. conda install spades.py

# to intall spades.py through biconda channel

1. conda install bcftools

# to install bcftools

1. conda install fastp

# to install fastp

1. conda install multiqc

# to install multiqc