Project 1; BASh Basic

79 #!/bin/bash

80 #NGS Practice Script-Kefeletswe Majoka

81 #print your name

82 echo "Kefeletswe Majoka"

83 #create directories

84 mkdir -p Kefeletswe

85 mkdir -p biocomputing

86 cd biocomputing || exit

87 #Download files

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

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

90 #Move.fna file to Kefeletswe folder

91 mv wildtype.fna ../Kefeletswe/

92 #Delete duplicate wildtype.gbk.1 file

93 #Delete duplicate wildtype.gbk.1 file

94 rm -i wildtype.gbk.1

95 #check mutant or wildtype in .fna

96 if grep -qi "tatatata" ../Kefeletswe/wildtype.fna; then echo "Mutant"; grep -i "tatatata" ../Kefeletswe/wildtype.fna > mutant\_lines.txt; echo "Mutant lines saved to mutant\_lines.txt"; else echo "Wild type"; fi

97 #count number of lines in wildtype.gbk(excluding LOCUS header)

98 grep -v "^LOCUS" ../Kefeletswe/wildtype.gbk | wc -l

99 grep -v "^LOCUS" ../biocomputing/wildtype.gbk | wc -l

100 grep -v "^LOCUS" ./biocomputing/wildtype.gbk | wc -l

101 grep -v "^LOCUS" ../biocomputing/wildtype.gbk | wc -l

102 #print sequence lenght from LOCUS line

103 lsildtype.gbk | wc

104 #print sequence length from LOCUS line

105 grep "^LOCUS" ../biocomputing/wildtype.gbk | '{gsub(/[^0-9]/,"",$3); print $3}'

106 grep "^LOCUS" ../Kefeletswe/biocomputing/wildtype.gbk | '{gsub(/[^0-9]/,"",$3); print $3}'

107 #Print source organism from SOURCE line

108 grep "^SOURCE" ../biocomputing/wildtype.gbk | cut -d' ' -f2-

109 #List all gene names and save to a file

110 grep '/gene=' ../biocomputing/wildtype.gbk | sed 's/\/gene="//;s/"//' > gene\_names.txt

111 echo "Gene names saved to gene\_names.txt"

112 #clear terminal space

Project 2: Installing Bioinformatics Software on the terminal

1 wget https://repo.anaconda.com/miniconda/Miniconda3-latest-Linux-x86\_64.sh

2 #activate base environment

3 conda activate base

4 #create conda environemt named funtools

5 conda create -n funtools

6 #activate the funtools environment

7 conda activate funtools

8 #install Figlet using apt-get

9 sudo apt-get update

10 sudo apt-get install filler

11 condo list | grep filler

12 apt list --installed | grep filler

13 sudo apt-get remove --purge filler -y

14 sudo apt-get autoremove -y

15 #install figlet

16 #install figlet with apt-get

17 sudo apt-get update

18 sudo apt-get install figlet -y

19 #check figlet installation

20 figlet MAJOKA

21 figlet Tshephe

22 which figlet

23 figlet am the best

24 #install bwa through the bioconda channel

25 conda activate funtools

26 conda install -c bioconda bwa

27 #verify installation

28 bwa

29 #install blast through the bioconda channel

30 conda install -c bioconda blast

31 #verifying installation

32 blastn -version

33 #install santos through the bioconda chann

34 #install samtools through bioconda

35 conda install -c bioconda samtools

36 #verify installation

37 samtools --version

38 #install bedtools

39 conda install -c bioconda bedtools

40 #check bedtoolls installation

41 bedtools --version

42 #install spades.py through bioconda

43 conda install -c bioconda spades

44 #verify

45 spades.py --version

46 #install bcftools through bioconda

47 conda install -c bioconda bcftools

48 #install fastq

49 conda install -c bioconda fastqc

50 #verify installation

51 fastqc --version

52 #install multiqc through bioconda channel

53 conda install -c bioconda multiqc

54 #creating space by cleaning conda caches and temporary files

55 conda clean -a -y && sudo apt-get clean && sudo apt-get autoremove -y && rm -rf /tmp/\* ~/Downloads/\*

56 #check space availability

57 df -h

58 #install multiqc

59 condo install -c bioconda multiqc

60 conda install -c bioconda multiqc

61 #verify multiqc installation

62 multiqc --version

63 #checking github

64 git --version

65 `gcloud projects list`

66 history

(base) kefeletswemajoka@cloudshell:~$