1 echo Gilbert

2 mkdir Gilbert

3 ls

4 mkdir biocomputing && cd biocomputing

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

6 ls

8 ls

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

10 ls

11 mv wildtype.fna ../Gilbert

12 ls

13 rm wildtype.gbk.1

14 ls

15 cd ../Gilbert

16 ls

17 grep "tatatata" wildtype.fnat

18 grep "tatatata" wildtype.fna

19 grep "tata" wildtype.fna

20 grep "tatatata" wildtype.fna > matchinglines\_outputs.txt

21 ls

22 cd ../biocomputing/

23 ls

24 tail -n +2 wildtype.gbk | wc -l

25 grep "^LOCUS" wildtype.gbk | awk '{print $3}'

26 grep "^SOURCE" wildtype.gbk | awk '{$1=""; print $0}'

27 grep '/gene=' wildtype.gbk

28 clear && history