COMPUTER OPERATING SYSTEM – BIOINFORMATICS ANALYSIS

Compare protein sequences of non-pathogenic strain and pathogenic strain using BLAST in Linux Ubuntu

· Install blast+

```
amizah@DESKTOP-E00L91N:~$ sudo apt-get update
[sudo] password for hamizah:
Hit:1 http://archive.ubuntu.com/ubuntu focal InRelease
Get:2 http://security.ubuntu.com/ubuntu focal-security InRelease [114 kB]
Get:3 http://archive.ubuntu.com/ubuntu focal-updates InRelease [114 kB]
Get:4 http://archive.ubuntu.com/ubuntu focal-backports InRelease [108 kB]
Get:5 http://security.ubuntu.com/ubuntu focal-security/main amd64 Packages [1178 kB]
Get:6 http://archive.ubuntu.com/ubuntu focal-updates/main amd64 Packages [1510 kB]
Get:7 http://security.ubuntu.com/ubuntu focal-security/main amd64 c-n-f Metadata [9132 B]
Get:8 http://security.ubuntu.com/ubuntu focal-security/universe amd64 Packages [677 kB]
Get:9 http://archive.ubuntu.com/ubuntu focal-updates/main amd64 c-n-f Metadata [14.7 kB]
Get:10 http://archive.ubuntu.com/ubuntu focal-updates/universe amd64 Packages [894 kB]
Get:11 http://archive.ubuntu.com/ubuntu focal-backports/universe amd64 Packages [20.8 kB]
Get:12 http://archive.ubuntu.com/ubuntu focal-backports/universe Translation-en [14.3 kB]
Fetched 4654 kB in 14s (334 kB/s)
Reading package lists... Done
namizah@DESKTOP-E00L91N:~$ sudo apt-get install ncbi-blast+
Reading package lists... Done
Building dependency tree
Reading state information... Done
ncbi-blast+ is already the newest version (2.9.0-2).
0 upgraded, 0 newly installed, 0 to remove and 101 not upgraded.
```

Download NC_000913.fasta and NC_002655.fasta

a. Create a folder "os project"

```
hamizah@DESKTOP-E00L91N:~$ ls
NC_000913.fasta NC_002655.fasta
hamizah@DESKTOP-E00L91N:~$ mkdir os_project
hamizah@DESKTOP-E00L91N:~$ ls
NC_000913.fasta NC_002655.fasta os_project
```

b. Move downloaded "NC_00913.fasta" and "NC002655.fasta" into the folder "os project"

```
hamizah@DESKTOP-E00L91N:~$ mv NC_000913.fasta NC_002655.fasta os_project
hamizah@DESKTOP-E00L91N:~$ ls
os_project
hamizah@DESKTOP-E00L91N:~$ cd os_project
hamizah@DESKTOP-E00L91N:~/os_project$ ls
NC_000913.fasta NC_002655.fasta
```

c. Change filename "NC_00913.fasta" to "ecoli-k12.fasta" and filename "NC_002655.fasta" to "ecoli-h7.fasta"

```
hamizah@DESKTOP-E00L91N:~/os_project$ my NC_000913.fasta ecoli-k12.fasta
hamizah@DESKTOP-E00L91N:~/os_project$ my NC_002655.fasta ecoli-h7.fasta
hamizah@DESKTOP-E00L91N:~/os_project$ ls
ecoli-h7.fasta ecoli-k12.fasta
```

d. Set up a database file for E.coli K12. The command to use is "makeblastdb" from the BLAST+ package

```
namizah@DESKTOP-E08L91N:~/os_project$ makeblastdb -in ecoli-k12.fasta -dbtype prot -title "E.coli K12 Database" -out ecoli-k12db -parse_seqids

Building a new DB, current time: 01/28/2022 06:08:38

New DB name: /home/hamizah/os_project/ecoli-k12db

New DB title: E.coli K12 Database

Sequence type: Protein

Keep MBits: T

Maximum file size: 10000000000

Adding sequences from FASTA; added 20 sequences in 0.081609 seconds.

hamizah@DESKTOP-E08L91N:~/os_project$ 1s
ecoli-h7.fasta ecoli-k12.fasta ecoli-k12db.phr ecoli-k12db.pin ecoli-k12db.pog ecoli-k12db.psd ecoli-k12db.psi ecoli-k12db.psq
```

e. BLAST "ecoli-h7.fasta" protein sequence against "ecoli-k12.fasta" using program "blastp" in blast+ package and export the query result as "h7vsk12.txt". Please note that you should use e-value 0.00001 for your blast query.

```
hamizah@DESKTOP-E00L91N:~/os_project$ blastp -db ecoli-k12db -query ecoli-h7.fasta -out h7vsk12.txt -evalue 0.00001
hamizah@DESKTOP-E00L91N:~/os_project$ ls
ecoli-h7.fasta ecoli-k12.fasta ecoli-k12db.phr ecoli-k12db.pin ecoli-k12db.pog ecoli-k12db.psd ecoli-k12db.psi ecoli-k12db.psq h7vsk12.txt
```

f. Use "awk" and "egrep" to extract the first 20 annotated proteins.

```
namizah@DESKTOP-E08L91N:~/os_project$ awk '/Query=/ ||/No hits/{print}' h7vsk12.txt | awk '{i++;line[i]=$0; if($0~/No hits/){print line[i-1]}}' | egrep -v "([Uu]nknown) | [Pp]utative | [Hh]ypothetical" | head -20 Query= AAG59188.2 thiamin biosynthesis, probable sulfur donor [Escherichia Query= AAG57887.2 lipoprotein-34 [Escherichia coli 0157:H7 str. E01933]
Query= AAG57887.2 pyridoxal/pyridoxal/pyridoxamine kinase [Escherichia Query= AAG57281.2 cytidine/deoxycytidine deaminase [Escherichia coli
```

• Brief description of final output

```
Query= AAG59188.2 thiamin biosynthesis, probable sulfur donor [Escherichia Query= AAG57587.2 lipoprotein-34 [Escherichia coli 0157:H7 str. EDL933] Query= AAG57537.2 pyridoxal/pyridoxine/pyridoxamine kinase [Escherichia Query= AAG57281.2 cytidine/deoxycytidine deaminase [Escherichia coli
```

The final output displays 4 protein sequences in the first 20 annotated proteins that present in the pathogenic strain *E.coli O157:H7* but not in the nonpathogenic strain *E.coli K12*.