Assignment Nr. 10

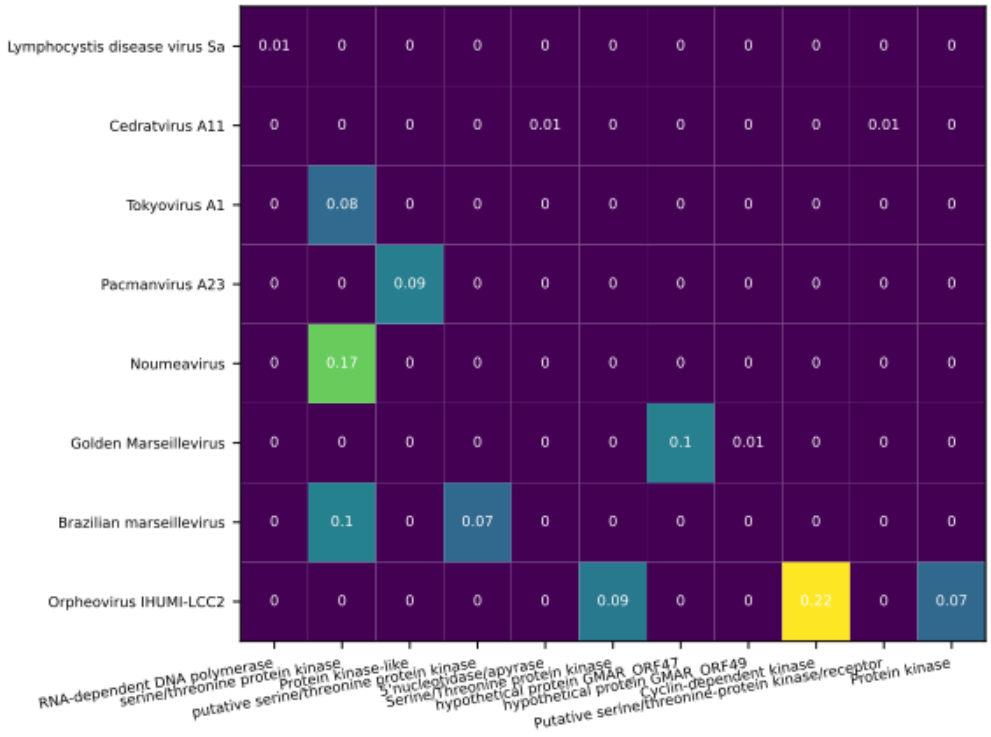
(Deadline 26.01.2020)

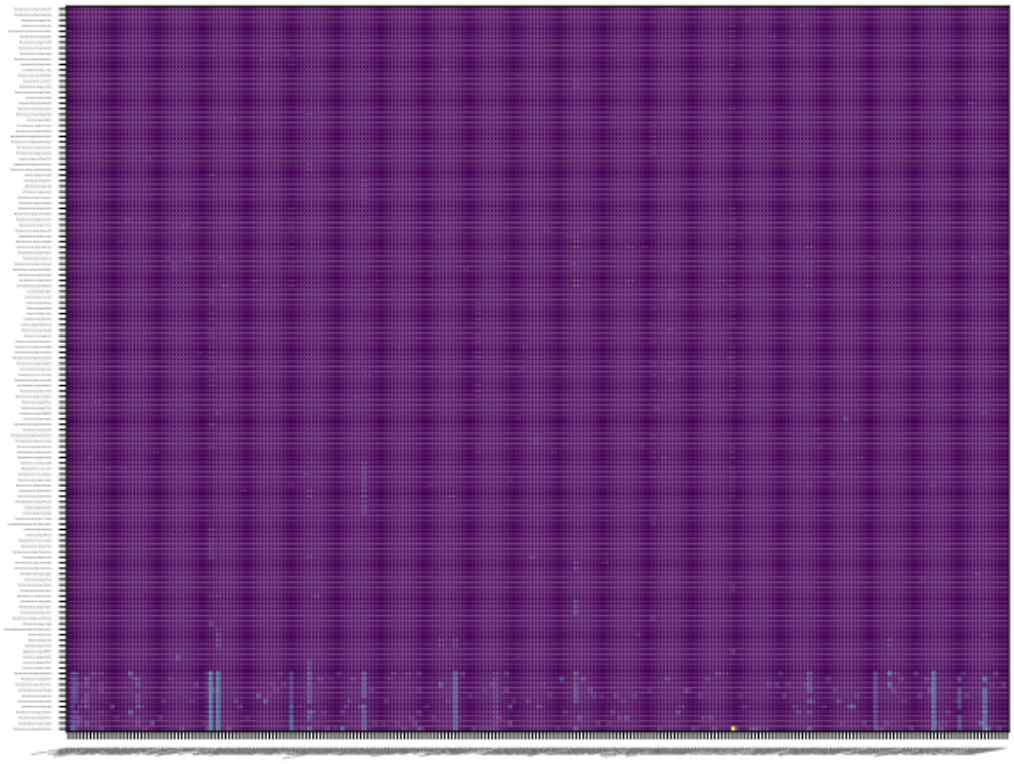
Task 5

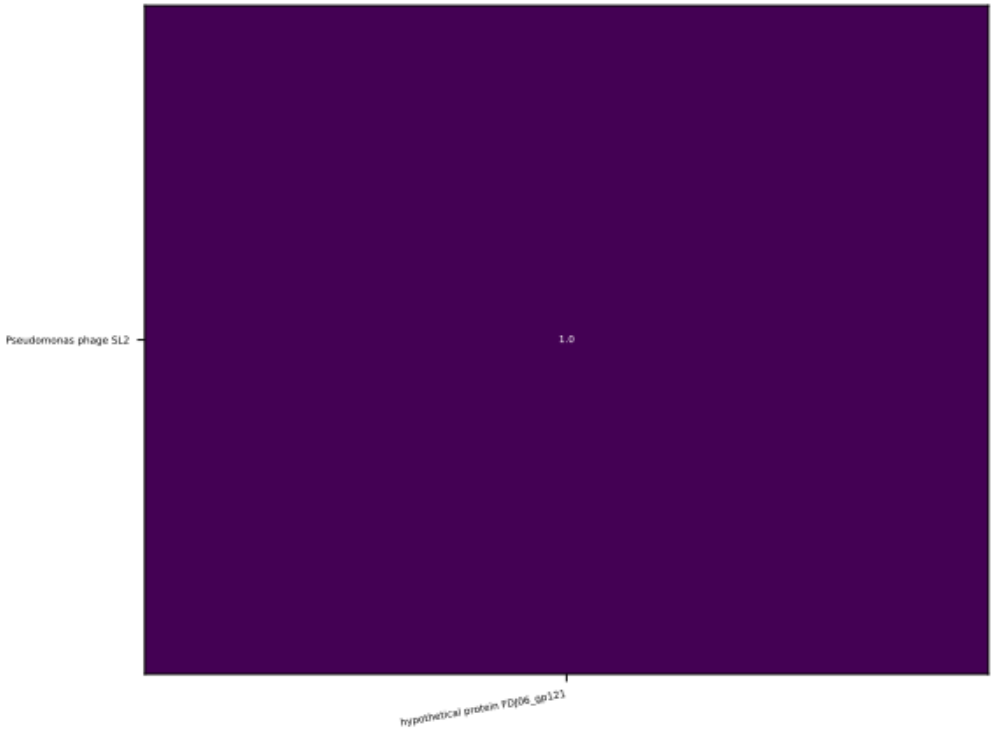
The 10 samplealignments got produced with the following commandline:

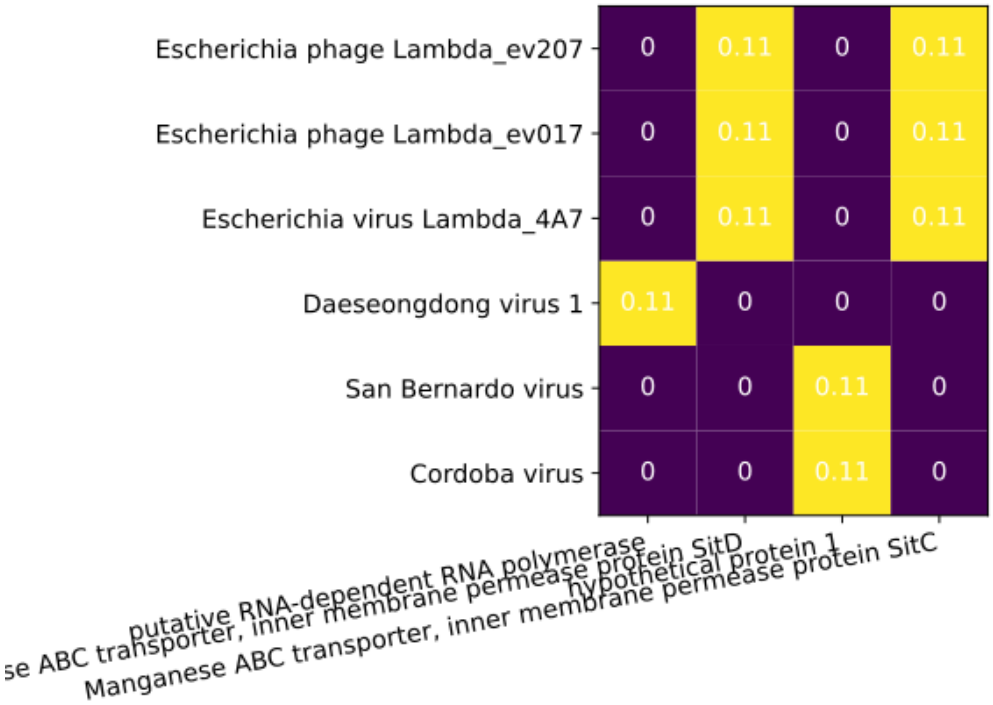
diamond blastx -q sample02.fasta -d viral -o sampleXXalignment.fasta -k0 -f6 stitle

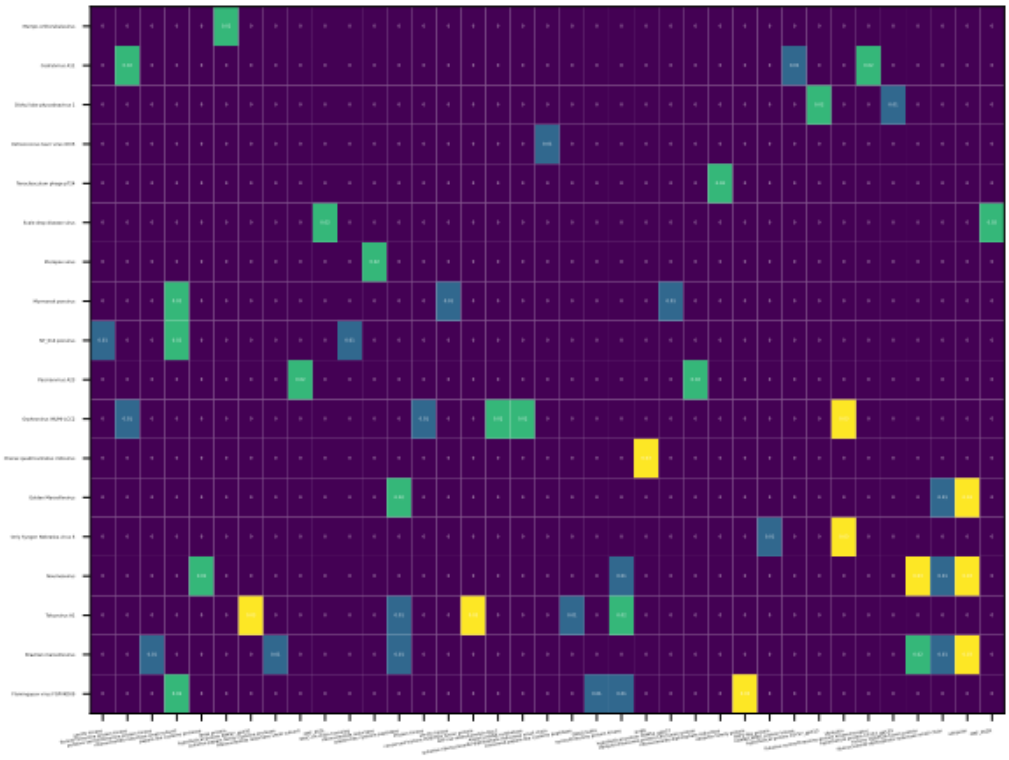
So because we got 10 fastq datafiles, we used the blastx mode for the alignment against the produced database called viral.dmnd. So to get all hits (at most 1) we use the -k0 comand and the -f6 stitle command to only get the names of the matches and not the sequences.






Pseudomonas phage SL2
1.0
hypothetical protein YDJ06_gp121


Escherichia phage Lambda_ev207
Escherichia phage Lambda_ev017
Escherichia virus Lambda_4A7
Daeseongdong virus 1
San Bernardo virus
Cordoba virus
0 0.11 0 0.11
0 0.11 0 0.11
0 0.11 0 0.11
0.11 0 0 0
0 0 0.11 0
0 0 0.11 0
se ABC transporter, inner membrane permease protein SitD
putative RNA-dependent RNA polymerase
Manganese ABC transporter, inner membrane permease protein SitC
hypothetical protein 1



So in the following tabel we summerized the viruses we think is the aligned one. For some samples no hits can be recogniced.

Sample Heatmap	Organism
1	Noumeavirus
2	no hit
3	no hit
4	Microbacterium phage nephthea
5	Phoydomonas phage SL2
6	Escheria phage Lambda$_e v207, Escheriaphage Lambda_e v017, Escheriavirus Lambda_4 A$
7	no hit
8	no hit
9	no hit
10	Nouveavirus