

1

1.a

DNA Identity Matrix

	Bat CoV	Bat CoV RATG13	MERS CoV	P-CoV	SARS-CoV2	SARS-CoV
Bat CoV	-	25.51	23.29	41.77	24.56	25.45
Bat CoV RATG13	25.51	-	30.44	75.94	92.68	67.57
MERSCoV	23.39	30.44	-	48.10	29.46	30.84
P-CoV	41.77	75.94	48.10	-	82.28	62.02
SARS-CoV2	24.56	92.68	29.46	82.28	-	65.37
SARS-CoV	25.45	67.57	30.84	62.02	65.37	-

The closest relatives are:

- SARS-CoV2 with RATG13 (92.68%)
- SARS-CoV2 with P-CoV (82.28%)

Protein Identity Matrix

	Bat CoV	Bat CoV RATG13	MERS CoV	P-CoV	SARS-CoV	SARS-CoV2
Bat CoV	-	18.44	18.55	30.77	18.56	18.22
Bat CoV RATG13	18.44	-	23.40	84.61	74.58	97.47
MERSCoV	18.55	23.40	-	23.08	26.06	26.47
P-CoV	30.77	84.61	23.08	-	73.08	84.62
SARS-CoV	18.56	74.58	26.06	73.08	-	73.94
SARS-CoV2	18.22	97.47	26.47	84.62	73.94	-

The closest relatives are:

- SARS-CoV2 with RATG13 (97.47%)
- SARS-CoV2 with P-CoV (84.62%)

1.b

The possible source of origin could be deduced with the sequence having the highest level of percentage identity.

- Possible source of origin for SARS-CoV2 is RATG13
- Possible source of origin for MERSCoV is P-CoV

2

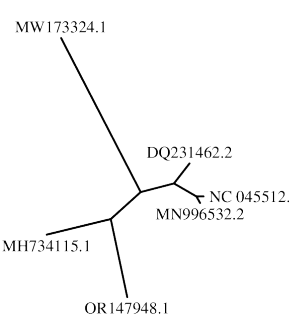


Figure 1: No bootstrap DNA pars tree

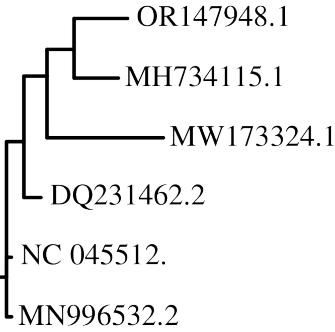


Figure 2: No bootstrap DNA pars gram

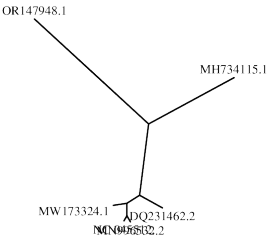


Figure 3: No bootstrap DNA ml tree



Figure 4: No bootstrap DNA ml gram

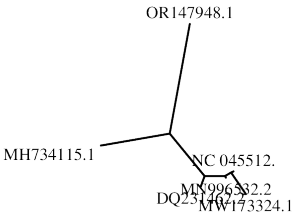


Figure 5: No bootstrap DNA dist tree



Figure 6: No bootstrap DNA dist gram

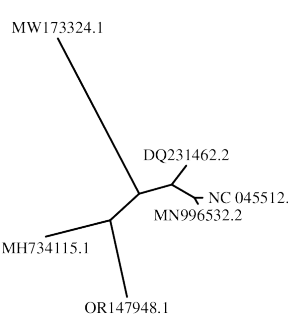


Figure 7: bootstrap DNA pars tree

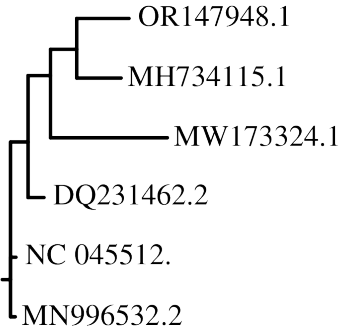


Figure 8: bootstrap DNA pars gram

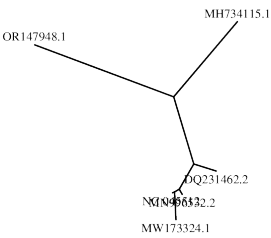


Figure 9: bootstrap DNA ml tree



Figure 10: bootstrap DNA ml gram

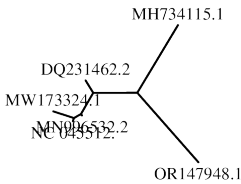


Figure 11: bootstrap DNA dist tree



Figure 12: bootstrap DNA dist gram

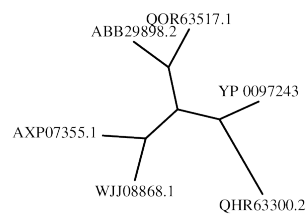


Figure 13: No bootstrap prot pars tree

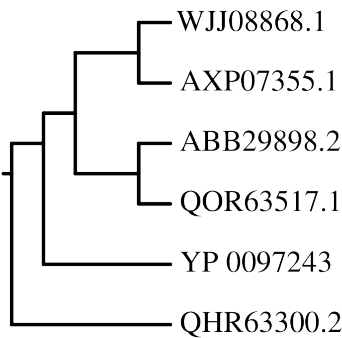


Figure 14: No bootstrap prot pars gram

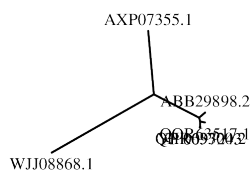


Figure 15: No bootstrap prot ml tree



Figure 16: No bootstrap prot ml gram

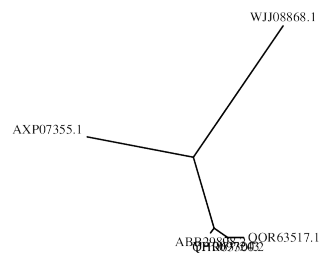


Figure 17: No bootstrap prot dist tree

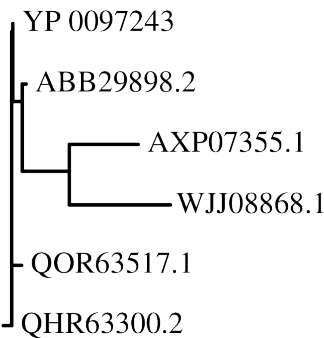


Figure 18: No bootstrap prot dist gram

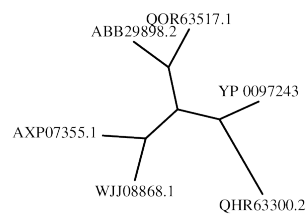


Figure 19: bootstrap prot pars tree

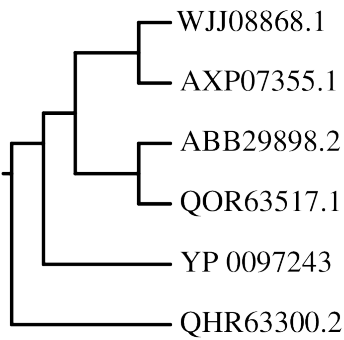


Figure 20: bootstrap prot pars gram

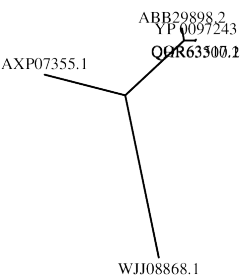


Figure 21: bootstrap prot ml tree

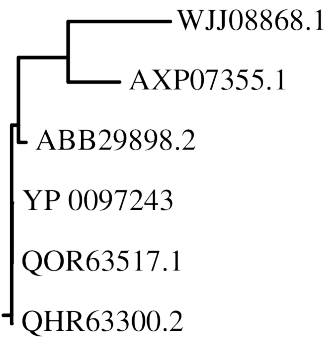


Figure 22: bootstrap prot ml gram

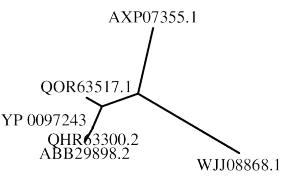


Figure 23: bootstrap prot dist tree



Figure 24: bootstrap prot dist gram

2.a

The trees obtained by different methods are mostly in agreement topology wise. We can come to this conclusion by observing that the relative depth between the sequences are almost always the same in case of all the trees.

2.b

- Yes, there are slight differences with and without bootstrapping. In some cases, the depth is not as high in the bootstrapped version. This means that bootstrapping avoids alignments by chance.
- Bootstrapping allows for the tree depth constructed to be more robust. It allows for the samples to better represent the variations in the group. The information it provides is that it allows us to infer the confidence of the depth of the sequences.

2.c

Yes, the inferences made in the previous question are in agreement with the trees generated. SARS-CoV2 and RATG13 are having close origin on the tree, and MERSCOV and P-CoV are also having close origin on the tree. This supports our previous findings.