ECES T580 Lab 5

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Lab 5.1.1

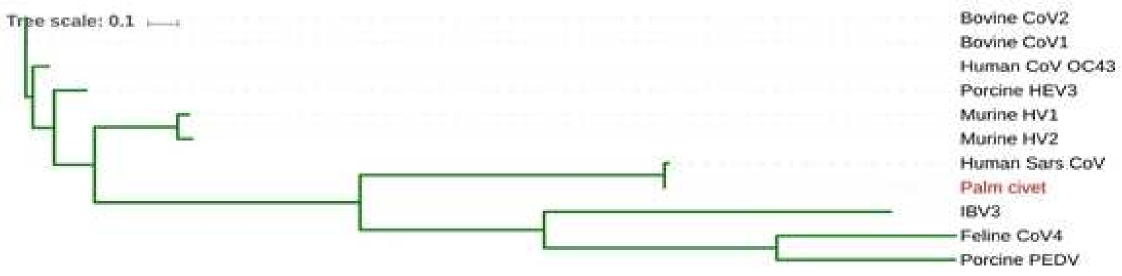
Background

SARS, a disease/illness that first appeared in China. It is a virus, and underwent mutations over a long period of time. The goal is to figure out what is the virus is related too

The pipeline consists of MAFFT, for quick alignment of multiple sequences with little computational burden. Some error but it works for our test case MAFFT will first align series of sequences, then we will pass the data onto readseq that will convert to a different data format (for running RAxML, "maximum likelihood"). From there we will take the data into iTOL where we will be able to visulize a tree

Here is the output from iTOL:

```
figure(1)
imshow('part1_tree.jpg')
```

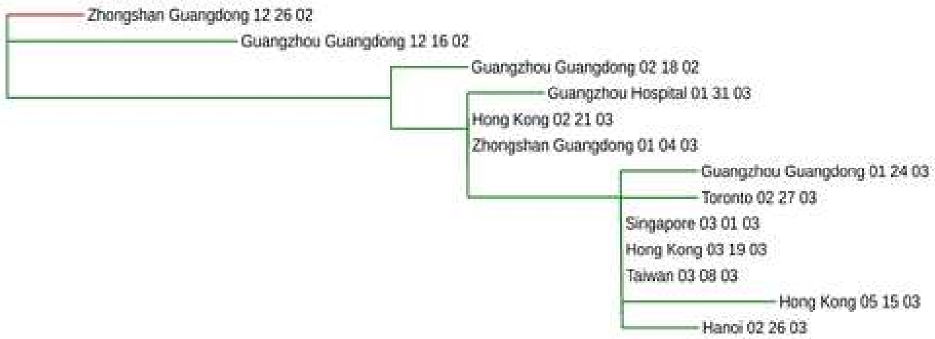


Upon analysis we can see that Palm Civet is most likely the closest relative to Human SARS

Lab 5.2.1

Run SARS Data Part 2 through the same pipeline and show results

```
figure(2)
imshow('part2_tree.jpg')
```


Zhongshan Guangdong 12 26 02
Guangzhou Guangdong 12 16 02
Guangzhou Guangdong 02 18 02
Guangzhou Hospital 01 31 03
Hong Kong 02 21 03
Zhongshan Guangdong 01 04 03
Guangzhou Guangdong 01 24 03
Toronto 02 27 03
Singapore 03 01 03
Hong Kong 03 19 03
Taiwan 03 08 03
Hong Kong 05 15 03
Hanoi 02 26 03

Upon analysis we can see that the epidemic most likely originated from Zhongshan Guangdong in 12/26/02

Import the data sequence using fastaread

```
[headers, sequences] = fastaread('SARS_Data_Part_2.fasta');
```

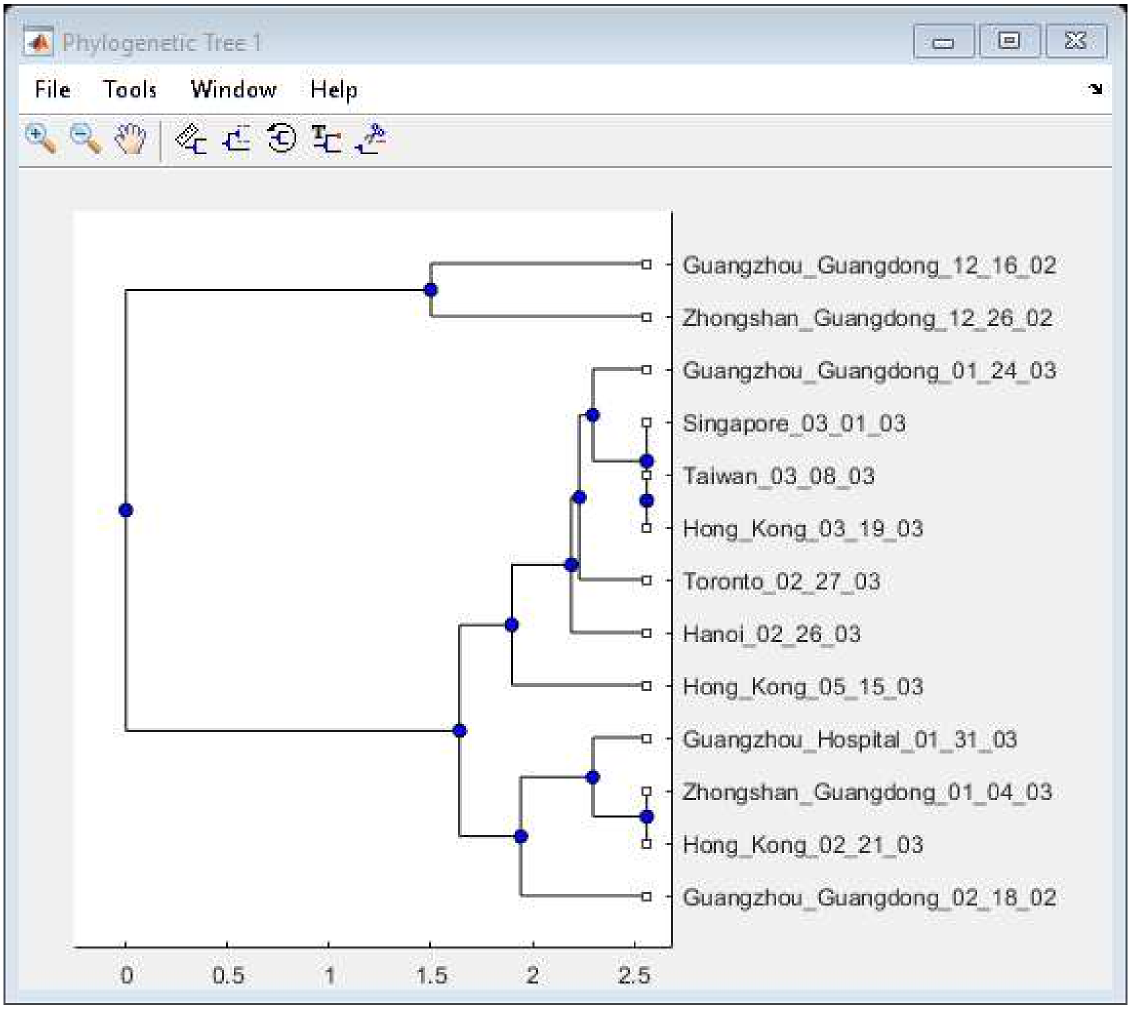
Calculate pairwise distance between sequences

```
D = seqpdist(sequences, 'Alphabet', 'NT','indels','pair');
```

Construct a phylogenetic tree from pairwise distances

```
phyloTree = seqlinkage(D,'average',headers)
view(phyloTree)
```

```
Phylogenetic tree object with 13 leaves (12 branches)
```


Phylogenetic Tree 1
File
Tools
Window
Help
Guangzhou_Guangdong_12_16_02
Zhongshan_Guangdong_12_26_02
Guangzhou_Guangdong_01_24_03
Singapore_03_01_03
Taiwan_03_08_03
Hong_Kong_03_19_03
Toronto_02_27_03
Hanoi_02_26_03
Hong_Kong_05_15_03
Guangzhou_Hospital_01_31_03
Zhongshan_Guangdong_01_04_03
Hong_Kong_02_21_03
Guangzhou_Guangdong_02_18_02
0
0.5
1
1.5
2
2.5

Upon analysis of this tree, we can see that the Zhongshan Guangdong 12/26/02 epidemic strain branched along with Guangzhou Guangdong 12/16/02 epidemic strain, and that they shared some common ancestor.

The difference between the RAxML model and the UPGMA model, in the UPGMA method, it makes the assumption that rate of mutations is constant over time,for all lineages in a tree. This means that all leaves of the tree have same distance from the root. Whereas, the RAxML shows sequences changing and mutating and varying length of times. Whereas the maximum likelihood model is seen to have root and branch distances varying, not utilizing this basic assumption of the molecular clock hypothesis

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