

## Tyler Bradley – ECES T580 Lab 5

### Lab 5.1.1

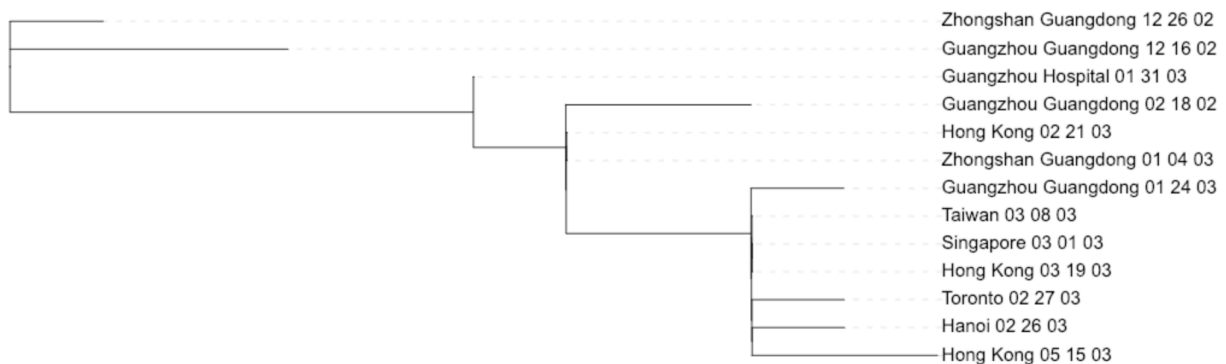
Tree scale: 0.1



The coronavirus that is most closely related to Human SARS CoV is Palm Civet.

### Lab 5.2.1 – Online Portion

Tree scale: 0.0001



The origin of the SARS epidemic appears to have begun at Gaungzhou Guangdong on Dec 16, 2002 but is also closely related to another strain of the norovirus from 12/26/02 in Zhongshan Guangdong. However, the 12/16/02 strain seems to be more closely related to strains sequenced in the early months of 2003.

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## Lab 5.2.1 Matlab Portion

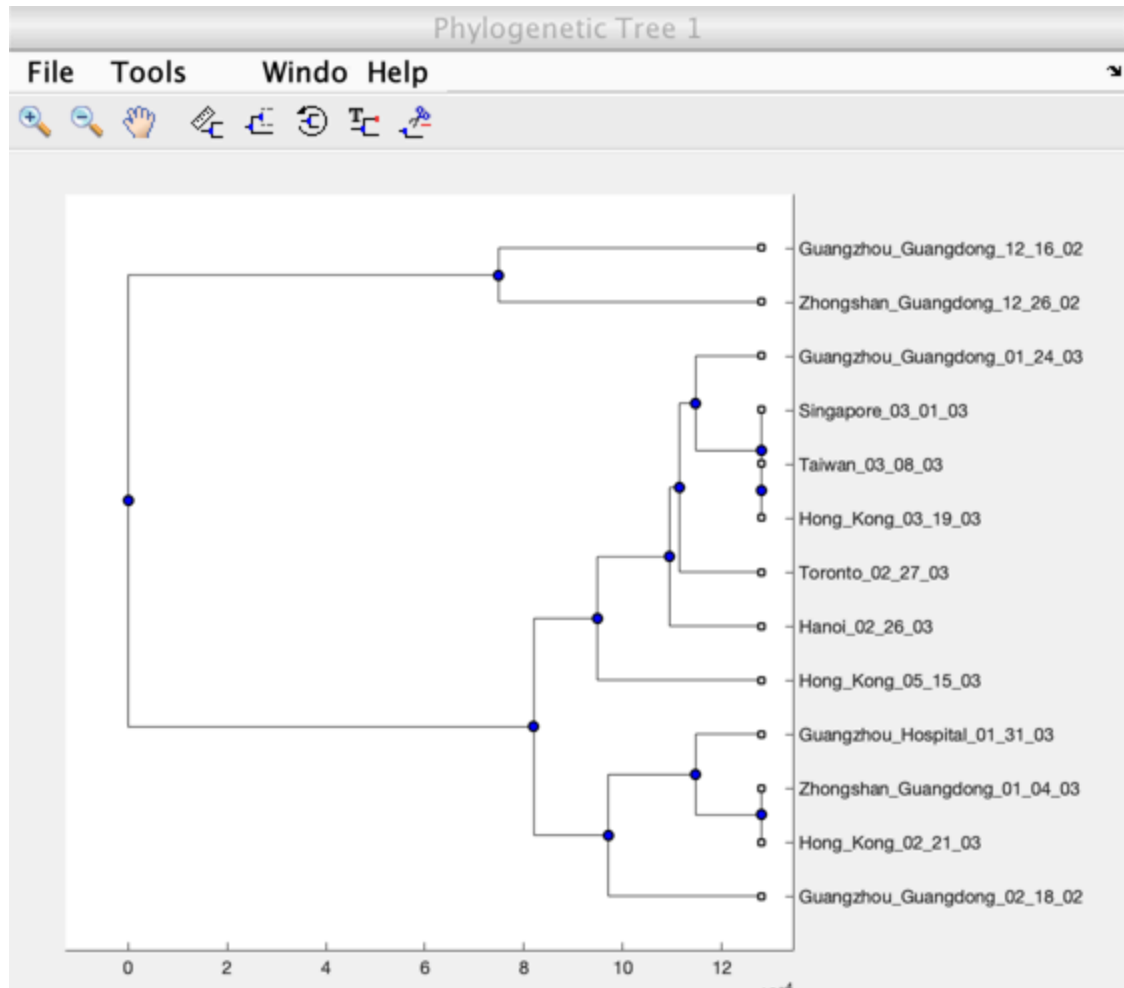
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seqs = fastaread("SARS_Data_Part_2.fasta");

seq_dist = seqpdist(seqs);

tree = seqlinkage(seq_dist, "average", seqs);

view(tree)

% Overall, the two tree building methods make the same major groupings
% of
% sequences. The two December 2002 sequences are separated from the
% rest of
% the sequences indicating that they are likely they starting point
% and the
% norovirus evolved from that point. However, way in which they are
% separated is slightly different. In the Cipres tree, it appears that
% the
% 12/16/02 sequence is more closely related to the future sequences,
% but in
% the matlab tree, they appear to be equally distant from the rest of
% the
% sequences. The rest of the groupings appear to be fairly similar.
% There
% are some apparent discrepancies that arise due to CIPRES use of
% actual
% branch lengths while matlab appears to normalize branch length in
% favor
% of more clear sub groupings. However, when looking closely, the
% shorted
% branch lengths on the sub nodes near the tree tips correspond with
% more
% closely related sequences in the matlab tree. So overall, there is
% good
% agreement between the two methods.
```



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