
Lab 5.2.1 Matlab Portion

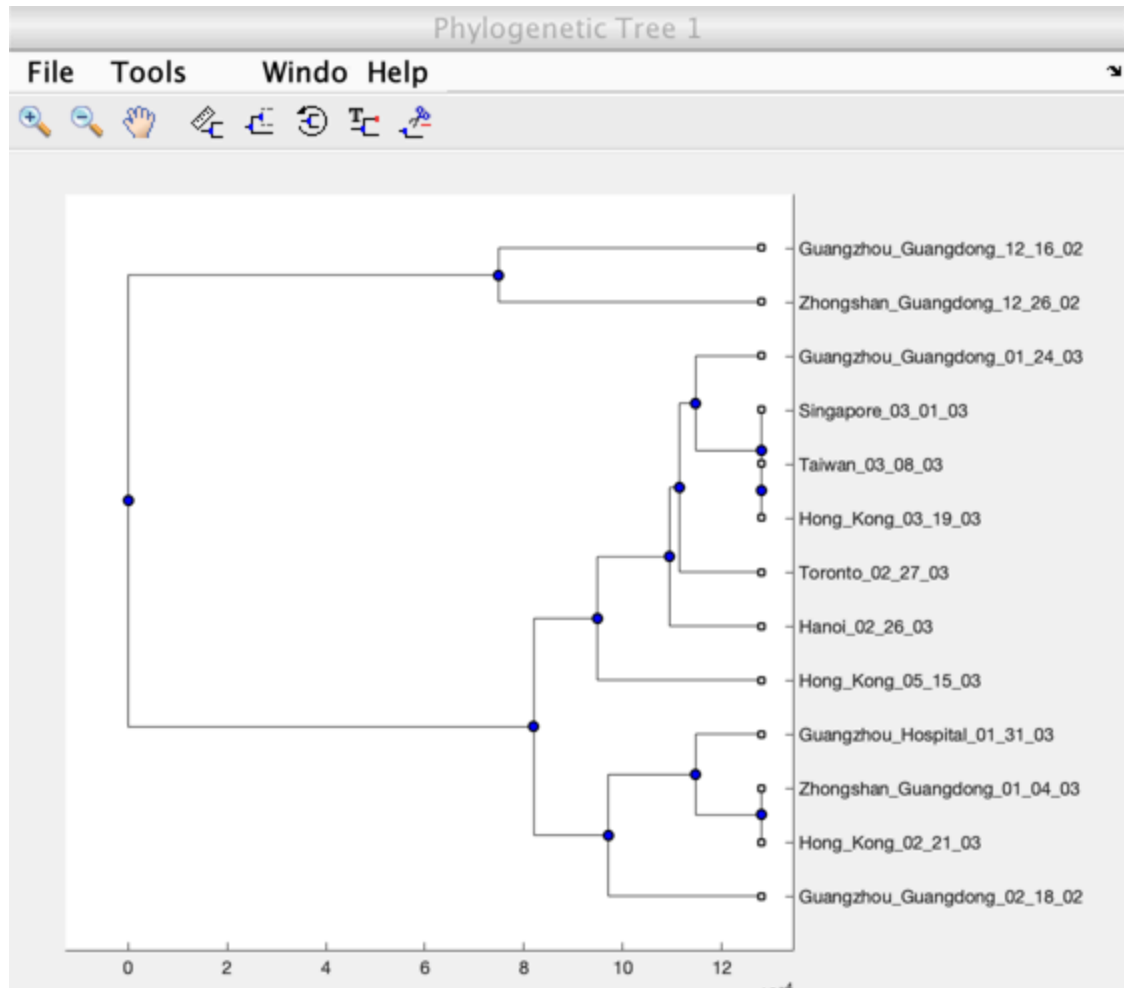
```
seqs = fastaread("SARS_Data_Part_2.fasta");

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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