Exercise 4: Phylogenetic tree worksheet

Answers to questions:
4.1 Why include more than one phage per cluster?

4.2 Would you expect clearer results if all of phages in a cluster were included?

4.3 Since some of these clusters have over 100 phages, is it reasonable to choose a subset of phages to represent the cluster? (for phage students- go to phagesdb and find out what is special about Crossroads)

4.4 Submit your phylogenetic tree onto the worksheet.

4.5 How would you annotate this tree?

4.6 Are all members of a cluster next to each other in this tree?

4.7 Which clusters are predicted to be the closest in evolutionary time (aka. the most similar)?

4.8 Which are predicted to be the farthest apart in evolutionary time?

4.9 Which branch is the least supported based on bootstrapping results?

4.10 Submit your phylogenetic network onto the worksheet.

4.11 How would you annotate this network?

4.12 Are all members of a cluster next to each other in this network?

4.13 Which are predicted to be the farthest apart in evolutionary time?

4.14 Describe similarities (if any) between the phylogeny.fr tree and the Splitstree network.

4.15 Describe differences (if any) between the phylogeny.fr tree and the Splitstree network.

4.16 What conclusions can be drawn from these analyzes using the capsid protein sequences?