**Computer Lab 5 – Phylogenetics I: Maximum Parsimony**

**Conservation Genetics (BIOL 4174 / 5174)**

Due date: 2/26/2018 at Midnight.

Submit this file via Blackboard.

Part I – Parsimony

1. Record your starting Treelength value here. What does this value represent?
2. Record your final treelength here. Did you find multiple trees with this same treelength value?
3. Find an example of each of the following:
   1. Autapomorphy
   2. Synapomorphy
   3. Homoplasy – reversal
   4. Homoplasy – convergence

**For each example, export the tree showing the character as a .pdf** (File 🡪 Save Tree as PDF…). Name each file by the example it represents (e.g., reversal.pdf, autapomorphy.pdf, etc.). Save these four .PDF files in the “lab\_5/character\_states” folder on your computer.   
  
The tree topology should be identical in all four examples – do not move around branches to force homoplasy, synapomorphy, etc. There are 684 characters in your data matrix, so this is unnecessary.   
  
Once you have saved all four files, zip your character\_states folder (right-click the folder 🡪 Send to 🡪 compressed (zipped) folder) and name the zipped file as username.zip. Submit this file via the provided assignment link on Blackboard.   
  
**For each example, list in this document which taxa are involved (e.g., which taxa show the homoplasious character in your homoplasy example?)**.

Part II – Maximum Parsimony in MEGA

1. What is the length of this tree? This number should be shown in the lower left corner of the Tree Explorer window, or it can be obtained by clicking the information icon (5th icon from the left).
2. How does this length compare to the tree you constructed by hand in Part I of this lab?
3. How many equally parsimonious trees were found by the program (Click the information icon (it looks like a lower case, italicized “i”) to find this number)?
4. Root the tree so that *Sphenodon* is sister to the ingroup. Insert a copy of the tree into your homework assignment (the easiest way to do this is in MEGA is to click on “Image 🡪 Copy to Clipboard.” You can then paste the tree into this document).
5. After making the 50% majority rule consensus tree, root it by *Sphenodon* again and paste a copy of the tree into this document.
6. Which groups of taxa have been collapsed into polytomies in your tree?
7. What do the values on nodes represent in your Majority Rule Consensus tree?
8. Which groups of taxa have been collapsed into polytomies in your tree? Why might there be more polytomies in this tree compared to the 50% majority rule tree?

Part III – Bootstrapping

1. Once again, root your tree on the branch leading to *Sphenodon*. Collapse any node with less than 50% bootstrap support (Compute 🡪 Condensed tree; set the cut-off value for the condensed tree to 50%; click OK). Insert a copy of the tree into your homework document.
2. How many clades were collapsed due to low support? After collapsing nodes with support of less than 50, do you still have any poorly supported clades in your tree? Which species are found in these clades? Why might these nodes be difficult to resolve?
3. If you performed the bootstrapping analysis again, would you expect the exact same values? If you are unsure, compare your values with a neighbor, or re-perform the analysis. Explain your answer.
4. Explain in your own words what a bootstrap support value indicates.

Part IV – Heuristic Search Methods

1. Did this method find a tree with a length that matches the one found by the branch and bound method? If not, what was the treelength?
2. How many equally parsimonious trees were found? How does this compare to your results using the branch and bound method?
3. Did any of your five runs find a longer tree? If yes, then answer the following three questions:
   1. What was the length of the tree?
   2. If multiple trees were found, make a 50% majority rule consensus tree and copy it into your homework document. If only a single most parsimonious tree was recovered, then copy that tree here. Make sure your tree is rooted by *Sphenodon*.
   3. Explain how this tree differs from the 50% majority rule consensus tree you calculated using the branch and bound method.