**Computer Lab 7 – Phylogenetics III:**

**Bayesian Methods and MCMC**

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

Due date: 3/12/2018 at Midnight.

Submit this file via Blackboard.

Part I – MrBayes

1. Now, use the charset command to insert another line of code to designate the rest of the alignment (characters 169 to 852) as belonging to the ATP6 gene. Provide the line of code you will use to designate the rest of the alignment as belonging to ATP6 in the space below:
2. Provide the line of code you will use to apply the GTR+I+G model to the ATP6 gene in the space below:
3. What did you decide upon for your burnin value?
4. Are the support values (i.e., Bootstrap values vs. Bayesian Posterior Probability) that you obtain for branches/nodes in your tree in PhyML and MrBayes equivalent to one another? Explain why or why not.

Part II – Simulating MCMC

1. Did your single chain take a while to ‘find’ the peak? If you were to use these values to infer the probability distribution of “x” and “y”, do you think these initial points would be informative?
2. Next, use the “burn-in” slider to remove these exploratory proposals. What value did you choose?
3. Try a few different values for the Proposal Size Window. How does this change how your chain samples parameter space? What consequences might there be to having too small or large of a proposal size window?
4. When sampling a more complex parameter space, did your chain get stuck on a single peak (local optimum), or was it able to find and explore all peaks?
5. When adding a second chain, did you notice that the main chain (shown in blue) was better able to “find” alternative peaks? Why or why not?