**Computer Lab 6 – Tree Building (Part 2)**

**Introduction to Models of DNA Sequence Evolution and Maximum Likelihood**

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

Submit this file via Blackboard.

**jModelTest:**

Answer the following questions for your helo-atp6.phy file:

* What model was selected by hLRT?
* What was the preferred AIC model?
* What was the preferred BIC model?
* Which of these models is the most complex?

Answer the following questions for your helo-atp8.phy file:

* What model was selected by hLRT?
* What was the preferred AIC model?
* What was the preferred BIC model?
* Which of these models is the most complex?

Answer the following questions for your helo-atp86.phy file:

* What model was selected by hLRG?
* What was the preferred AIC model?
* What was the preferred BIC model?
* Which of these models is the most complex?

Using what you know about AIC and BIC, explain why BIC may sometimes select a less complex model than AIC?

Why must the same tree be used to test all models in order to perform a hLRT?

**Maximum Likelihood Treebuilding:**

1. What command did you issue to run PhyML on the helo-atp6.phy file? Enter this command in the text box below:
2. What command did you issue to run PhyML on the helo-atp86.phy file? Enter this command in the text box below:
3. Look at the tree you generated from the gene ATP8. Do you notice anything strange about the placement of the snakes (*P. regius* and *B. constrictor*) in this tree? Why do you think this might have happened?
4. Does *Heloderma suspectum* form a monophyletic group in the atp8 tree? What about the atp6 tree? If it is not monophyletic, provide a better term to describe it (Hint: you may have to refer back to the lab 5 materials)
5. Compare your three trees generated in PhyML. How do the topologies of the three trees differ?
6. Compare the three trees generated using the “helo-atp86.phy” file (i.e., one of the PhyML trees and both of the RAxML trees). How do the topologies of the three trees differ? How do the bootstrap values compare? Provide two reasons why bootstrap values may differ among these trees.
7. Did the two different methods used in RAxML result in different trees or different bootstrap values? Give examples.
8. In your own words, explain the advantage of using a model-based method such as Maximum Likelihood rather than Maximum Parsimony for treebuilding.