Name _____

Integrative Biology 200B   Spring 2007
"PRINCIPLES OF PHYLOGENETICS: ECOLOGY AND EVOLUTION"

Quiz 1
You may use any books, notes, or references, but you must work independently of other people.
To keep the amount of writing under control, please confine the answers to the space provided (but write
clearly and large enough to see!); outlines and pictures are fine.

1. Define phylogenetic signal. Is the strength of phylogenetic signal for a binary trait related to our ability
to confidently reconstruct ancestral character states? You may explain your answer based on either
parsimony or likelihood approaches to ancestral reconstruction.

2. An icthyologist colleague comes to you for help. She is studying a clade of marine fish that have
diversified across a broad latitudinal gradient. She has collected live specimens from multiple locations
from tropical to polar regions, recording the latitude of collection and measuring (in the lab) the animal's
temperature optimum for swimming. Based on DNA from each sample, a fully resolved molecular
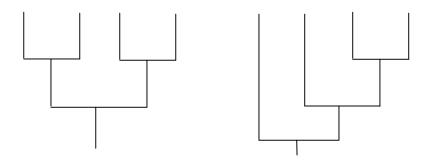phylogeny has been obtained for the group.

      a) What method would you recommend she employ to test the hypothesis that optimum
      swimming temperature is correlated with latitude of origin? What is the null hypothesis, and the
      key assumptions underlying your recommended method? Briefly explain how the method works,
      and how it provides an appropriate test of the hypothesis.

      b) What if the source locations were recorded only as 'tropical' and 'extra-tropical': what method
      could you recommend? Would it matter whether distribution was strongly conserved
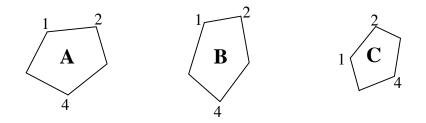   (phylogenetically speaking) in your choice of a recommendation?

3. Can a key innovation be considered an adaptation? If so, what kind of a selection process is going on?
Explain your answer.

4. You trace a binary character on a tree using parsimony, and that character is seen to have 2 to 4 shifts
from state 0 to state 1 under different reconstructions. How is it possible to have a range of values for
shifts from state 0 to 1 given the same length under parsimony?

5. How many possible labeled topologies correspond to each of these unlabeled topologies?

6. In morphometrics, which of these pentagons are the same shape, according to Kendall's definition? Why?

7. Assuming that you know the "true" tree, how would you determine if different exons from a gene have different rates of evolution?

8. You test for clade imbalance by comparing the difference in size between the two basal clades of your tree to that same difference in trees simulated either with a Random Partition or a Yule Process. Which null distribution do you expect to calculate a lower p-value? Why? Would you trust that p-value?

9. What is the difference between neoteny and progenesis? How can you tell in practice?

10. What is the difference between adaptation and exaptation? How can you tell in practice?