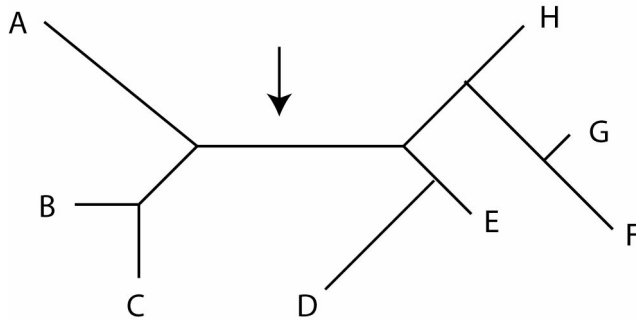Molecular Systematics Midterm
Spring 2004

1) Consider the tree below.

a) Illustrate the two nearest neighbor interchange branch swaps around the branch indicated (the central horizontal branch).

b) Draw the tree if it were rooted with "D" as the outgroup.

2) If you wish to, you may consult the tree appended to the end of the exam.
a) Are alpha hemoglobin and beta hemoglobin homologous? Is "homologous" the single best word to describe their relationship? What word would you recommend be used to describe their relationship?

b) If you were uncertain as to the homology of these globins, what kind of evidence would you look for to determine their relationship?

3) According to Zuckerkandl and Pauling, is each of the following a semantic, episemantic, or asemantic molecule?
a) Hemoglobin

b) The heme which is bound to hemoglobin

c) The iron atom which is bound to the heme which is bound to hemoglobin.

4a) Describe four models of DNA sequence evolution, indicate the relationship among these methods (i.e., if they are nested methods, indicate which is a special case of another method).

4b) Consider the four methods you described above. What assumptions can you identify that are *shared* by all of these methods?

5) Consider Bayesian analysis and maximum likelihood analysis. Both are likelihood methods.

a) Describe and distinguish between the concepts of probability and likelihood.

b) What is a prior probability?

c) What is Bayes Theorem?

c) What assumptions are shared by both Bayesian and maximum likelihood analysis?

d) Describe the Metropolis algorithm.

Name: _____

X) Consider the concept of branch lengths in the context of parsimony, distance, and likelihood analyses of DNA sequence data.

a) Is branch length a similar metric with each of these methods? If so, what is the definition of branch length that applies to each of these methods? If not, how do they differ?

b) Are there predictable relationships among branch lengths determined with different methods (assuming that the tree topology is similar)? If so, please identify at least two pairs of methods for which such a prediction could be made, explain what that relationship would be, and give an indication of why you expect that this should be the case. It is sufficient simply to say that method Y will always predict longer branches than method Y, or that method A would tend to apportion branch length equally while method B would tend to apportion branch length to some specific branches.