Quiz 2

You may use any books, notes, or references, but you must work independently of other people.

To keep the amount of writing under control, <u>please confine the answers to the space provided</u> (but write clearly and large enough to see!); outlines are fine, or use diagrams if they help.

1. (10 points) Briefly compare and contrast phylogenetic methods based on Maximum Likelihood and Parsimony. Pick two aspects of each method often thought of as an advantage or disadvantage that are interrelated, e.g. the same attribute might be seen as an advantage under one paradigm and a disadvantage in the other or one might be problem for one that is explicitly accounted for under the other.

2. (20 points total) What sort of comparative method would you apply to the following evolutionary questions (e.g., what kind of data would you want, how would you generate a null hypothesis, how would you judge statistical significance?):

a. (5 pts.) Are white-colored petals an adaptation for moth pollination in flowering plants?

b. (5 pts.) Does the evolution of multicellularity cause an enhanced rate of diversification in lineages?

c. (5 pts.) Has a particular clade of parasitic fungi closely co-evolved with its clade of host plants?

d. (5 pts.) There is a trend in birds and mammals towards increasing body size in higher latitutes (Bergmann's Rule).

3. (20 points) The town of Bikini Bottom has enough money to set aside one 10 hectare plot and has 4 candidate areas to choose from. Much of the money was raised in the "save the jellyfish" campaign. You have been hired to provide an

opinion on what to save and are expected to provide the historical, i.e. phylogenetic, perspective. You have one set of five species (A…E, where "B" is the beloved jellyfish) for which you have the cladogram (A (B (C (D E)))).

A survey of the areas found these species to be distributed as follows:
Jellyfish Fields- A,D,E
Crabby Canyon- C,D,E
Squid Ridge- A,B
Sponge Plaines- B,C,D,E

Use the Vane-Wright et al. method of root-weighting (you must calculate I, i, Q and W) and any other information that is contained in this question to make your recommendation. Another person is just counting species. How do your results compare? Use the space below to show work and briefly make your case as to what area to preserve.

4. (10 points) Recode the cladogram in question 3 into a matrix as if you were going to do a Brooks Parsimony Analysis.

5. (10 pts.) In biogeography, what are the major differences between Assumptions 0, 1 and 2 and what is the purpose of the RAC and how is it different from a TAC or a GAC?

6. (10 points) An editor of a journal wants you to place both Bremer support and Decay Analysis values on your cladograms. Pick one and explain briefly why you would use it. For the other, explain to that pesky editor why you decline to put those numbers in your figures.

7. (20 points) Short answers; briefly answer these short questions

a. (5 pts.) What would be the best consensus / tree-comparison method be for each of these situations and why?

   7 different maximum parsimony trees derived from a single matrix.

   1,000 trees in a ".t" file generated by Mr.Bayes from sampling tree space.

   5 trees from different studies with overlapping, but not identical taxa.

b. (5 pts.) If you search for the maximum parsimony tree for a given matrix using a normal heuristic search using TBR, a ratchet and a sectorial search, will you necessarily find the same tree every time? Why or why not?

c. (5 pts.) What are "nuisance" parameters in terms of ML or Bayesian phylogenetic estimation? Enumerate a few and explain what a "nuisance" parameter is.

d. (5 pts.) What are 'Items of Error' in reconciled trees?