

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. Word-processed answers are OK, as long as they are the equivalent length. **The Quiz is due at 3:30 sharp**, either in room 3083 VLSB, or by email to: BMishler@berkeley.edu. Relative point value is given -- 100 points total.

1. (10 points) Based on what you have learned in class, critique the following actual quotation. In your critique be sure to explain underlying concepts and fully express ideas about what characters are, what the components of a matrix are and how these relate to the purpose, goals and interpretation of phylogenetic analyses.

Posted to Taxacom by Richard Zander- "*Total evidence is not* [the answer to using both DNA and morphology], *since we are combining in one analysis molecular data on genetic continuity with morphological data from studies searching out conservative probably selectively linked traits. Combining apples and oranges (sic) give cole slaw.*"

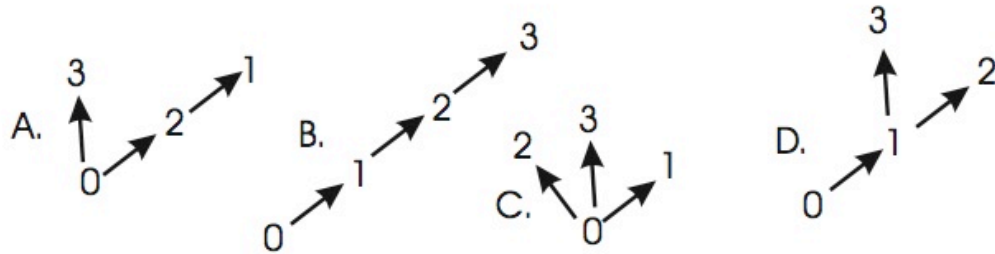
2. (10 points) Paedomorphic character states present a tremendous challenge to phylogenetic reconstruction whereas peramorphic characters are typically better "behaved." Why should this be the case? What assumptions might be incorporated into an analysis to counter spurious paedomorphic signal in tree topologies?

3. (10 points)

Given the tree and matrix at the bottom, optimize on the tree characters with the following attributes:

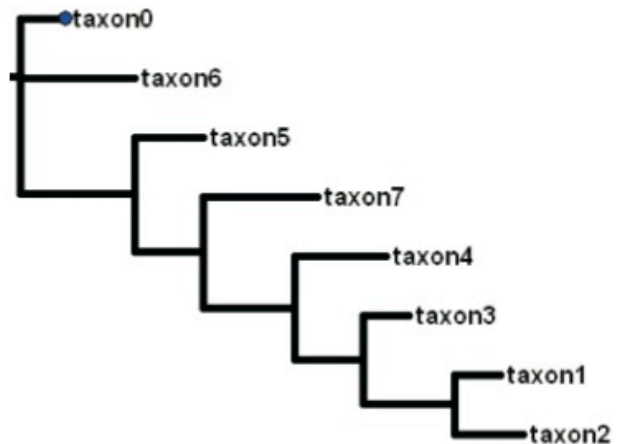
1. one informative character that is has a ci of 1.0
2. one character that has an ambiguous optimization. Show both ACCTRAN and DELTRAN possibilities.
3. one character that is an autapomorphy.

In regard to character 10, which of these (A,B,C,D below) shows the correct transformation of states on this tree?



Characters 0 - 10

| | 0 | 5 | 10 |
|--------|---|---|----|
| taxon0 | 0 | 0 | 0 |
| taxon1 | 0 | 1 | 1 |
| taxon2 | 0 | 1 | 1 |
| taxon3 | 0 | 0 | 1 |
| taxon4 | 0 | 1 | 0 |
| taxon5 | 0 | 1 | 0 |
| taxon6 | 0 | 0 | 0 |
| taxon7 | 1 | 0 | 0 |



4. (10 points) You work on an extinct group of organisms that are well represented in the geologic record. You decide to do a cladistic analysis of your group. You would like to include stratigraphic data in analyses, but how? Give at least two approaches to account for stratigraphic occurrences. What are the pros and cons of the different approaches?

5. (20 points) --Two competing analyses have been published addressing the same controversial phylogenetic question but present conflicting results. Based only on the attributes for each study as given below, compare and contrast what was done, what are some of the possible problems and what are some of the best qualities of each? What would you do to improve them? Given the information provided, which would you judge as the preferable analysis in this case?

Study A:

Data Analyzed: Mitochondrial DNA from COI, NADH-6 and 12S RNA genes.

Alignment: ClustalW (default parameters)

Analysis methods: NJ, ML, Parsimony for each gene and as a combined matrix.

Support measures/ data exploration: All analyses subjected to bootstrap and multiple method tree agreement.

Results presented: Strict consensus trees for each method and majority rule tree for all trees from all analyses combined. Selected adult morphological character mapped on and optimized on the majority rule tree.

Study B:

Data analyzed: Mitochondrial DNA from COI, nuclear DNA from CAD and 18S rDNA genes and 100 characters of adult morphology.

Alignment: by hand

Analysis methods: Parsimony of combined data. Using various character weighting schemes.

Support measures/ data exploration: Decay analysis. Sensitivity to character weighting. Comparisons of partitions using ILD.

Results presented: Strict consensus tree of each different analysis using a specified weighting scheme. Random tree selected from set of most parsimonious trees from the analysis that had the best ILD score is used to show optimizations of character transformations.

6. (10 points) What are the basic similarities and differences between Bayesian- and maximum-likelihood- based methods in statistics? What do these similarities and differences look like specifically in phylogeny estimation methods. (Examples of things to discuss: what is the final estimate saying? How is uncertainty assessed or represented? What are the assumptions of the two methods?)

7. (30 points: 5 points each) Briefly contrast the following pairs of terms (Use diagrams if they help)

character-state polarity vs. character-state ordering

evolutionary systematics vs. phylogenetic systematics

ontology vs. epistemology

orthology vs. paralogy

Manhattan vs. Euclidian distance

semaphoront vs. OTU