

"PRINCIPLES OF PHYLOGENETICS "**Quiz 1**

You may use any books, notes, or references, but you must work independently of other people. To help keep the amount of writing under control, outlines, bullet points, and drawings are fine. Please email to bmishler@berkeley.edu by **Midnight** Friday, 3/18.

1. [10 pts.] Explain how Markov Chain Monte Carlo methods work in Bayesian phylogenetic analyses. Also explain what MCMC convergence, burn-in, and mixing are, and why they are important.
2. [20 pts., 5 each] The following definitions were copied directly from the NCBI Blast Glossary (<http://www.ncbi.nlm.nih.gov/books/NBK62051/> accessed 12 Mar 16). For each provide an improved definition in your own words. Where possible make your definition applicable to morphological data as well. Briefly explain any problems with the original definitions that your new definitions have addressed.
 - a. Alignment. The process or result of matching up the nucleotide or amino acid residues of two or more biological sequences to achieve maximal levels of identity and, in the case of amino acid sequences, conservation, for the purpose of assessing the degree of similarity and the possibility of homology.
 - b. Homology. Similarity attributed to descent from a common ancestor. Homologous biological components (genes, proteins, structures) are called homologs. See also orthologs and paralogs.
 - c. Identity. The extent to which two (nucleotide or amino acid) sequences have the same residues at the same positions in an alignment, often expressed as a percentage.
 - d. Similarity. The extent to which nucleotide or protein sequences are related. Similarity between two sequences can be expressed as percent sequence identity and/or percent positive substitutions.
3. [10 pts] Compare and contrast strict, majority rule, and Adams consensus trees. Be sure to discuss generally how they are produced, what they are typically used for, how they compare in terms of resolution and efficiency, and what problems related to use and interpretation each may pose.
4. [10 pts] You are conducting a study to reconstruct the ancestral state of life form in angiosperms (for example, woody vs. herbaceous, or tree vs. shrub). Identify the steps you need to take, including the required data or other inputs to your analyses, and your choice of methods. Which step do you think your results will be most sensitive to (in other words, what information or analytic choices might have the most influence on obtaining alternative results).
5. [10 pts.] What is the Brownian motion model of trait evolution, and what kinds of trait does it apply to? What are the underlying assumptions of the model, and what is the pattern of simulated trait change over time that results from the model? Provide an example of an empirical question in comparative biology that you might ask, and how a model such as Brownian motion helps us to construct a statistical test that will answer that question.
6. [20 pts., 10 for each part]
 - a. Trait correlations are often used to test hypotheses of adaptive evolution. Succinctly explain how you could conduct a comparative test of trait correlations between two discrete traits, and between two continuous traits.
 - b. From a conceptual standpoint, how do these tests contribute to addressing hypotheses of adaptation? What other tests are needed for a complete assessment of adaptation?

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7. [10 pts.] What (if anything) is a species, in your opinion? Give reasons to back up your opinion, including why it matters to the community of biologists what species are.

8. [10 pts.] What are the roles that morphology should play in phylogenetics?