

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, please confine the answers to the approximate space provided; outlines and drawings are fine. You may handwrite or type your answers. You should email to bmishler@calmail.berkeley.edu by **9:00 pm**, this evening, May 2.

1. [20 pts.] Arguments over the relative importance (or even existence of) macro-evolutionary selection has been an ongoing debate for almost 50 years. Using your favorite taxon, (1) what macro-evolutionary patterns might you look for in either diversification or extinction data for your group, and (2) how might you test these patterns for macro-evolutionary signal?

2. [20 pts.] Dispersalist approaches to biogeographic questions have predominated the field since its inception. At greater time scales this model often gives rise to center of origin assumptions. What are some of the problems with center-of-origin arguments, and why should there be ‘problems’ with these assumptions at all? As evolutionists, don’t we all assume that new taxa are initially restricted to very small distributions and therefore would have dispersed from these point sources with time?

3. [20 pts.] Many ecological studies begin with the premise that modern-day communities and their interactions represent fully integrated systems that are often assumed to have evolved synchronously. This approach circumvents the temporal and spatial histories of the constituent organisms, historical interactions, and how a system may have changed with the addition or subtraction of key components. How might you test the premise that a particular interaction in a community has both evolutionary as well as an ecological significance?

4. [20 pts] What, if anything, is a species? List the main possible answers, and then indicate which you prefer yourself. In a couple of sentences, defend your personal choice.

5. [20 pts] There are a variety of situations where comparisons of two or more cladograms are essential to answering questions in comparative biology. Please identify **two** examples of cladogram comparisons from very different fields. For each example, clearly identify: (a) What are the terminal taxa for each cladogram? Are they identical, overlapping, or different? (b) What does each of the cladograms represent (e.g., are branches time calibrated)? (c) What is the hypothesis or question being addressed in comparing the two trees? (d) What kind of qualitative, quantitative, or statistical test is used to address the hypothesis?