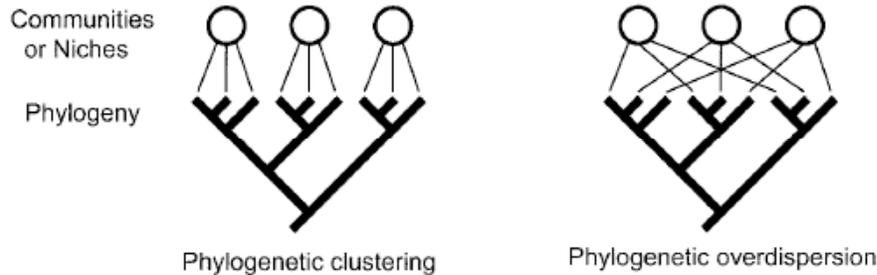


## "PRINCIPLES OF PHYLOGENETICS: ECOLOGY AND EVOLUTION"

**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 space provided (but write clearly and large enough to see!); outlines and pictures are fine. **Due at 3:30 sharp at Brent Mishler's office (4164 VLSB).** Points deducted for late delivery.

**1. (12 points)** Ecological filtering refers to a process whereby species co-occurring within communities tend to be phenotypically similar to each other. Filtering can lead to either phylogenetic clustering or phylogenetic overdispersion (see diagrams below). Explain a scenario leading to each outcome (hint: the answer has to do with phylogenetic signal).



**2. (12 points)** Studies of cospeciation are based on comparing the phylogenies for clades of interacting species (e.g., hosts and parasites). What is the role of branch length information in such comparisons? Does it matter if the branches are in relative time units, or if they are calibrated against absolute time?

**3. (12 points)** Explain two roles of phylogenetics in establishing conservation priorities? In each case, what is the conservation objective (implicit or explicit) and how can phylogenetic information help to accomplish that objective?

**4. (12 points)** It is widely believed that multi-drug therapy slows the rate of evolution in HIV relative to single-drug therapy. You have samples of many viral particles from one individual who is using only a single anti-viral and from the individual they contracted HIV from, who has been using multiple drugs. (a) What would you expect the phylogeny of these particles to look like? How would the amount of time since transmission affect the topology? (b) How would you test for the effect of multi-drug therapy on evolutionary rate against a null? Why is it critical that all the viral particle samples be taken at the same time (or pretty close to it)?

**5. (10 points)** You analyze a morphological data set using parsimony, and find one most parsimonious tree, three trees just one-step longer and five that are two-steps longer. You calculate the symmetric difference between the most parsimonious tree and all of the other trees. Do you expect this value to be greater for the one or two step longer trees? Why? What would it imply about tree space if you found a single one-step longer tree with a much larger symmetric difference from the most parsimonious tree than the two-step longer trees?

**6. (15 points each)** What sort of comparative method or approach would you apply to the following evolutionary questions (e.g., what assumptions would you make, what kind of data would you require, how would you generate a null hypothesis, how would you judge statistical significance?):

a. Did the early radiation of angiosperm lineages cause the diversification of the insects?

b. In the history of the Caribbean Islands, which two present-day islands were connected the longest?

c. True species-level selection occurred in the radiation of the birds?