

"PRINCIPLES OF PHYLOGENETICS "

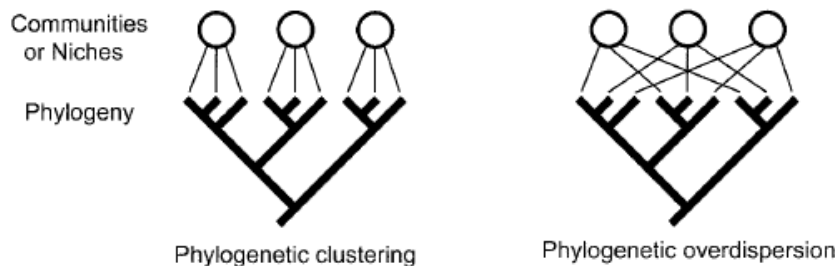
Quiz 2, May 5, 2014

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 (12:00 am)** this evening, 5/5.

1. [20 pts.] You have reconstructed the phylogeny for a taxon of flowering plants, *Floris*, consisting of 150 extant species. It is hypothesized that this group experienced a shift in diversification rates after their primary pollinators switched from bees to birds 40 million years ago.
 - a. Draw a lineage through time (LTT) plot that would support this hypothesis. Make sure to label the axes and indicate where the diversification shift occurs. Describe some of the caveats in using this approach.
 - b. The bird pollinators for these plants, *Wingus*, represent a monophyletic clade. How could you use this information to support or refute your initial hypothesis of diversification rate shifts?
 - c. What are the two alternative ways of interpreting an observed diversification shift?

2. [20 pts.] You have a contract to evaluate five valleys in a mountain range from a biodiversity standpoint and decide which two have the highest priority to preserve permanently as parks as a mitigation measure (the remaining three are likely to be developed for hydroelectric power). Consider your decision two ways, and give your criteria and the methods you would use: (A) using species diversity & endemism measures, and (B) using phylogenetic diversity & endemism measures.

3. [20 pts] 1. 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 that could lead to each outcome.



4. [20 pts] As we discussed in class, (1) biogeographic analysis of areas, (2) study of gene family evolution among genomes, and (3) studies of host-parasite coevolution often involve comparisons of different phylogenies, with tests for similarity in topology and/or timing.

- A) Identify important ways in which these three types of studies are similar and different.

B) Then describe a comparative method that is used in *each* field, and evaluate whether it is appropriate to use it for the others. If not, why not?

5. 20 pts.] You have the published phylogenies for taxa in Widgetidae, Thingoptera, and the *Resipsa*, which are ((W1,W2)W3), ((T1,T2)T3) and (R1,R2) (R3,R4)).

They are distributed in the following areas:

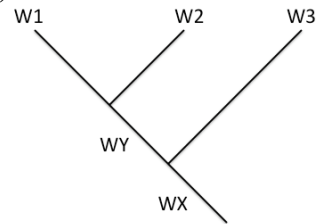
Atlantis- W1, T1, R2

Mu- W2, R1

Rutas- T2, R3

Lemuria- W3, T3, R4

Valinor- T3, R4



A. As a hint, above right is the topology for Widgetidae with the clades labeled and below is the MRP coding for Widgetidae and Thingoptera. Complete this matrix by coding the *Resipsa* clade and adding it to the matrix, then reconstruct the area relationships based on all these data using Brooks Parsimony Analysis (BPA).

[↓ add your columns here ↓]

	W1	W2	W3	Wx	Wy	T1	T2	T3	Tx	Ty
OUT	0	0	0	0	0	0	0	0	0	0
Atlantis	1	0	0	1	1	1	0	0	1	1
Mu	0	1	0	1	1	?	?	?	?	?
Rutas	?	?	?	?	?	0	1	0	1	1
Lemuria	0	0	1	1	0	0	0	1	1	0
Valinor	?	?	?	?	?	0	0	1	1	0

B. How many characters in the BPA matrix are NOT parsimony informative?

C. Give the resulting tree or trees and the strict consensus if appropriate.

D. What are the implications for missing and widespread taxa in this analysis?