

May 4, 2006: **Introduction to comparative methods for evolution, ecology, & behavior**

**A. Discrete-state characters.** Sometimes we are interested in examining how discrete-state characters evolve on a tree individually and together. These are characters that met the 'discrete-state' criteria for taxonomic characters that we discussed earlier.

1. A review of character mapping, and its basis.
  - Inferring history; Hypothetical Taxonomic Units (HTUs)
  - Homology reviewed
  - ACCTRAN vs. DELTRAN
  - equivocal assignments to HTUs
  - Possible errors in inference; what to do to correct or allow for these
2. Here are some types of hypotheses that can be tested:
  - polarity of character changes in one character
  - phyletic conservatism in one character
  - association of state changes in two characters
    - undirected (Ridley's test)
    - directed (Maddison's test)

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In class exercise

Assume the following data set of 12 taxonomic characters for eight tree species plus an inferred ancestor, and the distribution of three functionally important variables in these taxa.

(i) Construct a phylogenetic tree using the taxonomic characters. (ii) Point out which (if any) of the three following adaptive scenarios receives support from this tree.

functional variables:

taxa:	tax. characters:	fruit size:	fruit color:	fruit disperser:
one	1 0 1 1 0 1 1 1 1 0 0	L	RED	monkey
two	0 1 1 1 0 1 1 1 0 1 0	L	RED	monkey
three	0 0 1 0 1 1 1 1 0 1 0	L	GREEN	monkey
four	0 0 0 0 0 0 1 1 0 1 0	S	GREEN	monkey
five	1 0 0 0 0 0 1 0 0 1 0	S	GREEN	parrot
six	0 0 0 0 0 0 0 0 0 1 1	L	GREEN	monkey
seven	0 0 0 0 0 0 0 0 0 1 1	L	RED	monkey
eight	0 0 0 0 1 0 0 0 0 0 1	S	GREEN	parrot
Outgroup(s)	0 0 0 0 0 0 0 0 0 0 0	S	GREEN	parrot

A. Large fruits (L) evolved as an adaptive specialization (greater "reward") for monkey dispersal.

B. Monkeys evolved their preferences for fruits of certain trees because they are attracted to red colors.

C. Small fruits (S) evolved because parrots (given their particular food-size preferences) selected against trees with large fruit.

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## B. Evolution of quantitative traits on cladograms

1. The bad old way. Direct correlations of species values. Species as data points. Why not?

2. Advent of quantitative comparative approaches; importance of history (jobs!)

### Motives:

A. "remove" influence of history

B. Describe variation due to phylogeny by tracing on phylogenetic tree

3. Taxic approaches (compare sister groups):

A. ANOVA and ANCOVA -- nested using taxonomy; partition variance, "subtract" phylogenetic effects.

B. Autocorrelation -- based on spatial statistics; time from divergence, i.e., distance on a phylogeny (see example from Miles and Dunham paper); May or may not weight by branch length.

C. Independent contrasts (Felsenstein) -- assume separate paths, based on Brownian model; compare differences in value of traits between sister groups.

D. Regression -- general linear model approach.

4. Transformational approaches (reconstruct values for nodes, look at direction of change):

A. How to map quantitative characters on a tree?

B. Minimum evolution models

1. Distance Wagner approach (median state rule)

2. Squared-change parsimony (again assuming Brownian model)

3. Directional methods (Huey & Bennett; Losos)

## C. Tempo and mode issues (combining character evolution with cladogram comparisons):

Gradual versus punctuational: is change along branches uniform?

Rates in morphology?

--standard deviation or *coefficient of variation* [= 100(s/y)]

-- the *darwin*: change by a factor of  $e$  (=2.718) per million years; on a natural log scale that is a changes in one unit per million years; millidarwin, etc.

How to test hypotheses about rates? (e.g., molecular clocks?) --maximum likelihood tests (covered in earlier lab session)

How to test hypotheses about trends?

-- An example using number of pollinators in orchids