

Jan. 27, 2011. **Qualitative character evolution within a cladogram**

In this portion of the class, we are interested in examining how discrete-state characters evolve on a tree individually and together. These are characters that meet the 'discrete-state' criteria for taxonomic characters that we discussed earlier. Other quantitatively varying characters can also be studied, but they require different methods which we'll cover later.

When we do such mapping, we are inferring history; trying to use our knowledge of the observed twigs of the trees (semaphoronts, OTUs) to infer traits of hypothesized "ancestors" (Hypothetical Taxonomic Units (HTUs)). The historical concept of homology discussed in the first lecture both requires and makes possible these kinds of inference.

When we focus on the question of character evolution, we will assume that we have already obtained a phylogeny (with possible uncertainties). As we map the history of particular characters, we are not reevaluating the underlying phylogenetic hypothesis. Some have argued that you must not include a character for phylogeny reconstruction and then also map its ancestral states to test evolutionary hypotheses. What do you think?

Mapping of character states on a tree is an essential starting point for comparative methods related to phenotypic traits. The analysis of ancestral/derived states is central to phylogenetic approaches to questions of adaptation, divergent/convergent evolution, and correlated evolution. A typical adaptive hypothesis posits that trait X is an adaptation to selective pressure Y. For example: tough, evergreen leaves, termed sclerophylls, are an adaptation to semi-arid environments. This hypothesis may be tested in various ways, but one of the key predictions is that lineages with sclerophyll leaves first encountered semi-arid environments, and then evolved sclerophylly. If they evolved sclerophylly before encountering the hypothesized selective environment, then this trait must have evolved (and thus be an adaptation) in response to some other factor. This is one type of question that would lead you to conduct a comparative test.

### **I. Ancestral states under parsimony**

The simplest approach to mapping ancestral states is the parsimony principle: we seek the reconstruction that requires the fewest evolutionary 'steps' or transitions between character states. We don't know that evolution proceeded in this way, but the basic argument for parsimony is that we should not assume any additional evolutionary events, beyond the minimum number necessary to explain the observed patterns. After calculating the ancestral states for a character, we can then test a number of hypotheses regarding the number of steps, their distribution on a tree, the polarity of character change, and the sequences or associations of change in two or more characters.

The exact algorithm for calculating ancestral states by parsimony depends on the type of character and the assumed 'cost' of transition among different states:

- 1) Unordered traits have 2 or more states, and all transitions require only a single step;
- 2) Ordered traits have 3 or more states on an ordinal scale, and the number of steps is equal to the difference in state values (i.e., from 1 to 3 requires 2 steps);
- 3) Dollo traits: change is only allowed from ancestral to derived state (reversals require 'infinite' steps);
- 4) Arbitrary step matrices allow user to assign any desired cost structure to transitions.

In many cases, most parsimonious reconstructions (MPR) can be estimated visually, though it is easy to miss alternative equally parsimonious reconstructions when there are several gains and losses. Equivocal assignments to HTUs are quite frequent under parsimony when there is "close" homoplasy, so be aware. There are two ways to arbitrarily resolve equivocal assignments: ACCTRAN vs. DELTRAN.

To illustrate the mechanics of parsimony reconstruction, the formal algorithm for Fitch parsimony for unordered states is provided below. Note: In contrast with the maximum likelihood methods we will study next lecture, branch lengths are not incorporated in parsimony algorithms. One can calculate a branch length after the fact based on the number of characters that change on a branch, but they are not used in the process of determining the MPR.

A number of specific types of hypotheses can be tested with these character mappings:

- estimating phylogenetic conservatism (covered below)
- polarity of character changes in one character (trends)
- association of state changes in two or more characters (next lecture)

---

**Fitch parsimony algorithm** – ancestral reconstruction of an unordered trait (binary or multistate); simplified algorithm for bifurcating tree (no polytomies) with no internally fixed states.

**Set notation:**

- $\cap$  Intersection: the items shared by both sets
- $\cup$  Union: the combined list of items from both sets
- $\emptyset$  The null or empty set

**Definitions:**

downpass - an algorithm that starts at the terminal taxa and works downward through the ancestral nodes, so all daughter nodes must be visited before visiting a deeper ancestral node

uppass - an algorithm that starts at the root and progresses upwards to the terminals

MPR - Most Parsimonious Reconstruction

P,Q,M,N - nodes of the tree (see figure on board)

S - downpass state set

F - uppass state set

L - length of tree (number of changes)

$\leftarrow$  - assign RHS to LHS

Start with L = 0

**Algorithm 1:** Fitch downpass algorithm  
 if (N is terminal)  $D_N \leftarrow$  observed trait value  
 else {  
    $D_N \leftarrow D_P \cap D_Q$   
   if ( $D_N == \emptyset$ ) {  
      $D_N \leftarrow D_P \cup D_Q$   
      $L \leftarrow L + 1$   
   }  
 }

**Algorithm 2:** Fitch uppass algorithm  
 if (N is root)  $U_N \leftarrow D_N$   
 else {  
    $U_N \leftarrow D_S \cap U_M$   
   if ( $U_N == \emptyset$ )  $U_N \leftarrow D_S \cup U_M$   
 }

**Algorithm 3: Assign MPR at each node**  
 $MPR_{root} \leftarrow D_N$   
 $MPR_N \leftarrow U_M \cap D_P \cap D_Q$   
 if ( $MPR_N == \emptyset$ )  $MPR_N \leftarrow (U_M \cap D_P) \cup (D_P \cap D_Q) \cup (U_M \cap D_Q)$   
 if ( $MPR_N == \emptyset$ )  $MPR_N \leftarrow U_M \cup D_P \cup D_Q$

---

## 2. Is a trait ‘conserved’? Null models for the number of changes on a tree

After reconstructing the evolutionary history of a trait, you might wish to test a hypothesis about whether the trait has undergone an ‘unusually’ small or large number of transitions between alternative states. This is the question of phylogenetic signal: if the trait exhibits a small number of transitions, then it will be conserved over large portions of the tree and close relatives will tend to exhibit the same state (high phylogenetic signal = conserved trait). If the trait exhibits a large number of changes, then close relatives will frequently have different states (low phylogenetic signal = divergent/convergent trait).

Testing the hypothesis of phylogenetic signal requires that we compare the observed number of transitions to some null hypothesis, and ask whether the data is improbable, and thus significantly different from, the null. In this case, an appropriate null model could be constructed by asking how many changes would be expected in the trait if there was no phylogenetic signal, i.e. states of the trait were randomly arranged among the taxa so close relatives share the same state only by chance (not due to inheritance from a shared common ancestor) (Maddison and Slatkin 1991). This is an example of a non-parametric test (i.e., there is no elegant solution that can be derived analytically from the underlying statistical parameters). The significance of non-parametric tests can be solved using Monte Carlo methods, which simply means brute force computer simulation under the null model.

The basic logic of a Monte Carlo test is as follows:

- I. Choose a test statistic, T, in this case the number of evolutionary steps on a tree.
- II. Calculate T for the observed data; we’ll call this  $T_0$ .
- III. Choose a null model to obtain random permutations of the data in which the pattern

of interest is removed, but all other relevant aspects of the data are maintained. In this case, we can permute (= sample without replacement) the states of the character across the tips of the tree. What aspect of the data is randomized using this null? What aspects of the data are kept constant?

IV. Conduct 99, 199, 999, 1999, 9999, 19999 randomizations using the null model in III, calculating the test statistic for each of the null data sets, T1-9999. The number of randomizations depends on the complexity of the null model, the speed of your computer, the precision you desire for the significance value, and your patience. The total number of observations, N, will be the number of randomizations plus 1 for the observed data. In some cases, it will be possible to enumerate all possible permutations of a data set under the null model. In this case the total number of possible permutations is N, one of which is the observed value, and significance can be calculated as an exact test.

V. Add the observed value to the set of null values, and then sort the entire distribution to determine the rank of  $T_0$ , which we'll call R. In the case of ties,  $T_0$  should be placed closest to the middle of the rankings, i.e. at the highest rank if it is less than the median and at the lowest rank if it is greater than the median. So if  $T_0 = 5$  (bold case below) in a null distribution based on 9 randomized data sets:

4, 5, 5, **5**, 6, 6, 7, 7, 8, 9: R = 4 out of 10  
or 1, 2, 3, 3, 4, **5**, 5, 5, 6, 7: R = 6 out of 10

VI. Now, to calculate a significance value you have to decide between two alternative tests. If you are only interested in testing the hypothesis that  $T_0$  is lower than the null expectation OR that it is greater than the null expectation, you are conducting a one-tailed test. For example, you may want to know if a trait exhibits high phylogenetic signal, but you don't really care if it exhibits lower signal than random. This would correspond to a test that the rank of  $T_0$  is significantly lower than the median. On the other hand, if you want to test for  $T_0$  deviating from the null hypothesis in either direction, it is a two-tailed test. The p-value for significance under these alternatives is:

One-tailed low:  $P \leq R/N$

One-tailed high:  $P \leq (N+1-R)/N$

Two-tailed:  $\min(2R/N, 2*(N+1-R)/N)$

#### References:

Maddison WP, Maddison DR (2000) MacClade 4 (pdf manual), Sunderland MA: Sinauer, chapters 3, 4 and 22 (equivalent to chapters 4, 5 and 17 in published MacClade 3 manual).

Maddison WP, Slatkin M (1991) Null models for the number of evolutionary steps in a character on a phylogenetic tree. *Evolution* 45: 1184-1197.