Genetics/MBT 541
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Lecture 1
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Phylogeny methods, part 1
(Parsimony and such)
Methods of reconstructing phylogenies (evolutionary trees)

**Parsimony methods.** Tree that allows evolution of the sequences with the fewest changes. *Also compatibility methods: tree that perfectly fits the most states.*

**Distance matrix methods.** Tree that best predicts the entries in a table of pairwise distances among species. *Closely related to clustering methods.*

**Maximum likelihood.** Tree that has highest probability that the observed data would evolve. *Also Bayesian methods: tree which is most probable a posteriori given some prior distribution on trees.*

**Invariants.** Tree that predicts certain algebraic relationships among patterns in the data. *Mathematically fun though little-used as it ignores too much of the data.*
A tree we will be evaluating
A simple data set with nucleotide sequences

<table>
<thead>
<tr>
<th>Species</th>
<th>Characters</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>1 2 3 4 5 6</td>
</tr>
<tr>
<td>Alpha</td>
<td>T A G C A T</td>
</tr>
<tr>
<td>Beta</td>
<td>C A A G C T</td>
</tr>
<tr>
<td>Gamma</td>
<td>T C G G C T</td>
</tr>
<tr>
<td>Delta</td>
<td>T C G C A A</td>
</tr>
<tr>
<td>Epsilon</td>
<td>C A A C A T</td>
</tr>
</tbody>
</table>
Most parsimonious states for site 1
Most parsimonious states for site 2
Most parsimonious states for site 3
Most parsimonious states for sites 4 and 5
Most parsimonious states for site 6
Steps on this tree, all characters, for one choice of reconstruction on each character. There are 9 steps in all.
Steps on another tree. There are 8 in all.
Steps on another tree, 8 in all. This is just the previous tree, rerooted.
State reconstruction on an unrooted tree
Branch lengths, averaged over all state reconstructions. This is not the most parsimonious tree but the first one we saw.
Fitch’s algorithm (for nucleotide sequences):

To count the number of steps a tree requires at a given site, start by constructing a set of nucleotides that are observed there (ambiguities are handled by having all of the possible nucleotides be there).

Go down the tree (postorder tree traversal). For each node of the tree consider its two immediate descendants’ sets, $S$ and $T$, and

- If $S \cap T \neq \emptyset$, write it down as the set in that node,
- If $S \cap T = \emptyset$, write down $S \cup T$ and count one step.
Counting the numbers of state changes using Fitch’s algorithm.
**Sankoff’s algorithm**

A dynamic programming algorithm for counting the smallest number of possible (weighted) state changes needed on a given tree.

Let $S_j(i)$ be the smallest (weighted) number of steps needed to evolve the subtree at or above node $j$, given that node $j$ is in state $i$.

Suppose that $c_{ij}$ is the cost of going from state $i$ to state $j$.

Initially, at tip (say) $j$

$$S_j(i) = \begin{cases} 
0 & \text{if node } j \text{ has (or could have) state } i \\
\infty & \text{if node } j \text{ has any other state}
\end{cases}$$
Then proceeding down the tree (postorder tree traversal) for node $a$ whose immediate descendants are $\ell$ and $r$

$$S_a(i) = \min_j \left[ c_{ij} + S_\ell(j) \right] + \min_k \left[ c_{ik} + S_r(k) \right]$$

The minimum number of (weighted) steps for the tree is found by computing at the bottom node (0) the $S'_0(i)$ and taking the smallest of these.
An example of using Sankoff’s algorithm
Compatibility Method

Two states are compatible if there exists a tree on which both could evolve with no extra changes of state.

**Pairwise Compatibility Theorem.** A set $S$ of characters has all pairs of characters compatible with each other if and only if all of the characters in the set are jointly compatible (in that there exists a tree with which all of them are compatible).

(True for what kinds of characters?)

The compatibility test for sites 1 and 2 of the example data is:

<table>
<thead>
<tr>
<th>site 1</th>
<th>site 2</th>
<th>C</th>
<th>A</th>
</tr>
</thead>
<tbody>
<tr>
<td>T</td>
<td>X</td>
<td>X</td>
<td></td>
</tr>
<tr>
<td>C</td>
<td>X</td>
<td></td>
<td>X</td>
</tr>
</tbody>
</table>
Compatibility matrix for our example data set.
The graph of pairwise compatibility. There are two “maximal cliques”, one larger than the other.
Reconstructing the tree from the clique (1, 2, 3, 6). Each character splits one set into two parts, creating a new branch which divides the species according to their state in that character.
Fitch’s set of nucleotide sequences that have each pair of sites compatible, but which are not all compatible with the same tree.

<table>
<thead>
<tr>
<th></th>
<th>Alpha</th>
<th>Beta</th>
<th>Gamma</th>
<th>Delta</th>
<th>Epsilon</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>A</td>
<td>A</td>
<td>C</td>
<td>C</td>
<td>G</td>
</tr>
<tr>
<td></td>
<td>A</td>
<td>C</td>
<td>G</td>
<td>C</td>
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<td></td>
<td>A</td>
<td>C</td>
<td>C</td>
<td>G</td>
<td>A</td>
</tr>
<tr>
<td></td>
<td>A</td>
<td>C</td>
<td>C</td>
<td>G</td>
<td>G</td>
</tr>
</tbody>
</table>
The logic of the reconstruction of ancestral states. The shaded state is the one that has been reconstructed at the lower of these two nodes in the tree. To decide what to reconstruct above it, we choose the smallest of $c_{2i} + S(i)$. 
Assignment of possible states, in parsimonious state reconstructions, for the site used in the example of the Sankoff algorithm. The parsimonious reconstructions are shown by arrows, with the costs of the changes shown. The states that are possible at the nodes of the tree are those whose boxes in the array of numbers are solid, with the others having dotted lines.
Some references


Massachusetts (in press, out this summer) [The best possible book on phylogenetic inference]