

BIOL 471 – Methods in Systematics – Phylogenetic Inference Unit
Counting Steps & Ancestor Reconstruction using Parsimony

1. Score terminal species for character of interest.

Downward Pass

2. Starting at the tips of the cladogram, start with two sister species and assign the intersection or union of the two to the node below them.

An intersection is where both descendants of the ancestral node have the same state; therefore, that state is assigned to the ancestral node.

A union is where the two descendants of the ancestral node have different states; therefore, both are temporarily assigned to the node.

3. Work the same way from another pair of taxa, down the tree until all nodes have been assigned an intersection or union.

[COUNT THE NUMBER OF UNIONS after the downpass, this is the most parsimonious length of that character on the cladogram.]

Upward pass

4. Moving up the tree from the basal-most node (for simplicity-sake, assume that the state possessed by the most distant outgroup taxon is the state at the basal-most node), resolve any unions based upon the intersection with the lower node. If there is not intersection for a particular node on the up-pass, then your data are ambiguous for that node.

[THE STATES ASSIGNED TO NODES are one (not necessarily the only one) most parsimonious reconstruction of the state possessed by the hypothetical ancestor of that node's immediate descendants.]

Now apply your method to determine (1) which is the most parsimonious tree on the next page and (2) the states for each character for each hypothetical ancestor in each tree.

	char. 1	char. 2	char. 3
Species A (outgroup)	0	0	1
Species B	1	1	0
Species C	1	0	1
Species D	1	1	1

