

Name: \_\_\_\_\_

### Tutorial 1: Simple, Manual Cladogram Construction

1. We wish to infer relationships among the major groups of vertebrates.
2. In order to “root” the phylogenetic hypothesis (i.e., our cladogram), we will choose the snail as the sole member of our outgroup.

3. Below is a character-by-taxon matrix for seven characters and their states.

Character and Character State List:

0. VERTEBRAE PRESENCE: no (0); yes (1).
1. LEGS PRESENCE: absent (0); present (1).
2. ENDOTHERMY: absent or *cold-blooded* (0); present or *warm-blooded* (1)
3. FUR PRESENCE: absent (0); present (1).
4. MAMMARY GLANDS PRESENCE: absent (0); present (1).
5. THUMB (OPPOSABILITY): not opposable (0); partially or fully opposable (1).
6. TAIL PRESENCE: present (0); absent (1).

	VERTEBRAE	LEGS	ENDOTHERMY	FUR	MAMMARY GLANDS	OPPOSABLE THUMB	TAIL
Snail	0	0	0	0	0	-	-
Fish	1	0	0	0	0	-	1
Lizard	1	1	0	0	0	0	1
Bird	1	1	1	0	0	0	1
Cow	1	1	1	1	1	0	1
Monkey	1	1	1	1	1	1	1
Gorilla	1	1	1	1	1	1	0
Human	1	1	1	1	1	1	0

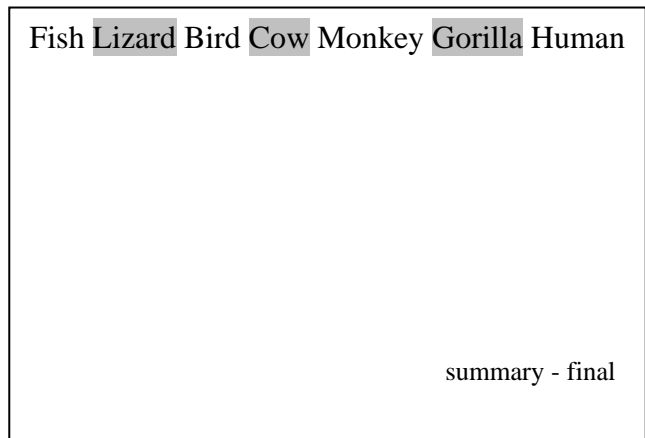
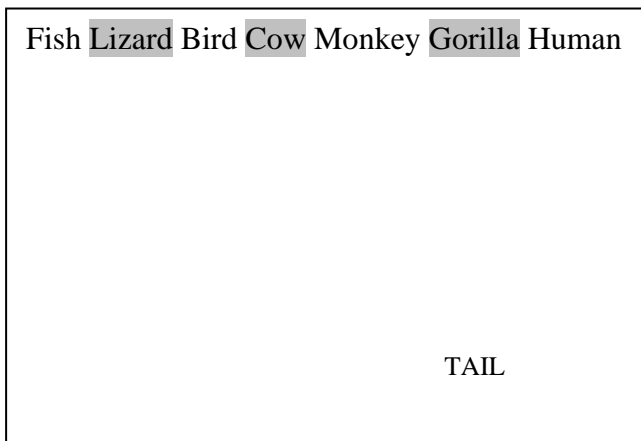
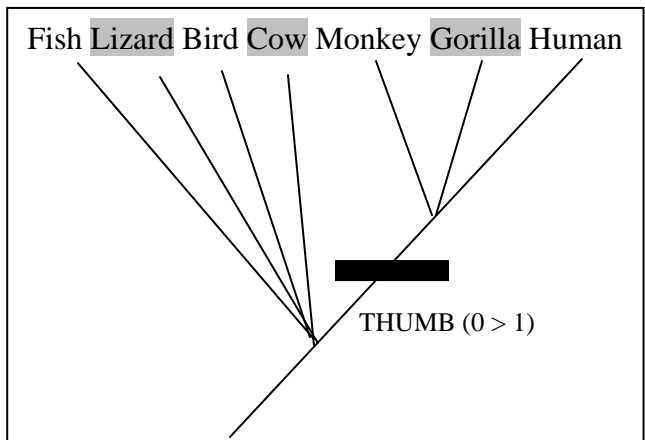
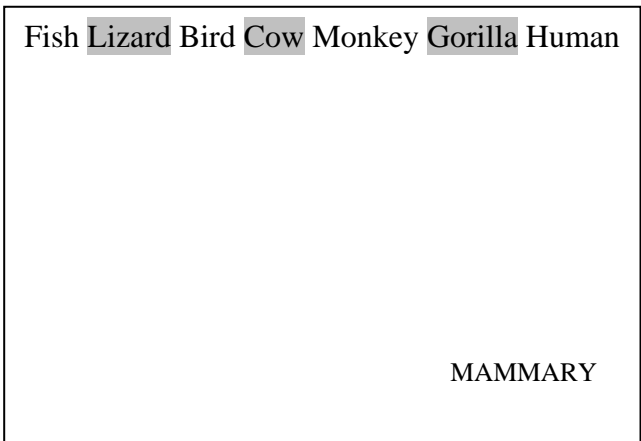
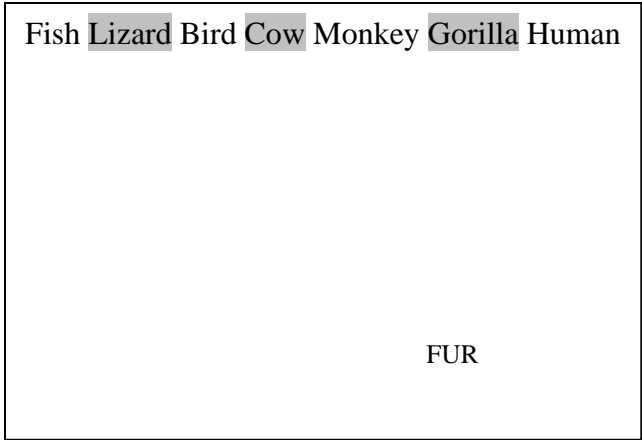
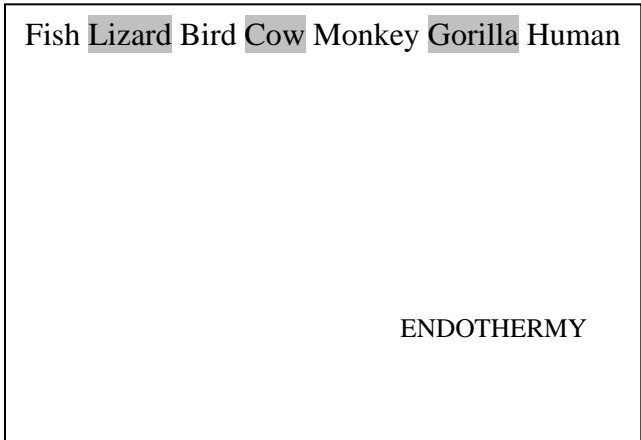
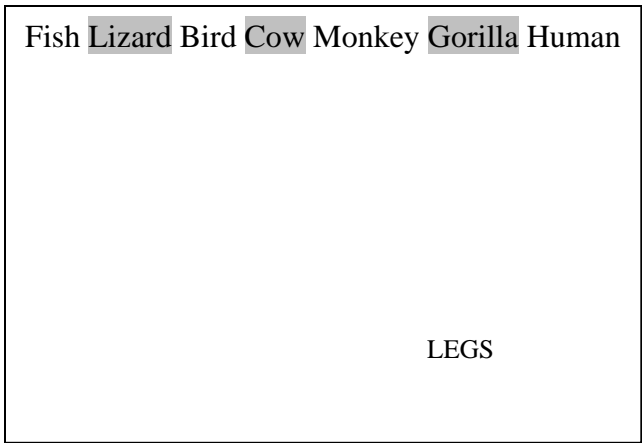
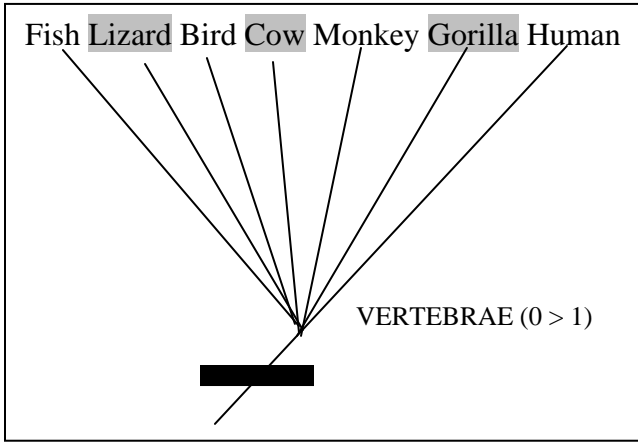
\*Note: a “-“ denotes that the character is inapplicable—i.e., not relevant—for that species.

4. In order to infer phylogeny, we will use the outgroup with the assumption that character states possessed by the outgroup are plesiomorphic.

States shared amongst members of ingroup (vertebrates) and the outgroup (snails) are symplesiomorphies (i.e., shared plesiomorphies) and are not basis for identifying clades.

Only synapomorphies (i.e., shared derived characteristics) point to clades or monophyletic groups.

5. ON THE NEXT PAGE: With each character treated separately, draw the cladogram suggested by each character. Use the principle of parsimony. When a character is uninformative with respect to certain relationships, draw those lineages as members of a polytomy (as opposed to dichotomy).



6. Now add two characters – WING PRESENCE (absent = 0; present = 1) and PEDALITY (quadrupedal = 0; bipedal = 1).

	VERTEBRAE	LEGS	ENDOTHERMY	FUR	MAMMARY GLANDS	OPPOSABLE THUMB	TAIL	WINGS	PEDALITY
Snail	0	0	0	0	0	-	-	-	-
Fish	1	0	0	0	0	-	1	-	-
Lizard	1	1	0	0	0	0	1	0	0
Bird	1	1	1	0	0	0	1	1	1
Cow	1	1	1	1	1	0	1	0	0
Monkey	1	1	1	1	1	1	1	0	0
Gorilla	1	1	1	1	1	1	0	0	0
Human	1	1	1	1	1	1	0	0	1

7. Map and label these two new characters as hashmarks onto your summary tree.

8. Answer the following questions:

*Is the presence of wings informative with regards to relationships in our cladogram?*

*Which kind(s) of inferred character transformation(s) is the origin of wings? (i.e., symplesiomorphy, synapomorphy, autapomorphy, apomorphy, and/or plesiomorphy)*

*Is the presence of bipedality (obligate bipedalism) a synapomorphy in our cladogram?  
 What is (are) the term(s) from lecture or your reading that would apply to this?*

## **Tutorial 2: Character State Optimization for Choosing Most Parsimonious Cladograms and Reconstructing Ancestral States.**

The method we will use here is called Fitch Optimization.

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.

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 Cladistics Tutorials 1 & 2 by Dr. Chris Hardy

	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

