

Exercise 1: The basic principles

1. Goals – understand the terms
 - a. Taxon
 - b. Branch
 - c. Node
 - d. Clade
 - e. Character
 - f. Character state
 - g. Evolutionary event
 - i. Gain
 - ii. Loss
 - h. Tree length
 - i. Parsimony
2. Steps (to be done with me)
 - a. Open MacClade
 - b. Open the file “Vertebrates 1 char”. Four windows open with the file.
 - i. Tree Window – this window contains the cladogram
 - ii. Tool palette – ignore this window or close it.
 - iii. Tree statistics window – this has an important parameter – the tree length
 - iv. Character window – this allows the mapping of the changes in character state in the displayed tree. There is a single char
 - c. A tree is displayed with 10 different taxa. A **taxon** is a group of phylogenetically related organisms at any level (species, genus, etc). *Note that this tree is not what we think is the “correct tree”; its just a tree with which to start.*
 - d. A **branch** leads to each taxon. In a cladogram, two branches always join at a **node**. Nodes also have branches which join at deeper nodes. A node and all the more superficial branches and taxa connected to this node is a clade. The basal node for a clade represents the hypothetical, last common ancestor of all the taxa in the clade.
 - e. There is only a single **character** to explore: the amnion, which is an important tissue in the developing embryo of some vertebrates. This character has two **character states**: 1) presence and 2) absence. The colored lines show the distribution of these states (yellow = absent, blue = present).
 - f. Notice that in this tree, the presence of an amnion has evolved three times, so we say that there have been three independent, **evolutionary events** in this phylogeny, each a **gain** of an amnion. Look at the **tree length** in the Tree statistics window. What is it? _____.
 - g. Grab the branch leading to birds and drag it to the branch leading to (birds + frogs + lungfish). Grab the branch leading to (snakes + crocodiles) and drag it to the branch leading to the node (mammals + lizards + turtles + birds + snakes + crocodiles). Notice that there are now two evolutionary events. 1) gain of amnion and 2) **loss** of amnion in (frogs + lungfish). We know that this latter is a loss because there is a hypothetical common ancestor of (frogs + lungfish) in which the amnion was present. So an evolutionary event can be a gain or a loss. The absence of an amnion in ray fin fishes and salamanders in this tree is not an

- evolutionary event because they do not have a hypothetical common ancestor that had the amnion. What is the tree length of this tree? _____.
- h. Now grab the branch leading to (frogs + lungfish) and move it to the branch leading to salamanders.
 - i. How many evolutionary events are there? _____
 - ii. What are these events? _____
 - iii. What is the tree length? _____
 - i. Given what you have discovered so far, how would you calculate the tree length?

 - j. We have looked at three different trees so far. We don't know which of these, if any, is the true tree. How do we make a decision on what our best estimate of the true tree is? Modern systematists make this decision by applying the **Principle of Parsimony**, which states something like “the best explanation is the simplest (or least complex)”. The first tree that we looked at required three independent, evolutionary events, the second required two, and the third required one. Which is simplest? The third. So if we apply the Principle of Parsimony then we chose the third tree as our best estimate of vertebrate phylogeny. Or we say that the third tree is most parsimonious. So, “most parsimonious” means “shortest tree length.”
 - k. Now grab the branch leading to turtles and drag it to the branch leading to birds. What did this do to the tree length? _____
 - l. Given this dataset with one character, is there a single shortest tree? How do we decide which of these shortest trees is our best estimate of the true tree?

Exercise 2 – Finding the shortest vertebrate tree

- 1. Goals – Finding the most parsimonious tree by hand.
- 2. Steps (to be done with partners)
 - a. Open MacClade
 - b. Open file “Vertebrates.” This dataset has the same taxa but 13 characters.
 - c. The character window has scroll bars that allow you to scroll through the 13 characters to explore the distribution of the states of each character on the tree.
 - d. Start with character 1, “Amnion.” Count the number of evolutionary events for this character. We did this above. Now look in the Character window and note the number of steps for the character “Amnion.” This is the number of evolutionary events for this character.
 - e. Scroll to the next character (“appendages”) and count the number of evolutionary events. Check the “steps” to make sure that you are correct. Describe these events
 - i. _____
 - ii. _____
 - iii. _____
 - f. Scroll through all thirteen thirteen characters and add up the steps for each character. This sum equals _____

- g. Now look at the tree length. What is it? _____
- h. So now in your own words, describe tree length.

- i. Move branches around until you find the shortest tree that you can find. This is your unsystematic attempt to find the most parsimonious tree. We are using a demo version of MacClade, so we cannot use the print function. Instead, Press command-shift-4, then press spacebar, then click in the window with the tree. This will save an image file named “picture1” to the desktop. Find this file and rename it “vert_tree_1”
- j. Can you find a different tree that is equally short. If so, save it and rename it “vert_tree_1b”

Exercise 3: Finding your own characters: The Caminalcules

- 1. Goal – learn how to code a character matrix in order to study the phylogenetics of a group of hypothetical animals – the Caminalcules
- 2. Steps
 - a. Build character matrix
 - i. The four different groups should use different sets of caminalcules
 - 1. Group 1: 1 – 12
 - 2. Group 2: 5 – 16
 - 3. Group 3: 5 – 12, 23 - 25
 - 4. Group 4: 5 – 12, 26 - 29
 - ii. Describe characters and assign each character state a number using excel
 - 1. characters can be discrete (e.g. presence/absence)
 - 2. or continuous characters can be made to be discrete (< 10 mm, 10-20 mm, >20 mm)
 - 3. decide if character states are ordered or not (lengths would be ordered, red/green/blue would not).
 - iii. Create a data matrix in MacClade
 - 1. the rows should be labeled, c1-c12. These are the taxa (individual caminalcules)
 - 2. the columns should be the characters.
 - 3. Fill in the matrix with the numbered code for the character state for each taxon
 - b. Analyze with MacClade
 - i. Find the shortest tree by hand.
 - ii. Save this tree as Camin_01
 - iii. Find the shortest tree using the parsimony tool.
 - iv. Save this tree as Camin_02
 - c. Compile everything into a Word document

Bio 205 – Lab 1 - Phylogenetics

