

## Dinosaur Practice Problem: Key for Steps 7 and 8

### Step #7: Use character matrix to analyze possible trees.

In this example, rather than making you analyze all 15 possible trees, we have drawn a subset of 5 trees to analyze. You should get the idea from these, but you can always set up the other 10 trees on your own if you like.

For each tree, you will need to determine where state changes must have occurred. In some cases, you will need to decide whether a convergence or a reversal is necessary; choose the option which puts fewer changes on the tree. (If the number of changes is identical, it doesn't matter which you choose.)

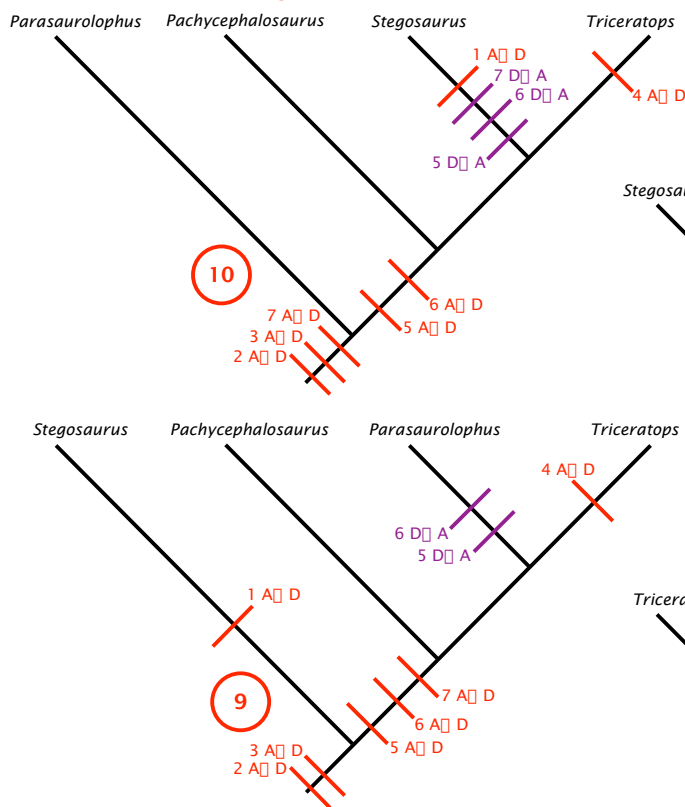
Review the trees in Figure 3 if you have questions. This process of analyzing trees may take a little time, but the more you can get figured out now, the more comfortable you will be with the procedure during lab.

Red represents a single change from ancestral to derived.

Purple represents a reversal from derived to ancestral.

Green represents a convergence: multiple changes from ancestral to derived.

The total number of changes required in each tree is in circled, in red.

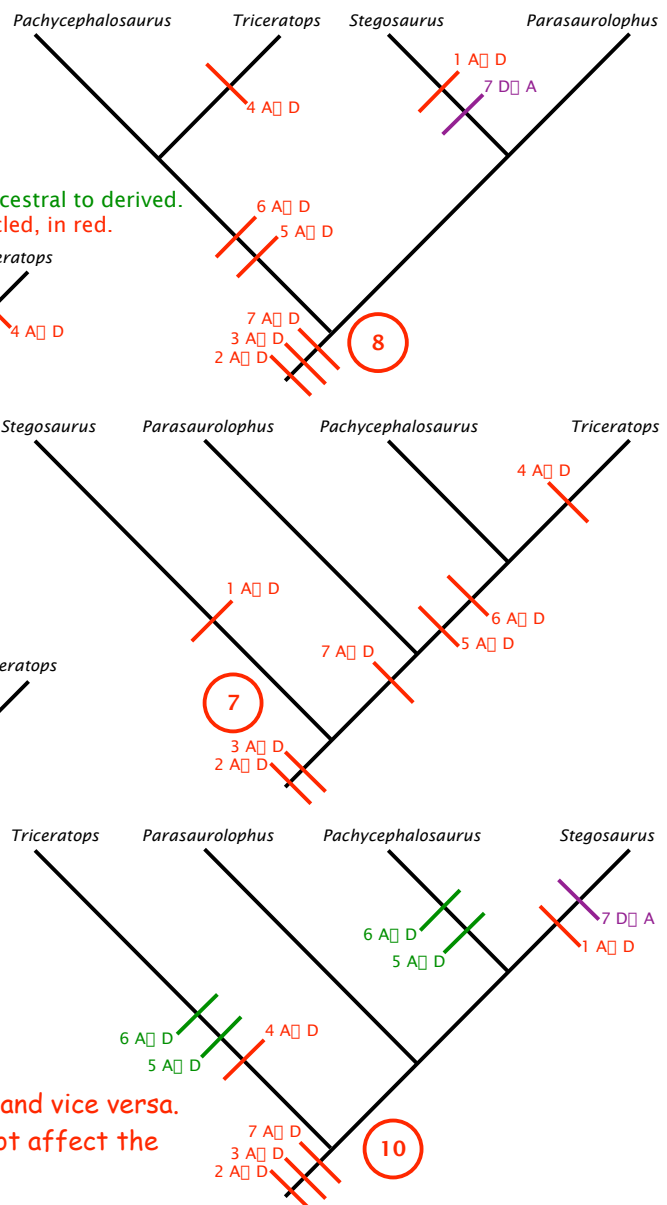


You could redraw the reversals as convergence, and vice versa. You might try this for practice; it may or may not affect the total number of changes in the tree.

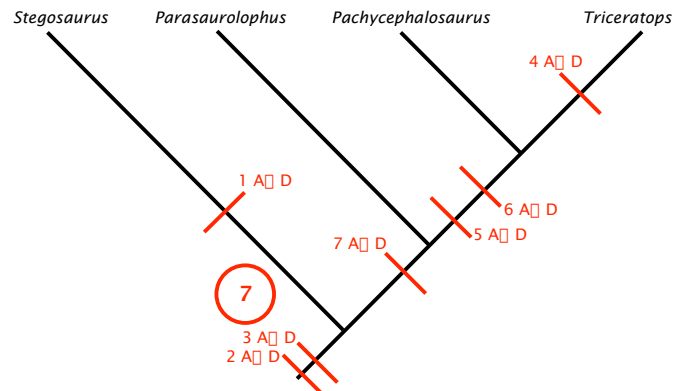
### Step #8: Determine which tree is most parsimonious.

After you have counted up the changes required for each tree, find the tree with the smallest number. Congratulations! If you haven't already, step back and look at how much each character contributed to your selection of that tree. Were there characters that had the same effect on all the trees? What are the implications of characters like those? Which characters were the most important in determining your phylogeny?

Jot down any questions you have about this procedure and bring them to lab. You can ask your lab instructor or TA about them, or just discuss them in your lab group.



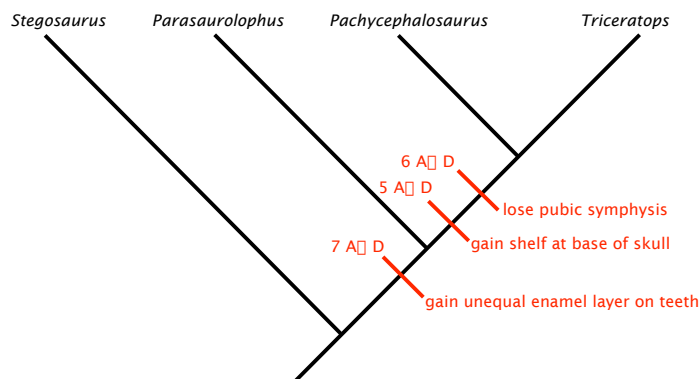
The most parsimonious tree is the one shown below. It requires only 7 changes, and no reversals or convergence.



You should quickly notice that including characters 2 and 3 on your trees did not affect the phylogeny. If you look back at the character matrix in Step 6, you'll see that these characters are derived for all four organisms: this is why they are not useful.

Characters 1 and 4 were also not helpful in creating a phylogeny; since only one organism has the derived character state for each of these characters, it does not help us group organisms with shared derived characters. If you look over your trees, you'll see that characters 1 and 4 are always out on the ends of branches, and so do not affect the overall tree.

Characters 5 and 6 have the same pattern of derived and ancestral states across these organisms. This means they do not provide us with different information from each other, but they do effectively support the same tree. Overall, characters 5, 6, and 7 were the only characters which helped us distinguish between the different possible trees. Here's a revised version of this tree with only the distinguishing changes marked:



Please bring any questions to lab with you!