# Tree Thinking

In classifying organisms, scientists use evidence from a variety of sources including morphology (appearance/structure), behavior, DNA, and fossils. Tree diagrams are models that represent how organisms likely evolved from common ancestors. This diagram is comparing species, but tree diagrams can be used to compare populations, subspecies, or other units of classification.
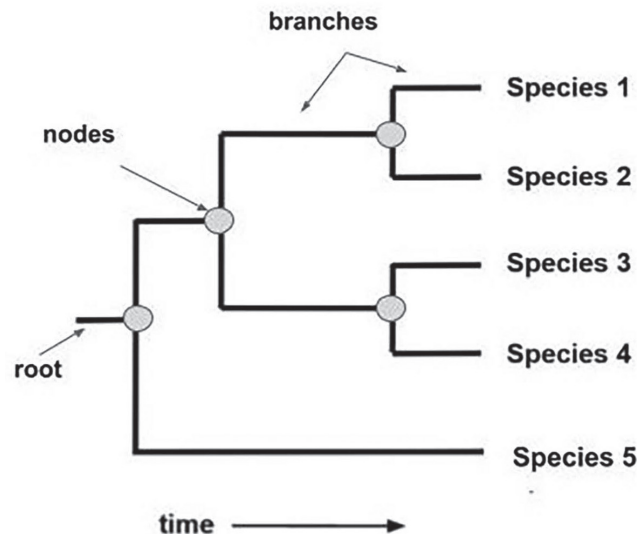

A tree diagram is read from the root to the tips of the branches.

How the branches connect shows how species evolved over time. Each node (gray circle) represents a split or divergence into two groups. This is considered a speciation event. That point of divergence is also representing the most recent ancestor for all of the groups descending from that node. Two species are *more* related if they share a *more recent* common ancestor. Species are less related if they have a less recent common ancestor, meaning their shared branching point is further away.

UNIT 4 | CHAPTER 11 • Lesson 9 • How can adaptation lead to new species?
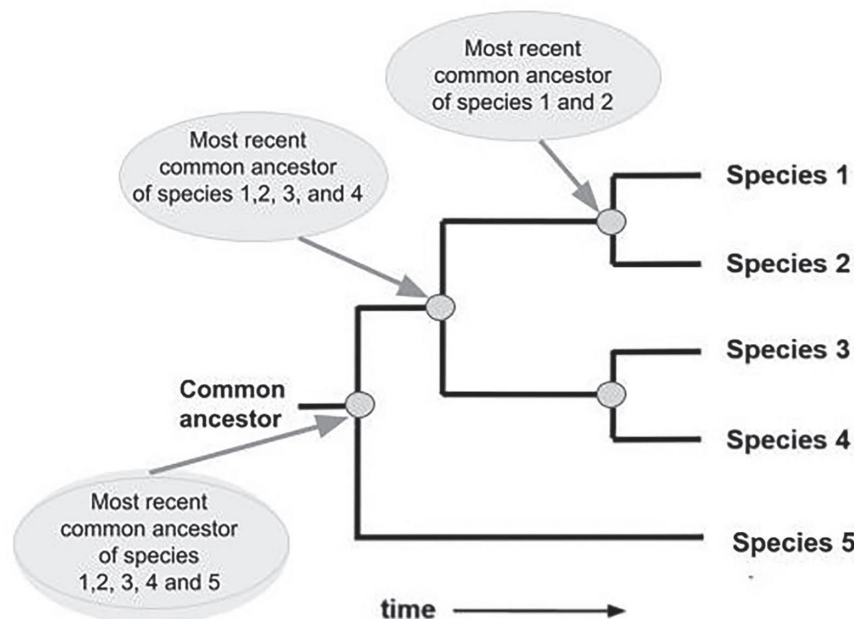
When reading a tree to understand relatedness, focus on the branching points where the nodes are located, not on the order of the species of interest. In fact, if you rotate, or pivot, the branches around the node, it does not impact the information. The two trees below show a different order of the species but not of the nodes. Both trees are showing the exact same relatedness between these species.
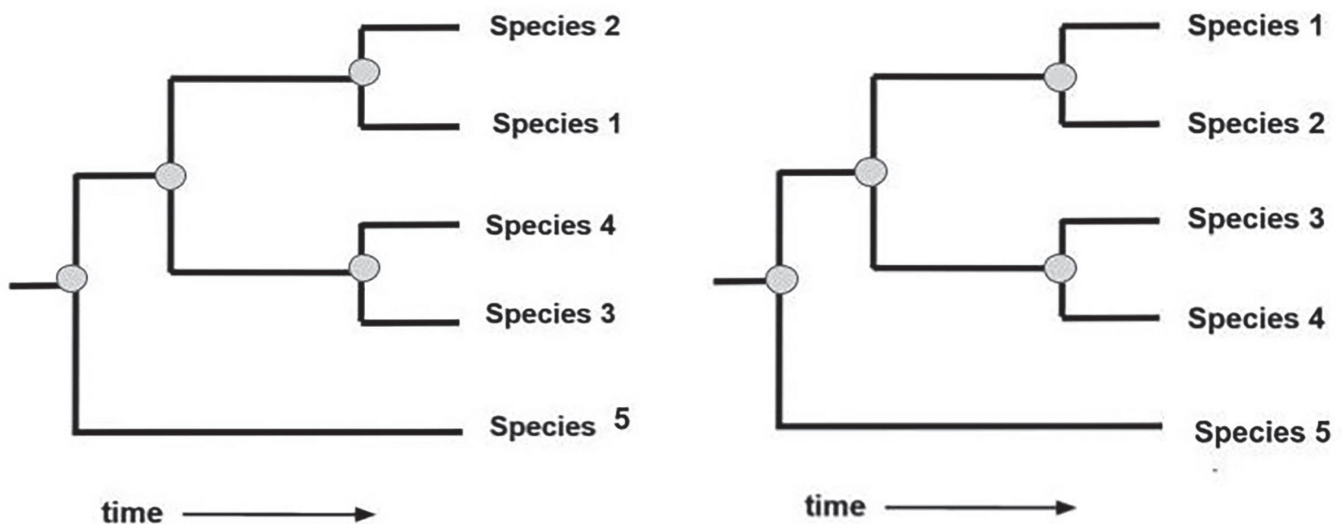
Tree diagrams can become more complex as scientists choose to include more or different information. In those cases, how the tree was constructed would be included. For example, the tree below shows the branch for species 3 not extending to the same length as the other species. This is one way to show that a species is now extinct. Other methods might include using a dashed instead of solid line or putting an "X" over the species name.