

Drawing Evolutionary Trees

The process of grouping organisms into species and other higher-level classifications is known as *systematics*. This process allows scientists anywhere to use consistent methods to document similarities among various plants, animals, and other living things. While historical methods relied on similarity of morphology (a *phenetic* approach), this can be misleading in cases where similar traits have evolved independently. The current method employed by most scientists is a *cladistic* approach, which also takes into account any information or hypotheses about which traits are likely to be *ancestral* versus more recently *derived*.

In the **Owls in Trees** investigation, you are seeking to create evolutionary hypotheses by drawing trees based on observable morphological traits and elements of owl calls that can be heard or seen with sound visualization software. What kind of similarities are you interested in, though? Since all bird species share certain traits such as four limbs, it is helpful to try to identify traits that are likely to be shared, derived traits (called *synapomorphies*), ones that may have arisen within the owls specifically, and that can differentiate subgroups which are likely to share a common ancestor.

Evolutionary trees (or *cladograms*) are not tricky to make if you know how to begin. Here are some step-by-step instructions to help you get started:

- 1) First, look at each of the species you are working with. Observe the characteristics of each one and form initial hypotheses about which are most closely related to one another. (If you have a species that you know is an *outgroup*, or further related from any of the species than they are from each other, this can help inform your initial hypotheses and selection of characteristics.)
- 2) Identify prominent traits, or *characters*, that might help you differentiate the species into broader groups. For simplicity, define your traits so that they only have two *character states*: *ancestral*, and *derived*. You may have to make inferences about the ancestral character states, for which you should be able to explain your reasoning. Once you choose these characters, list them in the columns of the table, or *character matrix*.
- 3) Next, list your owl species as the rows of your matrix. Looking at each species, work along the columns one-by-one to mark whether they have the ancestral, or derived state of each character. (Note: for simplicity, we use checkmarks to indicate the presence of derived traits, but software for generating *phylogenetic* hypotheses often uses the convention of 0 for ancestral and 1 for derived).

- 4) Add up the total derived characters present for each species as shown in the table below. This will help you get an idea of the relatedness of one species to another as you form your tree. Usually you will want to start your tree with the species that has fewest derived characters.

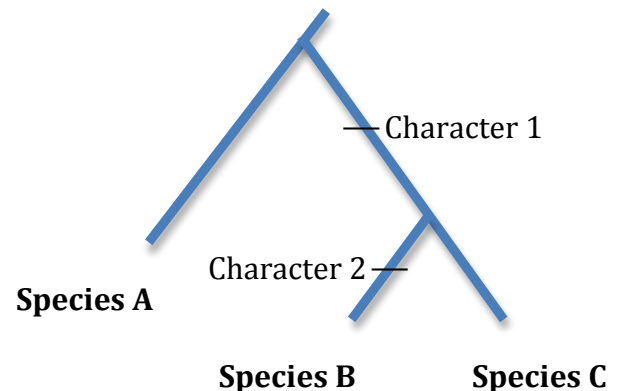
In this table, Species A appears to be the earliest diverging, possessing none of the derived characters we have identified as arising within the owl lineage.

	Character 1	Character 2	Character 3	Character 4	Character 5	Total
Species A						0
Species B	✓	✓		✓		3
Species C	✓					1
Species D	✓	✓		✓	✓	4

- 5) Start your tree with a simple upside-down *y* shape. At the end of one branch of this shape, place the species that shares the fewest traits in common with the other species (e.g., the outgroup, if you have one). There are methods of creating “unrooted” trees when you don’t have an outgroup, but here we will focus on “rooted” evolutionary trees.)

- 6) With the first species in place, then look for the species with the second lowest total of derived characters, which in our example is species C. Form a new node at the end of the second branch on which to place species C.

- 7) With each change in character state, you will form a node to make a new branch. Find the next most ancestral species and set a new node.



- 8) Continue adding nodes and branches until all species have their own branch. It may be helpful to label the characters along each branch to help you stay organized with the tree as shown on the figure above.

While creating your tree, there are several things you may wish to keep in mind. First, no species should be placed at the nodes. All surviving species (called *extant*) and *extinct* species (which no longer exist but we have evidence of from the fossil record) belong at the ends of branches. At times, you might find it necessary to split more than one species at a node because two of the species have a trait while the others do not. This is okay as long as you make sure that the character states support this splitting (e.g., you should not draw extra nodes that aren’t supported by a character found in your matrix).

Make sure to go back and check your tree. Can it be formatted more simply? The simplest tree that requires the fewest number of changes in the presence or absence of traits is called the most parsimonious tree. There are other ways than parsimony to determine the best tree, such as using prior knowledge about species histories, traits, or molecular evolution to determine the most likely tree. Often, the most parsimonious tree and the most likely tree are the same, so using a parsimony rule is a good first attempt at reconstructing evolutionary history.

Key Terms and Concepts

Ancestral

Character

Character state

Character matrix

Cladistic

Cladogram

Derived

Extant

Extinct

Node

Outgroup

Parsimony/Parsimonious

Phenetic

Phylogeny/Phylogenetic

Synapomorphy

Systematics

Resources to Learn More

Understanding Evolution Website:

http://evolution.berkeley.edu/evolibrary/article/phylogenetics_01

Tree of Life Web Project:

<http://tolweb.org/tree/phylogeny.html>