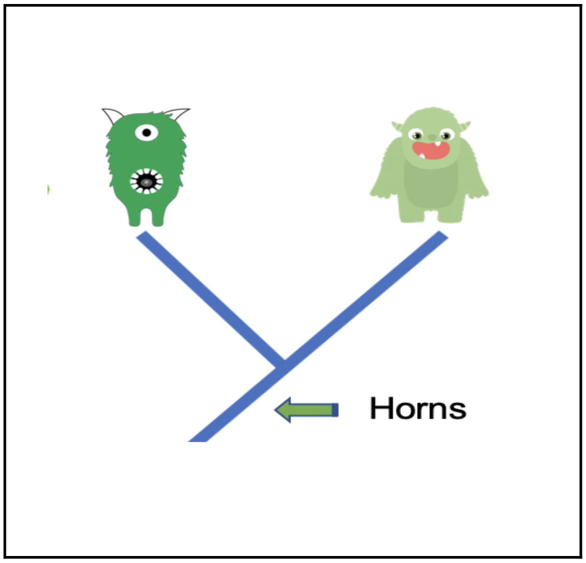
Creating a Monster Phylogeny

Format: In person or online



Part of a “monster phylogeny,” showing where horns evolved.

Author: Beth Shook

Time needed: 30-50 minutes

Learning Objectives

- Identify traits of characters and place them into a student-defined hierarchy to create a classification key
- Draw a corresponding phylogeny (evolutionary tree) for the characters
- Identify clades and corresponding primitive and derived characteristics using the phylogeny

Supplies Needed

- Ten imaginary character cards/tiles per group (each group can have the same set of ten or a unique assortment). Characters (attached) can be printed on cardstock or laminated, or tiles from a child’s memory/matching game can be used.
- Pencils with erasers
- Colored markers
- Blank paper
- Rulers (optional)
- Student worksheet (attached)

Readings

- Etting, Stephanie. 2019. Chapter 5: Meet the Living Primates. *Explorations*.

Introduction

A phylogeny is a diagram depicting evolutionary relationships among organisms (*taxa*). Phylogenies are sometimes referred to as evolutionary trees or cladograms. These “family trees” are developed based on analysis of physical traits, or, increasingly, genetic information, that provide clues about the evolutionary relationships between these organisms.

In this lab, students create a fictional phylogeny by first identifying traits shared among fictional characters and developing a (student-defined) classification key. Students then draw the phylogeny and identify common ancestors (nodes), contemporary *taxa* (tips), and clades. They mark where certain traits evolved on the tree. Lastly, students identify primitive and derived traits for some of the clades.

Steps

1. This activity may be assigned as either an individual or small group activity.
2. Instructors will distribute 10 character images to each student or small group. Each group can have the same set of 10, or each group can have a unique assortment of characters (this is often more enjoyable). Printables (attached) can be printed (on cardstock or laminated), or tiles from a child’s memory/matching game can be used. It is *not* recommended to use images of real animals as students may feel pressured to select the “right” biological answer. Instead, students should be encouraged to be creative.There is no perfect phylogenetic answer. This lab is more about experiencing the process and learning the concepts.
3. Before the activity, the instructor should spend some time introducing what phylogenies are and how they are drawn and labeled. Some of this information is provided in the “background” section of the student worksheet (attached).
4. The instructor should also review how to identify clades and primitive and derived characteristics. It can be beneficial to go through a simple example ahead of time, articulating the expectations for how to circle clades, write in where traits evolved, and identify primitive and derived traits.
5. Using the cards and the instructions in the student worksheet (attached), students develop a classification key and a corresponding phylogeny. This phylogeny should be appropriately labeled. Lastly, students will circle some clades and identify primitive and derived traits.
6. Instructors should collect the students’ phylogenies to check for accuracy. Afterward, they should go through an abbreviated version of one of the phylogenies (or use the example

attached) and check for students' understanding of primitive and derived traits. Do not reveal the example to the students before they turn in their phylogenies, as it may bias their work.

Review Questions

- What is the meaning of “phylogeny”?
- Which characteristics did you focus on when you were developing your tree? Why? In this case we don't know in what order the traits evolved in this group of *taxa* (they are fictional!). However, biologists want their phylogenies to reflect evolutionary history. What clues do biologists use to help them identify the order in which these traits evolved?
- How would your phylogeny change if you chose to focus on different aspects?
- What have you found to be the most helpful way to distinguish between primitive and derived traits for a given clade? Briefly describe how one trait on your phylogeny could be both a primitive and a derived trait.

Adapting for Online Learning

1 Not adaptable **2 Possible to adapt** 3 Easy to adapt

This activity does not require many supplies and could be adapted for online classes if students can print and cut out the imaginary characters (attached) or move the digital images around in an electronic document (e.g., Google Slides). This activity can be difficult for some students new to these concepts, so it is important that students follow the order of the steps and ask questions during the process. It is best to do this activity during a synchronous online session (live with an instructor) or provide a demonstration first.

For Further Exploration

The Understanding Evolution team. Phylogenetic systematics, a.k.a. evolutionary trees. https://evolution.berkeley.edu/evolibrary/article/0_0_0/phylogenetics_01

References

Etting, Stephanie. 2019. “Chapter 5: Meet the Living Primates.” In *Explorations: An Open Invitation to Biological Anthropology*, edited by Beth Shook, Katie Nelson, Kelsie Aguilera, and Lara Braff. Arlington, VA: American Anthropological Association. http://explorations.americananthro.org/

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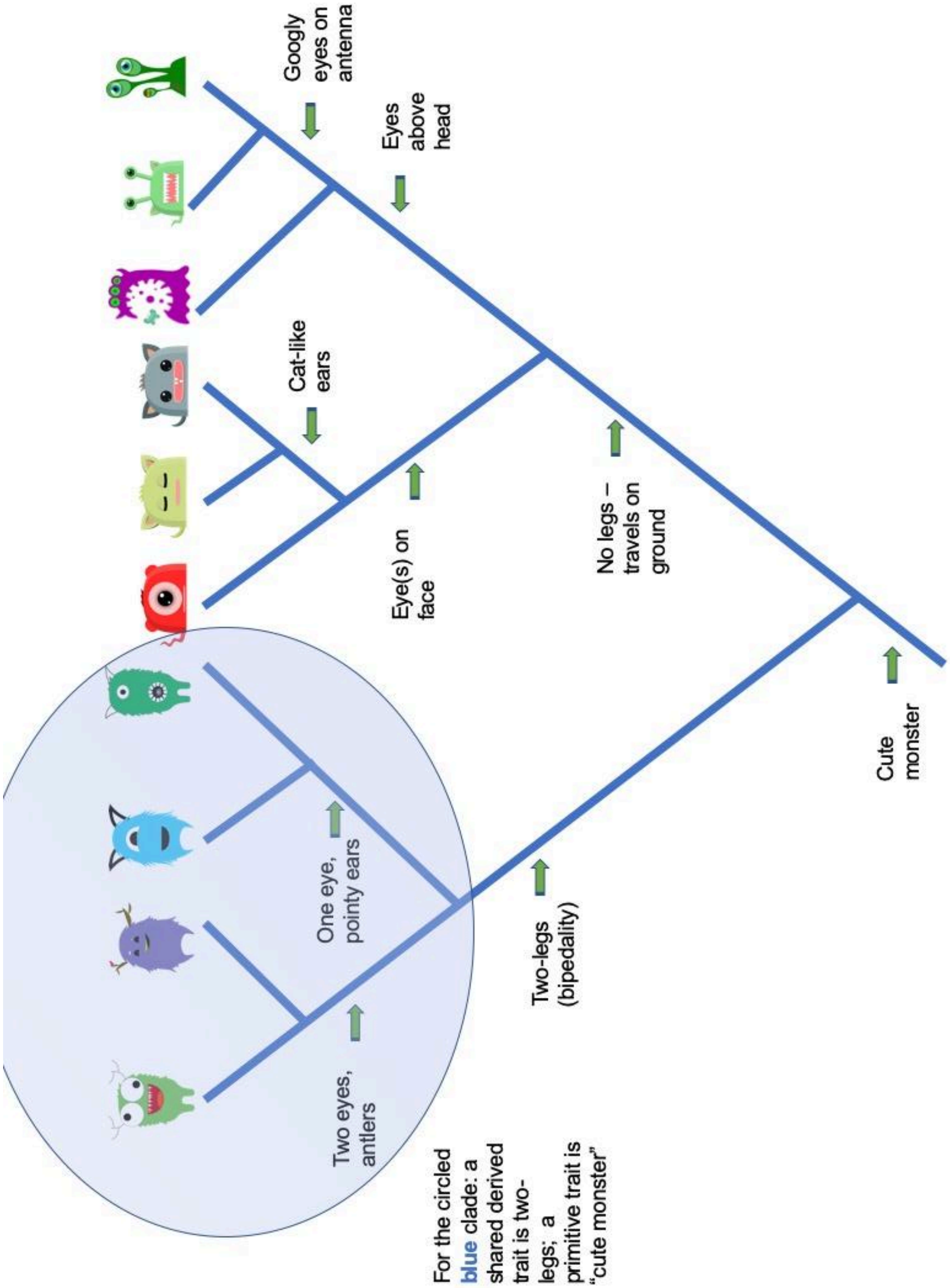
Example Phylogeny for Instructor

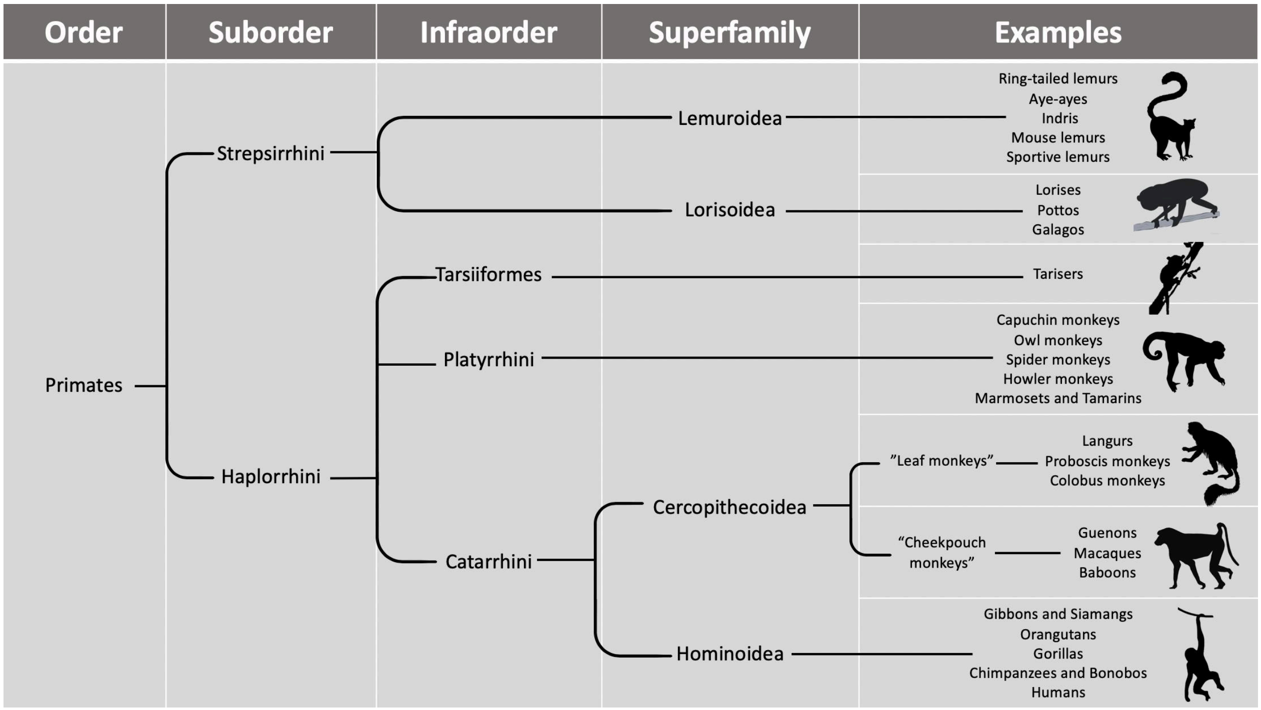


For the circled **blue** clade: a shared derived trait is two-legs; a primitive trait is "cute monster"

Creating a Monster Phylogeny: Worksheet

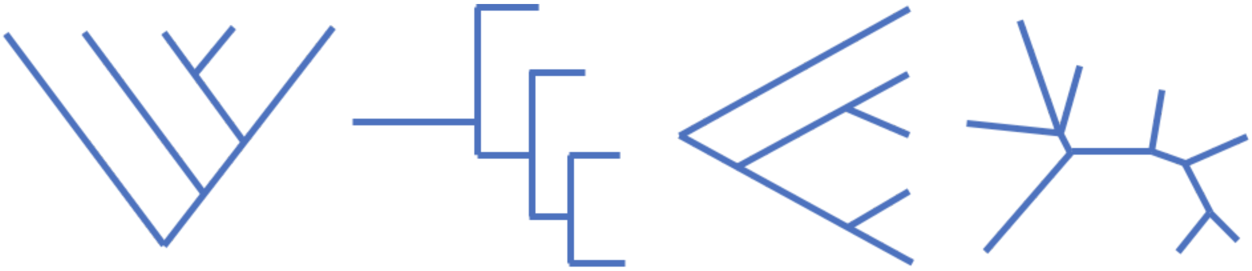
Background

A phylogeny is a diagram depicting evolutionary relationships among organisms (*taxa*). Phylogenies are sometimes referred to as evolutionary trees or cladograms. These “family trees” are developed based on analysis of physical characters, or, increasingly, genetic information, that provide clues about the evolutionary relationships between these organisms. An example phylogeny of the order *Primates* is provided below.

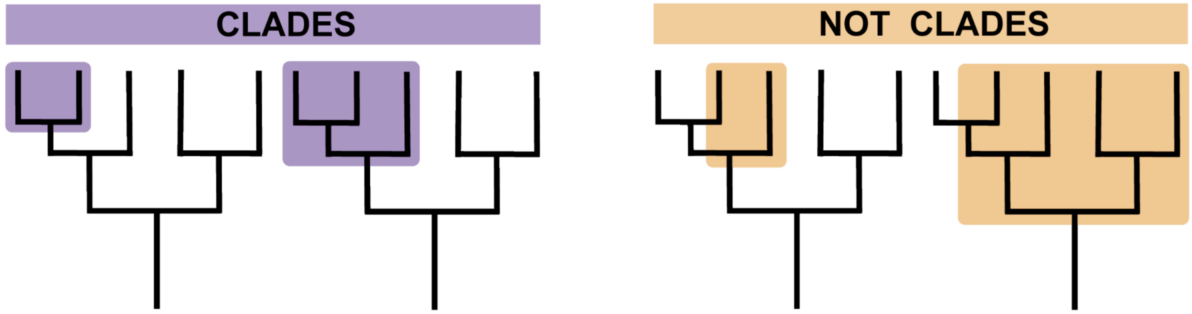


Each of the tips of the phylogeny represents a type of organism (*taxon*, singular for *taxa*). These are usually different species, but could be individuals. A *node*, where a phylogeny branches into two (or more) descendant branches, represents a common ancestor. Typically those in the field of cladistics (who create and study evolutionary trees and clades, as defined below) assume that when a lineage splits, it splits into exactly two groups. However, sometimes the data is insufficient to identify in which order the splits occurred.

Phylogenetic trees can be oriented in various directions, with the common ancestor at the bottom, side, or even spiraling out from the center.



Phylogenetic trees depict *clades*. A clade is defined as a common ancestor and **all** of its descendants (living and extinct). Phylogenies will include many clades—often with clades nested inside of other clades. In fact, the entire tree can be conceptualized as one clade—since they all share one common ancestor. Thus, when describing part of a phylogeny, it is important to clearly identify which clade is being discussed—members of a clade will often share a scientific name.



Cladistics assumes that characteristics (physical and/or genetic) will change over time. It is when these traits change that we are able to differentiate between lineages or groups. The original form of the trait (held by ancestors and relatives outside a designated clade) is considered "*primitive*" or *plesiomorphic*. Be careful not to assume primitive traits are more simple or inferior, though, as evolution does not imply improvement or increased complexity! Changed traits are referred to as "*derived*" or *apomorphic*. All members of a clade can be distinguished from all other *taxa* in the tree because they inherited a *shared derived trait* or traits that were novel to the common ancestor of that clade.

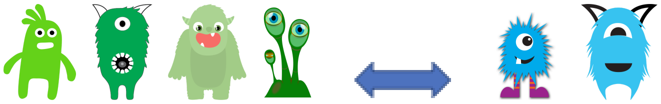
Steps

For this activity, you will use the 10 imaginary characters provided for you, to create a classification key and a corresponding phylogeny. You will need a couple sheets of blank paper, a pencil with an eraser (to draw your phylogeny and erase/move lines, if needed), and colored pens, to complete the activity.

To Build the Classification Key

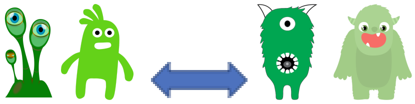
1. Lay out the 10 characters in front of you. Identify a character trait(s) that divides the 10 characters into two groups, for example: two legs versus four legs or green versus blue. The 10 characters do not need to be divided exactly in half; dividing them into one small and one large group based on the trait you select is equally fine. The precise trait(s) you select is not critical for this activity; what matters is that your categorization is strong. **Take careful notes along the way to document the new groups you made and the traits you used to divide them.**

   Example: Green versus Blue

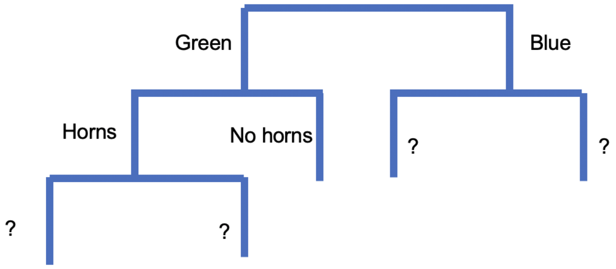
2. Repeat the process with each of the small groups, selecting a new trait each time. For example, you could now divide the green group by those with horns and those without. The number of individuals in each group does not matter—a group of five could be divided into one and four, or two and three. **Again, take careful notes along the way to document the new groups you made and the trait(s) you used to divide them.**

   Example: Horns versus No Horns

3. Continue dividing up all subgroups with two or more imaginary characters until each individual can be classified as unique by the traits it possesses. Again, take careful notes along the way!

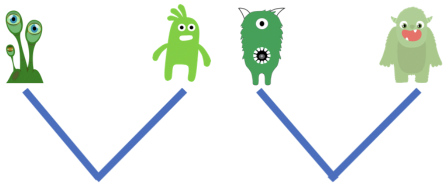
4. Now write out a simple key—it does not need to be perfect but it must be legible and clearly represent each of the divisions of your characters. At the bottom of the key, where all individuals have been separated, it may be helpful to give each character a name to help you distinguish it on both the key and the phylogeny. Here is an example of a key. Be sure to include the derived traits that you use to divide your characters next to the brackets.



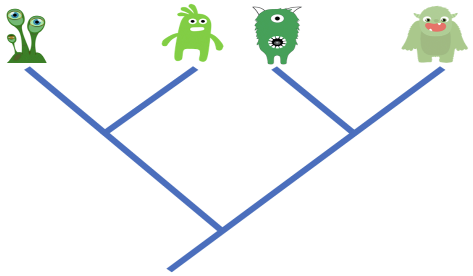
To Build the Phylogeny

5. Using a pencil and a new blank sheet of paper organized on a landscape layout (so the long edge is horizontal), list all 10 characters across the top of the page in the same order that they were at the bottom of your key (left to right). You may draw them or use an identifying name (e.g., green three-eyed monster).

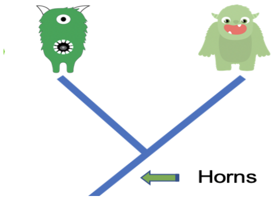
6. Starting just below the characters, draw lines down to connect the characters who are most closely related (share the most traits and were the last to be separated in the key.)



7. Continue connecting individuals/groups (at their node) to complete the phylogeny.



8. Label the phylogeny with all the traits from your key approximately where they evolved (just below the last common ancestor node).



9. Using three different colored markers, draw a circle around three distinct clades (one color for each clade).

10. To the side, or on the back of your finished phylogeny, answer the following questions based on your tree.
    a. Define clade.
    b. What are represented by the tips of the phylogeny?
    c. What are represented by the nodes of the phylogeny?
    d. For each of the three clades, name a *shared derived trait* and a *primitive trait*. Please record the color and corresponding trait; for example: *For the red clade, a primitive trait is three teeth and a shared derived trait is fur.*
    e. Are there any traits from your phylogeny that were identified as a primitive trait for one clade and a derived trait for another clade? Why does this occur?

11. When you are finished, label your phylogeny with your name and submit it to your instructor.