

Subject Code	BIO 1	Biology 1
Learning Guide Code	4.0	Classification of Organisms
Lesson Code	4.5	Constructing a Phylogenetic Tree or Cladogram
Time Frame		30 minutes



TARGET

After completing this learning guide, you are expected to:

1. determine how a phylogenetic tree or cladogram is constructed; and
2. construct a phylogenetic tree or cladogram based on a given set of characters.

HOOK

Below is an image of common utensils used in the kitchen. If you were to arrange them in your kitchen, how would sort them out? Would you arrange them by function? By shape? Or by make? What would be the best characteristic to sort them?



Scientists also need to sort and list characteristics of organisms being classified when constructing phylogenetic trees and cladograms; the more representative of relatedness the characteristic, the more effective the tree in showing evolutionary history.



When constructing phylogenetic trees or cladograms, lists of characters of organisms to be classified are generated. The lists would show whether the characters are shared by all organisms (assumed as ancestral characters) or not shared at all (assumed to be derived characters). An example of a list of characters is given below to illustrate this process.

Table 1 presents a group of organisms in columns and some characters in rows. An “X” mark in the column signifies that the organism possess that particular character.

Table 1. Character List of Five Selected Animals.

Character	Lamprey	Antelope	Bald Eagle	Alligator	Sea Bass
Lungs		X	X	X	
Jaws		X	X	X	X
Feathers			X		
Notochord	X	X	X	X	X
Gizzard			X	X	
Hair		X			

(Source: Bear et al., 2016)

The first step is to determine the character that is common to all of the organisms. This character is assumed as the ancestral condition - the notochord. Thus, the notochord should characterize the oldest ancestor at the base of any cladogram or tree to be constructed. The next step is to determine the next most common character among the organisms. In this case, the presence of jaws is shared by all except one of the organisms, the lamprey. This means that the lamprey is the outgroup, an organism that diverged early in the history of the group of organisms being investigated. The lamprey is then represented by a branch that is separated from the rest of the group.

If this process is continued, adding a branch to the tree based on the presence or absence of a character, you will eventually place all the organisms on separate branches (see Figure 1).

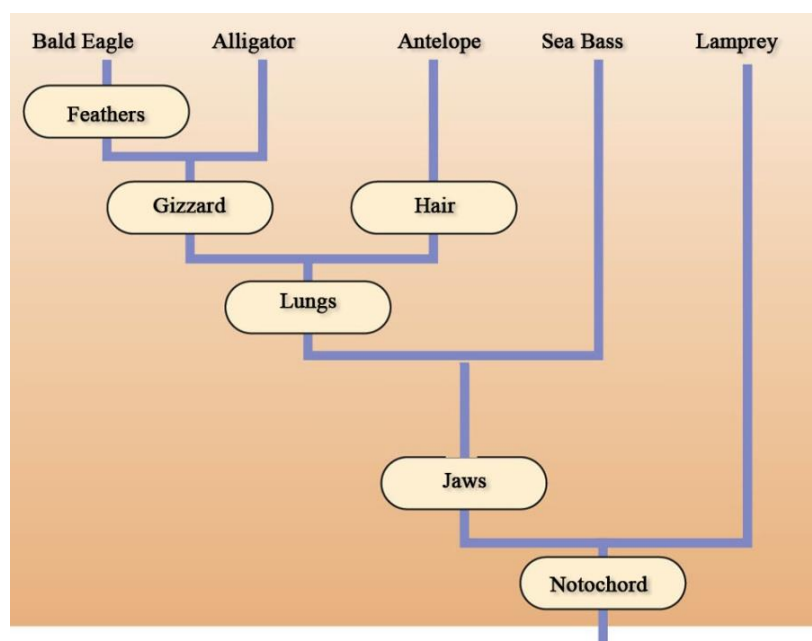


Figure 1. Cladogram created based on data in Table 1. Each shaded ellipse represents an ancestor possessing that trait, while the organisms on the opposite branch lack that trait. From *Taxonomy and Phylogeny* by Bear et al., 2016, <https://cnx.org/contents/24nI-KJ8@24.18:EmlvXoDL@7/Taxonomy-and-phylogeny>. CC 4.0

Points to remember:

1. When interpreting a tree or cladogram, the focus should be on the branches and the way they are connected to each other. They provide the important information, not the way the organisms or taxa are arranged at the top. The evolutionary relationship is not determined from the organisms' sequence at the top.
2. Tracing the branch points downwards or backwards will lead you to the most recent common ancestor of a group of organisms aligned at the top of the tree or the ends of the branches. For example, in Figure 1, the alligator and the antelope have a more recent common ancestor than the alligator and the sea bass.
3. A longer line does not mean a longer length of time. The lines just represent the direction of time from past to present or from ancient times to a more recent period. The lengths do not indicate the evolutionary time between branch points.
4. Trees or cladograms can be represented in different ways and still be identical.

Any set of inherited characters can be useful in generating cladograms. When characters are quantitatively representative of relatedness, the cladograms generated can be powerful tools for understanding organisms and for generating predictive hypotheses.



NAVIGATE

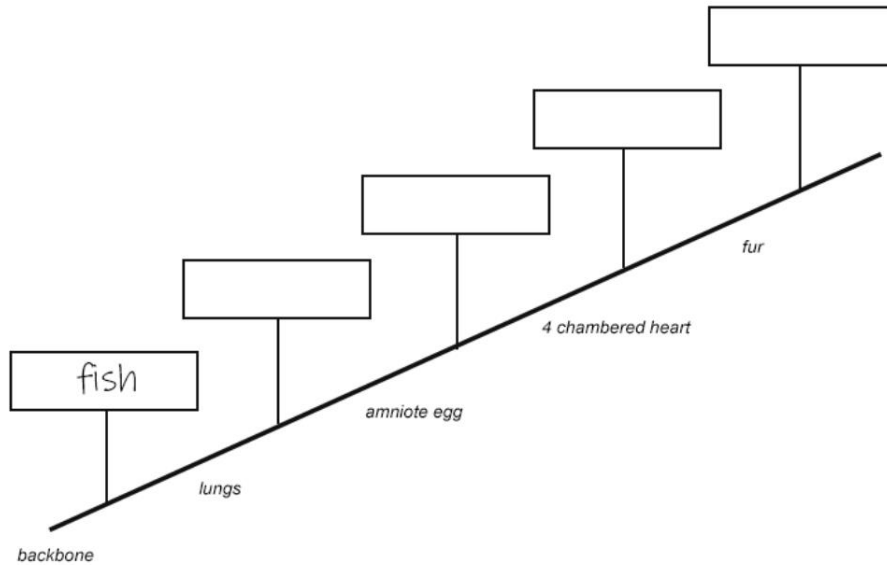
A. Creating an Animal Cladogram (What is a cladogram?, 2020)

Complete the characteristics chart for five species of animals below. Place an **X** for features that each animal has, and a **O** for features not exhibited in the animal. All of these animals have backbone, the first column is completed for you. (non-graded)

Table 2. Characteristics Chart of Five Vertebrates.

Animal	Traits				
	Backbone	Lungs	Amniotic Egg	4 Chambered heart	Fur
Fish	X				
Frog	X				
Lizard	X				
Bird	X				
Koala	X				

Convert the chart into a diagram. Each group, called a clade, has the traits below it on the diagram. When a group does not have a trait, it is called an outgroup. The first outgroup is fish, because it is the only one that does not have lungs. Complete the diagram below using the data in Table 2.



B. Create Your Own Cladogram (Muskopf, 2020)

To make your own cladogram, you must first look at the animals you are studying and establish characteristics that they share and ones that are unique to each group. For the animals on the table, indicate whether the characteristic is present (**X**) or not (**O**). Based on that chart, create a cladogram like the one above.

Table 3. Characteristics Chart of Five Animals

Animal	Traits				
	Cells	Backbone	Legs	Hair	Opposable thumbs
Slug					
Catfish					
Frog					
Tiger					
Human					



KNOT

Shared characters, whether ancestral or derived, are used by scientists in constructing phylogenetic trees and cladograms. Shared characters must first be listed and sorted before a tree can be constructed. And when classifying the organisms, the starting point must always be the character that is shared by most of the organisms. The tree generated would be a good tool for hypothesizing evolutionary relationships when the characters used are quantitatively representative of relatedness within a group of organisms.

References:

Bear, R., Rintoul, D., Snyder, B., Smith-Caldas, M., Herren, C., & Horne, E. (2016, May 14). *Chapter 4: Taxonomy and phylogeny*. Openstax CNX. <https://cnx.org/contents/24nI-KJ8@24.18:EmlvXoDL@7/Taxonomy-and-phylogeny>

Muskopf, S. (2020, March 9). *How does a cladogram reveal evolutionary relationships?*. Biology Libretexts. [https://bio.libretexts.org/Bookshelves/Ancillary_Materials/Worksheets/Book%3A_The_Biology_Corner_\(Worksheets\)/Evolution/How_Does_a_Cladogram_Reveal_Evolutionary_Relationships%3F](https://bio.libretexts.org/Bookshelves/Ancillary_Materials/Worksheets/Book%3A_The_Biology_Corner_(Worksheets)/Evolution/How_Does_a_Cladogram_Reveal_Evolutionary_Relationships%3F)

Reece, J.B., Urry, L.A., Cain, M.L., Wasserman, S.A., Minorsky, P.V. & Jackson, R.B. (2011). *Campbell Biology* (9th ed.). San Francisco, California: Pearson Benjamin Cummings.

What is a cladogram? (2020, April 4). Biology Libretexts. [https://bio.libretexts.org/Bookshelves/Ancillary_Materials/Worksheets/Book%3A_The_Biology_Corner_\(Worksheets\)/Evolution/What_is_a_Cladogram%3F](https://bio.libretexts.org/Bookshelves/Ancillary_Materials/Worksheets/Book%3A_The_Biology_Corner_(Worksheets)/Evolution/What_is_a_Cladogram%3F)

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