

Subject Code	BIO 1	Biology 1
Learning Guide Code	4.0	Classification of Organisms
Lesson Code	4.4	Interpreting Phylogenetic Trees and Cladograms
Time Frame		30 minutes



TARGET

After completing this learning guide, you are expected to:

1. identify and describe the parts of a phylogenetic tree;
2. differentiate a phylogenetic tree from a cladogram; and
3. analyse the evolutionary relationships among organisms based on a phylogenetic tree or cladogram.

HOOK

Family trees are commonly used to show relationships among individuals. The figure below shows an example of a simple family tree with three generations.

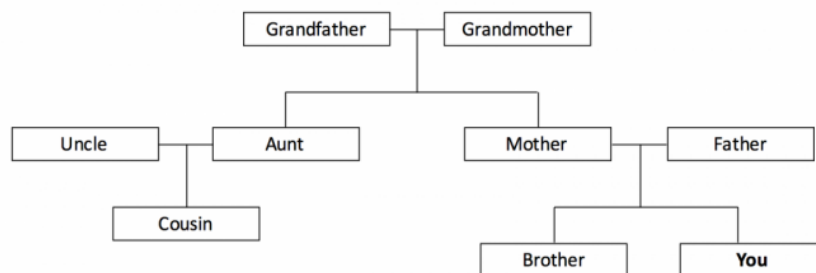


Figure 1. A simple family tree with three generations.

If you construct your own family tree, would it look the same as the one above?

Just like your family tree, relationships among different organisms can be represented using a branching diagram, the phylogenetic tree.



IGNITE

A **phylogenetic tree** is a branching diagram that represents the evolutionary history of a group of organisms (see Figure 2). It is constructed using various data derived from studies on morphology, fossil evidence and molecular evidence to establish relationships. Just like a phylogenetic tree, a cladogram also illustrates relationships among organisms (see Figure 3). The difference is that the branches in a cladogram are representatives of the relative amount of change or evolutionary time that has occurred between organisms whereas; branches in a phylogenetic tree can be proportional to the evolutionary time. To some biologists, the cladogram represents a hypothesis about the evolutionary history of a group, while phylogenies represent true evolutionary history. There really is not really much of a difference and the terms can be interchangeable. In any case, they both describe a tree

structure that represents the hypothesized evolutionary relationships within a group of organisms based on data from morphology, fossil evidence and gene sequences.

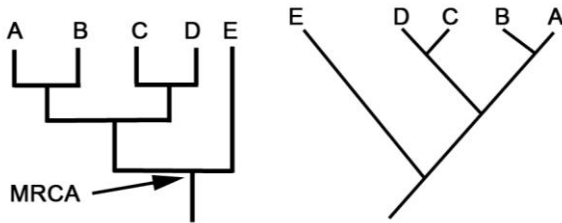


Figure 2. A phylogenetic tree showing five groups or species. MRCA means most recent common ancestor. From *Taxonomy and Phylogeny* by Bear et al., 2016, <https://cnx.org/contents/24nI-KJ8@24.18:EmlvXoDL@7/Taxonomy-and-phylogeny>. CC 4.0

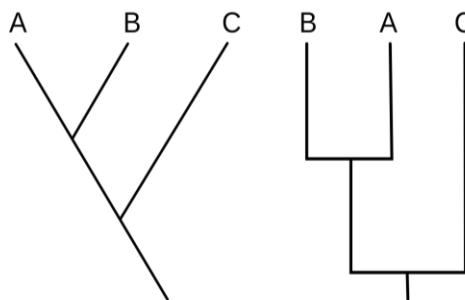


Figure 3. Two seemingly different, though identical, cladograms, illustrating the idea that neither shape, nor a particular arrangement of the terminal branches really matters. The only information included in the cladogram is the information on the nested pattern of the sister-group relationships. By Kouprianov, 2006, <https://commons.wikimedia.org/w/index.php?curid=1136977>. CC-SA 3.0

Parts of a Phylogenetic Tree / Cladogram

Organisms being classified are found at the tips of the tree's **branches**, and each organism or species is called a **taxon**. Their relationships are depicted in a series of two-way **branch points** (see Figure 4). The tree in Figure 4 shows a **root**; this means the most common ancestor of all the taxa in the tree is represented by a branch point within the tree (often drawn farthest to the left). Figure 4 shows the evolutionary relationship of five groups or taxa (A, B, C, D, and E). Branch points (1, 2, 3, and 4) represent the most common ancestor of the organisms found to the right of the branch points. For example, branch point 4 is the most common ancestor of Taxa C and D. Taxa A and B are **sister taxa**, groups of organisms that share an immediate common ancestor. A **basal taxon** (also called an **outgroup**) is a lineage that diverges early in the history of a group, and like taxon E lies on a branch that originates near the common ancestor of the group.

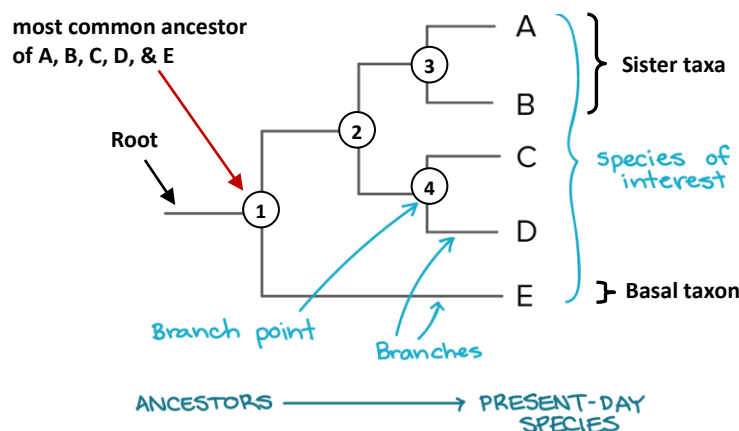


Figure 4. Parts of a phylogenetic tree. (image modified from Khan Academy, n.d.. CC BY 4.0)

A tree may also show a **polytomy**, a branch point from which more than two descendant groups emerge (see Figure 5). A polytomy shows that the evolutionary relationships among the taxa are not yet clear.

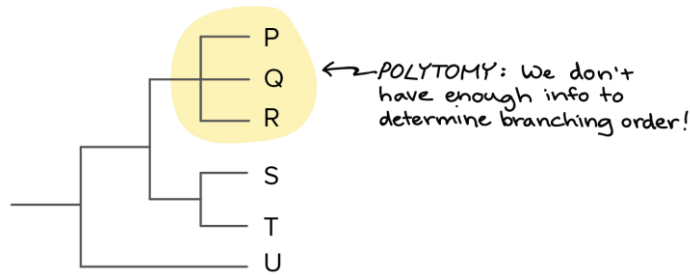


Figure 5. A phylogenetic tree with a polytomy. From *Phylogenetic Trees* by Khan Academy, n.d. <https://www.khanacademy.org/science/high-school-biology/hs-evolution/hs-phylogeny/a/phylogenetic-trees>. CC BY-NC-SA 4.0

A phylogenetic tree may be rotated around one of the branch points as a pivot without changing the relationships. Figure 6 shows trees illustrating the relationships among species A, B, C, and D. The trees are essentially the same. The point is to focus on the relationships and the branch points and not on the sequence of the species across the tops of the trees.

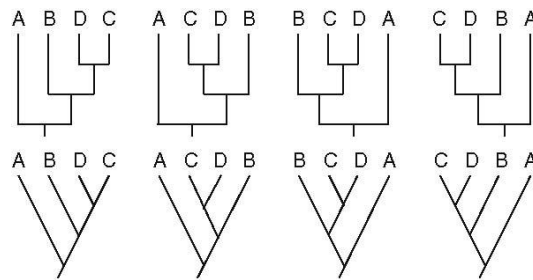


Figure 6. Different depictions of the same phylogenetic tree. All the trees depict the same relationships among organisms A, B, C and D. From *Taxonomy and Phylogeny* by Bear et al., 2016, <https://cnx.org/contents/24nI-KJ8@24.18:EmlvXoDL@7/Taxonomy-and-phylogeny>. CC 4.0

Cladistics

Cladistics is an approach to systematics wherein common ancestry is the primary criterion used to classify organisms. Species are placed into groups called **clades**, each of which includes an ancestral species and all of its descendants. There are major types of clades: monophyletic, paraphyletic and polyphyletic. A monophyletic group (clade) consists of an ancestral species and all of its descendants (see Figure 7).

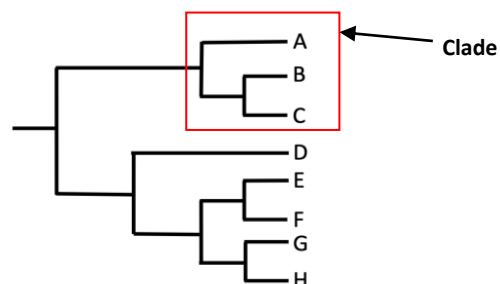


Figure 7. A phylogenetic tree showing a monophyletic group. The tree has eight groups showing a monophyletic group (clade) consisting of taxa A, B and C and their common ancestor. (image modified from Digital Atlas of Ancient Life, n.d. CCNC-SA 4.0)

A paraphyletic group consists of an ancestral species and some, but not all of its descendants (see Figure 8). A polyphyletic group includes taxa with different ancestors (see Figure 9).

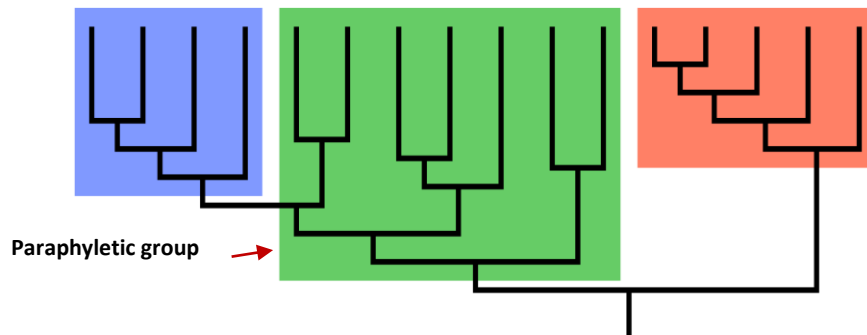


Figure 8. Cladogram (family tree) of a biological group. Examples of a clade are shown by the blue and red subgroups. A paraphyletic group is exemplified by the green subgroup; it excludes the blue branch, even though they came from a common ancestor. From *Clade* by Life of Riley, 2010, <https://en.wikipedia.org/wiki/Clade>. Public Domain

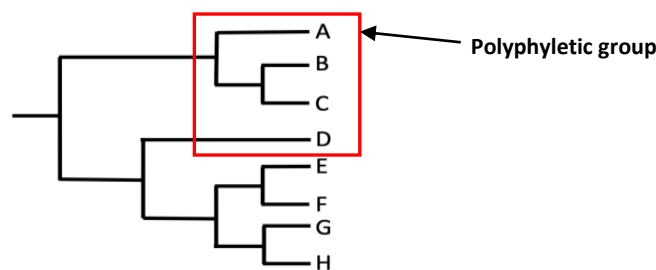


Figure 9. A tree showing a polyphyletic group. Some members of the group have different ancestors; A, B and C share a common ancestor, while D has a different ancestor. (image modified from Digital Atlas of Ancient Life, n.d. CC NC-SA 4.0)

Cladograms or phylogenetic trees are constructed based on a comparison of morphological or molecular characteristics of organisms, either ancestral or derived. Characteristics originating in an ancestor of the taxon are **shared ancestral characters**. Those that are not found in their ancestors but are present in the descendant taxa are **shared derived characters**.

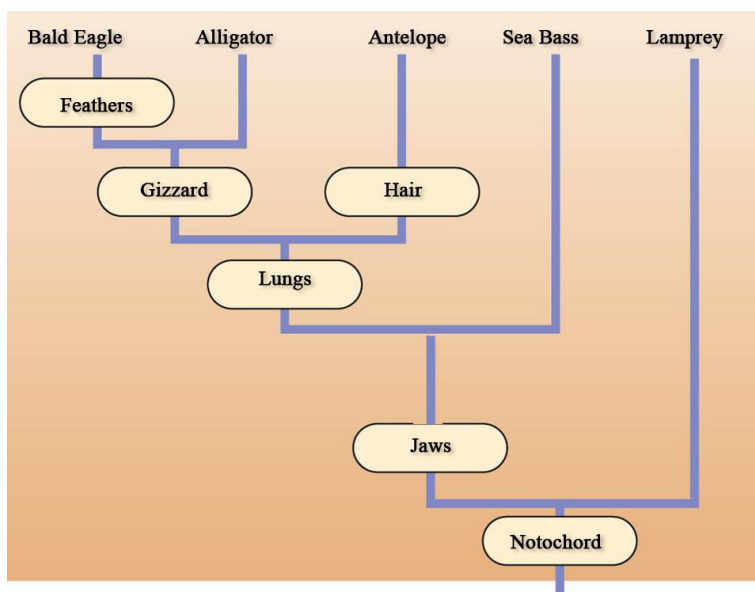


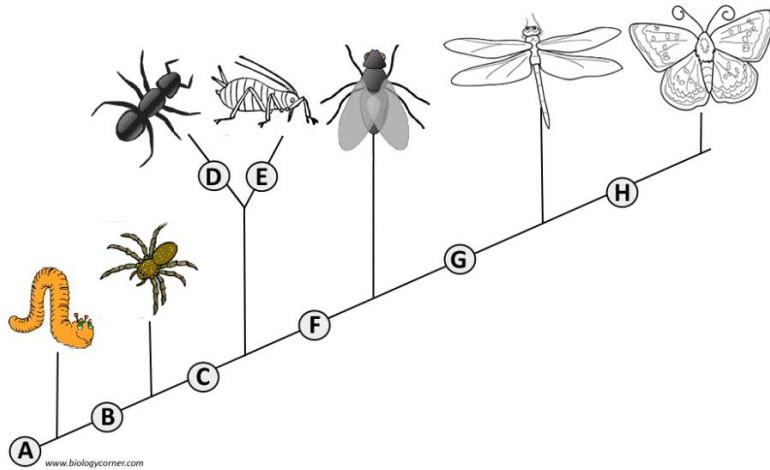
Figure 9. A cladogram constructed based on shared ancestral / derived characters. Each shaded ellipse represents an ancestor possessing that trait, while the organism(s) on the opposite branch lack that trait. From *Taxonomy and Phylogeny* by Bear et al., 2016, <https://cnx.org/contents/24nI-KJ8@24.18:EmlvXoDL@7/Taxonomy-and-phylogeny>. CC 4.0



NAVIGATE

Analyzing the Cladogram (Muskopf, 2020)

Examine the sample cladogram, each letter on the diagram points to a derived character, or something different (or newer) than what was seen in previous groups. Match the letter to its character. *Note: this cladogram was created for simplicity and understanding, it does not represent the established phylogeny for insects and their relatives. (non-graded)*



1. ____Wings
2. ____6 Legs
3. ____Segmented body
4. ____Double set of wings
5. ____Legs
6. ____Crushing mouthparts
7. ____Curly antennae
8. ____Cerci (abdominal appendages)



KNOT

A phylogenetic tree or a cladogram is a branching diagram that represents the evolutionary relationships of organisms. The organisms are classified based on shared ancestral characters or shared derived characters. These characteristics can include external and internal morphology, fossil characteristics and molecular characteristics. Still phylogenetic trees and cladograms are still hypotheses. They can be revised and updated as new data become available and included in the analysis.

References:

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