

Evolution and Biodiversity Laboratory

Systematics: Reconstructing Phylogenies

by Dana Krempels and Julian Lee

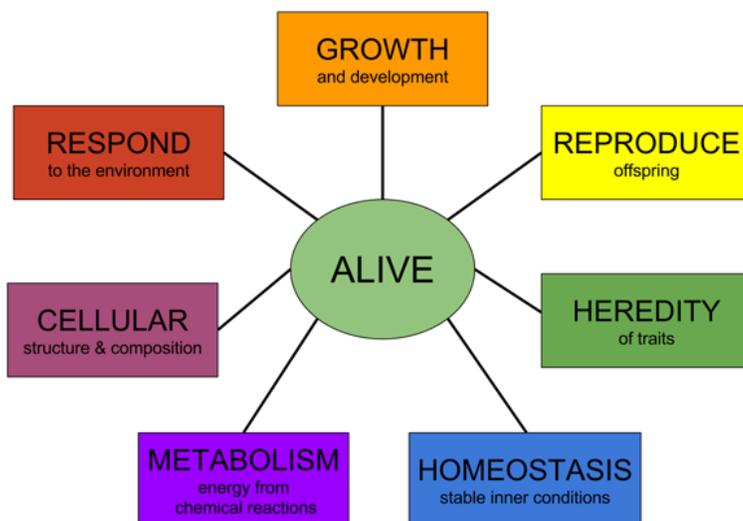
Plentiful evidence confirms that **extant** (presently living) and **extinct** (no longer living) species evolved from previously existing **ancestral species**. We know that this involved **descent with modification** of **traits** (= **characters**) from one generation to the next.

- A **primitive character** (**plesiomorphy**) shows little or no change from the same character in an ancestor
 - A **symplesiomorphy** is a primitive character shared between two or more taxa
- A **derived character** (**apomorphy**) has changed in appearance and/or function relative to the same character in an ancestor
 - A **synapomorphy** is a derived character shared between two or more taxa

I. Symplesiomorphies vs. Synapomorphies

All living things share certain characteristics that define them as living things.

To be considered alive, a thing must exhibit



- **cellular composition**
- **metabolism**
- **homeostasis**
- **response to its environment**
- **growth and development**
- **reproduction**
- **heritability of traits (DNA)**

Figure 1. The seven criteria of life

By Chris Packard - Own work, CC BY-SA 4.0,
<https://commons.wikimedia.org/w/index.php?curid=59184218>

These seven shared traits are **primitive** to all living things because they were also present in the common ancestor of all living things.

They are **symplesiomorphies** that define life.

Consider:

- Would your knowing that a living thing has **DNA** allow you to distinguish it from other living things?
- Would your knowing that a living thing can maintain **homeostasis** allow you to distinguish it from other living things?
- Would your knowing that a living thing can **reproduce** allow you to distinguish it from other living things?

Simple answer: No.

Symplesiomorphies are not informative or useful when one is trying to separate a large group of organisms into smaller, less inclusive groups.

Synapomorphies are informative and useful when one is trying to separate a large group of organisms into smaller, less inclusive groups. A synapomorphy unique to the individuals in a particular taxon makes them *different* from members of other taxa.

Synapomorphies inherited from a common ancestor indicate relative recency of common descent.

The more synapomorphies two taxa have in common, the more recently they evolved from a common ancestor.

II. Homologous vs. Analogous characters

If the similarity of a character in two separate taxa can be attributed to their presence in a common ancestor, then those two characters are said to be **homologous**.

For example, the **forelimb bones** of all tetrapod (four-legged) vertebrates are homologous to one another, because they all evolved from the same bones in a common tetrapod ancestor.

Although the bones may have evolved very different sizes, shapes, and functions, they all developed from the same embryonic sources and have evolved from the

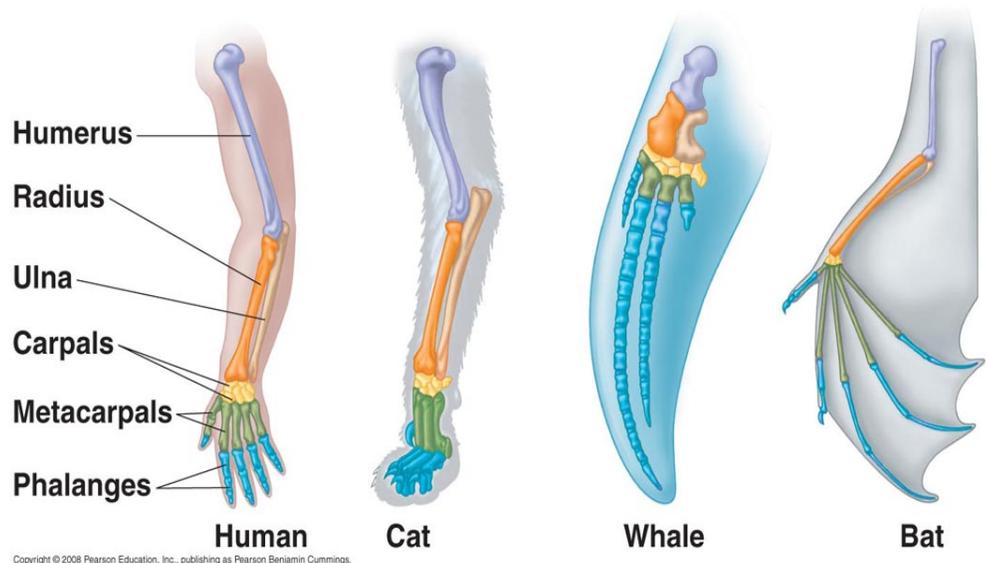
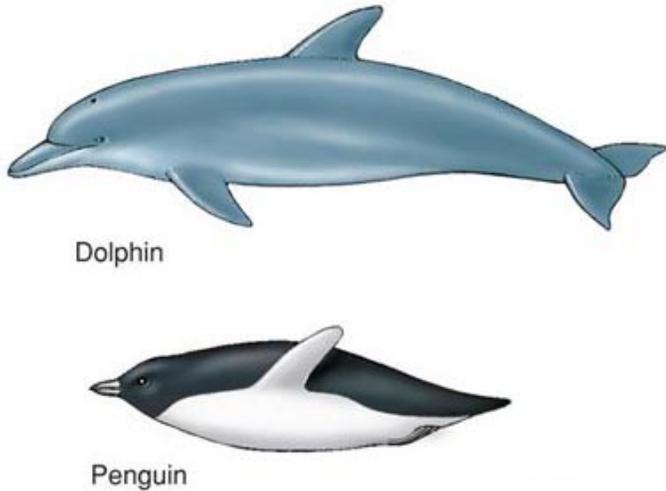


Figure 2. Homologous vertebrate limb bones

same ancestral tetrapod limb bones

Not all physical similarities are homologous. Unrelated taxa often have evolved superficially similar morphologies in response to *similar natural selection pressure*.



For example, a penguin and a dolphin share a streamlined, fusiform shape well adapted for fast swimming. However...

- the penguin's body evolved from that of an ancestral, flying bird.
- the dolphin's body evolved from that of a four-legged, terrestrial mammal.

The superficial similarity of penguin and dolphin is a result of **convergent evolution**.

Figure 3. Convergent fusiform bodies of dolphin and penguin

Characters that have evolved similar form and function from disparate ancestral sources are said to be **analogous**. Analogous characters are sometimes called **homoplastic characters** or **homoplasies** (from the Greek *homo*, "alike" and *plas*, "shape").

Don't let the similarity of the terms "homoplastic" and "homologous" confuse you!

III. Modern Systematics: The Cladistic System

The **Cladistic System** (from the Greek *clad*, "branch") is a biological classification system in which organisms are classified exclusively on the basis of **recency of descent from a common ancestor as determined by synapomorphies**.

A. Phylogenetic Trees

A **phylogeny** is a history of the natural evolutionary descent of extant and extinct taxa from ancestral forms. The cladist attempts to reconstruct phylogenies by comparing the **character states** of extant and extinct forms.

Phylogenies can be represented as treelike diagrams showing how various extant taxa branched from common ancestors and from each other. Such a diagram is called a **phylogenetic tree** or **evolutionary tree** (Figure 4).

- A phylogenetic tree shows putative evolutionary relationships.
- A phylogenetic tree constructed with cladistic methods is called a **cladogram**.
- A **clade** is a group of organisms believed to have evolved from a common ancestor.
- **Taxa** (clades) are represented as **branches** that bifurcate from **nodes**.
- A node represents the **hypothetical common ancestor** of the taxa on the branches above it on the tree.

- A node also represents the taxonomic unit (order, family, genus, etc.) containing the taxa represented by the branches.
- Nodes are considered *hypothetical* ancestors (also known as **hypothetical taxonomic units**, or **HTUs**) because they cannot be directly observed.
- The base or **root** of the tree represents the hypothetical common ancestor of all taxa on the tree.

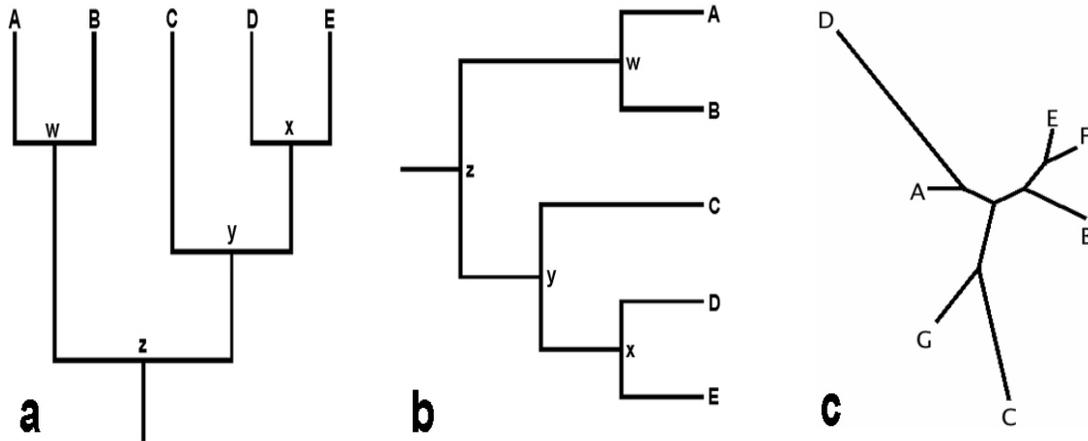


Figure 4. Different graphic representations of phylogenies. Whether a tree is upright, on its side, or drawn as a spiral, the information is essentially the same. Nodes represent common ancestors of taxa (branches) above them on the tree, and endpoints represent descendant taxa.

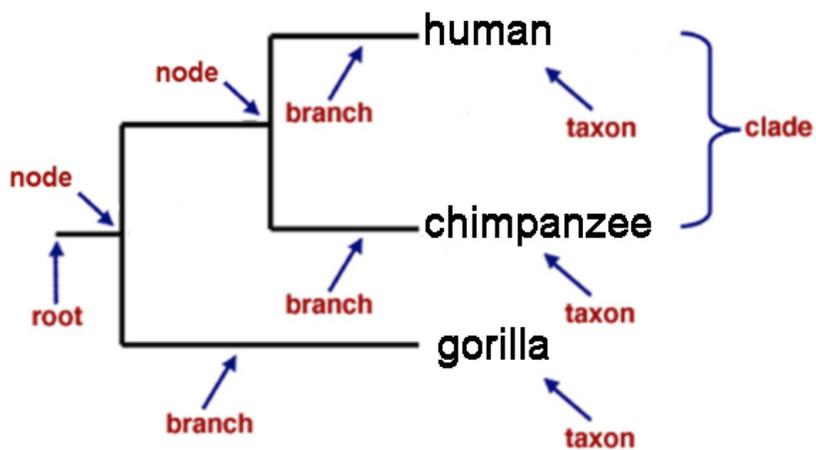


Figure 5. A phylogenetic tree. The taxa included are “human,” “chimpanzee,” and “gorilla.”

- Each node represents the common ancestor of the taxa to the right of it on the tree.
- All taxa descended from a common ancestor comprise a **clade**.
- Human and Chimpanzee comprise a single clade.
- Human/Chimpanzee/Gorilla comprise another, more inclusive clade.
- The more inclusive the clade, the higher its taxonomic rank.
- Branches diverge from nodes (ancestors), and represent a genetic unit descended from the ancestor at that node.
- Two lineages branching from the same ancestor arose at the same geological time
- The root represents the common ancestor of all taxa included on the tree.

B. The Rules of Modern Systematics

The Cladistic System of classification was first published by German zoologist **Willi Hennig** in 1950. It is an objective and quantitative method of modern classification, and it is to its tenets that we—and the vast majority of modern systematists--adhere.

There are rules.

Rule #1: The branches at every node can be rotated.

The branches do not imply any sort of order; they indicate only recency of common descent. In Figure 5, the node under human and chimpanzee could be rotated so that chimpanzee is on top and human is below. The information on the tree would not change with rotation of the node.

Rule #2: Two lineages branching from a single ancestor node are known as sister taxa.

Further specialization after a branch point is irrelevant. Therefore, it would be incorrect to say that humans evolved more recently than chimpanzees, or that humans should be placed in their own family simply because they seem so different from chimpanzees. *Taxonomic groupings are based on common ancestry only, not subjective perceptions of specialization.*

Rule #3: There is no such thing as a “most highly evolved” taxon.

All extant species are descended from successful ancestors, and are evolved to survive and reproduce in the context of their specific environment. Evolution is a process. It has neither a goal nor a subjective value system.

Rule #4: No extant nor extinct taxon can be considered ancestral to any other extant or extinct taxon.

Nodes represent hypothetical ancestors, not taxonomic units. When an ancestral lineage diverges to become two separate taxa, the ancestral lineage (hypothetical ancestor) is considered extinct, even if one of the descendant taxa is (or might be) virtually the same as that hypothetical ancestor.

Living species did not evolve from other living species.

Humans did not evolve from monkeys.

Humans and monkeys share a common ancestor.

C. Rooted and Unrooted Trees

Rooting a tree is determining the location of the hypothetical common ancestor with respect to the other taxa on the tree.

In a **rooted tree**, each node represents the most recent common ancestor of the taxa branching from it. Rooted trees are directional, with all taxa evolving or radiating from that single common ancestor at the root.

Because we have seen only rooted trees so far, this might seem like a no-brainer. But raw phylogenetic data often yield *unrooted* trees.

In an **unrooted tree** (Figure 6) there is no hypothetical ancestor, and no directionality to the tree. The tree shows only the putative evolutionary relationships of the taxa on the tree, without the evolutionary directionality implied by an ancestor.

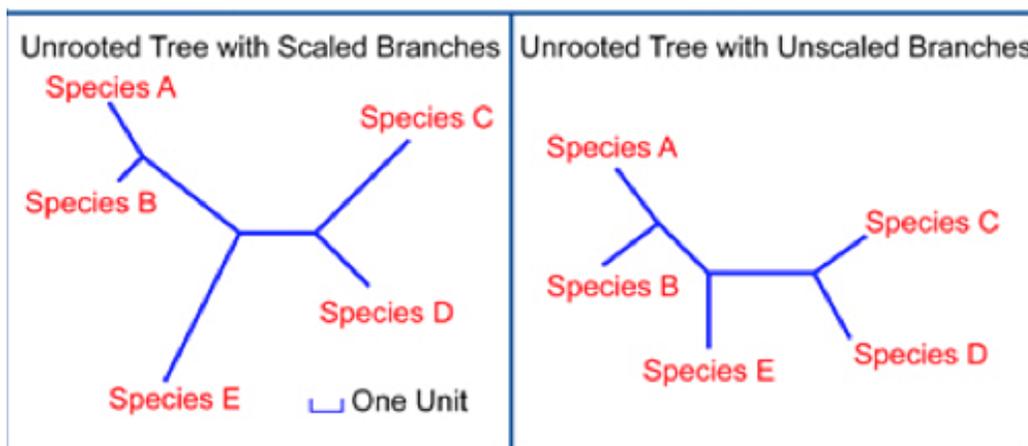


Figure 6. Trees can be rooted or unrooted (Source: <http://www.ncbi.nlm.nih.gov/About/primer/phylo.html>)

Unrooted trees are not as informative as rooted trees.

In order to root a tree, one must consider a taxonomic unit that is

- closely related to the taxon being studied
- phylogenetically *outside* taxon being studied.

This closely related group is known as the **outgroup**.

Contrast this with the **ingroup**, the taxa being classified in a study.

The outgroup serves as a reference group to allow identification of primitive characters.

Characters common to both the outgroup and the ingroup are considered primitive to the entire assemblage. For example, if you were trying to determine relationships among various species of Canidae (dog family), you might use a bear (Ursidae) as your outgroup (Figure 7) to determine which characters are primitive. The taxa most similar to the outgroup should (hypothetically) be the first to branch off from the common ancestor. (The rest of the relationships can be organized by identifying ingroup synapomorphies.)

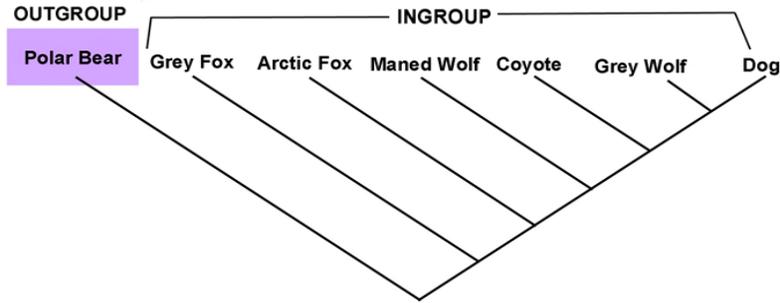


Figure 7. Hypothetical phylogeny of canid taxa, with member of Ursidae (Polar Bear) as outgroup. Characters common to the bear and the canids should not be used to construct less inclusive canid taxa.

D. Monophyly, Polyphyly, Paraphyly

A phylogenetic tree is not constructed randomly.

A **clade** is said to be **monophyletic** if it includes an ancestral species and all of its descendants. The systematist uses synapomorphies to determine recency of common descent and true common ancestries. This is not always easy. In some cases, when new data are applied, a taxon once thought to be monophyletic turns out not to be.

A **paraphyletic** taxon fails to include all descendants of a particular common ancestor.

A **polyphyletic taxon** includes members that have descended from more than one different ancestor, but the common ancestor of those different ancestors has not been included. These are illustrated in Figure 8.

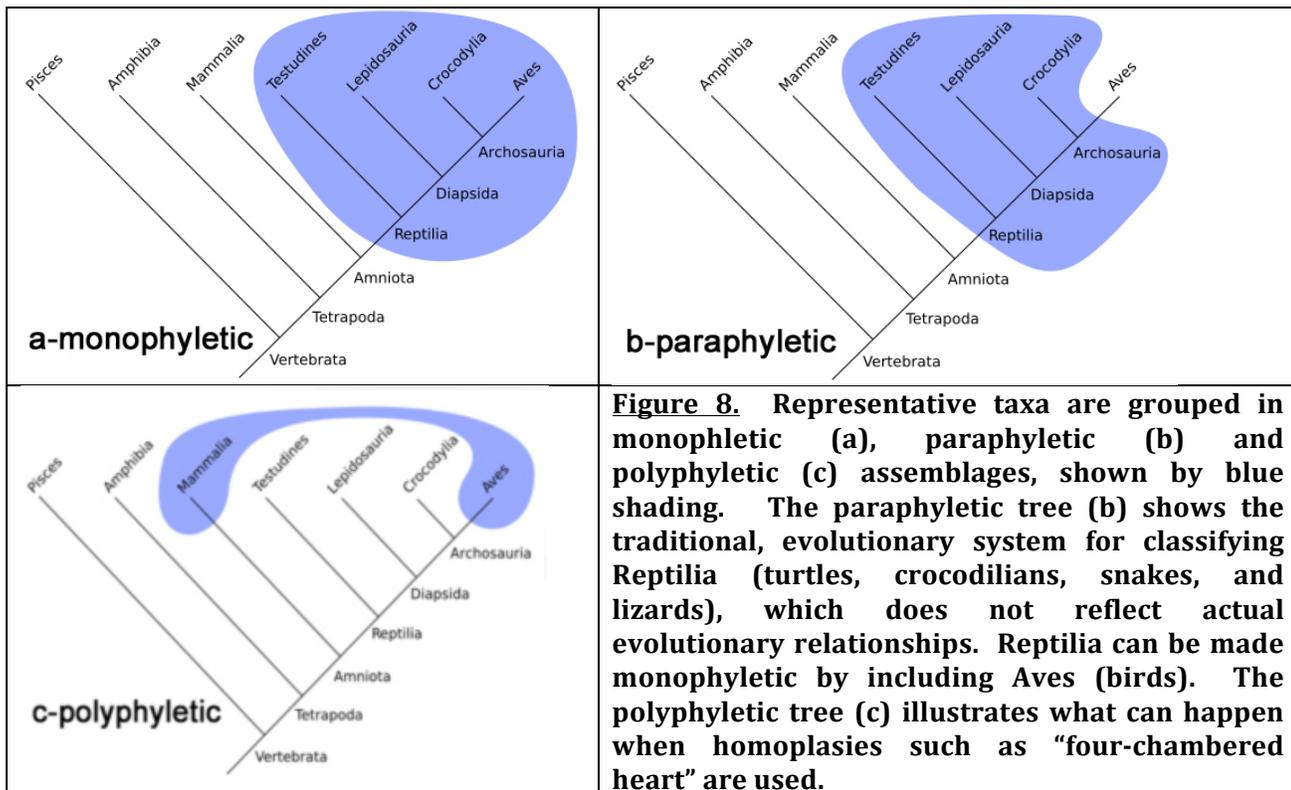


Figure 8. Representative taxa are grouped in monophyletic (a), paraphyletic (b) and polyphyletic (c) assemblages, shown by blue shading. The paraphyletic tree (b) shows the traditional, evolutionary system for classifying Reptalia (turtles, crocodilians, snakes, and lizards), which does not reflect actual evolutionary relationships. Reptalia can be made monophyletic by including Aves (birds). The polyphyletic tree (c) illustrates what can happen when homoplasies such as “four-chambered heart” are used.