



## Phylogeny, Taxonomy, and Nomenclature - a Primer

Phylogeny, taxonomy, and nomenclature are important concepts for how scientists study and conserve Life on Earth, including amphibians. Our goal here is to declutter these concepts and to highlight what these terms mean, how they are related, why biologists rely on these ideas, and how understanding them is important for using AmphibiaWeb.

**Phylogeny:** A phylogeny, or a phylogenetic tree, is a hypothesis (a scientist's "best guess") of evolutionary relationships among species. We refer to the phylogeny of all species as the Tree of Life. Phylogenetic trees show the hypothesized relationships among species as a branching pattern of ancestors and descendants. In these trees, **lineages** (branches) emerge from **nodes** (where branches meet) that represent the ancestors of currently living organisms (Figure 1). Lineages emerging from the same node, or ancestor, are more closely related to each other than either are to other lineages in the phylogeny. The end of a branch, whether it be a family (as in [the family tree](#)) or a species or a specific individual, is called a **tip** or a leaf (see Fig. 1). Sections of branches that do not lead directly to a tip are "internal branches" that simultaneously represent descendants and ancestors in the phylogeny; that is, they descend from ancestral nodes and lead to descendant nodes.

### Why is understanding phylogeny important?

Phylogenies show us the evolutionary relationships among species, allowing us to study how certain traits (e.g., color, venom, body size) evolve. Scientists study how traits change along branches in a phylogeny to understand how animals diversify and adapt to their environments over time. Phylogenies also provide vital information for conservation. By understanding evolutionary relationships among species, we can try to predict which lineages may be most vulnerable to human-caused environmental degradation like climate change or pollution. Some conservation biologists also try to focus on conserving the greatest evolutionary diversity, ensuring that we protect species that represent many different branches of the Tree of Life rather than protecting many closely related species.

**How are phylogenies made?** Phylogenies can be estimated based on any information about organisms. We could compare differences and similarities in size (e.g., big versus small animals) or color (e.g., green versus black animals), and, in fact, animals were originally grouped based on aspects of their physical appearance or behavior. For example, reptiles and amphibians were historically considered a single group because they were all seen as "creeping animals" (*herpeton* is Greek for a creeping animal). We now think of this way of organizing reptiles and amphibians as inaccurate because more rigorous analyses of anatomy and genetics revealed that reptiles are more closely related to mammals than to amphibians.

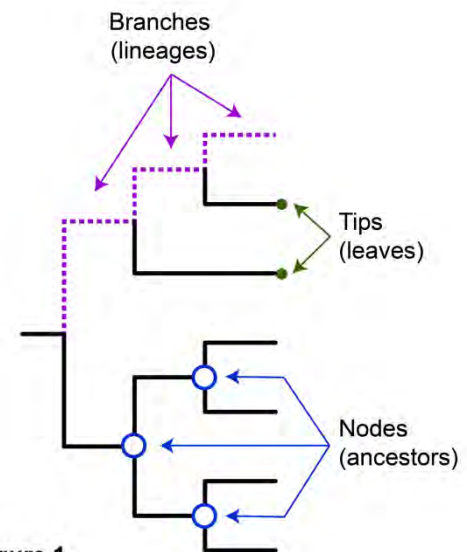


Figure 1.



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Today, scientists estimate relatedness (phylogeny) among organisms primarily using differences in DNA sequences of living animals and in the anatomy of their fossil ancestors. For an example of how scientists compare DNA sequences, see Figure 2, which is an alignment of mitochondrial DNA from five *Rana* species. A simple way to assess relatedness is to count the number of differences in DNA sequences, such as a C versus a T at a particular site (column), between species. View the full DNA sequences on GenBank with the following links: *Rana palustris* [KX269207.1](#), *Rana pipiens* [KY677811.1](#), *Rana clamitans* [KY677765.1](#), *Rana catesbeiana* [KY677760.1](#), *Rana sylvatica* [KY677767.1](#).

The relationships displayed within a tree are scientists' "best guess" as how these lineages are related based on the data used in the analysis. As additional data accumulate through new methods and as new species are discovered, these analyses may give different results. This leads to changes in estimates of relationships among studies depending on which types of data and analyses are used. Thus, it is best to consider the phylogeny as representing our current understanding and that it could change with new discoveries.



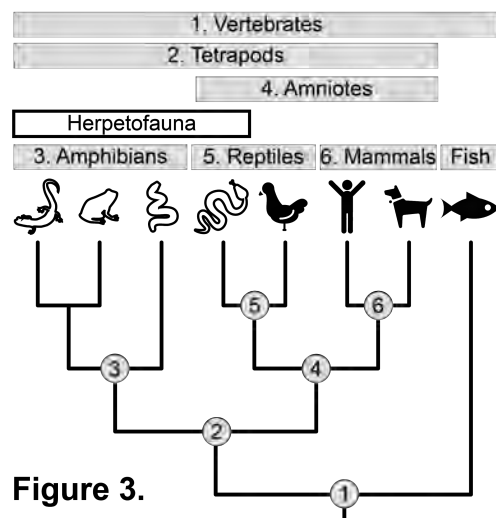
**Figure 2.**

Note that **A**, **C**, **T**, and **G** stand for one of the building blocks (nucleotides) of DNA: **A**denine, **C**ytosine, **T**hymine, and **G**uanine.

For more information on how to read and use phylogenies, see [Understanding Evolution](#).

### Key Phylogenetic Terms:

**Monophyly:** When a group of lineages in the Tree of Life includes an ancestor and all of its descendants. This group is called *monophyletic* (meaning "one branch") or a **clade**. Clades can be grouped within each other in a hierarchy. For example, in Figure 3, salamanders and frogs are both monophyletic groups, which are contained along with caecilians in the clade "Amphibians" (ancestral node = 3); amphibians, along with the reptile, mammal, and fish clades, are contained within the clade known as "Vertebrates" (ancestral node = 1). Note that other clades are present in this tree.



**Figure 3.**

**Paraphyly (non-monophyly):** If a group of organisms includes an ancestor and only some of its descendants, that group is called *paraphyletic* or *non-monophyletic*. Scientists care about

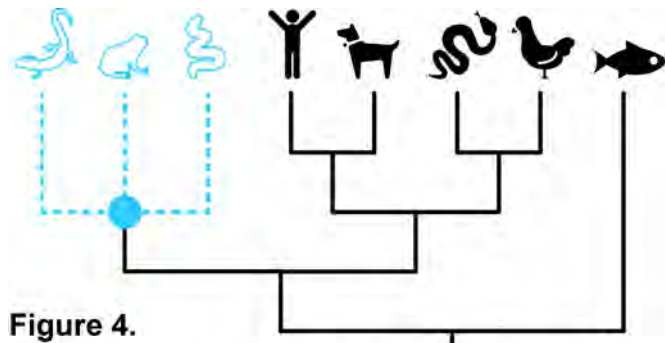


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distinguishing paraphyletic and monophyletic groups because monophyletic groups provide information about how evolution has occurred (which lineages emerge from which nodes) whereas paraphyly does not. Herpetology, the study of amphibians and non-bird reptiles - together known as “herpetofauna” or “herps” - is the study of a paraphyletic group because the group excludes mammals and birds, which are in fact reptiles. A group containing herps, birds, and mammals would be monophyletic, and this collection of animals would have a common ancestor at node 2 (Figure 3). This clade is known as the “Tetrapods.” Understanding that reptiles are a monophyletic group containing birds helped us find out that feathers evolved from scales, which were present in other reptiles but are absent in amphibians.

**Polytomy:** When an ancestral branch has just two descendants, we call that splitting pattern a dichotomy. If the ancestral branch has more than two descendants, it is a polytomy (meaning cut into many parts). A polytomy means that the relationships among these descendants are uncertain. In Figure 4, frogs, salamanders, and caecilians are shown as a polytomy, meaning that we don’t know which two are most closely related (share a common ancestor). Uncertainties in phylogenetic trees can exist because we have not yet been able to collect enough data to clearly disentangle the relationships among those lineages.

**Taxonomy:** The way we classify lineages and clades within the Tree of Life into named groups is called a taxonomy. Today, biologists generally agree that we should group organisms based on how they are related to each other through evolution. This means that the taxonomy we use should reflect shared ancestry (that is, phylogeny), ideally by organizing individuals and species into monophyletic groups.



**Figure 4.**

Note: we actually know that amphibians are not a polytomy; salamanders and frogs are more closely related to each other than to caecilians.

Taxonomy is organized as a hierarchy. AmphibiaWeb predominantly uses four nested taxonomic levels that describe clades on the Tree of Life: **order**, **family**, **genus**, and **species** (Figure 5). When appropriate (see [Taxonomy considerations](#)), we also use **subgenus** or **subfamily** names that provide additional evolutionary information regarding subsets of lineages within certain clades.

A good example is the [Northern Leopard frog](#), whose scientific name is *Rana pipiens*. The Northern Leopard frog’s genus name is *Rana* and its species name (or, “specific epithet”) is *pipiens*. This species falls into the broader family-level clade of Ranidae, known as the true frogs, which is within the order Anura (Figure 5). The genus *Rana* is very large (>100 species), so we sometimes also use subgenus groupings to help classify relationships among these species. The subgenus name of the Northern Leopard frog is *Pantherana*, which literally means “leopard frog”; *Pantherana* also includes other closely related species like the [Pickerel frog](#) (*Rana palustris*) and a newly-discovered species, the [Atlantic Coast Leopard frog](#) (*Rana*

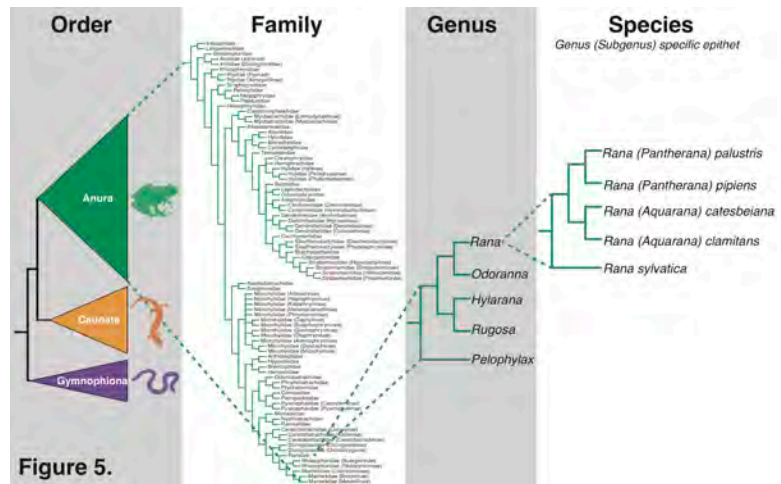


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*kauffeldi*). Another well known member of the family Ranidae is the [American Bullfrog](#) (*Rana catesbeiana*), which falls into a different subgenus called *Aquarana*, which means “water frog”. [Green frogs](#) (*Rana clamitans*) are also in the subgenus *Aquarana*. A member of the genus *Rana* that currently has not been assigned a subgenus is the [Wood frog](#) (*Rana sylvatica*).

**Nomenclature:** Rules for how we curate names for lineages and clades. Nomenclature does not necessarily reflect evolutionary relationships or biology, but is simply a set of rules for maintaining stable *taxonomy*. AmphibiaWeb promotes long-term stability in nomenclature and taxonomy because it helps easily

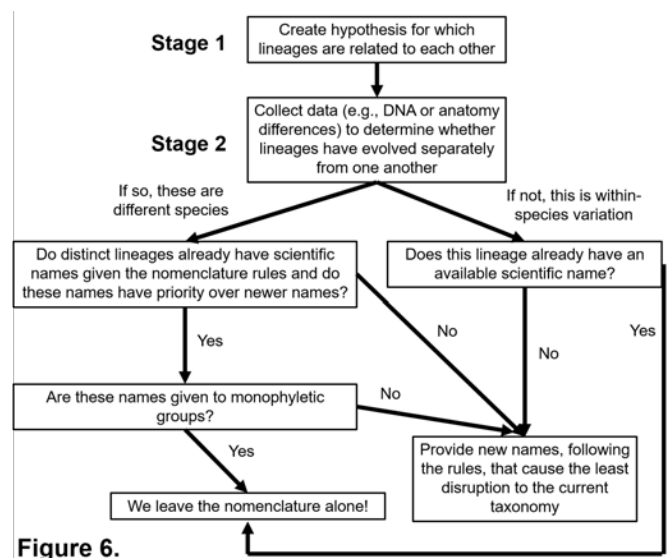
organize information about species. This means that we prefer to keep names of lineages or taxonomic clades constant over time, even as we gather new information about them. AmphibiaWeb chooses to accept or reject proposed taxonomic changes for specific lineages depending on whether the proposed changes both provide useful information for classifying organisms and promote the taxonomic stability of the group. A



common misconception is that the newest taxonomy is the best taxonomy. Scientists are technically free to adopt or reject newly published taxonomic changes. AmphibiaWeb adheres to a number of criteria to help our community work with the most biologically-informed and useful taxonomy and nomenclature. You can see AmphibiaWeb’s various taxonomy and nomenclature criteria [here](#) and the International Code of Zoological Nomenclature, which provides rules on how to name species, [here](#). For an example of a decision tree for changing nomenclature, see Figure 6 adapted from [Hillis \(2019\)](#).

### Why do phylogenies change over time?

We get more data (we add information about lineages): Perhaps the most common change in phylogenies happens when we get new data about lineages that change our understanding of their relationships. For example, phylogenies used to be based mostly on anatomy but they are now often based on combined assessments of DNA





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and anatomy, which have helped resolve previously unknown relationships within the Tree of Life.

Species get added (we find new lineages!): [New amphibians are being discovered all the time!](#) [In fact, 2–3 new amphibians are added to the amphibian tree of life every week.](#) As new species are discovered, we place them into the Tree of Life. Sometimes including these species changes how we previously understood relationships among lineages and may require reorganizing taxonomy.

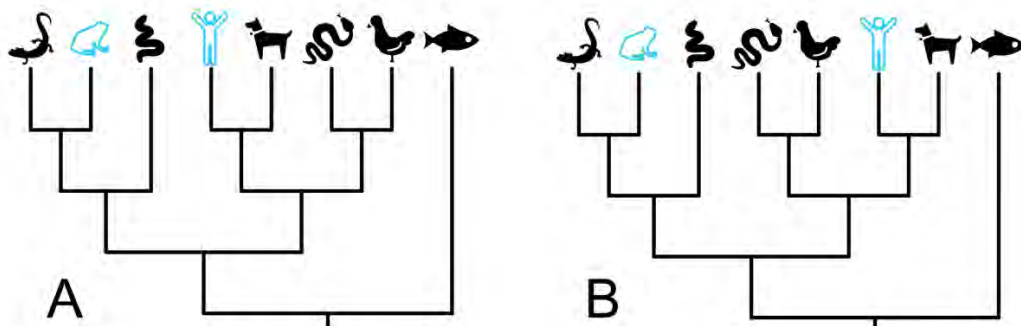
Species get split (we find out one lineage is actually two or more different lineages!): Sometimes one amphibian species is actually two or more different species that occupy different areas or habitats in the original species' range. When this “cryptic diversity” is revealed, taxonomists often split that species into multiple species.

Species get lumped (we find out two or more lineages are the same): Sometimes two or more amphibian species are just one amphibian species, which might live in different places, look different, or simply have different names even though we didn't know much about them. When it is discovered that multiple species are actually just different looking versions of the same species, these lineages can be lumped into one lineage. When multiple species are lumped into one, the species names are synonymized (in the same way that two or more words mean the same, two or more species names mean the same) and only the older species name prevails.

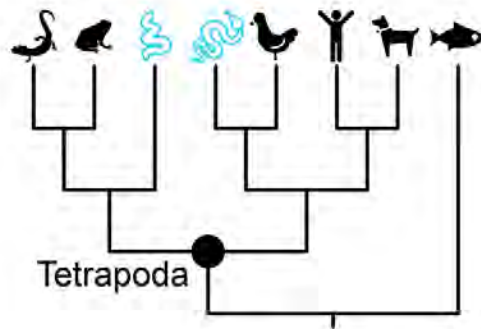
### Practice Questions

**It takes a bit of practice to correctly read a phylogeny, a skill we call “tree-thinking”. Here are a few exercises to hone your skills.**

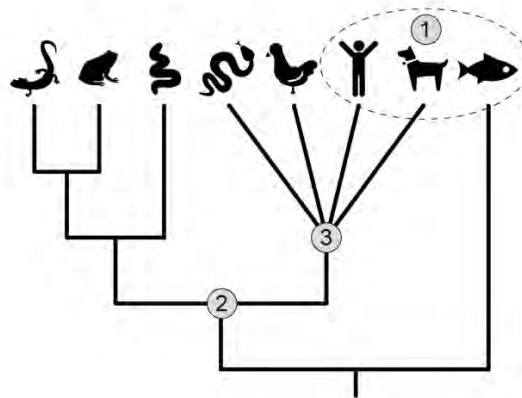
1. True or False: phylogeny A shows that humans and frogs are more closely related than phylogeny B.



2. Tetrapoda is the name of the clade of vertebrate animals with four limbs. Although the common ancestor of Tetrapoda (represented by the labeled node below) had four limbs, limbs have been evolutionarily lost several times in lineages that descended from this ancestor. Two limbless lineages are represented in our phylogeny: snakes and caecilians. Based on the relationships among the lineages within Tetrapoda, how many times did limblessness evolve in this phylogeny?

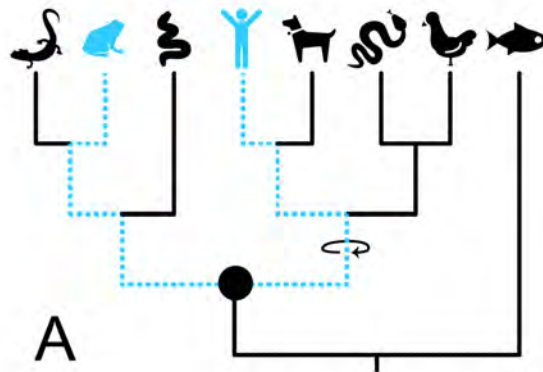


3. For each labeled group on the phylogeny below (indicated by either an ancestral node or a group of descendants), note whether the set of lineages could be described as a monophyletic group, a paraphyletic group, or a polytomy. Hint: there is at least one of each!

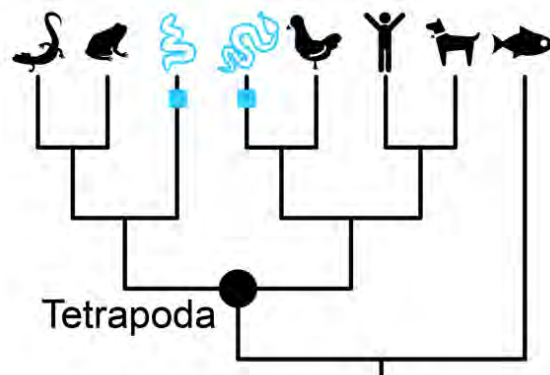


## Answers

- False! These trees actually depict the same phylogeny. Imagine *rotating* the branch leading to black dot (Tetrapoda) in each phylogeny. Rotating branches around their connecting node changes how the phylogeny looks but does not alter any relationships among lineages in that tree. Evolutionary distance between two lineages is measured by tracing from one tip to the common ancestor of both tips (node) and back up to the other tip. Follow the dotted lines to trace the ancestry between frogs and humans in both trees to see that *the evolutionary distance is the same*.

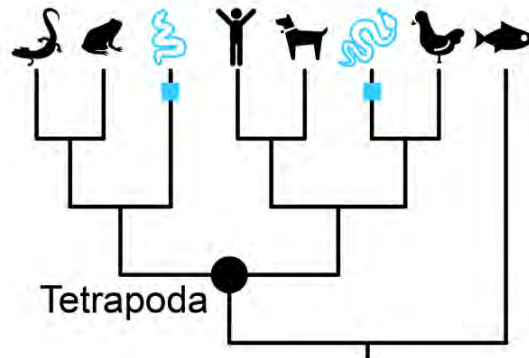


- The two lineages in this phylogeny that have lost their limbs (snakes and caecilians) are found in different clades of the tree. Thus, there are *two origins of limblessness* in each of these phylogenies. Here we depict these two events with blue squares on the branches leading to these two clades, indicating that limblessness evolved in an ancestor lineage of each of these clades.

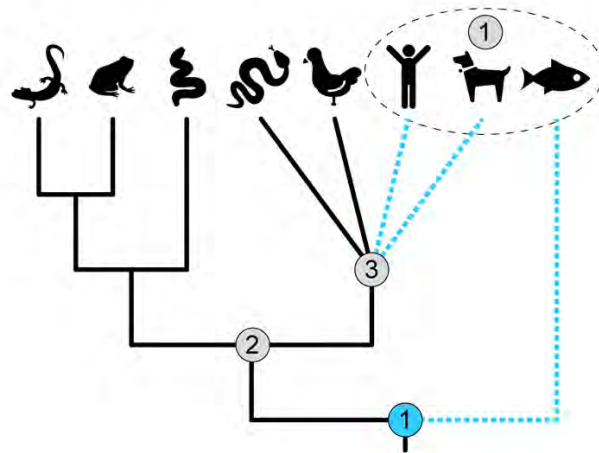


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Note that the phylogeny below is exactly the same as the one above, and thus depicts the two origins of limblessness. The only difference between the phylogeny above and below is that we have rotated one branch to change the right-to-left order of the tips, as was done in Question 1. (Compare this phylogeny with the one on the previous page)



- In this phylogeny, number 1 indicates a *paraphyletic* group (humans, dogs, and fish) because it includes an ancestor but not all of its descendants (amphibians, reptiles, and birds). Number 2 indicates a *monophyletic* group, or a *clade*, because it includes an ancestor and all of its descendants. Number 3 indicates a *polytomy*. Even though the relationships among lineages that descended from node number 3 are unclear, node 3 also indicates a *clade*, or a *monophyletic* group.







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Icons used in these figures were downloaded from [NounProject](#) (human: Vladyslav Severyn; snake: Dumitriu Robert; dog: bmijnlieff; fish: alex setyawan; chicken: iconsmind.com; salamander: Andrea Novoa; frog: Tatiana Belkina; caecilian: Georgiana Ionescu)

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