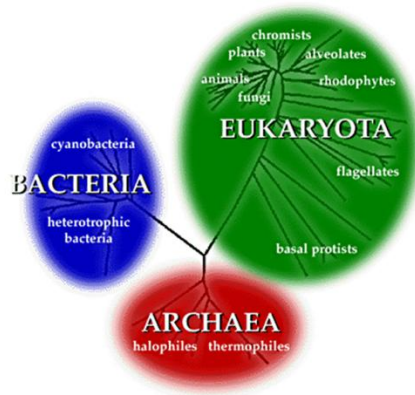


Cladistics and Phylogeny

We have been looking at how scientists classify organisms based on morphology and shared characteristics. We can use Linnean Ranks or Dichotomous Keys to help us classify organism.

A third method, developed based on research by Carl Woese is called the “Domains of Life”:

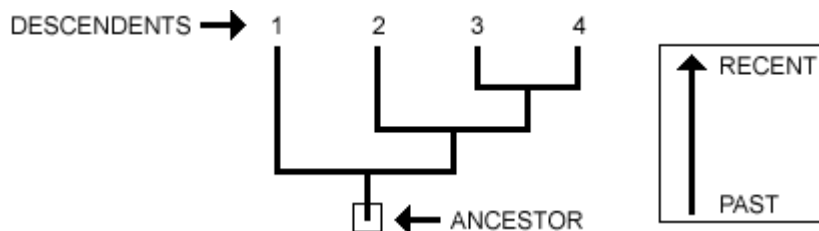


The three domains of Life: Bacteria, Archaea and Eukaryota encompass all life form present and past on Earth. This organization of organisms suggests that all three domains share a relationship, *a common ancestor* and can be exemplified by a family tree.

The Family Tree:

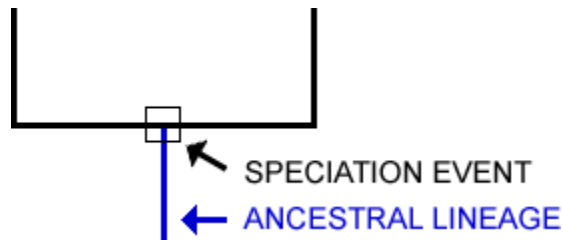
A family tree or a **phylogeny** can be constructed by studying inherited characteristics and historical evidence of a given species. The underlying hypothesis of phylogenetic trees is that it will exemplify evolutionary relationships between and amongst organisms.

Understanding a phylogeny is a lot like reading a family tree. The root of the tree represents the ancestral lineage, and the tips of the branches represent the descendants of that ancestor. As you move from the root to the tips, you are moving forward in time.

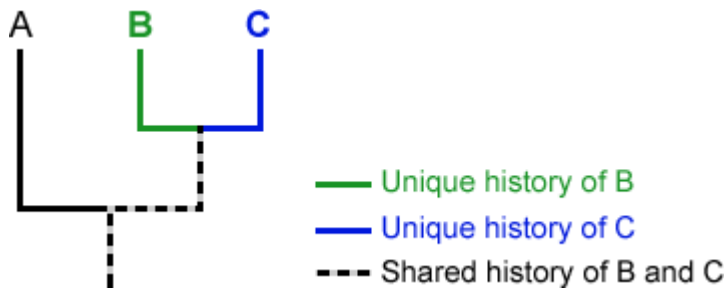


Understanding Phylogenies:

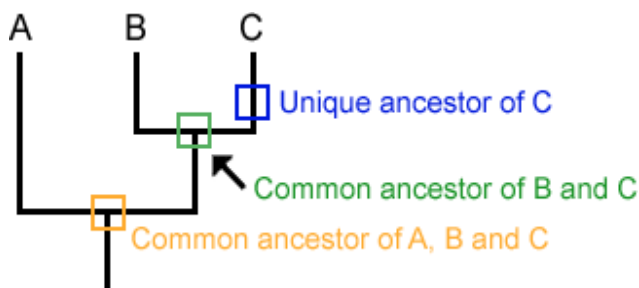
Speciation occurs when a lineage splits; it is represented as branching on a phylogeny. When a speciation event occurs, a single ancestral lineage gives rise to two or more daughter lineages. These daughter lineages are called **sister taxa**.



Phylogenies trace patterns of shared ancestry between lineages. Each lineage has a part of its history that is unique to it alone and parts that are shared with other lineages



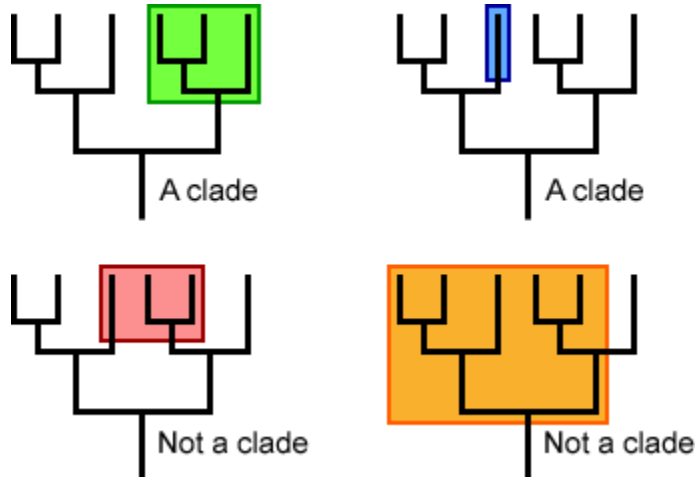
Similarly, each lineage has ancestors that are unique to that lineage and ancestors that are shared with other lineages — common ancestors.



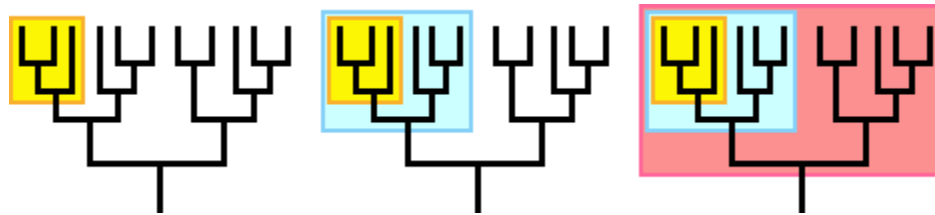
In phylogenetics a group of organisms that includes all the descendants of a *common ancestor* and that ancestor is called a **clade** or a **monophyletic group**.

A clade is a grouping that includes a common ancestor and all the descendants (living and extinct) of that ancestor. Using a phylogeny, it is easy to tell if a group of lineages forms a clade. Imagine clipping a single branch off the phylogeny — all of the organisms on that pruned branch make up a clade.

A group that does not contain all descendents of a common ancestor is called a **paraphyletic group**.



Clades are nested within one another — they form a nested hierarchy. A clade may include many thousands of species or just a few. Some examples of clades at different levels are marked on these phylogenies. Notice how clades are nested within larger clades.

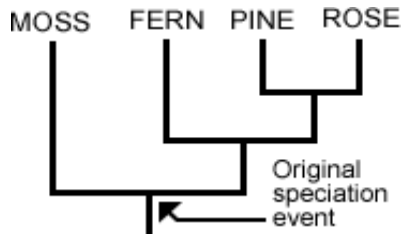


So far, we've said that the tips of a phylogeny represent descendent lineages. Depending on how many branches of the tree you are including however, the descendents at the tips might be different populations of a species, different species, or different clades, each composed of many species.

Trees, Not Ladders:

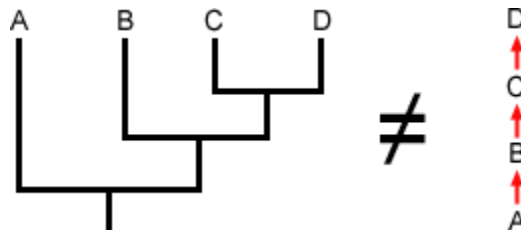
Sometimes, biologists have committed themselves to the erroneous idea that life can be organized on a ladder of lower to higher organisms.

Similarly, it's easy to misinterpret phylogenies as implying that some organisms are more "advanced" than others; however, phylogenies don't imply this at all.

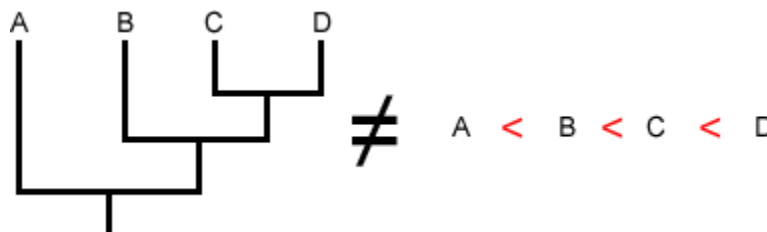


Here are some general rules about phylogenies:

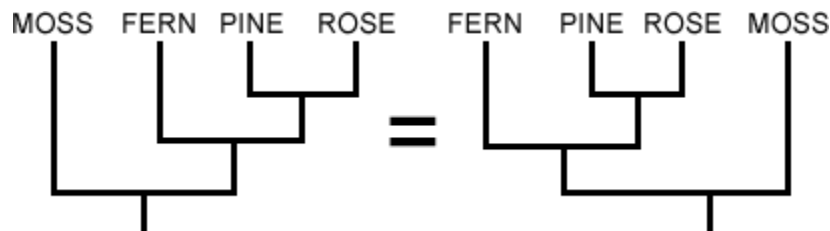
1. Evolution produces a pattern of relationships among lineages that is tree-like, not ladder-like.



2. Just because we tend to read phylogenies from left to right, there is no correlation with level of "advancement."



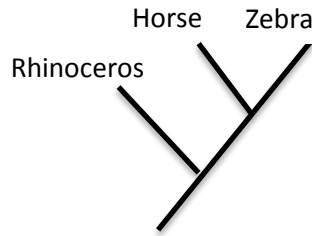
3. For any speciation event on a phylogeny, the choice of which lineage goes to the right and which goes to the left is arbitrary. The following phylogenies are equivalent:



Biologists often put the clade they are most interested in (whether that is bats, bedbugs, or bacteria) on the right side of the phylogeny.

The Passage of Time:

Node: A speciation event

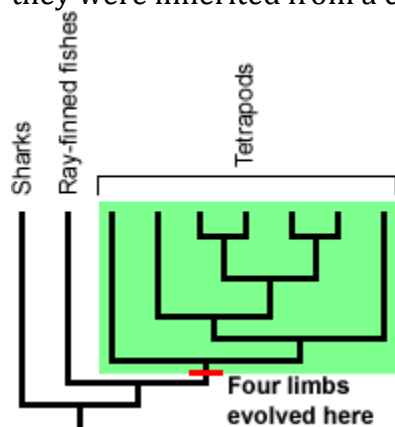


Taxonomy Today:

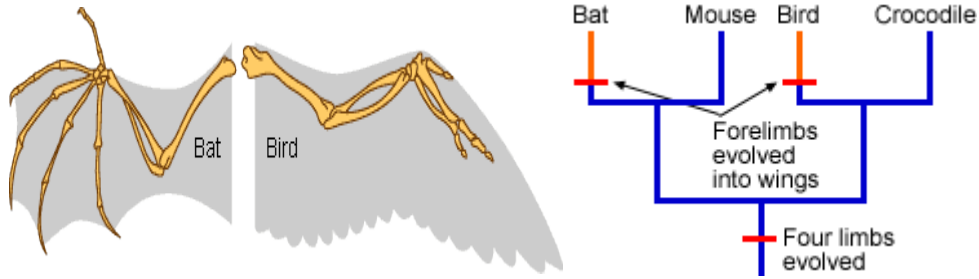
To build a phylogenetic tree, biologists collect data about the characters of each organism they are interested in. Characters are heritable traits that can be compared across organisms, such as physical characteristics (morphology), genetic sequences, and behavioral traits.

Homology Vs Analogy:

Since a phylogenetic tree is a hypothesis about evolutionary relationships, we want to use characters that are reliable indicators of common ancestry to build that tree. We use homologous characters — characters in different organisms that are similar because they were inherited from a common ancestor that also had that character.



Analogous characteristics — is having separate evolutionary origins, but are superficially similar because they evolved to serve the same function. Analogies are the result of convergent evolution.



Bird and bat wings are *analogous*. Bird and bat forelimbs are *homologous*.

Traditional vs Phylogeny:

Homework:

“Tutorial” hand out

+ Extra questions Handout

Note: there will be a quiz Friday. Will cover dichotomous keys, phylogenetics, prokaryotes, protists, viruses.