Understanding phylogenies

Reading phylogenetic trees
A phylogeny is the evolutionary relationships among organisms. The terms phylogeny, evolutionary tree, phylogenetic tree and cladogram can be used interchangeably for the purposes of this class.

Understanding a phylogeny is a lot like reading a family tree. The root of the tree represents the ancestral lineage (a continuous line of descent) and the tips of the branches represent the descendents of that ancestor. Branches represent populations through time. As you move from the root to the tips, you are moving forward in time.

When a lineage splits (speciation), 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. The location on the phylogenetic tree where this splitting occurs is called a node.

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.
A **clade** is a grouping that includes a common ancestor and all the descendents (living and extinct) of that ancestor. A clade is also called a **monophyletic group** or a lineage. 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. **Paraphyletic groups** are groups that contain a common ancestor and some, but not all, of its descendents.

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 the phylogenies below. Notice how clades are nested within larger clades.

Groups that occupy adjacent branches on a tree are called **sister taxa** or **sister groups**. A **taxon** (taxa, pl.) is any named group of organism (e.g., the reptiles, Felidae, beetles, *Homo sapiens*), whether or not it forms a clade. Sister groups are clades that are each other's closest relatives. On a phylogeny, sister groups occur anytime a single ancestral lineage gives rise to two daughter lineages: the daughter lineages are sister groups, and since they arose from the same ancestor at the same time, sister groups are always the same age.

An **outgroup** is a lineage in a phylogenetic analysis that falls outside the clade being studied. All members of the clade being studied will be more closely related to each other than to the outgroup, so the outgroup will branch off at the base of that phylogeny.
So far, we've said that the tips of a phylogeny represent descendant 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. Often, one sees phylogenies that include polytomies, nodes with more than two descendant lineages, creating a "starburst." This can mean one of two things:

- **Lack of knowledge**
  Usually, a polytomy means that we don't have enough data to figure out how those lineages are related. By not resolving that node, the scientists who produced the phylogeny are telling you not to draw any conclusions — and also to stay tuned: often gathering more data can resolve a polytomy.

- **Rapid speciation**
  Sometimes a polytomy means that multiple speciation events happened at the same time. In this case, all the daughter lineages are equally closely related to one another. The researchers who have reconstructed the tree you are examining should tell you if they feel that the evidence indicates that this is the case.

**Trees, not ladders**
Several times in the past, 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.

In this highly simplified phylogeny, a speciation event occurred resulting in two lineages. One led to the mosses of today; the other led to the fern, pine, and rose. Since that speciation event, both lineages have had an equal amount of time to evolve. So, although mosses branch off early on the tree of life and share many features with the ancestor of all land plants, living moss species are not ancestral to other land plants. Nor are they more primitive. Mosses are the cousins of other land plants.

So when reading a phylogeny, it is important to keep three things in mind:

1. **Evolution produces a pattern of relationships A B C D among lineages that is tree-like, not ladder-like.**
2. Even though 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.

**Misconceptions about humans**
The points described above cause the most problems when it comes to human evolution. The phylogeny of living species most closely related to us looks like this:

It is important to remember that:

1. Humans did not evolve from chimpanzees. Humans and chimpanzees are evolutionary cousins and share a recent common ancestor that was neither chimpanzee nor human.

2. Humans are not "higher" or "more evolved" than other living lineages. Since our lineages split, humans and chimpanzees have each evolved traits unique to their own lineages.

**Test your understanding**

1. On the diagram below, draw a circle around 3 different monophyletic groups.
2. On the diagram below, draw a circle around 1 paraphyletic group.
3. Five of these six trees describe exactly the same relationships among taxa 1 through 6. Identify the tree that is different from the other five. Circle the part of the tree that is different from the others.

![Trees Diagram]

4. The cladogram below is of a group of fish called cichlids. What does the phylogeny tell us about cichlid speciation?

![Cladogram]

**Building a phylogenetic tree**

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

A **shared character** is one that two lineages have in common, and a **derived character** is one that evolved in the lineage leading up to a clade and that sets members of that clade apart from other individuals.
Shared derived characters can be used to group organisms into clades. For example, amphibians, turtles, lizards, snakes, crocodiles, birds and mammals all have, or historically had, four limbs. If you look at a modern snake you might not see obvious limbs, but fossils show that ancient snakes did have limbs, and some modern snakes actually do retain rudimentary limbs. Four limbs is a shared derived character inherited from a common ancestor that helps set apart this particular clade of vertebrates. However, the presence of four limbs is not useful for determining relationships within the clade in green above, since all lineages in the clade have that character. To determine the relationships in that clade, we would need to examine other characters that vary across the lineages in the clade.

The characters used need to be homologous characters — characters in different organisms that are similar because they were inherited from a common ancestor that also had that character. An example of homologous characters is the four limbs of tetrapods. Birds, bats, mice, and crocodiles all have four limbs. Sharks and bony fish do not. The ancestor of tetrapods evolved four limbs, and its descendents have inherited that feature — so the presence of four limbs is a homology.

Bird and bat wings are analogous — that is, they have separate evolutionary origins, but are superficially similar because they evolved to serve the same function. Analogies are the result of convergent evolution, a process in which two distinct lineages evolve a similar characteristic independently of one another. This often occurs because both lineages face similar environmental challenges and selective pressures. Analogous traits are not used in a phylogeny because they do not come from a common ancestor.

Characters are placed on the tree using lines to indicate where they occurred.

The tree-building process is based on the principle of parsimony. The parsimony principle is basic to all science and tells us to choose the simplest scientific explanation that fits the evidence. In terms of tree-building, that means that the best hypothesis is the one that requires the fewest evolutionary changes.
Test your understanding

5. To the trees below, add the character “ability to fly”. Examine both trees with the new character. Which tree is more parsimonious and why?

6. Build a tree
Using the table of traits below and using the principle of parsimony, construct a phylogeny for the vertebrates. What do you have to know about the traits in order to construct the phylogeny?

<table>
<thead>
<tr>
<th></th>
<th>Vertebrae</th>
<th>Bony skeleton</th>
<th>Four limbs</th>
<th>Amniotic egg</th>
<th>Hair</th>
<th>Two-post-orbital fenestrae</th>
</tr>
</thead>
<tbody>
<tr>
<td>Rodents &amp; rabbits</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>Sharks &amp; relatives</td>
<td>Yes</td>
<td>No</td>
<td>No</td>
<td>No</td>
<td>No</td>
<td>No</td>
</tr>
<tr>
<td>Crocodiles &amp; relatives</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td>No</td>
<td>Yes</td>
</tr>
<tr>
<td>Ray-finned fish</td>
<td>Yes</td>
<td>Yes</td>
<td>No</td>
<td>No</td>
<td>No</td>
<td>No</td>
</tr>
<tr>
<td>Primates</td>
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<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>Amphibians</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td>No</td>
<td>No</td>
<td>No</td>
</tr>
<tr>
<td>Dinosaurs and birds</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td>No</td>
<td>Yes</td>
</tr>
</tbody>
</table>

From studying fossils and outgroups closely related to the vertebrate clade, you hypothesize that the ancestor of vertebrates had none of these features.

Focus on a group of lineages that have a shared derived trait and hypothesize a relationship for them. Add in additional groups by examining other shared derived traits. You may have to make several separate sketches initially to visualize the relationships and then collect them together into one tree at the end.

Phylogenetic Tree of the Vertebrates:

This exercise was modified from The University of California Museum of Paleontology’s Understanding Evolution website: http://evolution.berkeley.edu/evolibrary/article/evo_01