

LABORATORY #2 -- BIOL 111

Biodiversity Taxonomy/Phylogeny

In your first few lectures you heard a number of times, about the vast **diversity of life** that has evolved over the past ~ 3.5 billion years. We discussed life in its major **domains**, Bacteria, Archaea, and Eukarya and spent a bit more time on the major groups within Eukarya—plants, animal, fungi, and protists. We explained the idea of **natural selection** as the major force creating this diversity and mentioned Darwin and Wallace as the major contributors to this scientific hypothesis. We looked at the “family tree” of birds known as **honeycreepers**, and hypothesized why, despite being overall similar, they have notably different beaks! They descended from a common ancestor, and show selection for beaks that helped them eat different prey, reproduce, and maintain this helpful variation. This is the explanation for evolution and for extinction.

Something to ponder.... While the diversity of animals seems nearly endless, today the earth is experiencing the greatest mass extinction in its long history. Currently, species are going extinct at a rate of approximately 30,000 species a year. **During this lab period, 20 species will probably go extinct, mostly due to habitat loss and degradation of the environment.** Most of these are considered small and unimportant by most persons. However, they probably play a crucial role in the functioning of the ecosystem. Continued loss of species will someday pass a threshold where the effects of wiping out biodiversity for human needs will have a very large effect on the earth and all creatures on it.

Animal Diversity and Scientific Names (“Taxonomy”)

In order to make sense of animals and animal diversity, humans have studied living and dead animals, including fossils, in a number of ways. We discussed just 3 ways, in class. Scientists have **observed** as much as possible with their eyes, they have studied **the ways in which animals develop** (embryology) and they have studied the **genes (DNA) of animals**. Centuries of these studies have allowed humans to put animals into categories and to name them. And remember...scientists are always trying to do better...and if technology advances, some animals may be re-categorized!

Most organisms have familiar names, such as the red maple or the brown-headed cowbird. However, these familiar names are often misleading. Many different species are called the same thing in different parts of world (American **Robin**/New Zealand **Robin**), and many identical species are called different names (**orca/blackfish/killer whale**). Formal latin names are used by scientists to establish a unique name for each species on the earth. Each latin name is made, approved and used by scientists worldwide. Every species name consists of two parts: the first part is the generic name (or genus, e.g., *Homo*); the second part is the specific epithet (or species, e.g., *sapiens*). This Linnaean binomial system of nomenclature was introduced by Carrolaus Linnaeus in the 18th century and has been in use ever since. The study and practice of naming organisms is known as **taxonomy**.

Larger groups contain smaller groups, which contain even smaller groups and so on. This is similar to the old Kingdom system (which became problematic and is no longer used.).

For example, the taxonomy of corn (*Zea mays*) looks like this:

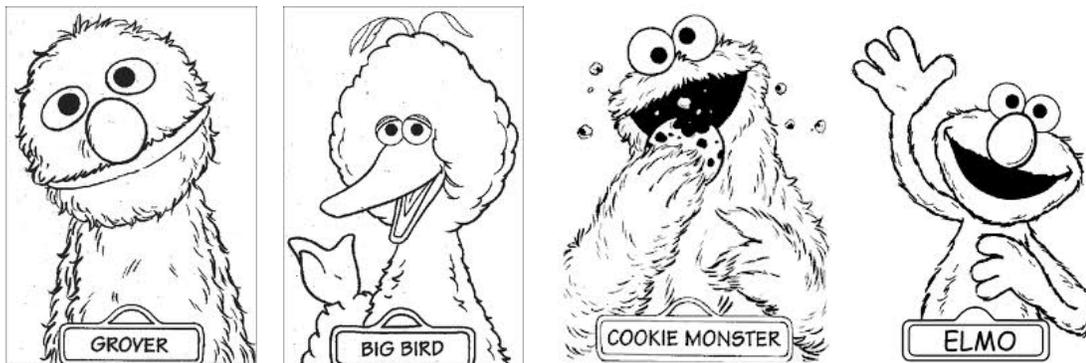
Plantae contains Anthophyta
Anthophyta contains Monocotyledons
Monocotyledones contains Commelinales
Commelinales contains Poaceae
Poaceae contains *Zea*
Zea contains *mays*
Mays

Note that the genus and species names are always *italicized* (or underlined), and the species is not capitalized.

Naming animals and categorizing animals go hand in hand. One way of categorizing living things is by use of that “family tree” system we have discussed. In biology, these family trees are called **phylogenetic trees** or **phylogenies**. Phylogenetic trees are just one explanation of how animals are related. Depending on the characteristics you focus on, many more than one tree may be constructed to explain the way in which different animal life forms evolved. Let's practice with a silly example.

Lets Practice!

How to do this? Here's a really simple example: using this technique we can estimate the relative relatedness of Grover, Elmo, Cookie Monster and Big Bird.



All belong to a larger group called “muppets”, which are the artistic creation of Jim Hensen. Think of one original muppet body plan. Then consider that all existing muppets are decedents of this first muppet. The 4 muppets above all differ from that original muppet because of modifications selected to survive in their environment, but they share a common ancestor, the original muppet.

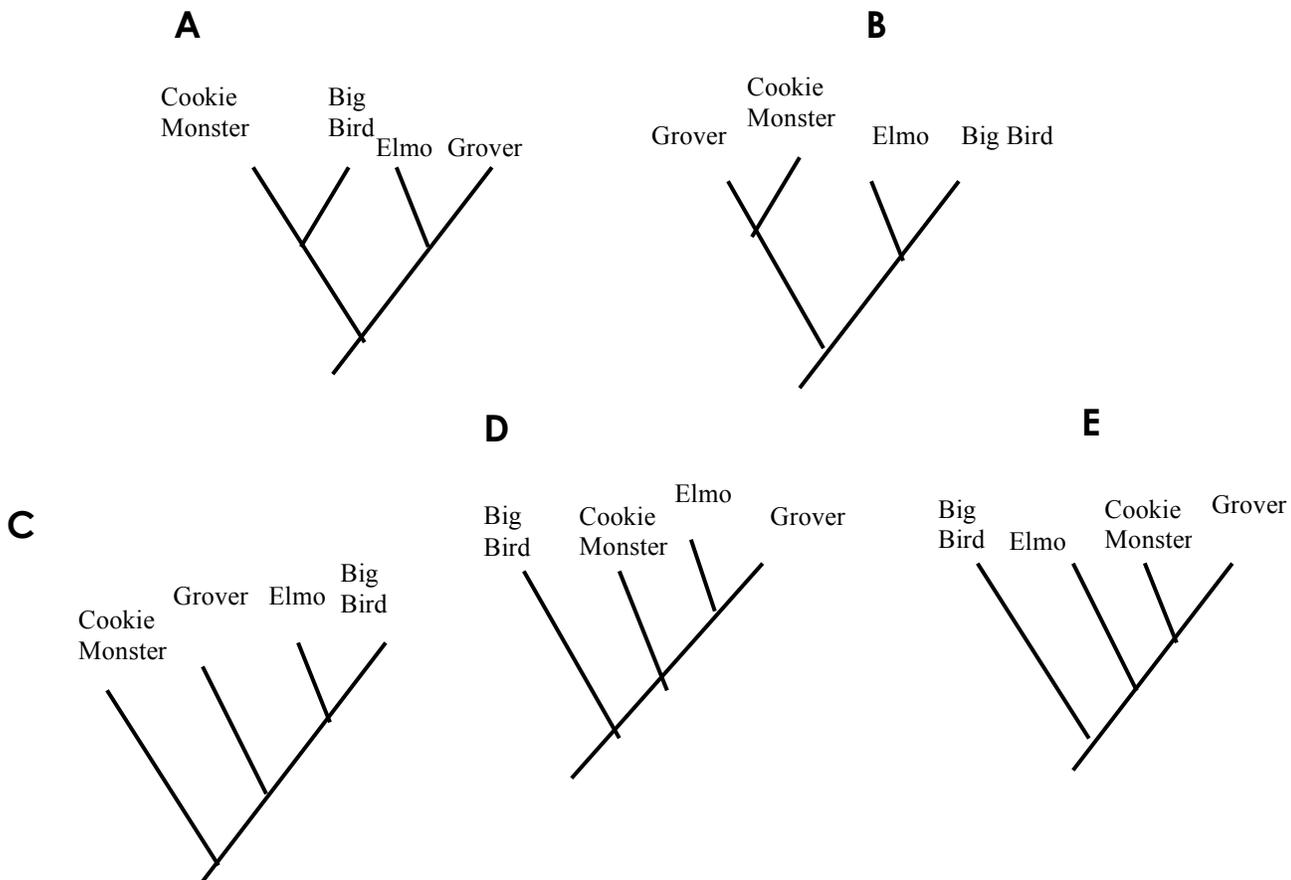
If we consider 3 characteristics of the 4 modern muppets. (Scientists would call these **apomorphies**) we might be able to make sense of how each muppet might fit into the historical tree of life for muppets.

Let's consider: **1) feathers**

2) rug-like skin

3) skinny arms

Each tree below represents a possible scheme for relatedness of Grover, Big Bird, Elmo, and Cookie Monster. If we place a number representing the 3 characteristics above on each tree, below the muppet that shows the characteristic we can test each tree for it's ability to explain how modifications may have been acquired. **Your instructor will demonstrate on the board.**



Note that on the most likely tree, a characteristic (1,2,3) should only appear once. It will take fewer "steps" to explain the animals' relatedness. We call this the most **parsimonious** tree. You will be doing this analysis for the organisms listed in lab today. This technique is called "phylogenetic analysis." You will choose the most **parsimonious** tree. The remaining trees are "less preferred", i.e., they have more "steps" to explain descent with modification.

Phylogeny is the genealogy, or family tree, of an organism. In other words, phylogeny is the hypothesis of how an organism evolved. Each phylogeny contains the significant traits (called **apomorphies**) that make it similar to or different from closely related organisms. Apomorphies are indicated with a hash mark through the associated branch on the phylogeny. All organisms above that hash mark have or had that particular trait.

There are three types of apomorphies. A **plesiomorphy**, is an ancestral or primitive trait. A hash mark indicating a plesiomorphy is placed on the base of a phylogeny indicating that all organisms above are united in having or having had this trait at one time. A **synapomorphy** is a trait that unites some, but not all, groups within the phylogeny. This trait is the most helpful in showing who is related to whom. A hash mark indicating a synapomorphy is placed at the base of some, but not all, groups within the phylogeny. An **autapomorphy** is a trait that only one group possesses, making this group different, and separating it from the others. A hash mark indicating this is placed at the base of an individual group. Your instructor will demonstrate this on the board.

To determining the most likely relationships between groups of organisms, one must first consider that there are lists of rules indicating which traits are considered “good” traits. As in, which traits result in a significant evolutionary change? Those that do are the important traits to consider.

In addition, we utilize the **principle of parsimony** to identify the phylogeny representing the most likely series of evolutionary events. That is, we look for the simplest tree. Why? It is assumed that it is easier (and hence more likely) to get from point A to point B through few steps rather than through many.

Procedure—More practice! Pretend the plastic dinosaurs are fossils or are somehow remains/specimens available to study!

One of the many ways to develop a phylogeny is to draw a character matrix.

1. To do so, assign a name for each member in the group. Place the names in rows.
2. Now, look for the associated apomorphies or traits. Identify at least one trait that all members share. This is your **plesiomorphy**. List it as a column heading.
3. Identify several traits that multiple, but not all, members share. These are **synapomorphies**. List these traits as additional column headings. Remember, these are the most important traits, as they show relatedness, so be sure to have several!
4. Now add a few **autapomorphies**. Again, these are traits that only one member of the group has. They are interesting, but don't really tell us a lot about how groups are related. Add these to the column headings.

- 5.** Now you are ready to fill in your matrix. For each intersecting box between a group member and a trait, indicate whether the member does or does not have that trait. A symbol X indicates the member has the trait, whilst a symbol -- indicates the member does not have that trait.
- 6.** Draw the associated phylogeny, placing the traits on the tree as hash marks. Remember, hash marks indicate that EVERYONE above it has the trait! Count up the number of evolutionary events.
- 7.** Now start to reorganize your group members to make your phylogeny more parsimonious. As in, reorganize to reduce the number of evolutionary events. The fewer events, the better, or more parsimonious, your phylogeny becomes!

Your instructor will lead you through this using Sesame Street characters. Then, we'll release you to do it on your own using dinosaur toys.

2. Neatly draw **three** phylogenies using the apomorphies identified in question #1. Be sure to label all apomorphies and indicate the number of **significant evolutionary events** in each phylogeny. You will likely see ways to improve each time you make your trees!

Which phylogeny (of these three) is the most parsimonious? **CIRCLE IT AND LABEL IT AS THE MOST PARSIMONIOUS!** (8 pts)

3. In reference to your most parsimonious phylogeny, provide a table indicating which apomorphies are **plesiomorphies**? Which are **autapomorphies**? Which are **synapomorphies**? (2 pts)

Plesiomorphies	
Synapomorphies	
Autapomorphies	