

Bio 3A Lab: Classification and Phylogenetic Systematics

Objectives

1. Understand the difference between a system of classification and a phylogeny, and how they are related.
2. Understand the basic method used in cladistic analysis.
3. Generate simple phylogenies based upon this method.
4. Compare traditional and cladistic classifications.

Systems of Classification

Classification of "things" seems to come naturally to the human species. You do it on a regular basis. Enter any kitchen and you'll find the pots and pans grouped together, the spices in a single cabinet, the dinnerware stacked neatly by type. Within a certain category there are sub-categories. Open the silverware drawer. The overall category: Eating Utensils. Within this category we find sub-categories, such as spoons, forks, knives, and chopsticks. Look closer and each of the sub-categories are further subdivided. Within spoons there are soup spoons, teaspoons, sugar spoons, serving spoons. This type of classification system is called a **hierarchy**. You may have used a similar method to organize your thoughts before writing a paper (the outline), or, if you are familiar with organizational structure of your computer, think of the root directory. In the culinary example above, we could organize our objects in the following way:

Major Category: *Kitchen Items*

1st Sub-category: *Silverware*

2nd Sub-category: *Spoons*

Final Sub-category: *Soup spoons* (or any of the others)

A natural outcome of this kind of thinking was the sorting of plants and animals into hierarchical groups. You should know that this kind of sorting was originally begun before the concept of evolution was elaborated. Carl von Linne' (*a.k.a. **Carolus Linneaus***) was one of the first to put forth a coherent method for organizing organisms. He was, in fact, a botanist, and his original work dealt with plants. Later, he worked on animals. In Linne's time there was a real need to organize the plants and animals in some coherent way. People were traveling extensively and bringing back or reporting hundreds (and soon thousands) of new organisms. Museums began to fill up, and you had to handle all of this new material. Linne', and those who followed, gave us a framework for sorting out the potential mess.

Thus, the first plant and animal classification systems were created primarily for convenience. In other words, for the convenience of the user, just like your kitchen classification system. In using such a system, we usually work from the "top down." For

instance, you purchase a new type of soup spoon. In finding the proper place for it, you will a) enter the kitchen, b) go to the silverware drawer, c) look at the spoon area, d) place the new soup spoons into the soup spoon sub-category. Another example is found in the library. To find a reference to the moons of Jupiter, you might have to drop through several hierarchical categories such as science, astronomy, solar system, planets, Jupiter, and moons. In fact, learning to use the library means learning the librarian's classification system. Creating systems and classifying organisms is called taxonomy (the process of grouping, a **taxon** is a group). The idea as you can see is probably as old as the human brain.

Following the growth of evolutionary theory, it became clear that a classification system could do much more. It could indicate the evolutionary relationships between organisms. Classifying organisms based upon relatedness is called **systematics**, and on the surface it may appear rather straightforward, even simple. In some cases, it may be; for instance, you probably have no trouble grouping birds together as a single related taxon. However, when the first specimens of the platypus were sent to the British museum, taxonomists were unsure whether they were birds or mammals. Today, heated debates rage on concerning the relationships of various groups of organisms. Moreover, there is considerable controversy over how we should go about quantifying our measurements of similarity. When I show you a bird, you look at it, and create a quick mental "scorecard" of characteristics. The first character that you note is probably the presence of feathers. Next, you might look at the characters of the feet or beak, or color patterns on the body. When you have assessed the suite of characters, you do a quick mental calculation, and decide that it is a cardinal.

At this time, there are a few competing methods used in systematics. The major competitor is called **cladistic analysis**. In a nutshell, cladistic analyses attempt to group taxa based upon recently evolved (**derived**), shared characteristics. The attempt is to determine the common ancestry of the groups. The method is, by far, the most rigorous and objective of the systematic methods.

Cladograms

As we postulate relatedness, we can begin to illustrate in a diagram. In this case, the diagram is called a **cladogram**.

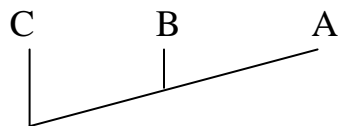


Figure 1. Sample cladogram with three operational taxonomic units, A, B, and C

In Figure One, group A has more derived characters in common with group B than with group C. A and B are more closely related to each other, than to group C.

As you might guess, you could draw cladograms for all sorts of things; and the single most important part of the analysis would be the selection of characters. In the "real systematic world" this is touchy business. The characters chosen must be **homologous**; that is they must represent common evolutionary origins. For instance, looking at the characteristics of the humerus in three species of higher primates would be perfectly acceptable, as the humerus is homologous in this group. However, characters of the wings of bats and flies is clearly disallowed, since those structures are clearly not related (they are **analogous**, similar

function, different origins). Next, the character must be evolutionarily new to the group (or groups). So far we have called such characters "derived", but cladists have their own nomenclature. They call such evolutionary novelties **apomorphies**. Primitive characters are called **plesiomorphies**. You will recall that the method of grouping was based upon shared, derived characters (shared apomorphies). There is a word that covers that, as well, **synapomorphies**: shared derived characters. And, of course, there's a word for shared primitive characters: **symplesiomorphies**.

Okay, let's try to put some of this to use. One problem that systematists face is determining the direction of the evolutionary transformation. Another way of saying this, we need to know whether the particular character is present in the common ancestor do decide whether it is primitive or derived. This direction is referred to as **polarity**. This determination may be very difficult. The usual method for this determination is to compare the group of interest to a taxon that is known to be primitive. This is called **outgroup comparison**. If we wanted to determine the affinities of lizards, horses and humans, we could use amphibians as a logical outgroup. Lizards, humans and horses share a very important derived character, the amniotic egg. Amphibians have a generally more primitive egg type. At this time we can construct an initial cladogram like the one seen in Figure Two.

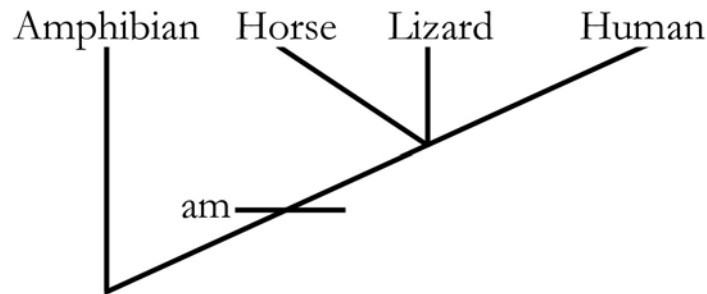


Figure 2. Initial cladogram showing relationships among the groups horses, lizards, amphibians and humans

Humans, horses and lizards are all arising from the same node, since we only know at this time that they form a group separate from the amphibia. We need to "resolve" the node, and determine the affinities within our sample group. In the above cladogram the horizontal line marked "am" indicates that groups above that point possess an amniotic egg. Now let's consider another character, the presence of hair. A score sheet for this character is shown in Table One.

Group	Hair
amphibians	-
lizards	-
horses	+
humans	+

Table 1. Score sheet for the characteristic "hair"

Using these data we can clarify the cladogram, and represent those affinities based upon our character analysis, as shown in Figure Three.

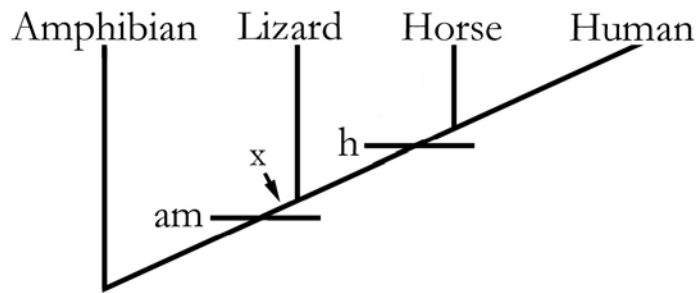


Figure 3. Cladogram for OTU's shown in Figure two using two character states

There could be an alternative interpretation of this diagram. What if some hypothetical ancestor of lizards (the "x" on the diagram) had hair? Then hair in horses and humans would be primitive, and the loss would be derived in lizards. However, the cladistic method always assumes that evolutionary novelties probably occur in the fewest number of steps (unless the data clearly indicate otherwise). For instance, the appearance of hair in horses and human lineage requires only one step. But the alternate hypothesis requires that hair be evolved in lizards, horses and humans, and then lost in lizards (two events). Thus we should accept the first hypothesis. This reliance on the "path of least resistance" is called the **rule of parsimony**, or **Occam's Razor**¹.

Procedure 1: Classification of inanimate objects.

Let's try a bit of cladistic analysis with some hardware store items. You will be give four different type of screws. The object of this exercise is to determine the relationships (phylogeny) among these three of them (one will be the outgroup).

The screws are labeled A B C and D. We are interested in the relationships between A B and C, with D as the out group. You must derive sets of character states for each of your species. Enter your data on the sheets provided in lab.

1. Choose five character states to analyze. Try to avoid easily modified characters like color. Use characters such as heads shape, thread counts, etc...
2. Determine the presence or absence of the characters among each of your species
3. Use the outgroup method to determine polarity. Circle those characters that you have determined are derived.
4. Determine the number of shared derived characters between all possible pair-wise combinations of your species, i.e. group A and B, group B and C, etc... Enter these numbers in the spaces provided.
5. Construct a cladogram using the rule that species with the greatest number of shared characters are most closely related. Remember to minimize the number of steps.
6. Construct a classification from your cladogram. Call the group containing the three related species a family. Within the family, the two species most closely related should form a single genus; the other species should form a second genus. On your cladogram circle the family, genera and species. Before you go on to procedure 2, compare your cladograms with

others in the class. If there are differences, how can you account for them?

Monophyly and Cladistics

Classification based upon the cladistic analyses is quite different from the type of simplistic "organizational classification" we discussed at the beginning of this lab. The fact that organisms are grouped together by shared derived characteristics implies a common origin for the group. Groups which share a common origin (i.e. have more derived characters in common with each other than with other such groups) are said to be monophyletic (*along a single lineage*). In the cladogram shown in Figure Four, several different, monophyletic groups are circled. Two things should be obvious from this illustration. First, any number of lineages that can be rooted back to a single branch qualify as monophyletic. Second, the groupings form nested sets within each other. These nested sets are the basis for hierarchical classification.

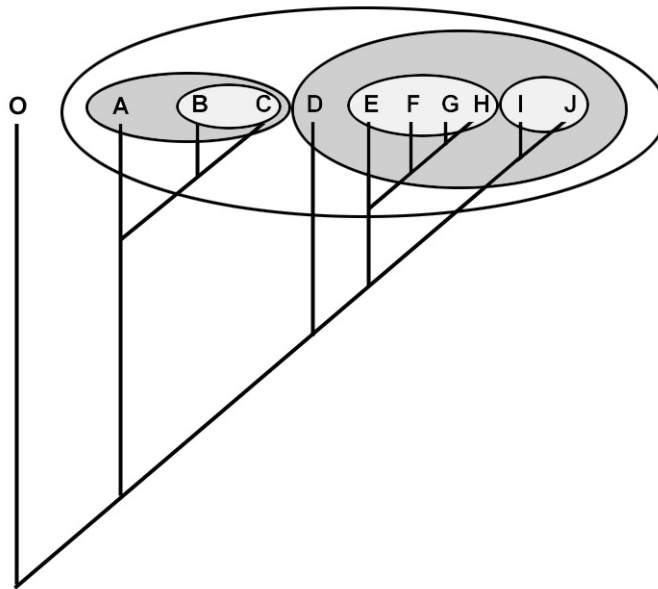


Figure 4. Sample cladogram showing nested sets and monophyletic groups

Procedure 2: Vertebrate Classification and Diversity

The Traditional Vertebrate Classification

In the lab you will find an array of vertebrates and their parts. Alfred Sherwood Romer was one of the most famous vertebrate biologists of the twentieth century. He used a system of classification similar to that described early in this lab. In lab you will be provided with Romer's Synoptic Classification of the Vertebrates. Using the Romer's characteristics, classify the vertebrate specimens in the lab to class. Pay particular attention to the descriptions Romer uses for each group.

Procedure 3: A Nested Sets Approach (classification by monophyletic groups)

In the answer section of the lab you will find the names of several taxa listed in a diagram. The names are similar to those used in our Romerian classification system (the traditional approach). In the following exercise we'll group these taxa by synapomorphies. On the

diagram, you should draw a circle around the group whose members display the listed character(s). This should give you 11 circles, with no lines crossing (i.e. nested sets).

Synapomorphic characteristics of vertebrates for use in nested sets analysis

- 1 hair and mammary glands present
- 2 feathers present
- 3 amniotic membrane present
- 4 pectoral and pelvic appendages present: limbs and girdles
- 5 paired fins (or limbs) with a base of muscle and bone
- 6 lung present (or swim bladder)
- 7 pelvic claspers present in males
- 8 jaws and paired appendages present
- 9 skeleton of cartilage or bone, brain and pharyngeal muscles
- 10 notochord (at some developmental stage)
- 11 distinct head region incorporating anterior end of notochord

When you're done compare this nested set system with the traditional one presented by Romer. You should find agreement in some areas, disagreement in others. Illustrate the relationships in a phylogenetic tree based upon the "traditional" grouping and a cladogram based upon the nested sets grouping. Discuss the differences between these in a few paragraphs.

¹ William of Occam (1284-1347) was an English philosopher and theologian. His work on knowledge, logic and scientific inquiry played a major role in the transition from medieval to modern thought. He based scientific knowledge on experience and self-evident truths, and on logical propositions resulting from those two sources. In his writings, Occam stressed the Aristotelian principle that entities must not be multiplied beyond what is necessary. This principle became known as Occam's Razor, a problem should be stated in its basic and simplest terms. In science, the simplest theory that fits the facts of a problem is the one that should be selected. (http://zebu.uoregon.edu/~js/glossary/occams_razor.html)

Name: _____

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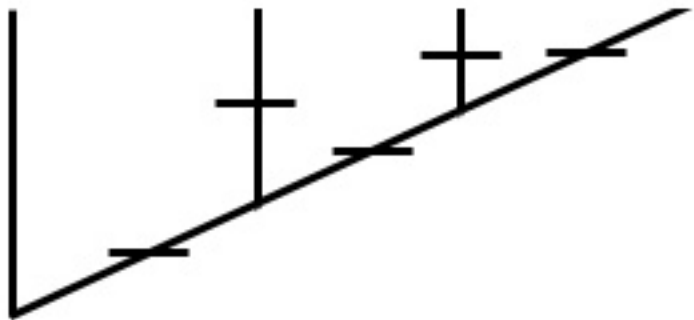
Procedure 1: Cladogram for Inanimate Objects

	Operational Taxonomic Units			
Character States	RED	BLUE	GREEN	YELLOW
a.				
b.				
c.				
d.				
e.				
f.				
g.				
h.				

Pair-wise comparisons of synapomorphies

Pair	RED	BLUE	GREEN	YELLOW
RED				
BLUE				
GREEN				
YELLOW				

Complete your cladogram here, include the character states:



On your cladogram circle a proposed family in red, the proposed e genera in blue and the species in green.

Procedure 2. Traditional (Romerian) Grouping of the Vertebrates

List species and characteristics (as shown in Romer) in this table:

Urochordates (outgroup)

Subphylum Vertebrata

Class Agnatha

Class Chondrichthyes

Class Osteichthyes

Class Amphibia

Class Reptilia

Class Aves

Class Mammalia

Procedure 3. Nested Sets approach

Draw circles around the groups displaying the characteristics (label circles)

		Traditional "Romerian" Classification	
Urochordates Hagfishes Lampreys Chondrichthyes Ray-finned fishes "Lobe-finned" fishes	Non-amniotes	Urochordates	
		Agnatha	
		Chondrichthyes	
		Osteichthyes	
		Amphibia	
		Amphibians "Reptiles" Birds Mammals	Amniotes
Aves			
Mammalia			

Now, illustrate the proposed evolutionary relationships in a phylogenetic tree based upon the "traditional" grouping and a cladogram based upon the nested sets grouping. Discuss the differences between these in a few paragraphs.