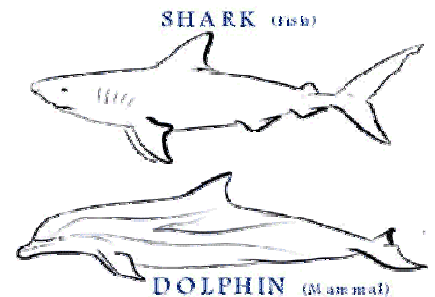


Lab Section: \_\_\_\_\_ Name: \_\_\_\_\_

## Pre-lab Homework Lab 9: Tracing Phylogeny

1. What are the 3 domains and 6 kingdoms of living organisms?
2. Define the following terms in your own words:
  - Phylogeny:
  - Taxonomy:
  - Derived trait:
2. **Figure 14.16** in your text shows how structural differences can be used to determine evolutionary relationships. Structures that developed from a common ancestor are called homologous structures. One difficulty in identifying homologous structures is that sometimes structures are similar but are not due to common ancestry. These are analogous structures. What are analogous structures and why do they occur?

3. Upon comparing sharks and dolphins you notice that both have dorsal fins that stick up out of their backs. Do you think these dorsal fins are homologous or analogous? Why? Recall: dolphins are mammals like us.





Name: \_\_\_\_\_ Date/Lab time: \_\_\_\_\_

## Lab 9: Tracing Phylogeny

### LAB SYNOPSIS:

- We will develop a taxonomic classification and phylogenetic tree for a group of imaginary organisms called **Caminalcules**.
- We will construct a phylogenetic tree of vertebrates from data given.
- We will be answering questions while watching a video on the evolution of whales.

**OBJECTIVES:** After successfully completing this lab, a student will be able to:

- Explain the connection between an organism's taxonomy and its evolutionary history.
- Describe the process used to develop evolutionary trees.
- Distinguish between analogy and homology when examining traits on evolutionary trees.

This exercise is modified from that of Robert P. Gendron, Indiana University of Pennsylvania.  
[http://www.southfloridamuseum.org/Portals/0/History-Museum/Resources/Evol\\_lab.pdf](http://www.southfloridamuseum.org/Portals/0/History-Museum/Resources/Evol_lab.pdf)

### Overview:

**Classification-** The action or process of classifying something according to shared qualities or characteristics.

Humans classify almost everything. For example cars can be classified anywhere from sports cars, to luxury cars to minivans. They can be further classified based on engine, weight class, type of fuel, as well as the purpose for which they are used. Classification is valuable in understanding and communicating the purpose and uses of various types of cars.

**Taxonomy-** The science of finding, describing, naming and classifying living organisms.

**Systematics-** The science of describing the evolutionary relationships of organisms.

Scientists classify organisms based on the evolutionary relationships (phylogeny). Phylogeny is implied by shared features (homologies). For example, biologists classify all organisms that share the characteristic of having a backbone as "vertebrates." The backbone is a characteristic that defines the group. If, in addition to a backbone, an organism has gills and fins it is a fish (a subcategory of the vertebrates). This fish can be further assigned to smaller and smaller categories down to the level of the species. The classification of organisms in this way aids the biologist by bringing order to what would otherwise be a bewildering diversity of species (there are probably at least 10 million species, of which only about one million have been named and classified).

Fish, humans and wolves all share the feature of having a backbone. But humans and wolves are also mammals (warm blooded, with hair and mammary glands). Sharing more characteristics indicates that they are more closely related to one another than they are to fish.

In the 1700's, Carolus Linnaeus ) developed a hierarchical classification scheme, still in use today (Table 1). This method groups all living organisms into categories based upon their distinguishing features.

An organism's form (morphology), internal organization (anatomy), physiology (function), reproduction (sexual features and functions) are used to group similar organisms into six groups called kingdoms.

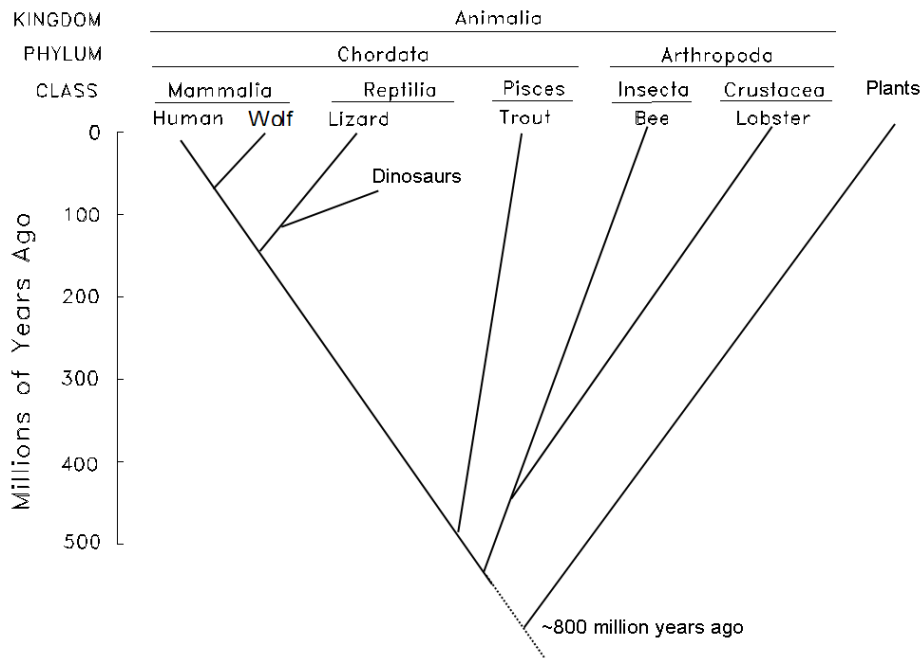
Figure 1 illustrates how four species are classified using this taxonomic system. Recall that genus and species names should be *italicized* or separately underlined.

DOMAIN	Eukarya			
KINGDOM	Animalia			Plantae
PHYLUM	Chordata		Arthropoda	Angiospermophyta
CLASS	Mammalia		Insecta	Monocotyledoneae
ORDER	Primate	Carnivora	Hymenoptera	Liliales
FAMILY	Hominidae	Canidae	Apidae	Liliaceae
GENUS	<i>Homo</i>	<i>Canis</i>	<i>Apis</i>	<i>Alium</i>
SPECIES (common name)	<i>sapiens</i> (humans)	<i>lupus</i> (wolf)	<i>mellifera</i> (honeybee)	<i>sativum</i> (garlic)

**Figure 1: Classification of four species using the Linnaeus taxonomic system.**

Thanks to the work of Darwin, it is now recognized that taxonomic classifications are actually **reflections of evolutionary history (phylogeny)**. For example, Linnaeus put humans and wolves in the class Mammalia within the phylum Chordata because they share certain characteristics (e.g. backbone, hair, warm-blooded, etc.). We now know that these similarities are not a coincidence; both species inherited these traits from the same **common ancestor**. In general, the greater the resemblance between two species, the more recently they diverged from a common ancestor. Thus when we say that the human and wolf are more closely related to each other than either is to the honeybee we mean that they share a common ancestor that is not shared with the honeybee.

Another way of showing the evolutionary relationship between organisms is in the form of a **phylogenetic tree** (see Figure 2 below):



**Figure 2: Phylogenetic tree.**

**Phylogenetic tree-** (evolutionary tree) a branching diagram showing the inferred evolutionary relationships among various biological species as based on homologies.

The vertical axis in this figure represents time. The point at which two lines separate indicates when a particular lineage split. For example, we see that mammals diverged from reptiles about 150 million years ago. The **most recent common ancestor** shared by mammals and reptiles is indicated by the point labeled **A**. The horizontal axis represents, in a general way, the amount of divergence that has occurred between different groups; the greater the distance, the more different their appearance. Note that because they share a fairly recent ancestor, species within the same taxonomic group (e.g. the class Mammalia) tend to be closer to each other at the top of the tree than they are to members of other groups.

**Homologies**- having the same evolutionary origin but not necessarily the same function; (the wing of a bat and the arm of a man are homologous)

**Analogies**- structures having similar function or superficial appearance, but not necessarily sharing a common evolutionary origin; (the wing of a bat and the wing of bird). Similarities are due to convergent evolution.

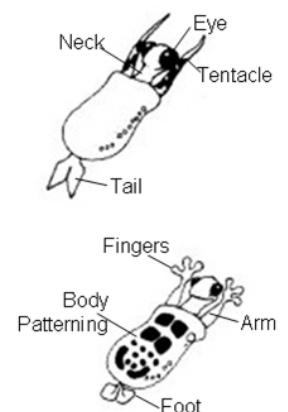
**Convergent evolution**- the independent evolution of similar structures due to similar natural selection pressure.

Homologies in morphology, anatomy, embryology and DNA sequences can all be used to build a phylogenetic tree. However some species resemble each other because they independently evolved similar structures in response to similar environments or ways of life, not because they share a recent common ancestor. This is called **convergent evolution** because distantly related species seem to converge in appearance (become more similar). Examples of convergent evolution include the wings of bats, birds and insects, or the streamlined shape of whales and fish. At first glance it might appear that whales are a type of fish. Upon further examination it becomes apparent that this resemblance is superficial, resulting from the fact that whales and fish have adapted to the same environment. The presence of hair, the ability to lactate and warm blooded clearly demonstrate that whales are mammals. To help avoid mistating analogous for homologous structures, the taxonomist must take into account a whole suite of characteristics, not just a single one.

The **fossil record** can also be helpful for constructing phylogenetic trees. For example, bears were once thought to be a distinct group within the order Carnivora. Recently discovered fossils, however, show that they actually diverged from the Canidae (wolves, etc.) fairly recently. The use of fossils is not without its problems, however. The most notable of these is that the fossil record is incomplete. For example, organisms with shells or bony skeletons are more likely to be preserved than those without hard parts (like worms).

### **Exercise 1: The Taxonomic Classification of Living Caminalcules**

We will model the process of systematics by classifying different species of Caminalcules. Caminalcules (Cami for short) are made-up “organisms” useful for studying the process of classification. We do these exercises with artificial organisms so that you will approach the task with no preconceived notion as to how they should be classified. This will allow you to deal with problems such as convergent evolution just as a taxonomist would. With real organisms you might already have a good idea of how they should be classified and thus miss some of the benefit of the exercise.



In this exercise, you will create a classification of the 14 extant (not extinct) Caminalcule species.

Procedure:

1. Obtain a packet of containing 14 Caminalcules (count them to confirm). Each of the 14 species of extant (not extinct) Cami is represented by a number Note the variety of appendages, shell shape, color pattern, etc.
2. Carefully examine the 14 living species and note the many similarities and differences between them. In the space below, create a hierarchical classification of these species, using the format in Figure 3. Instead of using letters (a, b, ...), as in this example, use the number of each Caminalcule species. Keep in mind that Figure 3 is just a hypothetical example. Your classification may look quite different than this one.

PHYLUM CAMINALCULA											
CLASS 1						CLASS 2					
ORDER 1						ORDER 2			ORDER 3		
FAMILY 1				FAMILY 2		FAMILY 3			FAMILY 3		
GENUS I		GENUS II		GENUS III	GENUS IV		GENUS V			GENUS VI	
a	g	h	d	b	j	l	e	k	c	f	i

**Figure 3: Hypothetical classification of living Caminalcules.**

1. Determine Genera

Taxonomists group organisms based on shared characteristics. Group the 14 different species of Cami into separate genera (plural of genus). The members of a genus will have some similar characteristics. Caminalcules numbered 19 and 20 for example are clearly more similar to each other than either is to any of the other living species so we would put them together in their own genus.

A. How many different genera of Cami did you find? \_\_\_\_\_

B. Which Cami are in each genera? Indicate the species' number. (each piece has a number in its corner) The table supplies 5 genera but you should indicate only those you and your group found (add more if necessary)

	Genus I	Genus II	Genus III	Genus IV	Genus V	Genus VI
The # of the species						

2. Determine Families

Look through your genera. Do any of them share features that might put them into the same family?

A. How many different families did you find? \_\_\_\_\_. Indicate the classification below.

	Family A	Family B	Family C	Family D	Family E
The # of the Genus					

### 3. Determine Orders Classes and Phyla

Do you see any similarities that might allow you to further classify orders classes phyla? Depending on how you organize the species, you may only get up to the level of order or class. You do not necessarily have to get up to the level of Kingdom or Phylum.

### **Exercise 2: Caminalcule Phylogeny**

A phylogenetic tree of the Caminalcule lineages has been constructed for you. These green Camis represent extinct species as based on fossil evidence.

**Lineage-** A line of descent from a common ancestor.

Note the lineages, branch points and the changes in characteristics through a lineage.

**Ancestral characteristics-** a character inherited from a common ancestor. For example; humans, birds and reptiles all have lungs. Lungs are an ancestral characteristic in these groups

**Derived characteristics-** a character inherited only within a subgroup of descendants. For example: the common ancestor of humans and fish had gills not lungs. Lungs are a derived characteristic in the lineage that gave rise to humans (but NOT in the common ancestor to humans and fish).

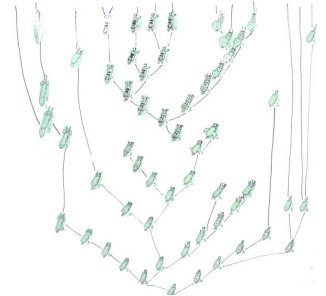
#### Procedure:

Determine the placement of the extant species of Cami at the top of the phylogenetic tree. To do this, note the form of the most recent ancestor and match its characteristics to the 14 extant Cami species.

1. List from left to right the number for each Cami

Camis that are closely related to one another will share a common ancestor. Do the results support your classification from exercise 1? Why? Why not? You may need to answer the questions below before addressing this question.

-----  
 Note the time scale on the Cami phylogenetic tree. It shows the time of major divergences (branch points) of the varied Cami groups. Use the Cami phylogenetic tree to explain convergent evolution, divergence, and vestigial structures in the questions below.



Questions:

1. Pick two extant Cami. Look over their evolutionary lineage and indicate which characteristics look to be derived and which look to be ancestral.
  
2. You will notice that some **lineages** (e.g. the descendants of species 56) branched many times and are represented by many living species. What kinds of environmental conditions might lead to rapid branching (rapid diversification)?  
Hint: our own mammal lineage underwent rapid diversification following the extinction of the dinosaurs ~65 million years ago.
  
3. Some lineages (e.g. the descendants of species 58) changed very little over time. What kinds of environmental conditions might result in very little change over time? Hint: organisms like horseshoe crabs and cockroaches are “living fossils” as they seem very little changes from their ancient fossilized forms.
  
4. Some Caminalcules went extinct without leaving descendents. In the real world, what factors might increase or decrease the probability of a species going extinct?



5. Find two examples of **convergent evolution** among the Caminalcules. This means finding cases where two or more species have a similar characteristic that evolved independently in each **lineage**. The wings of bats, birds and bees is an example of convergence since the three groups did not inherit the characteristic from their **common ancestor**. Write your answers in complete sentences (e.g. "Species *x* and *y* both have \_\_\_\_\_ but their most recent common ancestor, *z*, did not").
  
6. List two real-world examples of convergent evolution (ones that we have not already talked about in the lab manual). What might have caused the convergence?
  
7. Describe two examples of **vestigial structures** that you can find among the Caminalcules. These are structures that have been reduced to the point that they are virtually useless. Ear muscles and the tail bones are examples of vestigial structures in our own species.
  
8. Explain how vestigial structures can provide clues about a species' evolutionary past. Use vestigial organs found in humans to support your explanation.

**Exercise 3: Cladograms**

**Cladogram-** A diagram depicting patterns of shared characteristics among species. Implies evolutionary relationships.

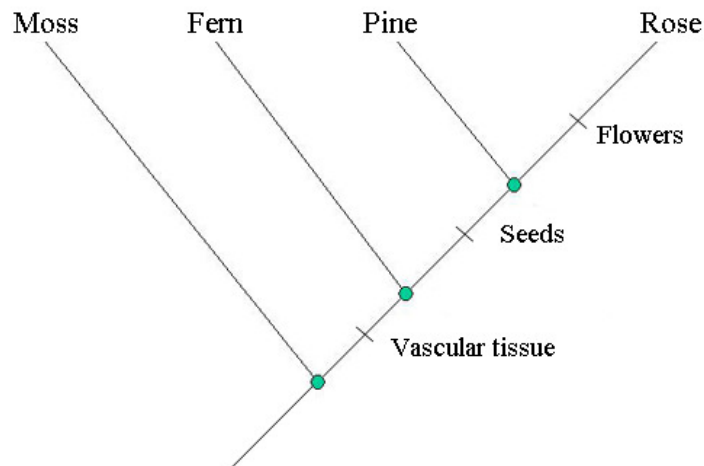
In this exercise, you will work with a real-world data set to build a cladogram of some groups of animals. The basic idea is very similar to the phylogeny in Exercise 2, except cladograms only show evolutionary relationships. Cladograms do not show an evolutionary time scale as seen in phylogenetic trees.

The data used in a cladogram is binary (1 means present, 0 means absent). The below example shows how plant data can be used to determine a simple plant cladogram.

**Binary data table for plants**

Organism	Vascular tissue	Chlorophyll	Seeds	Flowers	Total derived traits
Moss	0	1	0	0	1
Pine tree	1	1	1	0	3
Rose	1	1	1	1	4
Fern	1	1	0	0	2
<b>Total shared traits</b>	<b>3</b>	<b>4</b>	<b>2</b>	<b>1</b>	<b>na</b>

1. Determine the “outgroup”. The outgroup is the organism with the fewest number of derived traits. This is the group all other groups are compared to.
2. Starting with a diagonal line, the out-group is placed on the first branch. Just past the first branch, the most common derived trait is listed; in this case vascular tissue, which is composed of tube-like cells. The branching point or node on a cladogram marks the point where shared derived characters arose.
3. Next, the second most common derived trait is determined, which in this case is seeds. Ferns lack seeds and are thus placed on the second branch. The third most common derived trait is flowers. Pine trees do not have flowers and are thus placed on the third branch. Flowering plants are placed at the end.



⇒ Based on the data given, where would the chlorophyll trait be placed on this tree?

You will now use the data below to construct a cladogram showing the evolutionary history of animal groups.

Table: Animal Phylogeny Characteristics

Group	Backbone	Hair	Milk	Feathers	4 limbs	Wings	Diapsid skull	Complex placenta	Dorsal fin	Bird-like hips	Total derived traits
Hagfish	1	0	0	0	0	0	0	0	0	0	
Great white shark	1	0	0	0	0	0	0	0	1	0	
Eagle	1	0	0	1	1	1	1	0	0	1	
Velociraptor (dinosaur)	1	0	0	?	1	0	1	0	0	1	
Geko lizard	1	0	0	0	1	0	1	0	0	0	
Human	1	1	1	0	1	0	0	1	0	0	
Dolphin	1	1	1	0	1	0	0	1	1	0	
<b>Total shared traits</b>											<b>na</b>

Diapsid skulls- skull type that has a set of holes in addition to the set for the eye sockets.

Procedure:

1. Use the data table to draw a phylogeny of the evolution of vertebrate animals (on a separate sheet of paper).
2. Fill in the last row for the “total shared traits”. The higher numbers typically represent traits that evolved earlier. Ex. 7 organisms share the backbone trait. Thus all organism derived from that branch will probably have a backbone. The number of traits, highest to lowest, often tells you the order in which those traits evolved.
3. Fill in the last column for the “total derived traits”. Start with the organism that has the fewest total derived characteristics. This organism thus shows the most ancestral traits. It is called the “outgroup”. All other organisms will branch off its lineage.
4. Look for organisms that are similar to the outgroup except for one, or a few, differences. These differences indicate a branch point.
5. Organisms that share many features are usually more closely related. Look for differences. These indicate branch points.

Construct your cladogram below.

Questions:

1. How many different branches did you create? \_\_\_\_\_
2. What are 2 examples of analogous structures on this evolutionary diagram?
3. Biologists think that dolphins and humans are somewhat closely related. What support can you see for this hypothesis? Try to use the idea of a derived trait to answer this question.
4. Many paleontologists (people who study fossil remains) think that velociraptors (remember Jurassic Park 2???) had feathers. What evidence does your tree have for this hypothesis?
5. Most current taxonomy is done by comparing DNA sequences. Computers compare 1000's of nucleotides to generate a best guess tree. Why might this be a useful method for determining evolutionary relationships?

### **Exercise 5: Great Transformations**

**Video:** Great Transformations (2001). Runtime ~60 min.

“What underlies the incredible diversity of life on Earth? How have complex life forms evolved? The journey from water to land, the return of land mammals to the sea, and the emergence of humans all suggest that creatures past and present are members of a single tree of life.”

Read these questions prior to watching the video and answer them during the video.

1. What are some of the characteristics that all mammals have (including whales and dolphins!)?
2. What was unusual about the skull fragment that Dr. Gingerich found?
3. What did *Basilosaurus* have that other whales seem to have lost?
4. What is the big difference between how fish swim and how whales and dolphins swim?
5. What is a characteristic shared by land animals?
6. What characteristic does *Acanthostega* have that makes it so surprising?
7. What hypothesis does Dr. Clacks put forward on the evolution of limbs in animals?
8. What seems to have happened in the Cambrian explosion?
9. What underlying genetic mechanism seems to have allowed this?
10. How are the genes of fruit flies helping us to understand how evolution can occur?
11. Post video: Discuss with your group and indicate what you all found most interesting from this video?