Determining and Representing Phylogeny

Objectives:
- Learn how to create and interpret cladograms
- Learn some vertebrate skeletal anatomy
- Practice measuring using the metric system

Concepts: A **phylogeny** is the evolutionary history of a taxon. A **phylogenetic tree** is a diagram that shows the history and evolutionary relationships among members of a taxon. A **cladogram** is one type of phylogenetic tree; in a cladogram, taxa that share derived, homologous characters are represented as sharing a common ancestor.

Any cladogram is a hypothesis. With a particular selection of taxa and characters, numerous cladograms are possible. So how do is it decided which cladogram is the best supported? The more characters that fit the pattern of the cladogram, the more supported the hypothesis. Also, an assumption often followed in cladogram construction is that of **parsimony**. One should try to make the simplest cladogram that accounts for all the data. For example, all else being equal, a cladogram in which a derived character evolves just once is considered more likely than a cladogram in which the character evolves several times.

Problem: Construct a cladogram showing the evolutionary relationships among the taxa listed in Table 1. First, decide which taxa have which characters and put the results in Table 1.

TAXA CHARACTERS	dog	kangaroo	lizard	trout
hair				
placenta				
bony limbs				
vertebra				

Table 1: Characters of selected vertebrate taxa

In making a cladogram from the available data, one of the first things to do is to choose the **outgroup**. The outgroup is a taxon that is related to the other taxa, but is not a member of the group formed by the other taxa. Here, trout is the outgroup. It's related to the other three taxa (all 4 are vertebrates) but the others are all more closely related to each other than to the trout. (Trout lacks lungs and bony limbs, which the other three all have.)

To determine whether a character is **ancestral** or **derived** compare the character in the ingroup with that of the outgroup. Assume that the character in the outgroup is ancestral. If the character is different in the ingroup, then it is considered derived --[i.e., as evolution took place, the character has changed from its ancestral state to its derived state.[Use 'A' to symbolize the **a**ncestral character and a 'D' to symbolize a **d**erived character. (Campbell et al. use the term 'primitive' rather than 'ancestral.' However, 'primitive' tends to have a negative connotation and 'ancestral,' meaning 'similar to that of the ancestors' is descriptive, but neutral.)

Fill in the Table 2 to reflect whether the characters are ancestral (A) or derived (D).

Table 2: Polarity of characters of selected vertebrate taxa

TAXA / CHARACTERS	dog	kangaroo	Lizard	trout
hair				
placenta				
bony limbs				
vertebra				

Draw a cladogram below that conforms with the data in the Table 2. Label the cladogram with the shared, derived characters in the appropriate places.

Introduction: There are about 50,000 species of vertebrates, all of which share common ancestry. Your assignment today will be to determine the evolutionary relationships of 7 vertebrates, based on a set of characters listed below.

Methods: Collect data from the skeletons of the 7 species in the table below. Look at each skeleton and fill out the following character table.

Table 3: characteristics of selected vertebrates

TAXA CHARACTERS	Rabbit	Dog	Rat	Cat	Turtle	Chimpanzee	Human
Complete eye socket?							
Eye socket faces forwards or sideways?							
# of cervical vertebrae							
Radius and ulna fused or separate							
Digitigrade / plantigrade ?							
Quadraped or biped?							
Claws or nails?							
Incisors Present or absent							
Canines Present or absent							
Length of longest incisor (mm)							
Length of longest canine (mm)							
Incisor/canine length ratio							
Bears live young?							
# of vertebrae in tail							
Length of head (mm)							
Height of head (mm)							
Length/height ratio of head							
Other							

Results:

You have quite a bit of information in Table 3. This may be more information than you need to determine the phylogeny of these 7 species. Also, some of the data may not be helpful in determining phylogeny. Just as other scientists must do, you will have to choose which characters are useful in determining phylogeny, and which are not.

First, decide which characters are most **useful** for discriminating evolutionary relationships. You might consider how difficult it would be from a genetic and/or developmental standpoint for a particular character to change/mutate from one state to another. For example, you could easily imagine a species evolving a somewhat longer canine, but it is probably a much more complicated (and hence less likely) step to go from lacking canines to having canines (or vice versa). List the characters you think are most useful in the first column of Table 4.

Second, choose your outgroup and polarize (i.e. determine whether ancestral or derived) the characters you've chosen as useful. List the taxa in the top row; identify the taxa that will be your outgroup.

Table 4: Data Matrix of Character States of Vertebrates

Character	States	Outgroup (turtle)	rabbit	rat	rat	cat	chimp	human
	A= D=	A						
	A= D=	A						
	A= D=	A						
	A= D=	A						
	A= D=	A						
	A= D=	A						
	A= D=	A						
	A= D=	A						
	A= D=	A						
	A= D=	A						
	A= D=	A						

Third, use Table 5 to summarize your data from Table 4. For each pair of taxa, record the number of derived characters that are shared.   Think again about what you are being asked to do: Record the number of DERIVED characters that are shared, and Derived characters ONLY.

Table 5: Data Matrix of Shared Characters in Vertebrates

Taxon	turtle	rabbit	dog	rat	cat	chimp	Human
Turtle							
Rabbit						Do not fill in any of the gray spaces.	
Dog							
Rat							
Cat							
Chimp							
human							

1. Draw a cladogram that you think is best supported by the data that you have collected and organized. Remember, the greater the number of shared, derived, homologous characters, the more closely related are the two taxa. Include the derived characters in the appropriate places on the cladogram

Repeat the three steps under '**Results'** and make a second cladogram.   Rationale: While you were making decisions in filling in the above tables, you might have wondered if you were choosing the most appropriate characters or outgroup.   So repeat the process, and this time choose some of the alternate characters and/or an outgroup that you at first discarded.

Discussion and Conclusions:
Write the answers to these on a separate sheet of paper.

1. For each of the two cladograms, write a paragraph that explains why and how you decided that this was a plausible cladogram. (i.e. address why you chose the characters and/or outgroup you did.)

2. Finally, decide which of the two cladograms you think is more likely to be correct.
   Defend your answer.

3. The cladogram you have made is a hypothesis.
   a. What are some ways you could test this hypothesis ?

   b. With your method of testing the hypothesis in mind, make a prediction about what the results of the test should be if the hypothesis is true.