Geo 302D: Age of Dinosaurs

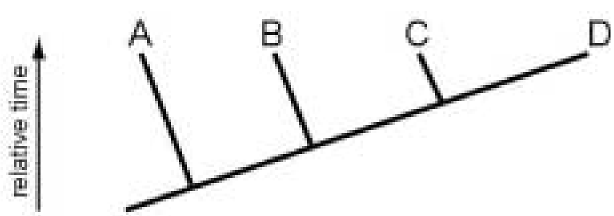
LAB 4: Systematics

Systematics is the comparative study of biological diversity, with the intent of determining the relationships between organisms. Humankind has always tried to find ways of organizing the creatures that surround us into categories or classes. Linnaeus was the first to utilize a working system of hierarchical classification, in 1758. It is his classification scheme which most of you are familiar with, as it is still taught in its basic form in grade schools. The system is based upon the organization of life forms into groups based upon their overall similarity.

In this course we use **phylogenetic systematics**, also called **cladistics**. This technique is used by most professional biologists, zoologists, and paleontologists. In this system, organisms are grouped together on the basis of shared ancestry. A result of using this system is that the ranks (e.g. Kingdom, Phylum, Class, Order, etc.) which many of you were forced to learn in previous science classes are impractical and do not necessarily reflect evolutionary relationships between organisms. Therefore, they are not used in cladistic methodology.

Cladograms

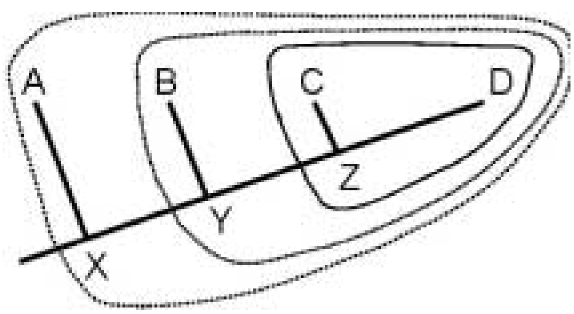
Cladistics uses branching diagrams called **cladograms** (or trees) to visually display the hypothesized relationships between **taxa** (a **taxon** is any unit of biological diversity; taxa is the plural form of the word). Look at the cladogram below. Relative time runs vertically. A, B, C, and D represent different taxa. They are out at the terminal tips of branches on the tree, so they are called **terminal taxa**. The points on the tree where branches meet are called **nodes**. A node represents the point of divergence between evolutionary lineages. The node also represents the **most recent common ancestor** between the two lineages splitting at that point.



How do you read a cladogram? Take a look at the cladogram above again. Taxon A branches off first. This tells you that A split from the lineage leading to the group (also called a **clade**) composed of B + C + D + their most recent common ancestor, before the lineages leading to B, C, and D each began to diverge. The node from which A splits off is where you should see the last organism that gave rise to both A and the group [B+C+D+ their most recent common ancestor]. Any two groups which share a more recent common ancestor with each other than with any other group are called **sister taxa**. Group [B+C+D+ their most recent common ancestor] and A are each other's sister taxon.

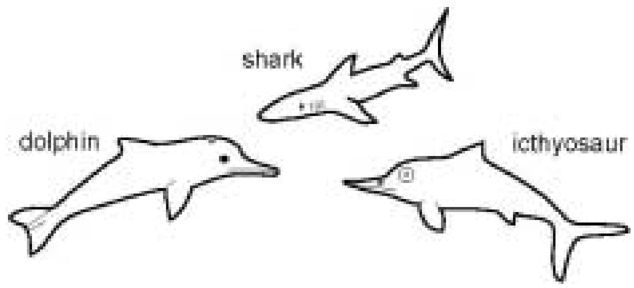
Likewise, you can see that B branched off from the lineage leading to C and D after their split with A, but before C and D diverged. This means that B shares a most recent common ancestor with group [C+D+ their most recent common ancestor]. B and [C+D+ their most recent common ancestor] are therefore sister taxa, and are more closely related to each other than either is to A.

You can probably already see that using terminology like [B+C+D+ their most recent common ancestor] gets lengthy and confusing. To get around this we give names to the groups at the nodes. See the cladogram below. A, B, C, and D are still terminal taxa, but now we also give the larger clades to which they belong the names X, Y, and Z. Now we can say that A and Y are sister taxa, and it still means the same as saying, "A and the group [B+C+D+ their most recent common ancestor] are sister taxa". **IMPORTANT!** X, Y, and Z are the names of clades, NOT the names of the organisms at each node! The groups X, Y, and Z are circled, showing how each clade is nested within others.

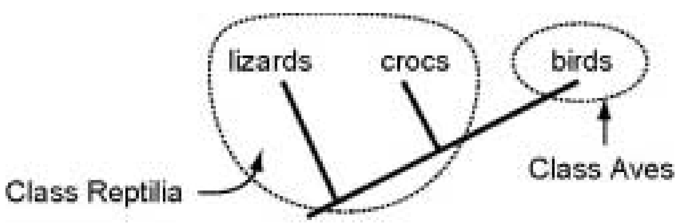


Types of groups

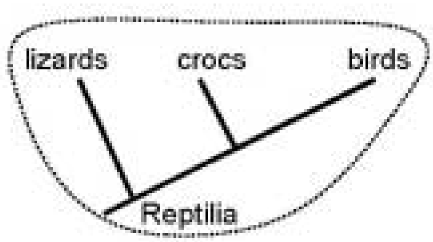
There are certain kinds of groups created by classification. In the figure below you see a dolphin, a shark, and an extinct form of marine reptile called an icthyosaur. They all have streamlined bodies for moving easily through water, their forelimbs are modified into flattened paddles for steering, and their tails are flattened to make a powerful means of propulsion. It is conceivable that you might look at these three animals and group them together on the basis of their overall similarity. But, the dolphin is a mammal, the shark is a fish, and the icthyosaur is a reptile. Any group created that contains only these three animals would be considered **polyphyletic**. A **polyphyletic group** is any group made up of organisms which do not share a recent common ancestor. !! No systematist recognizes polyphyletic groups as natural taxa.



The traditional, Linnean classification system recognized **paraphyletic groups**. A **paraphyletic group** is made up of an ancestral organism and some, but not all, of its descendants. For example, the cladogram below consists of lizards, crocodiles, and birds as terminal taxa. The birds and crocodiles are actually more closely related to each other (share a more recent common ancestor) than either is to lizards. In Linnean classification, lizards and crocodiles are lumped together in the Class Reptilia. Birds were placed in their own class, Class Aves. This means that "Reptilia" in a Linnean sense is paraphyletic. It contains an ancestral organism, plus lizards and crocodiles, but excludes some of the ancestor's descendants, the birds.



Evolutionarily speaking, birds are reptiles. They are very specialized in form and function, but they are still descended from reptiles. Cladistics does not recognize paraphyletic groups as naturally occurring taxa. Cladistics only recognizes **monophyletic groups**. **A monophyletic group is composed of an ancestor and <u>all</u> of its descendants**. The cladogram with lizards, crocs, and birds is shown below. "Birds" is merely one monophyletic group nested within a larger monophyletic group called Reptilia.



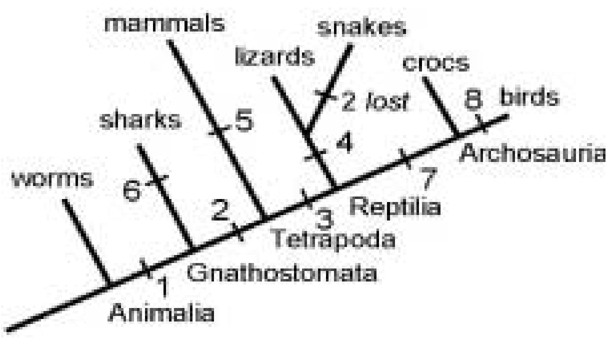
Determining relationships

Cladists are faced with the daunting task of trying to establish the inter-relationships of all organisms on Earth, both living and extinct. To achieve this goal, they look at organisms in detail and use the characters they possess to determine relationships. There are several terms and types of characters for which you are responsible.

- **apomorphy**: a character
- **plesiomorphy**: a primitive character. A taxon has a plesiomorphic character simply because it inherited it from its ancestors.
- **autapomorphy**: a derived (new) character that is present in only one taxon.
- **synapomorphy**: a shared, derived character. This is a derived character which is present in more than one taxon. **In cladistics you can only group organisms together on the basis of their synapomorphies**.

<u>**Exercises**</u>

Below you see a cladogram showing relationships between lizards, crocs, birds, mammals, earthworms, sharks, and snakes. For now, assume this cladogram depicts the true evolutionary relationships between these taxa. The following characters (apomorphies) were used to figure out relationships. They are mapped onto the cladogram.



1. jaws
2. legs
3. flat scales
4. forked tongue
5. hair
6. multiple rows of teeth
7. mandibular fenestra
8. feathers

Worms are primitive animals, with none of the traits seen in the others. “Jaws” (1) is a derived condition relative to worms, and is shared by all members of the monophyletic group Gnathostomata. This means “jaws” is a synapomorphy for Gnathostomata. The next character, “legs” (2) is not found in sharks, but it is shared by members of Tetrapoda (the clade [mammals +lizards +snakes +crocs +birds + their most recent common ancestor]). Therefore, “legs” is a synapomorphy for Tetrapoda. “Jaws” is no longer derived at this level. Because members of Tetrapoda already inherited their jaws from a more distant ancestor, “jaws” is a plesiomorphy for Tetrapoda. “Multiple rows of teeth” (6) is possessed only by sharks. It is derived compared to the worm, and is unique to sharks. This is an autapomorphy of the clade “sharks”.

As you can see, character 2 “legs”, is lost in snakes. The loss of characters happens often through the course of evolution. This does not mean that snakes are not tetrapods. They are descended from tetrapod ancestors that had legs, but snakes secondarily lost them in the course of adapting to a particular lifestyle. The loss of legs is an autapomorphy of snakes.

1. Give all characters which are plesiomorphic for Archosauria.

2. List all the autapomorphic characters you see on the cladogram above.

3. Who is the sister taxon to lizards?

4. Are “mammals” more closely related to “sharks” or Reptilia?

   Why?

5. Tetrapoda is the sister taxon to whom?

Making a data matrix

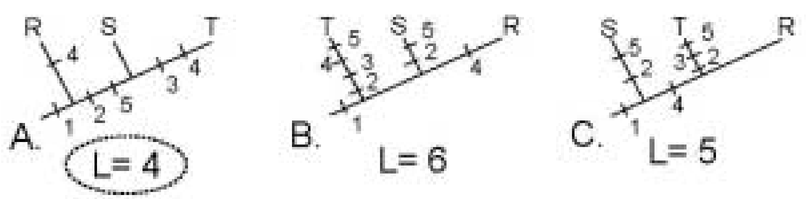
How does a cladist make a cladogram? First you pick taxa to work with. Then you pick characters that fulfill several criteria. The characters should be 1.) heritable, 2.) independent of one another, and 3.) unambiguous. You also pick an **outgroup**. The outgroup is a taxon that you feel represents the likely primitive condition for all of your taxa of interest (called the **ingroup**). This has the effect of polarizing your characters in the matrix, or in other words, it lets you know which characters are actually primitive and which are actually derived.

You then create a **data matrix**. Taxa go on one axis, and characters go on the other. Below is the matrix used to create the cladogram on page 4. On this particular data matrix, “0” stands for “character absent”, and “1” stands for “character present”. Some cladists use “0” to mean a character is primitive, and “1” to mean a character is derived with respect to the presence or absence of the character in the outgroup. You then examine the taxa and score the matrix based upon your observations. From this you can construct the cladogram by working your way up the tree by building more and more derived taxa.

	worm	shark	mammal	snake	lizard	croc	bird
1	0	1	1	1	1	1	1
2	0	0	1	0	1	1	1
3	0	0	0	1	1	1	1
4	0	0	0	1	1	0	0
5	0	0	1	0	0	0	0
6	0	1	0	0	0	0	0
7	0	0	0	0	0	1	1
8	0	0	0	0	0	0	1

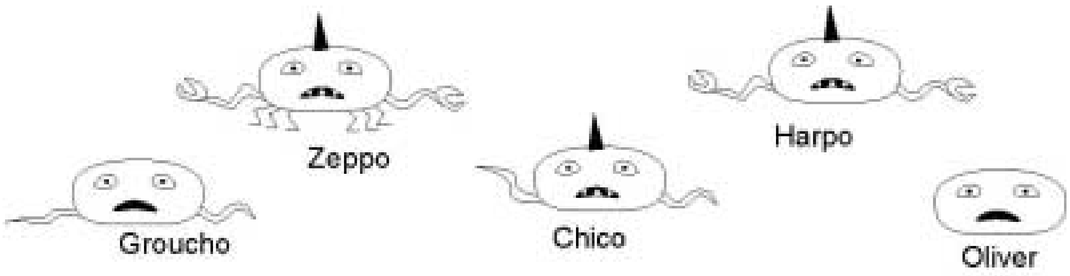
Sometimes an analysis yields more than one possible set of relationships. In the example below there are three terminal taxa (R, S, and T), and five characters (1-5). There are only three possible combinations of relationships, and these are shown. The characters are mapped on the cladograms. Cladists use the **Principle of Parsimony** to decide which tree is most likely correct. Parsimony assumes that the least complicated path is more likely to be the correct one. Cladists determine which tree is least complicated by counting the number of character state changes or steps (the number of times characters must be added or removed from a tree) in each. The tree with the fewest changes is considered the most parsimonious, and it is chosen as the correct tree. **Cladists use only synapomorphies to determine relationships. Plesiomorphies and autapomorphies are not counted.**

	R	S	T
1	1	1	1
2	0	1	1
3	0	0	1
4	1	0	1
5	0	1	1



!! Do not count plesiomorphies nor autapomorphies !!

6.) You are chief astrozoologist on a Mars mission. After prospecting for several days, you assemble a collection of life forms. It is now your job to determine the evolutionary relationships between these organisms. Use the list of characters given with the matrix below. You decide Oliver should be your outgroup, because it appears to be the least specialized, and therefore most primitive. Fill in the matrix. **Use "0" to represent the primitive state, as possessed by Oliver. "1" indicates a derived state**.



	Oliver	Groucho	Zeppo	Chico	Harpo
1.eyes					
2.mouth					
3.tentacles					
4.horn					
5.pincers					
6.legs					
7.teeth					

7. Construct a cladogram based upon your matrix. Map all your characters.

8. How many steps are there on your tree? Should you count characters 1 and 2?