Geo 302D: Age of Dinosaurs

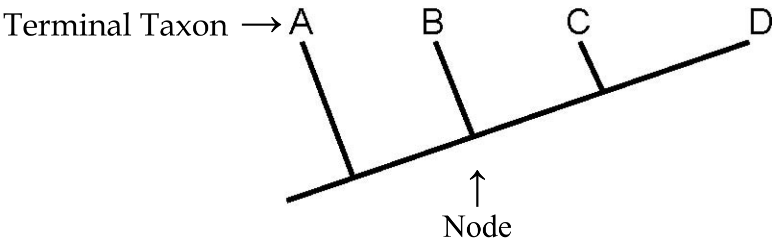
LAB 4: Systematics Part 1

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 organisms into categories. Carolus Linnaeus was the first to utilize a working system of hierarchical classification in 1758. It is his classification scheme that most of you are familiar with because 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**, which is 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 learned in previous science classes, are impractical and do not necessarily reflect evolutionary relationships among 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. A, B, C, and D represent different taxa. They are 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, which are represented by the branches. The node also represents the **most recent common ancestor** between the two lineages splitting at that point.

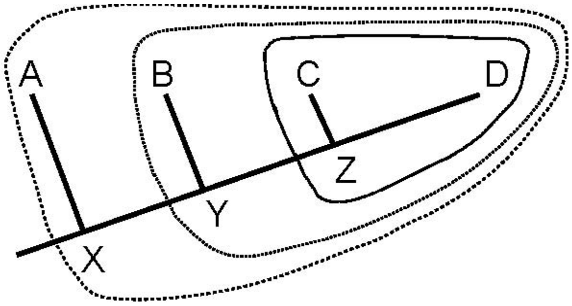


How do you read a cladogram? Take a look at the cladogram above again. Taxon A branches off first. This tells you that A split from the lineage leading to the group (also called a **clade**) composed of B + C + D + their most recent common ancestor, before the lineages leading to B, C, and D each began 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.

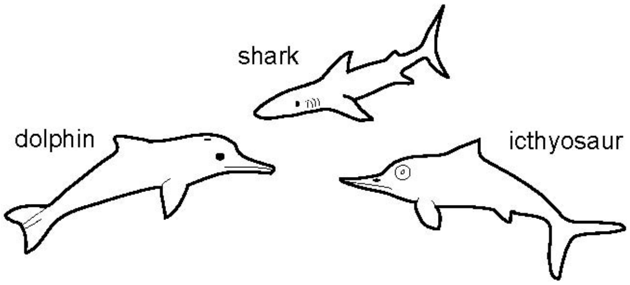
Likewise, you can see that B branched off from the lineage leading to C and D after their split with A, but before C and D diverged. This means that B shares a most recent common ancestor with group [C+D+ their most recent common ancestor]. B and [C+D+ their most recent common ancestor] are therefore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

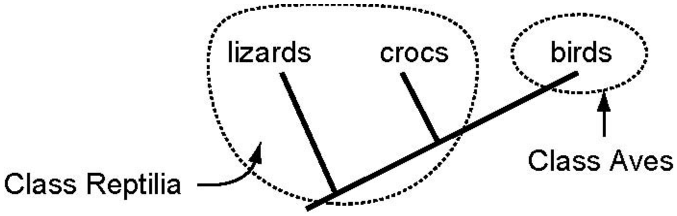


Types of groups

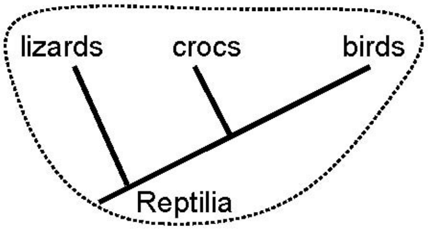
There are certain kinds of groups created by classification. In the figure below you see a dolphin, a shark, and an extinct form of marine reptile called an ichthyosaur. They all have streamlined bodies for moving easily through water, their forelimbs are modified into flattened paddles for steering, 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. However, 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. !! Polyphyletic groups are not natural groups because they do not reflect shared ancestry.



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 groupings as natural groups. Cladistics only recognizes **monophyletic groups**. **A monophyletic group (or taxon) 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.



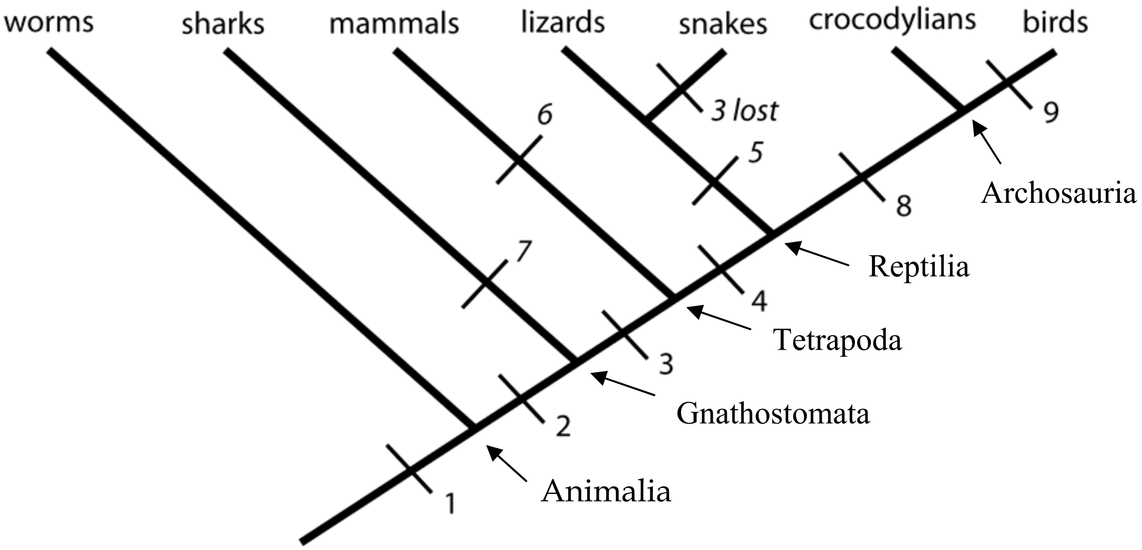
Determining relationships

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

- **apomorphy**: a derived character
- **plesiomorphy**: a primitive character.
- **autapomorphy**: a derived (new) character that is present in only one taxon.
- **symplesiomorphy**: a shared, primitive character. These characters are not informative when attempting to reconstruct relationships of taxa.
- **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**.

Exercises

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

All taxa present in this cladogram possess "cells" (0). Therefore, this character is a symplesiomorphy of the cladogram: it tells us nothing about the relationships of these organisms. Worms are primitive animals, with none of the traits seen in the others. "Jaws" (2) 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" (3) 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" (7) 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 3 “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.

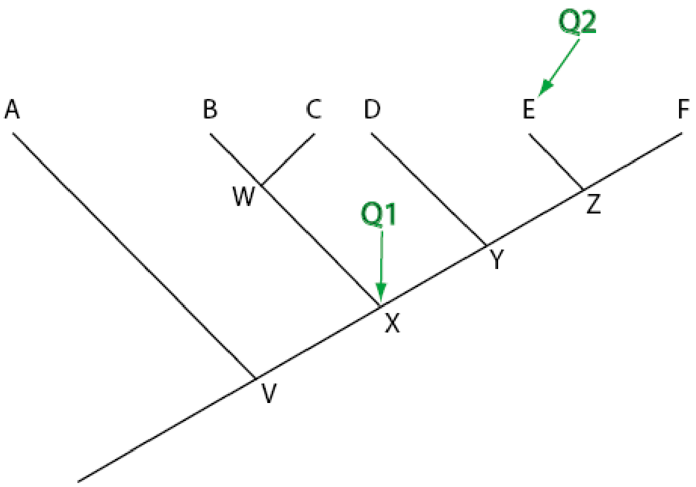
2. List all the autapomorphic characters you see on the cladogram above.

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?



6. a. Q1 designates a(n):
   a. apomorphy
   b. branch
   c. node
   d. terminal taxon

   b. What else does Q1 represent?

7. a. Q2 designates a(n):
   a. apomorphy
   b. branch
   c. node
   d. terminal taxon

8. Label the type of group present in each cladogram below: