Humans classify almost everything, including each other. This habit can be quite useful. For example, when talking about a car someone might describe it as a 4-door sedan with a fuel injected V-8 engine. A knowledgeable listener who has not seen the car will still have a good idea of what it is like because of certain characteristics it shares with other familiar cars. Humans have been classifying plants and animals for a lot longer than they have been classifying cars, but the principle is much the same. In fact, one of the central problems in biology is the classification of organisms on the basis of shared characteristics. As an example, biologists classify all organisms with a backbone as "vertebrates." In this case 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.

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 several million species ‑ of which about one million have been named and classified.) The field devoted to the classification of organisms is called **taxonomy** [Gk. taxis, arrange, put in order + nomos, law].

This view of taxonomy changed dramatically when **Charles** **Darwin** published *On The Origin of Species* in 1859. In his book Darwin presented convincing evidence that life had evolved through the process of **natural selection**. The evidence gathered by Darwin, and thousands of other biologist since then, indicates that all organisms are descended from a common ancestor. In the almost unimaginable span of time since the first organisms arose (about 3.5 billion years) life has gradually diversified into the myriad forms we see today.

As a consequence of Darwin's work it is now recognized that taxonomic classifications are actually **reflections of evolutionary history**. For example, Linnaeus put humans and wolves in the class Mammalia within the phylum Chordata because they share certain characteristics (e.g. backbone, hair, homeothermy, etc.). We now know that this similarity is 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** (Gk. phylon, stock, tribe + genus, birth, origin):



Figure 2

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.

**The Classification and Evolution of Artificial Organisms**

In this lab you will develop a taxonomic classification and phylogenetic tree for a group of imaginary organisms called Caminalcules. There is a number in parentheses indicating the geological age of each specimen in millions of years. Most of the fossil Caminalcules are extinct, but you will notice that a few are still living (e.g. species #24 is found among the living forms but there is also a 2 million year old fossil of #24 in our collection).

**Exercise 1. The Phylogeny of Caminalcules**

Using a large sheet of paper, construct a phylogenetic tree for the Caminalcules. Use a meter stick to draw 20 equally spaced horizontal line on the paper. Each line will be used to indicate an interval of one million years. Label each line so that the one at the bottom of the paper represents an age of 19 million years and the top line represents the present (0 years).

Cut out all the Caminalcules (including the living species). Put them in piles according to their age (the number in parentheses). Beginning with the oldest fossils, arrange the Caminalcules according to their evolutionary relationship. Figure 4 shows how to get started.

73

74

58

**?**

**?**

**?**

19

18

17

Millions of Years Ago

## Figure 4

**Hints, Suggestions and Warnings**

a. Draw lines faintly in pencil to indicate the path of evolution. Only after your instructor has checked your tree should you glue the figures in place and darken the lines.



b. Branching should involve only two lines at a time:

Like this Not this

c. Some living forms are also found in the fossil record.

d. There are gaps in the fossil record for some lineages. Also, some species went extinct without leaving any descendants (remember the dinosaurs, Fig. 1).

e. The Caminalcules were numbered at random; the numbers provide no clues to evolutionary relationships.

f. There is only one correct phylogenetic tree in this exercise. This is because of the way that Joseph Camin derived his imaginary animals. He started with the most primitive form (#73) and gradually modified it using a process that mimics evolution in real organisms. After you complete your phylogeny compare it with Camin's original.