



CLASSIFICATION OF LIVING THINGS

Classifying living organisms, the study of taxonomy and phylogeny trees

Taxonomy is the study of the principles behind **classification**. Classification is the process of sorting living organisms into groups. This involves studying individual **species** to find similarities, enabling categories to be set up.

The current system of classification was devised by **Carl Linnaeus** over 250 years ago. It uses eight **taxa**:

Taxonomic rank	Named taxonomic group example	
	Latin	English
Domain	Eukaryotae	Eukaryotes
Kingdom	Animalia	Animals
Phylum	Chordata	Chordates
Class	Mammalia	Mammals
Order	Primate	Primates
Family	Hominidae	Great apes
Genus	<i>Homo</i>	<i>Homo sapiens</i>
Species	<i>sapiens</i>	(human)

The **species** is the most basic unit of classification. Each member of the species is essentially the same, although there may be some variation. Members belonging to the same **genus** show many similarities, as many of the species are primarily the same, although there is more diversity. As you venture up the taxa, the similarities become less and less, and the groupings diversify more and more.

The easiest ways to remember the different taxa are using a *pneumonic* such as:

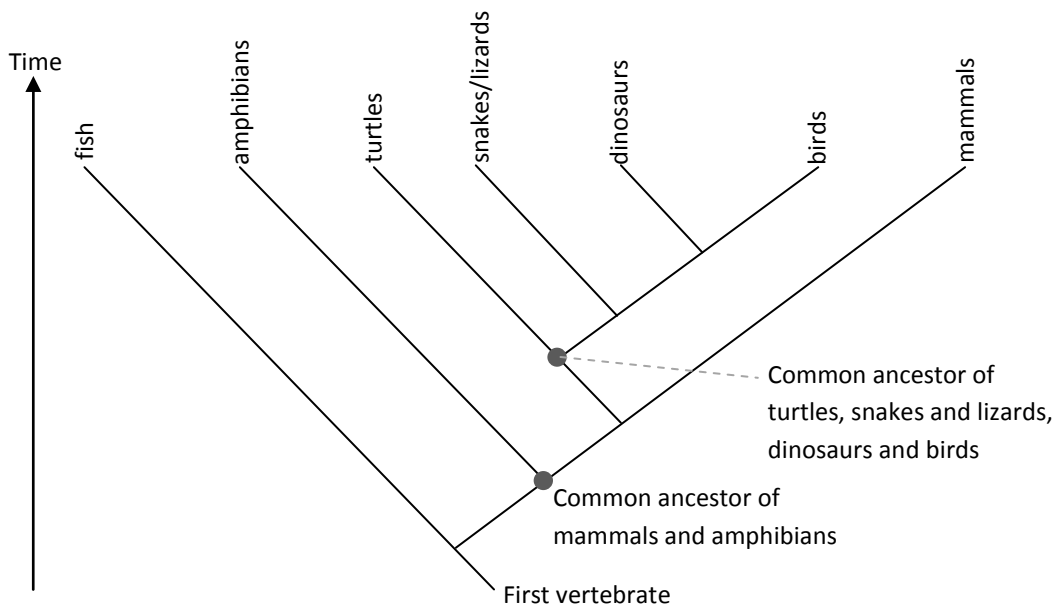
“Dennis keeps playing cards on Fred’s green stool”

“Do kinky people call often for good sex?”

A species name has a specific way of being written. It should be written in italics, with the genus beginning with a capital letter, and the species all in lower case, such as *Homo sapiens*. When handwriting, it is done by underlining the genus and species, rather than using italics, such as Homo sapiens.

PHYLOGENY

The practice of **phylogeny** is grouping together organisms that share a common **ancestor**. The more recent the ancestors, the more similarities there will be between the species.

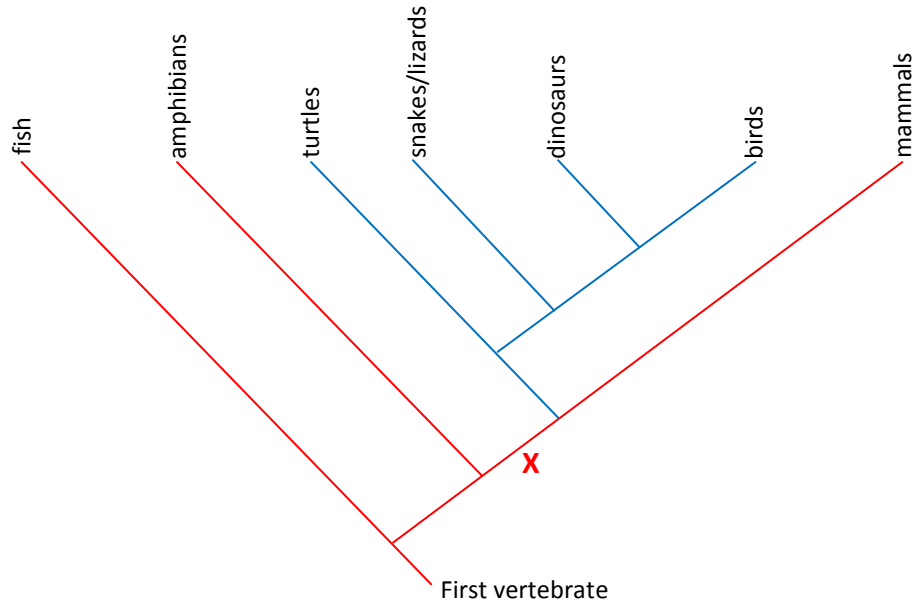


The tree divides as time progresses. As the tree splits, a **common ancestor** between future divisions and paths is present. For example, there are two common ancestors shown on this tree. One common ancestor is shared by the mammals and amphibians. Another is shared by the turtles, snakes and lizards, dinosaurs and birds. The turtles, dinosaurs, snakes and lizards all belong to the reptile group.

A good classification system should be:

- ✓ easy and clear to assign organisms to groups
- ✓ containing a wide range of groups (i.e. not just “Yes” or “No”)
- ✓ using groups which are classifiable (i.e. everything can be categorised)

Using the phylogeny tree system, we give organisms sharing a common ancestor the term **monophyletic**. Snakes, lizards, dinosaurs and birds are all monophyletic, as they share a common ancestor.



Reptiles, however, are *not* monophyletic, because the reptile group in general does not have one common ancestor. Instead, they are **polyphyletic**. There is no single ancestor that includes all reptiles without including other groups too.

We can use phylogeny to make predictions about past events. For example, using the tree above, if we know that turtles, snakes and lizards, dinosaurs, birds and mammals all have an *amniotic egg* (can survive on land), but fish and amphibians do not, we can tell that the amniotic egg was evolved at point X.

A DICHOTOMOUS KEY

Using a **dichotomous key** is a way of identifying and naming a specimen you have found. The key provides a series of questions. Each question has two answers, most often “Yes” and “No”. The answer to each question will either lead to another question or to the name of the specimen. E.g. for the example shown here:

- | | |
|--|--|
| 1 Are the buds paired? | yes – go to 2
no – go to 4 |
| 2 Are the buds black? | yes – ash
no – go to 3 |
| 3 Are the buds green? | yes – sycamore
no – horse chestnut |
| 4 Are the buds pointed and longer than they are wide? | yes - beech
no – go to 5 |
| 5 Are the buds bunched together at the tip? | yes – English oak
no – sweet chestnut |

