**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*:

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

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