

**LECTURE 1 NOTES**

**Week 1.1**

**25/7/16**

**BIOLOGICAL CLASSIFICATION SYSTEMS**

All life originated from a unicellular ancestor about 4 billion years ago. Due to natural selection and isolation of random variants led to the evolution of about 30 million species. A species is defined as an set of organisms that are able to produce offspring.

It is entrenched into our very nature that we have a desire for order and understanding, therefore by classifying, we can understand evolutionary affinities (phylogeny), biodiversity assessment, ecological impact, management and extrapolate information from closely related species to understand more about other species (including but not limited to ourselves).

**Taxonomy and Systematics**

Taxonomy	Systematics
<ul style="list-style-type: none"> <li>• Common names are unreliable</li> <li>• Example of Australian ‘oaks’: Tasmanian oaks (<i>Eucalyptus</i>), she-oaks (<i>Casuarina</i>), desert oaks (<i>Acacia</i>), silky oaks (<i>Grevillea</i>). None are oaks (<i>Quercus</i>) and most are not even close relatives.</li> <li>• An agreed upon name for each species</li> </ul>	<ul style="list-style-type: none"> <li>• Reveals evolutionary relationships</li> <li>• Classification should reflect those relationships</li> <li>• Creates a hierarchical system that organises our understanding</li> </ul>

**The father of taxonomy**

Linnaeus (1707) is considered the pioneer of the modern binomial classification naming system where each species is known by a genus and species name.

- Names are *italicised*
- Genus name is capitalised
- Species name is lower case
- Organisms are arranged in a taxonomic hierarchy
- E.g *Mus musculus* (the common mouse) and *Homo sapiens* (Human)

**Taxonomic hierarchies**

Common Name	Human	Common Chimpanzee	Grey Wolf	Tiger Snake	Monarch Butterfly
<b>Domain</b>	Eukaryota	Eukaryota	Eukaryota	Eukaryota	Eukaryota
<b>Kingdom</b>	Animalia	Animalia	Animalia	Animalia	Animalia
<b>Phylum</b>	Chordata	Chordata	Chordata	Chordata	Arthropoda
<b>Class</b>	Mammalia	Mammalia	Mammalia	Reptilia	Insecta
<b>Order</b>	Primates	Primates	Carnivora	Squamata	Lepidoptera
<b>Family</b>	Hominidae	Hominidae	Canidae	Elapidae	Nymphalidae
<b>Genus</b>	Homo	Pan	Canis	Notechis	Danaus
<b>Species</b>	Homo sapiens	Pan troglodytes	Canis lupus	Notechis scutatus	Danaus plexippus

**We classify organisms using specific, often descriptive, hierarchical naming systems**

## Taxonomy codes

- There are distinctly separate rules for the naming of:
  - Algae, plants and fungi
  - Animals
  - Bacteria
  - Viruses
- As codes are separate, two species can share the same name
- Renaming/splitting/joining species are typically received negatively by the research or otherwise-interested community
- Names have an authority (person who first provided the name at the end of the species)

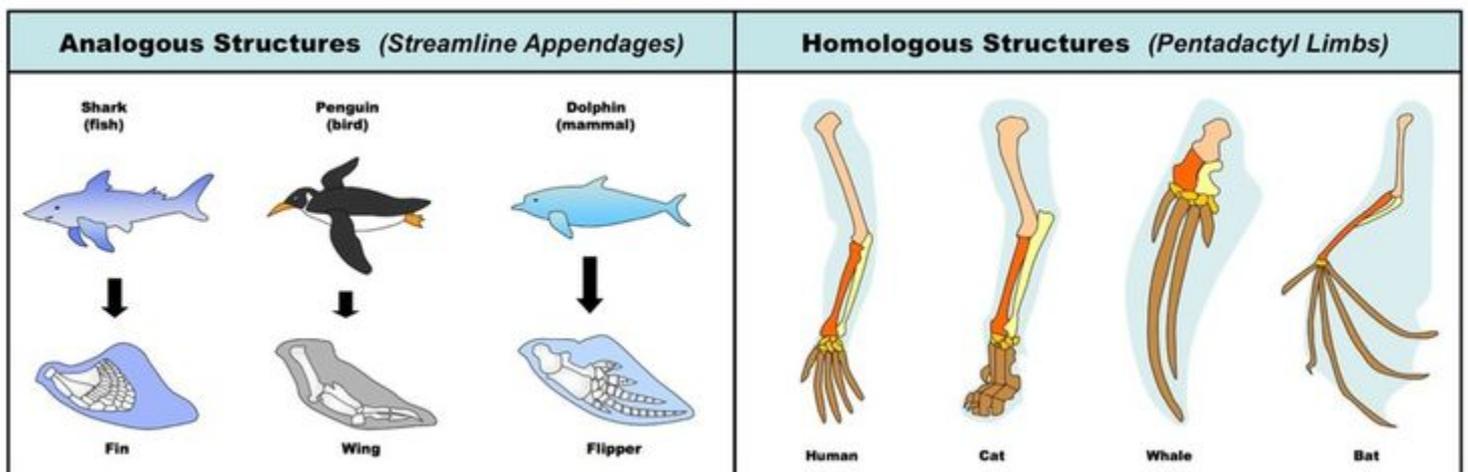
## Basis for biological (“natural”) classification

- Closely related organisms are more similar than distantly related organisms.
- This should be reflected in the nomenclature and taxonomic organisation of groups.
- Groups should be monophyletic: a single common ancestor for all members in that group not shared with any other species.
- Established on visible traits:
  - Morphology, e.g. tetrapods or vertebrates, amphibians vs reptiles
  - Reproductive parts, e.g. flowering plants vs conifers
- More recently inferred from molecular evidence:
  - DNA, RNA, proteins and secondary metabolites

## Cladistics (Systematics)

- Infers evolutionary relationships on the basis of ancestral and derived traits.
- Identifies branch points (i.e. +/-) in evolution
- One challenge is the there is an incomplete fossil record (or completely missing fossil record) for comparisons

## Analogous vs Homologous Traits



- **Homologous** traits have a common origin/ancestor
  - may be difficult to recognize because of divergence
- Traits may be lost or reduced and not obvious
- **Analogous** traits may result from convergence, called homoplasies

**Parsimony**

The method of constructing a tree (cladogram) with the least number of steps. Starts with a comparison organism (outgroup) and uses defining features (jaws, lungs, warm-blooded, mammaries) to create a evolutionary tree.

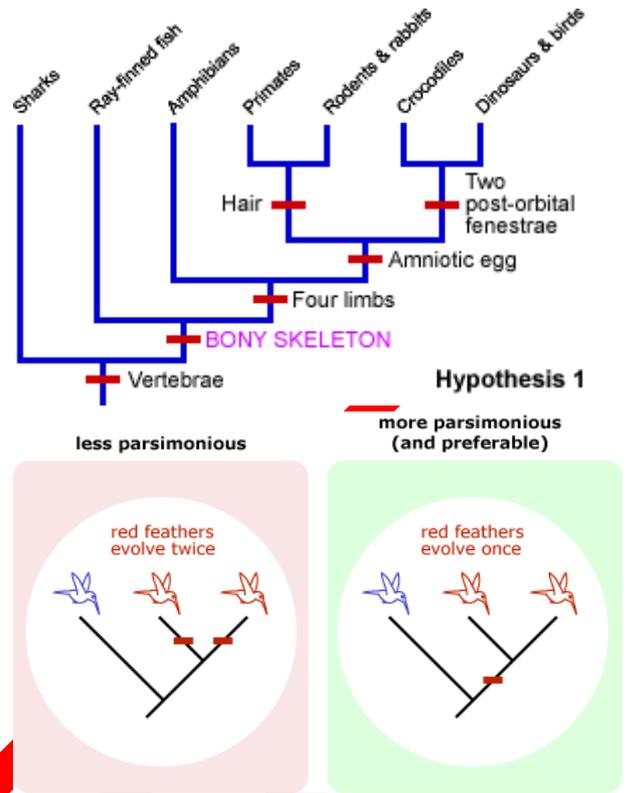
The ideal cladogram is the more parsimonious (fewest character changes) relationship between the taxa.

Groups can be inverted around a node and retain the same information and same evolutionary path.

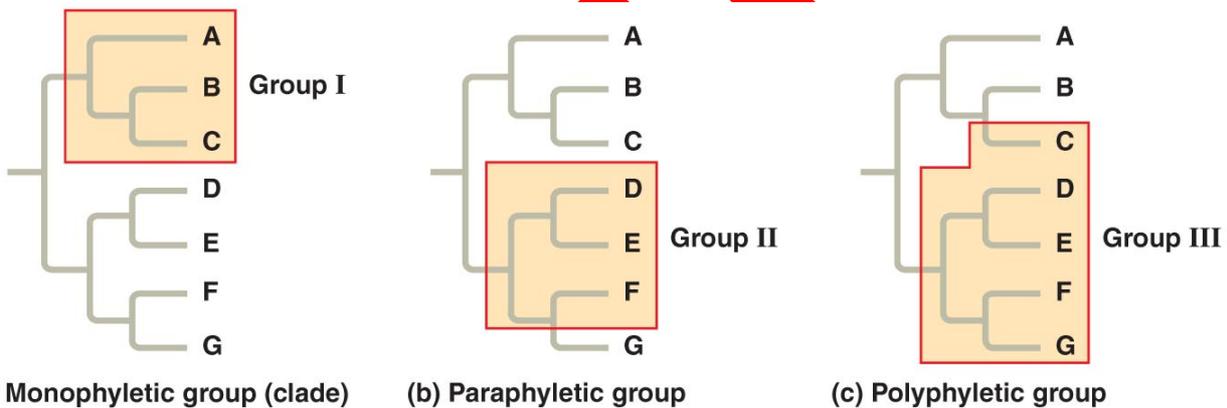
**DNA and constructing phylogenies**

DNA contains a large amount of neutral (no fitness effect) variation, providing some advantages in comparing organisms.

More distantly related organisms have less similar DNA and using molecular data, we can produce evolutionary relationships based of the % divergence between organisms.



**Mono vs para vs polyphyletic groups**



**We classify organisms using classification schemes that reflect evolutionary relationships.**

**These schemes are based on homologous traits, including morphology and since the advent of molecular biology methods using DNA sequences (or sometime RNA, proteins or other molecules).**