

CLADISTICS

Content Statements:

- A3.2.1 Need for classification of organisms
- A3.2.2 Difficulties classifying organisms into the traditional hierarchy of taxa
- A3.2.3 Advantages of classification corresponding to evolutionary relationships
- A3.2.4 Clades as groups of organisms with common ancestry and shared characteristics
- A3.2.5 Gradual accumulation of sequence differences as the basis for estimates of when clades diverged from a common ancestor
- A3.2.6 Base sequences of genes or amino acid sequences as the basis for constructing cladograms
- A3.2.7 Analysing cladograms
- A3.2.8 Using cladistics to investigate whether the classification of groups corresponds to evolutionary relationships
- A3.2.9 Classification of all organisms into three domains using evidence from rRNA base sequences

CLASSIFICATION SCHEMES

Classification systems are used by scientists to give organisational structure to the study of living organisms. They allow for organisms to be named according to a globally recognised scheme and make it easier to sort information about organisms and predict evolutionary links. Traditional classification schemes were based on morphology (identifiable structures), but newer schemes are based on molecular sequence comparison.

TAXONOMIC CLASSIFICATION

Conventionally, organisms have been classified by arranging into groups (called *taxa*) according to **common characteristics**. Each taxa functions as a hierarchical unit – the more taxa organisms share, the more similar they are considered to be. However, there are many limitations involved with classifying according to taxa:

- Taxonomic ranks set an arbitrary limit on the number of groupings by which organisms can be classified
- Fixed ranks do not reflect the gradation of variation (diverging populations may be hard to distinguish)
- Organisms may appear similar due to convergent evolution and not be related (analogous structures)

TAXA:

Domain

Kingdom

Phylum

Class

Order

Family

Genus

Species

PHYLOGENETIC CLASSIFICATION

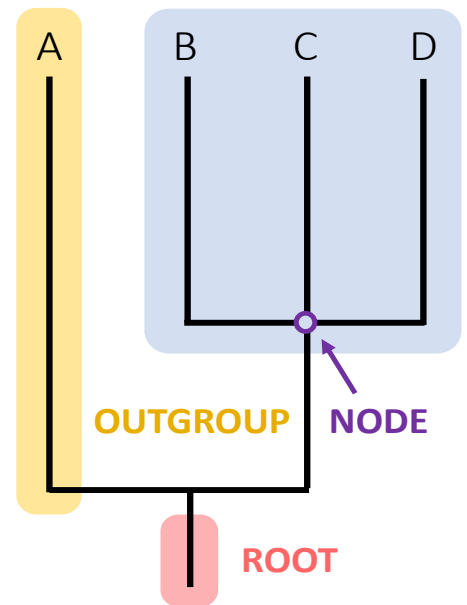
Due to the limitations associated with taxonomic systems based on structure, scientists now commonly use **evolutionary relationships** as a basis for classification. Evolutionary patterns are determined by comparing the molecular sequences of organisms. Over time, mutations will accumulate within a given sequence. The number of differences between two comparable sequences denotes the degree of evolutionary divergence (more differences = less related). The base sequence of genes (DNA) or the amino acid sequence (proteins) can be used – although amino acid sequences will demonstrate a slower rate of change due to degeneracy. The determination of evolutionary relationships is called **phylogenetics** and has the overall benefit of being more specific (can reflect gradations of variation) and less subjective (unlikely to result in misclassification).

CLADOGRAMS

Cladistics is a method of classifying organisms into groups of species called **clades**. Each clade consists of an ancestral organism and all of its evolutionary descendants. Members of clades will possess shared characteristics as a result of their shared evolutionary lineage. Clades can be organised into branching tree diagrams called **cladograms**. All cladograms contain numerous features to show divergence patterns:

- **Nodes:** Branch points representing divergence from an ancestor
- **Root:** Common ancestor for all the organisms in the cladogram
- **Outgroup:** Most distantly related species (i.e. a reference point)

Cladograms show a probable sequence of evolutionary divergence – the *fewer nodes* between groups, the *more closely related* they are. The most objective evidence for placing organisms in clades is from **molecular sequences**, although morphological traits are also viable.



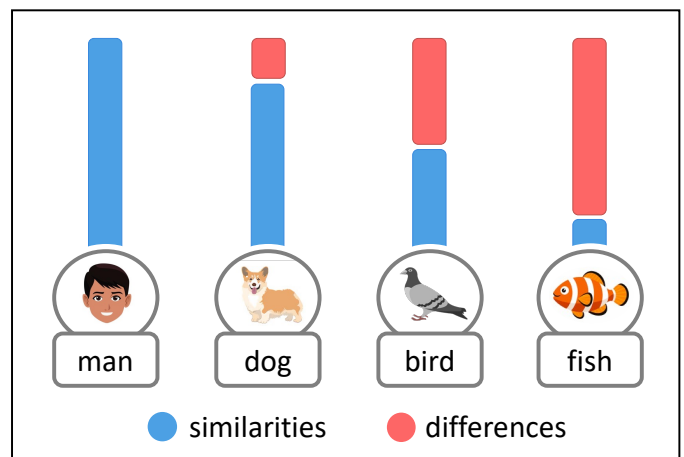
MOLECULAR CLOCK

Some genes or protein sequences may accumulate mutations at a relatively constant rate (e.g. 1 mutation per 1000 bases every generation). If this rate of change is **stable** and **reliable**, scientists can calculate a time of divergence according to the number of sequence differences. This method of estimating time is called a molecular clock and is used to form **phylograms** (where branch lengths are proportional to time). However:

- Different genes or proteins may change at different rates (mutation rates are *rarely* stable and reliable)
- The occurrence and intensity of selection pressures may alter the frequency of any sequence changes
- Over long periods, earlier changes may be reversed by later changes (limiting accuracy of predictions)

Because of these limitations, the molecular clock can only give estimates that are typically not very precise.

	# mutations											
fish	F	A	A	A	V	F	T	F	G	F	P	6
bird	F	S	T	A	R	F	R	P	P	H	V	4
dog	F	S	T	A	A	F	R	G	G	F	I	2
human	F	S	T	A	A	F	R	F	G	H	I	0
Consensus	F	S	T	A	A	F	R	F	G	H	I	



RECLASSIFICATION

Phylogenetic analysis has led to the reclassification of species to better match evolutionary patterns. For example, **figworts** are a family of flowering plants (*Scrophulariaceae*) that were reclassified after analysing chloroplast DNA – reducing the number of figwort species by more than half. All living organisms were also separated into **three domains** (*Eukarya*, *Bacteria* and *Archaea*) based on analysis of rRNA base sequences. The archaean cells were found to possess certain features that were more in common with eukaryotic cells:

- *Archaea* lack a nucleus and have circular DNA – which are characteristic features of all prokaryotic cells
- *Archaea* have histone-like proteins and lack peptidoglycan in their cell walls (similar to eukaryotic cells)