

TOPIC 5.4: CLADISTICS

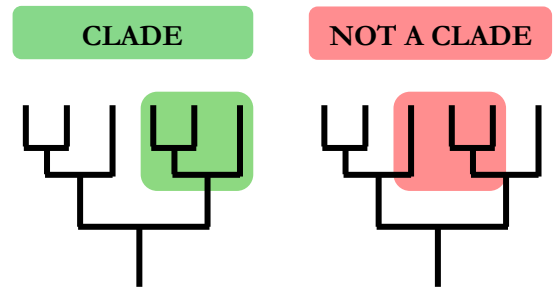
Clades

Cladistics involve classifying organisms into groups of species (**clades**)

- A clade consists of a single common ancestor and all descendants

Cladograms are tree diagrams where each branch point represent the splitting of two new species groups from a common ancestral species

- Each branch point (node) represents a speciation event
- The more nodes between groups, the less related the groups are



Structural Evidence

Historically, cladograms have been constructed based on structural characteristics, however this **not** always a reliable method for establishing evolutionary connections

- Related species may have distinctive (*homologous*) features
- Unrelated species may have similar (*analogous*) features

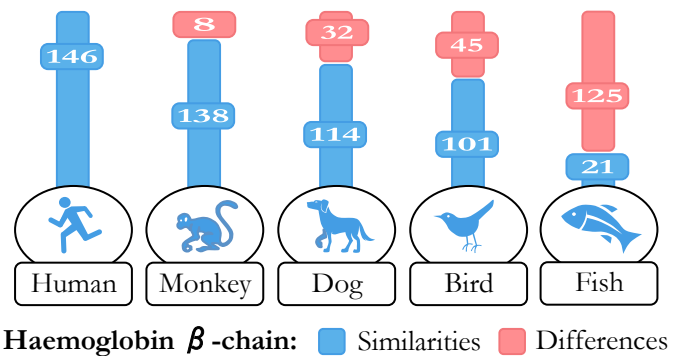
HOMOLOGOUS	ANALOGOUS
Structures look different	Structures look similar
Due to different selection pressures	Due to common selection pressures
Species do share a common ancestry	Species do not share a common ancestry
Evidence of <i>divergent</i> evolution	Evidence of <i>convergent</i> evolution
E.g. Pentadactyl limb	E.g. Fins (whale vs shark)

Molecular Evidence

Cladograms are now being generated via a comparison of biochemical evidence (i.e. DNA or amino acid sequences)

- Related species will have sequences with more similarities
- Amino acid sequences will accumulate differences at a slower rate to DNA sequences (due to degeneracy)

If a sequence accumulates mutations at a constant rate, the time of divergence can be calculated based on the number of mutations between the two species (molecular clock)



Cladograms

Structural Data: Compare characteristics via a table

	Lungs	Endothermic	Hair / skin
Fish	-	-	-
Lizard	✓	-	-
Bird	✓	✓	-
Rodent	✓	✓	✓

Molecular Data: Compare sequences via multiple alignment

fish	F	A	A	A	F	Q	F	G	F	T	I	Mutations	
lizard	F	S	T	A	A	R	P	P	H	T	V		3
bird	F	S	T	A	A	R	G	G	H	T	I		1
rodent	F	S	T	A	A	R	F	G	H	T	I		0
Consensus	F	S	T	A	A	R	F	G	H	T	I		

Example: Humans and Other Primates

