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Homology - similarity due to shared ancestry

Analogy - similarity due to convergent evolution (homoplasy)

CLADE - A monophyletic grouping that includes an ancestral species and all of its descendants.

⇒ CLADES can be distinguished by their SHARED DERIVED CHARACTERS

① Monophyletic Group (CLADE)
- ancestral species and all of its descendants.

② Paraphyletic Group
- ancestral species and some BUT not all descendants.

③ Polyphyletic Group
- some of its members have different ancestors.

(2)

- shared Derived Character is an evolutionary novelty to a clade

OUTGROUP - species or group of species from an evolutionary lineage that is known to have diverged before the lineage that includes the species we are studying.

Branch length

- (1) can indicate genetic change
- (2) can indicate time

Constructing Trees

- (1) Maximum Parsimony
- (2) Maximum Likelihood (algorithms)

Maximum Parsimony

- the hypothetical tree that require the fewest number of evolutionary events to have occurred

Branch point (NODE)

- represents the divergence of 2 evolutionary lineages from a common ancestor.

Sister TAXA

- groups of organisms that share an immediate common ancestor (node)

ROOTED

- branch point drawn furthest to the LEFT represents the most recent common ancestor of all taxa in the tree.

Basal TAXON

- lies on a branch that originates very close to the common ancestor.

Polytomy - more than 2 branches emerging from a branch point (node) with evolutionary relationships still unclear