

(adopted from Gloria Rendon, NCSA)

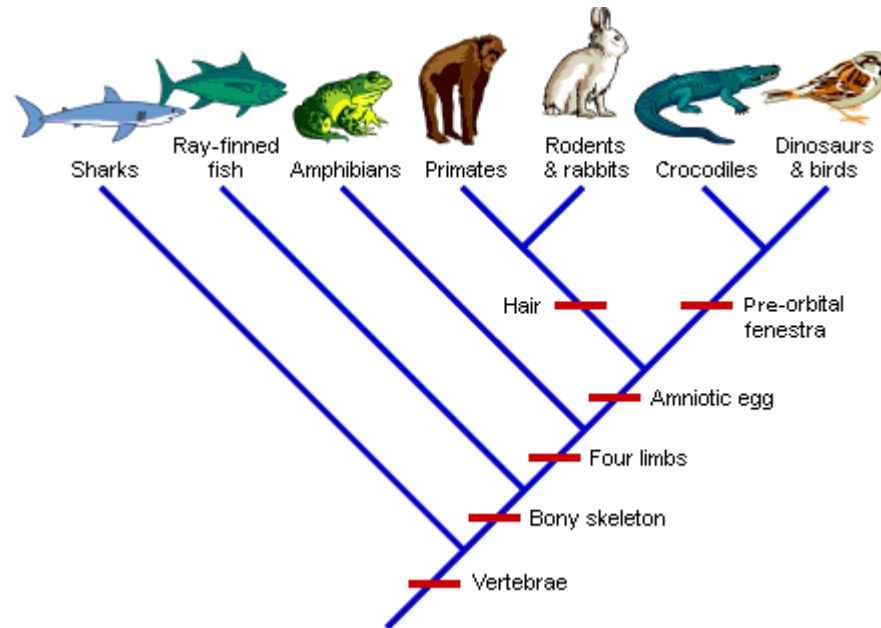
PHYLOGENETIC TREES

A **phyletic lineage** is an unbroken series of species arranged in ancestor to descendant sequence, with each later species having evolved from the one which immediately preceded it.

Phylogeny is the study of relationships among different groups of organisms and their evolutionary development. Phylogeny attempts to trace the evolutionary history of all life on the planet. It is based on the phylogenetic hypothesis that all living organisms share a common ancestry.

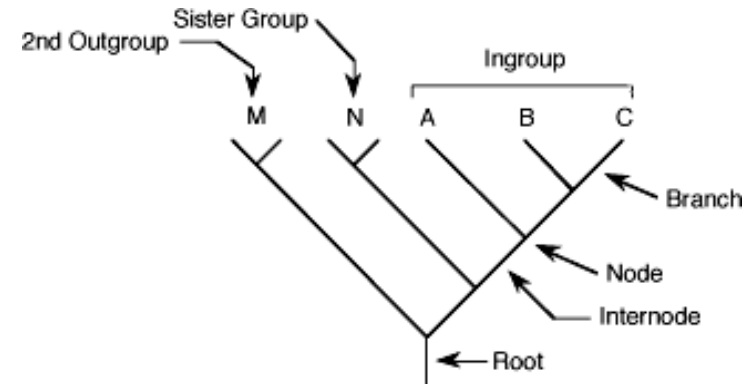
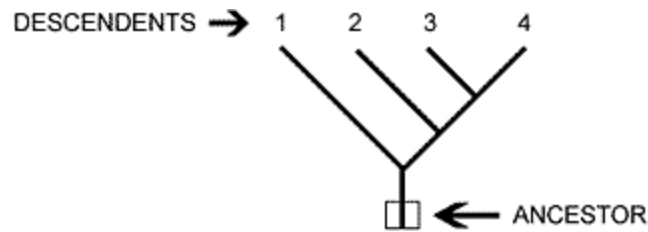
Reading phylogenetic trees: A quick review

(Adapted from evolution.berkeley.edu)



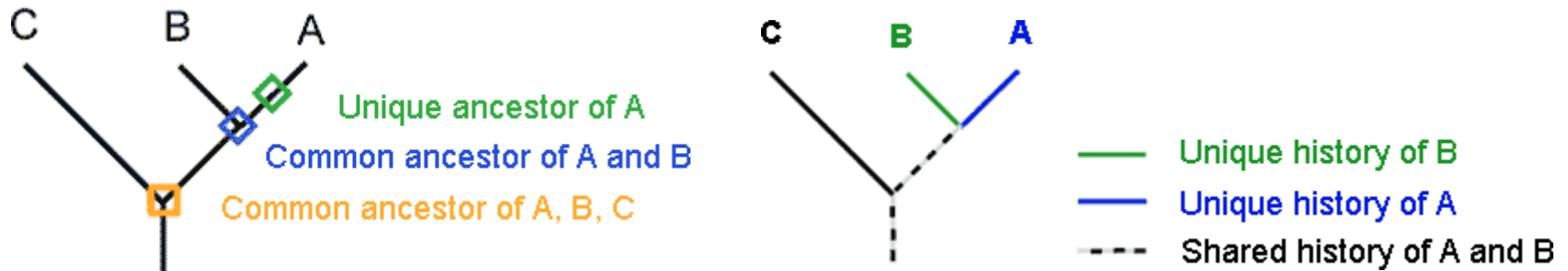
- A phylogeny, or species/evolutionary tree, represents the evolutionary relationships among a set of organisms or groups of organisms, called taxa (singular: taxon) that are believed to have a common ancestor.

Tips, Internal Nodes, Edges



- The tips of the phylogenetic tree represent groups of descendent taxa (often species)
- The internal nodes of the tree represent the common ancestors of those descendents.
- The tips are the present and the internal nodes are the past.
- The edge lengths in some trees correspond to time estimates – evolutionary time.

Sister Groups and a common ancestor



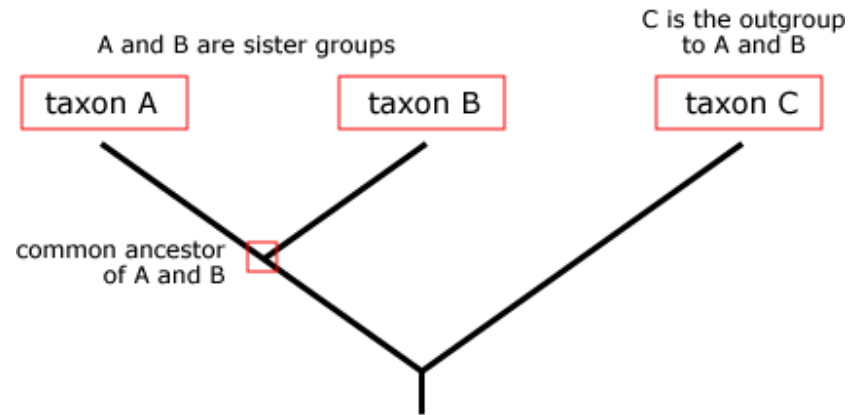
- Two descendents that split from the same node are called sister groups.
- In the trees above, species A & B are sister groups — they are each other's closest relatives; which means that:
 - i) they have a lot of evolutionary history in common and very little evolutionary history that is unique to either one of the two sister species and
 - ii) that they have a common ancestor that is unique to them.

Equivalent trees



- For any speciation event on a phylogeny, the choice of which lineage goes to the right and which one goes to the left is arbitrary.
- These three phylogenies are therefore equivalent.

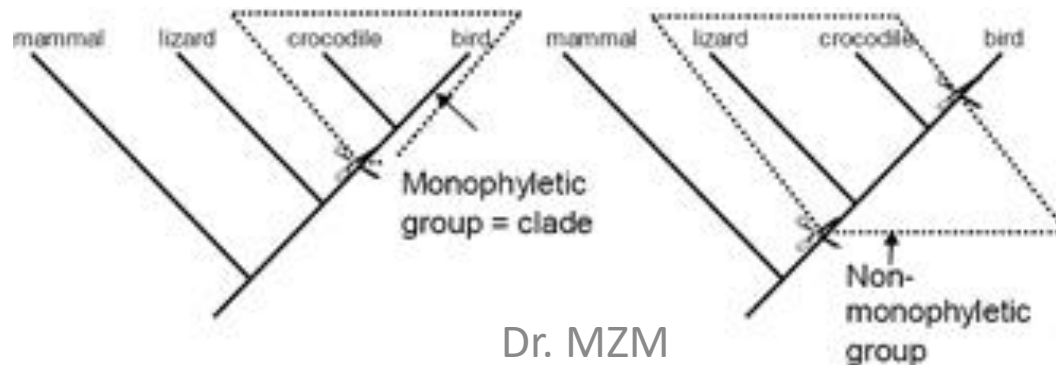
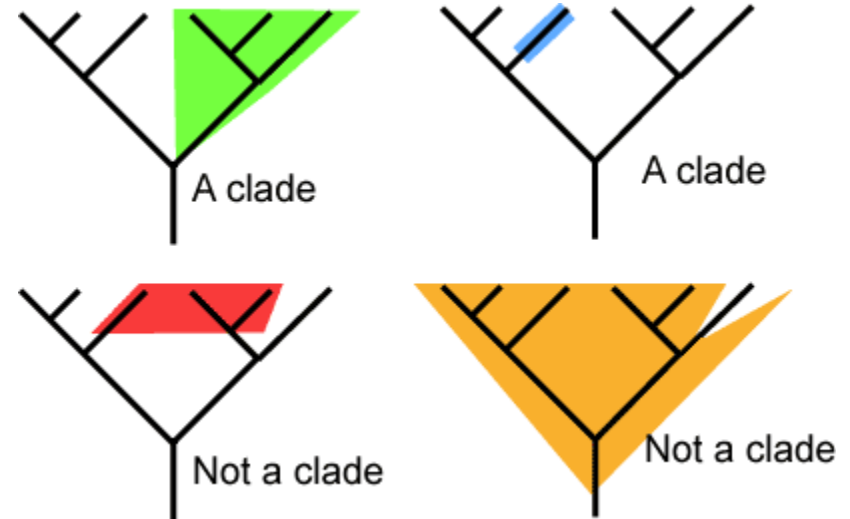
Outgroup

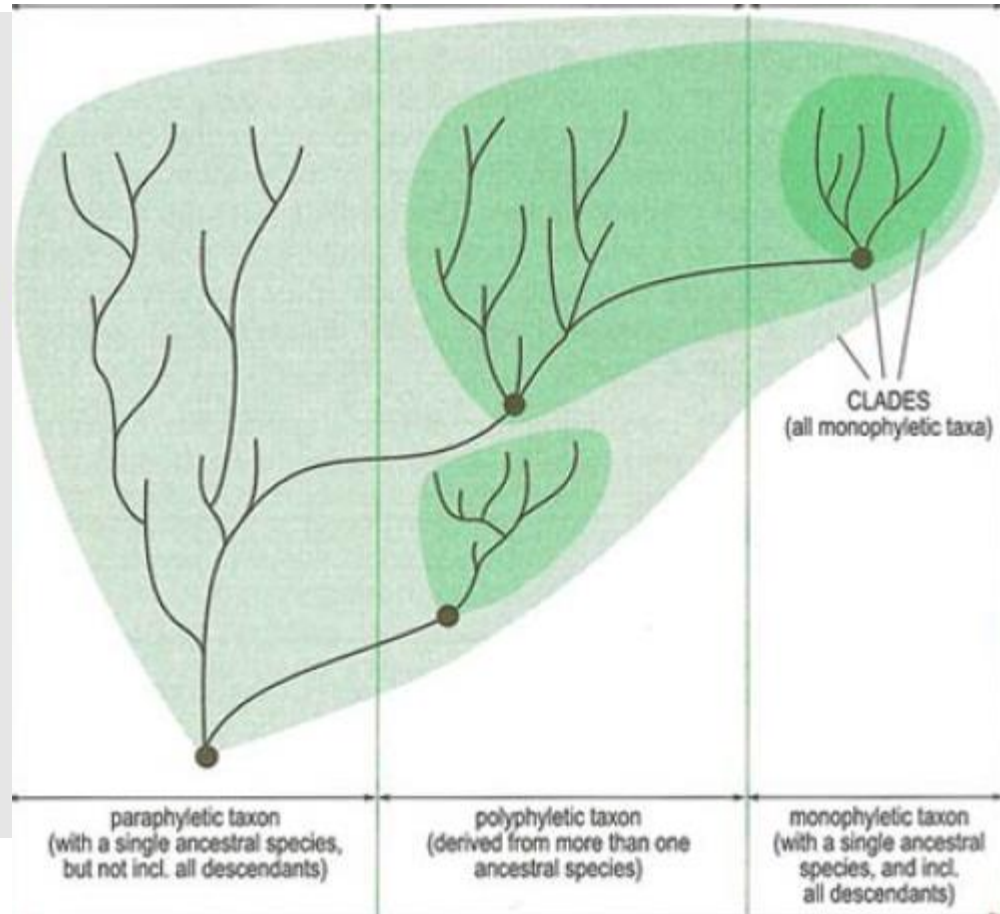
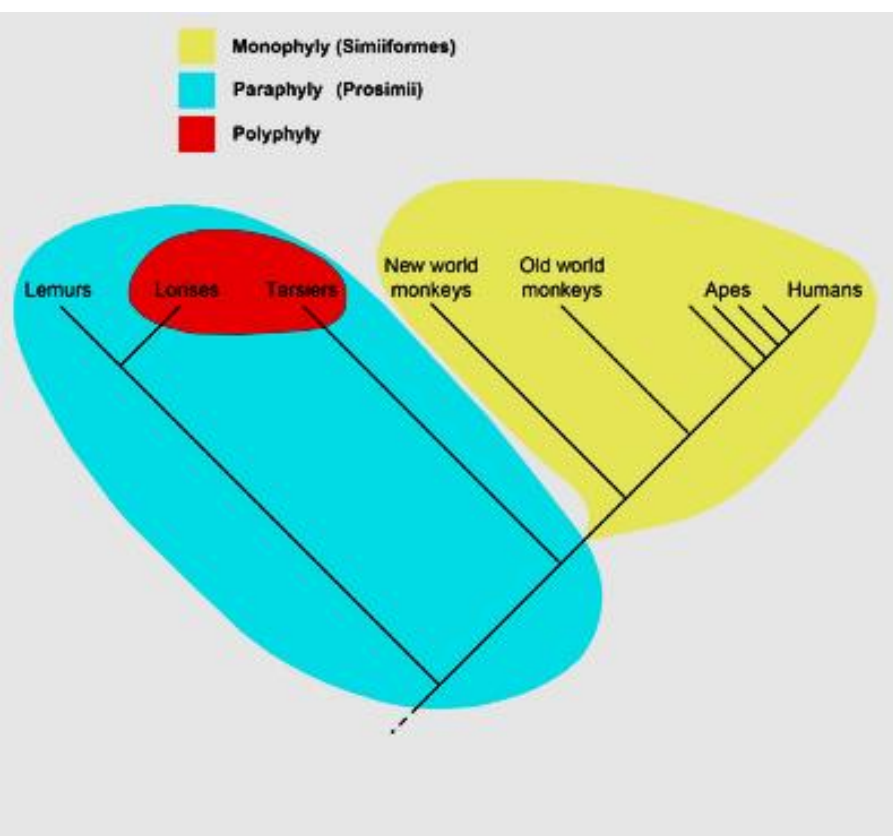


- Many phylogenies also include an outgroup — a taxon outside the group of interest.
- All the members of the group of interest are more closely related to each other than they are to the outgroup. Hence, the outgroup stems from the base of the tree.
- An outgroup can give you a sense of where on the bigger tree of life the main group of organisms falls. It is also useful when constructing evolutionary trees.

Branches and clades

- Evolutionary trees depict clades.
- A clade is a group of an ancestor and all descendants.
- You can think of a clade as a branch of the tree of life.
- Some examples of clades and non-clades in a phylogenetic tree are shown here.

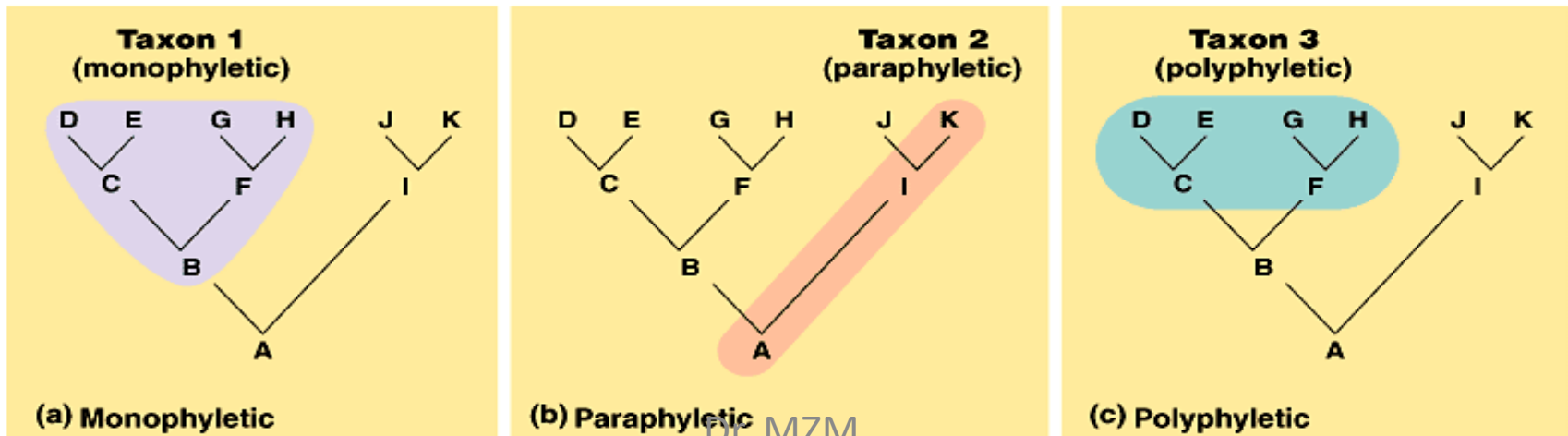




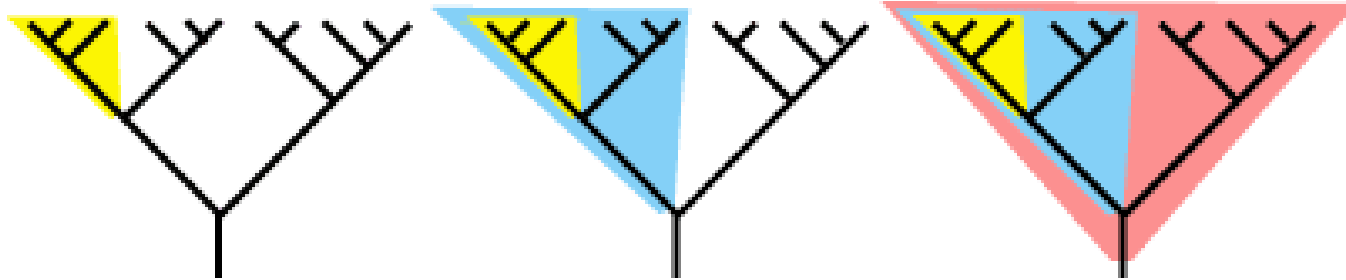
Monophyletic pertains to a taxon that is derived from a single ancestral species. ***only legitimate cladogram type!*** Or Monophyletic is a group of organisms that includes the ancestor and all the descendants.

Polyphyletic pertains to a taxon whose members were derived from two or more ancestors not common to all members. Or Polyphyletic is a group of organisms that does not include the most recent common ancestor.

Paraphyletic pertains to a taxon that excludes some members that share a common ancestor with members included in the taxon. Or Paraphyletic is a group of organisms that includes the ancestor and only a few of the descendants

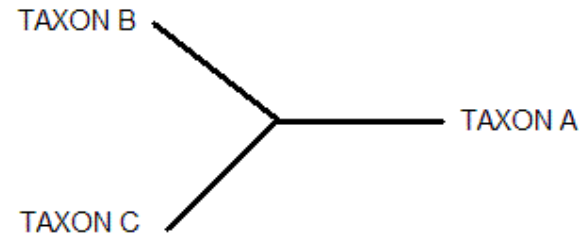
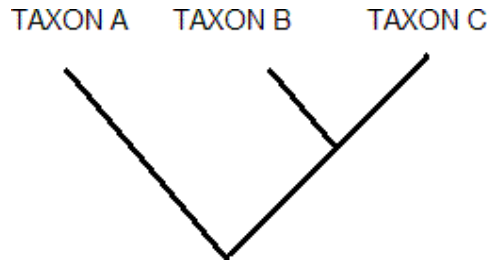


More on clades. Nested clades



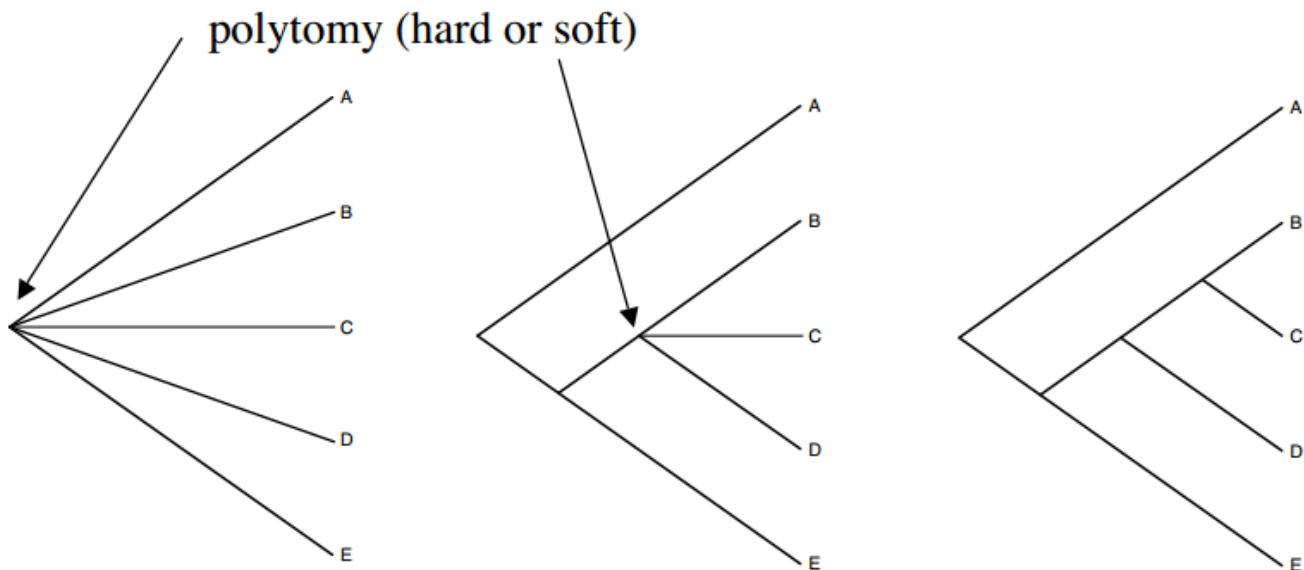
- Clades can be nested within one another
- A clade may include many thousands of species or just a few.
- Some examples of clades at different levels are marked on the phylogenies above.

Types of trees: unrooted vs. rooted



- A **rooted** phylogenetic tree is a tree with a unique root node corresponding to the (usually [imputed](#)) most recent common ancestor of all the entities at the leaves (aka tips) of the tree. A rooted tree is a **binary tree**.
- Unrooted** trees illustrate the relatedness of the leaf nodes without making assumptions about common ancestry. An unrooted tree has a node with three edges; the rest of the nodes have up to two edges.

Common Tree Terms

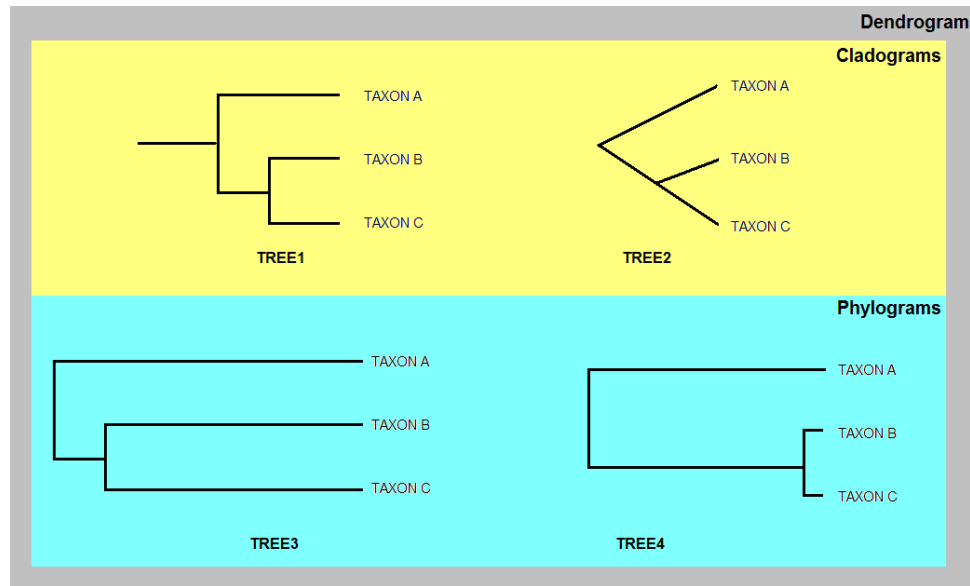


Star tree
completely unresolved

Nonbinary tree
partially unresolved
multifurcating

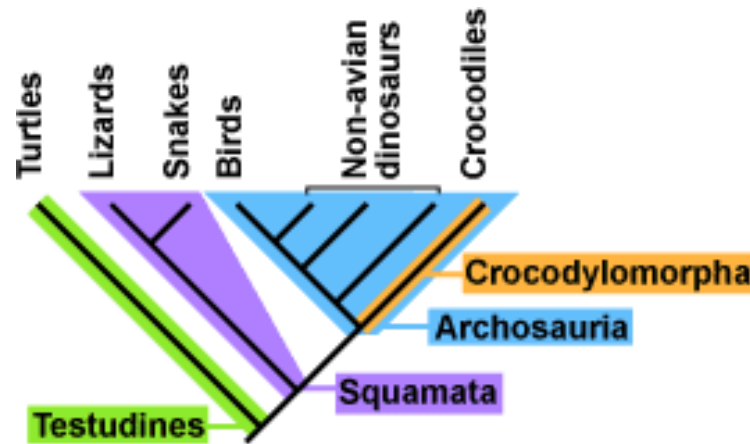
Binary tree
completely resolved
fully bifurcating

Dendrogram, cladogram, phylogram



- Dendrogram is the 'generic' term applied to any type of diagrammatic representation of phylogenetic trees. **All four trees depicted here are dendrograms.**
- Cladogram (to some biologists) is a tree in which branch lengths DO NOT represent evolutionary time; clades just represent a hypothesis about actual evolutionary history
TREE1 and TREE2 are cladograms and TREE1 = TREE2
- Phylogram (to some biologists) is a tree in which branch lengths DO represent evolutionary time; clades represent true evolutionary history (amount of character change)
TREE3 and TREE4 are phylograms and TREE3 ≠ TREE4

Phylogenetic Trees and classification



- Phylogenetic trees classify organisms into clades.
- By contrast, the [Linnaean system of classification](#) assigns every organism a kingdom, phylum, class, order, family, genus, and species.
- The phylogenetic tree depicted here identifies four clades

Phylogenies: Trees of Life

Linnaeus: Linnaean System of Classification

Based on similarity of traits

Hierarchical:

Kingdom

Phylum

Class

Order

Family

Genus

Species

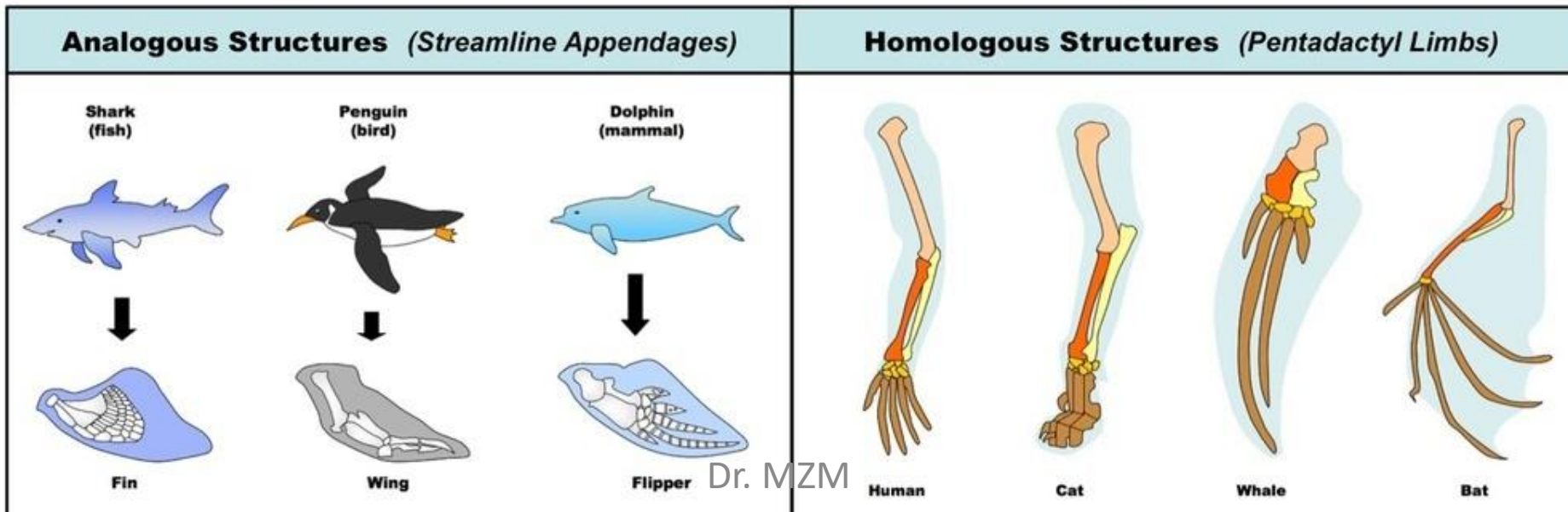
Kings **P**lay **C**hess **O**n **F**ine **G**rained **S**and

Keep **P**ots **C**lean **O**therwise **F**amily **G**ets **S**ick

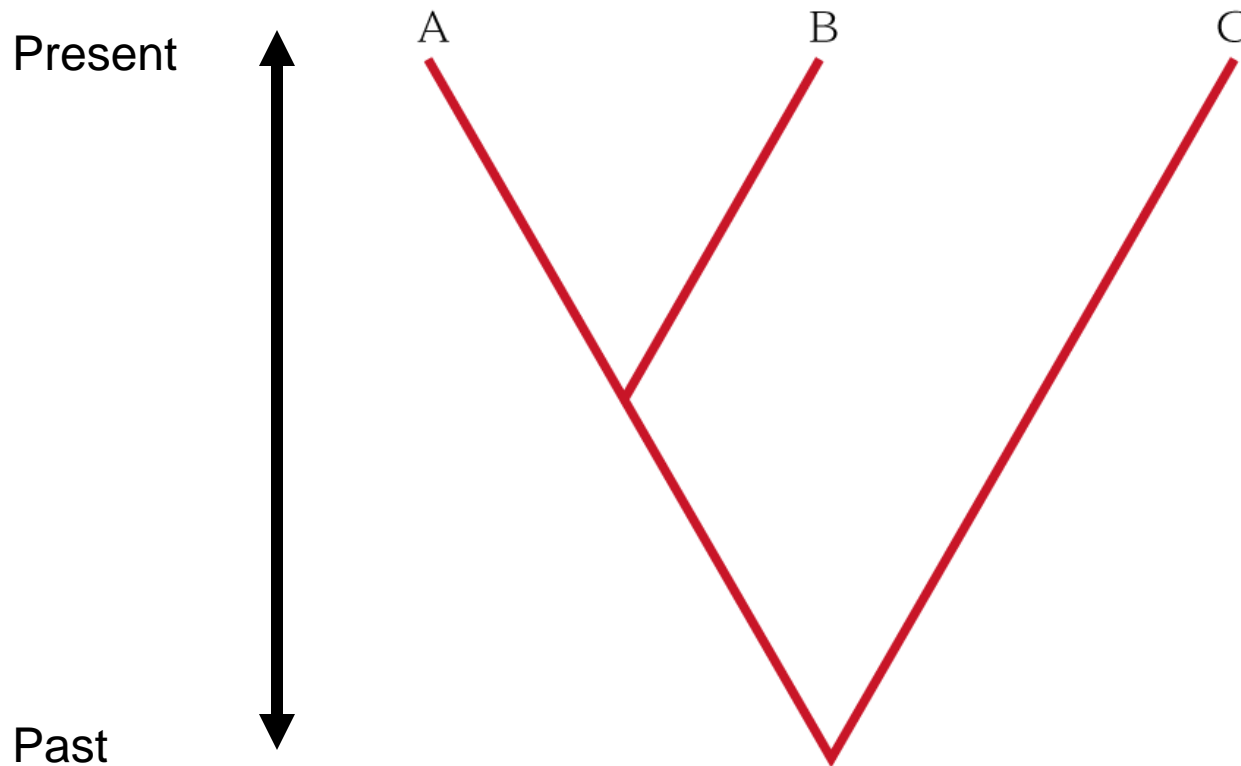
Inheritance or Convergence?

Homologous = Similar because of common decent (share a recent common ancestor) – Inheritance.

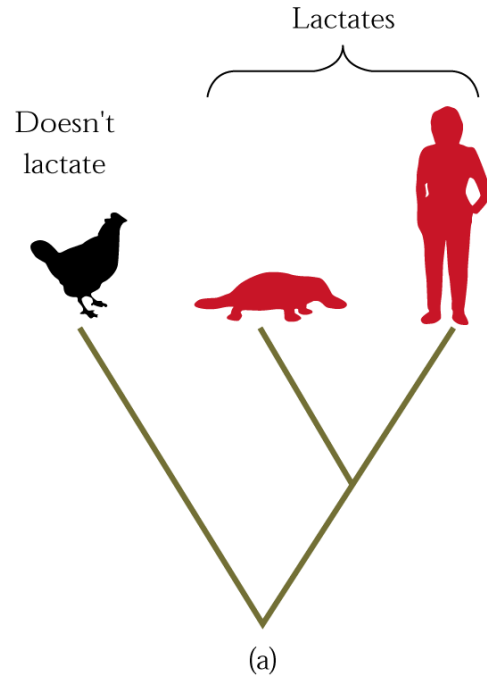
Analogous = Similar because of adaptation to the same or similar environmentally stable problem (Bird and Bat wings) - Convergence.



Phylogenies use homologous structures (traits) and must avoid analogous structures

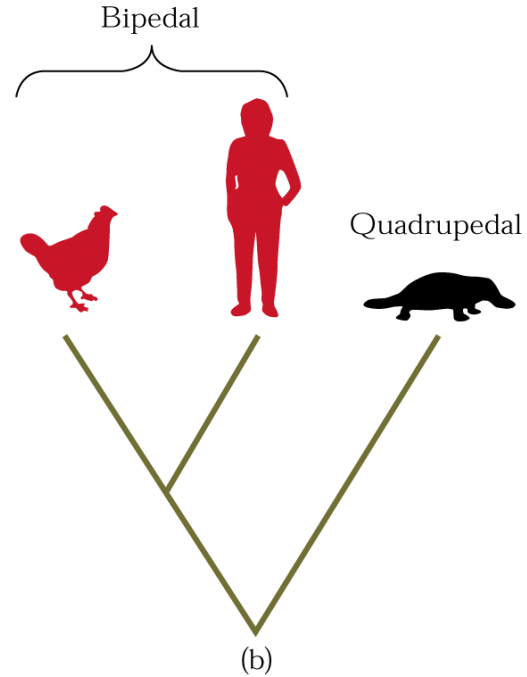


Yes



**Derived Trait
(last common ancestor)**

No



**Analogous Trait
(convergence)**