# Phylogenetic Trees terminology with example

Phylogeny A phylogeny is a tree that shows the evolutionary relationships among a group of organisms (living or extinct). Molecular phylogeny use molecular sequence data nucleotide or protein sequence which are orthologous to infer the evolutionary relationship among organisms.

Taxon: A taxon is a generic name for a taxonomic group. It act as a unit of classification Examples are species, but also populations, genera, families, orders, phyla, and so on. The plural is taxa. Each leaf on a phylogenetic tree represents a taxon.

Phylogenetic Tree: A tree is a acyclic directed graph that represents evolutionary relationships among taxa. Here, graph is a technical mathematical term that stands for a set of nodes and a set of edges that connect pairs of nodes. A tree is a special graph is connected and has no cycles. A graph is connected when there is a path from any node to any other node. A graph has no cycles when there is only one unique path (without backtracking) between any two nodes.
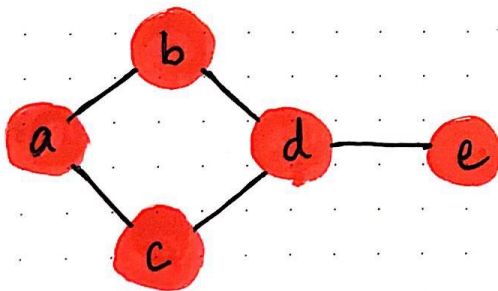
A graph with at least one cycle is known as a cyclic graph.
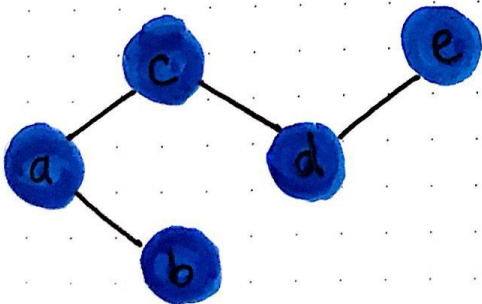
a graph with no cycles in it is known as an acyclic graph.

Node: A node in a phylogeny represents a taxon or a common ancestor for a set of taxa. The terminal nodes of the trees are are also refered to as operational taxonomic unit (OUT). Node are connected with each other with vertices also called as edges. The degree of a node is the number of edges that are connected to it.

Leaf A leaf is a node with degree one. In a phylogeny, a leaf usually represents a single present-day taxon. We will typically have a DNA sequence measured for each leaf. Internal Node An

internal node is node with degree greater than one. Internal nodes represent common ancestors. We typically do not have DNA data for internal nodes.
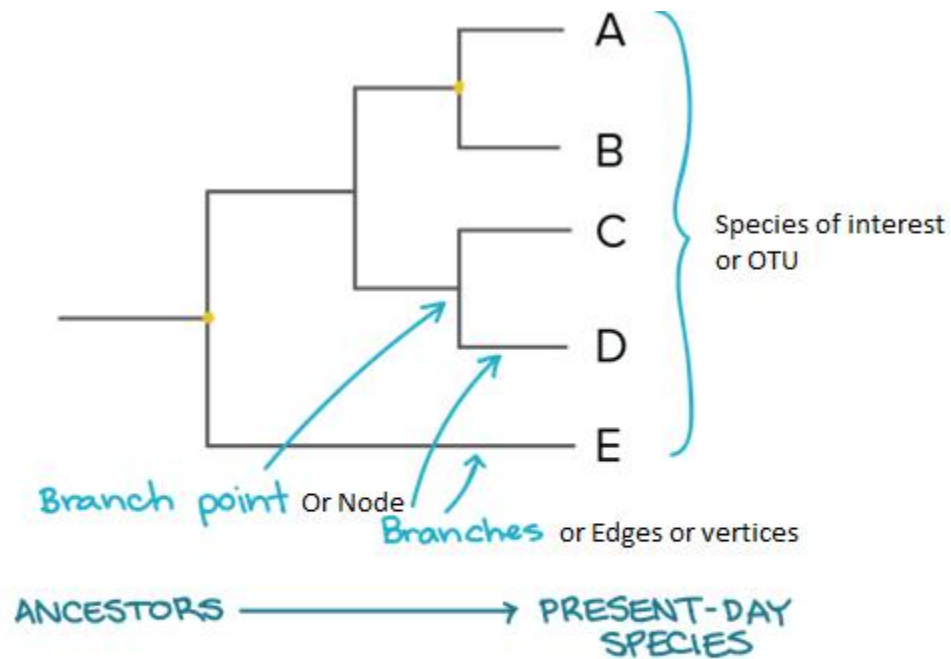

Edge An edge is the part of a graph that connects two nodes, and is represented by a line. An edge is also called a branch. An edge represents the evolutionary transition from an ancestral taxon to a descendant taxon.

Topology A tree topology represents all of the evolutionary relationships, but does not represent time or genetic distance. The topology is the graph and the leaf labels. The left/right orientation does not affect the topology.

Root: The root of a tree is the node that represents the common ancestor of all taxa in the tree.

Rooted Tree: A rooted tree is drawn so that time is represented by a single direction. This direction may be up, down, right, or sometimes even left, but the root is at the oposite end of the graph from the leaves.

Unrooted Tree: An unrooted tree is drawn without reference to the direction of time. An unrooted tree represents all of the rooted trees consistent with it. The root would typically be on one of the edges of the tree.

Rooted tree   **Unrooted tree.**
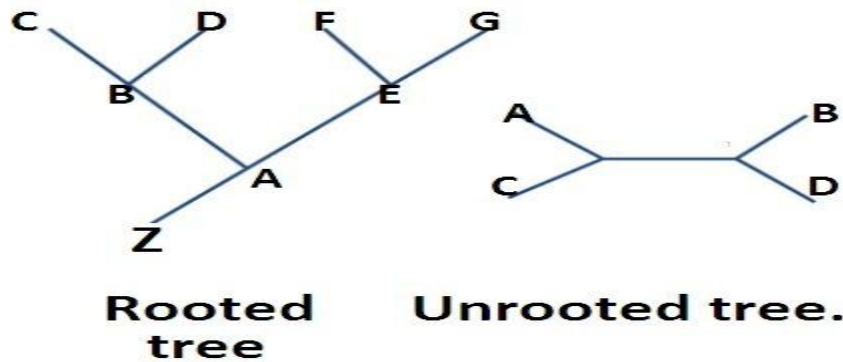
Binary Tree: A binary tree is a tree that represents an evolutionary history where all speciation events produce two ancestors from one. In a rooted binary tree, leaves have degree one, the root has degree two, and all other internal nodes have degree three. In an unrooted binary tree, all internal nodes have degree three. Trees that are not binary are said to contain polytomies, or nodes with more than two descendants. If there are n leaves, there are n − 1 internal nodes in a rooted binary tree and n − 2 internal nodes in an unrooted binary tree.

Binary Tree
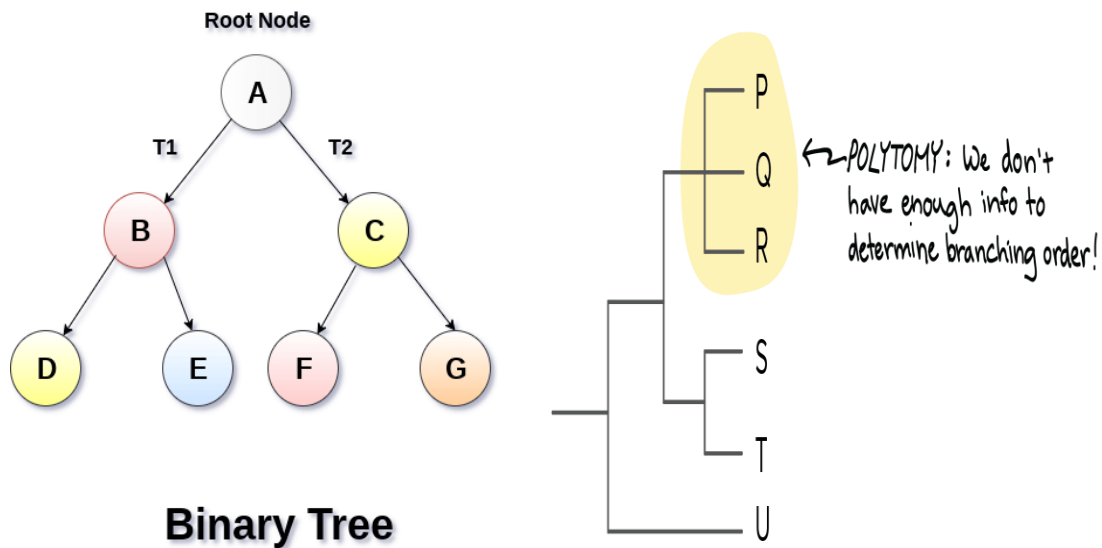
Clade : In a rooted tree, a clade is a group of leaves that form a monophyletic group meaning they have a common ancestor that is not a common ancestor for any other leaf in the tree. In an unrooted tree, a clade would be any group of taxa that can be separated from the rest by removing a single edge.

Monophyletic taxon : A group composed of a collection of organisms, including the most recent common ancestor of all those organisms and all the descendants of that most recent common ancestor. A monophyletic taxon is also called a <u>clade</u>.
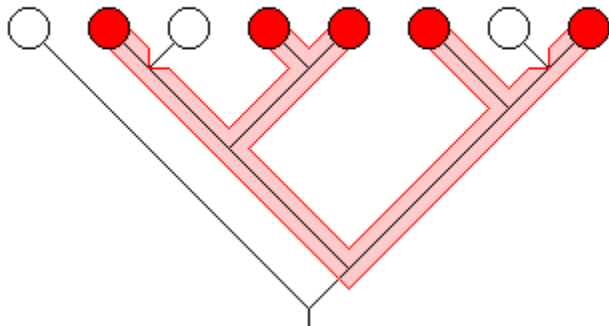
Monophyletic taxon (clade) :
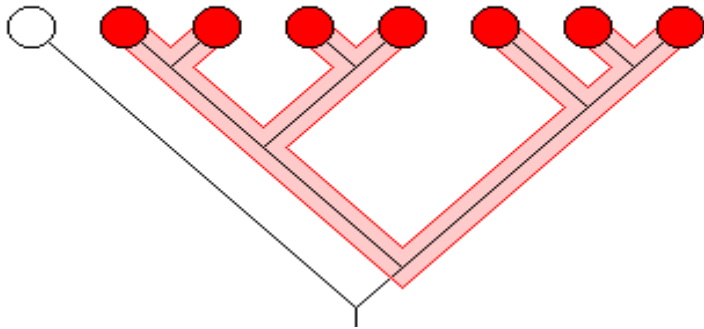
Examples : Mammalia, Aves (birds), angiosperms, insects, etc.

Paraphyletic taxon : A group composed of a collection of organisms, including the most recent common ancestor of all those organisms. Unlike a monophyletic group, a paraphyletic taxon does not include all the descendants of the most recent common ancestor.

Paraphyletic taxon :

Examples : Traditionally defined Dinosauria, fish, gymnosperms, invertebrates, protists, etc.

Polyphyletic taxon : A group composed of a collection of organisms in which the most recent common ancestor of all the included organisms is not included, usually because the common ancestor lacks the characteristics of the group. Polyphyletic taxa are considered "unnatural", and usually are reclassified once they are discovered to be polyphyletic.

Polyphyletic taxon :
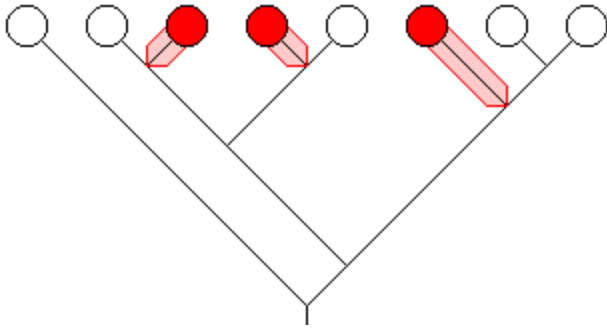
Examples : marine mammals, bipedal mammals, flying vertebrates, trees, algae, etc.

Split : A split is a partition of the taxa (leaves) into two nonempty sets. Each edge in a tree represents a split.

Subtree : A subtree is a subset of a tree that is a tree. Typically, we think of subtrees as defined by a root and all of the descendant nodes and descendent edges, but we can also get subtrees by pruning away nodes and edges. Edge Length An edge length is a number associated with an edge. The number may represent time or it may represent a measure of expected genetic distance.
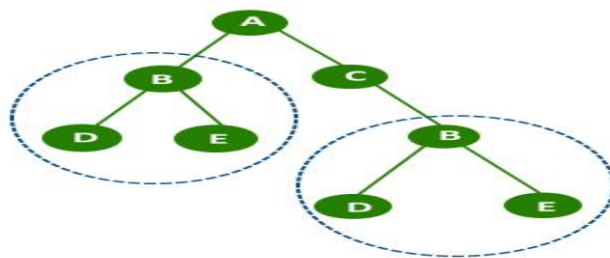
Ultrametric Tree : An ultrametric tree is a rooted tree with edge lengths where all leaves are equidistant from the root. Often, ultrametric trees represent the molecular clock which states that the rate of mutation is the same across all lineages of the tree. UPGMA produce ultrametric tree produce ultrametric tree.
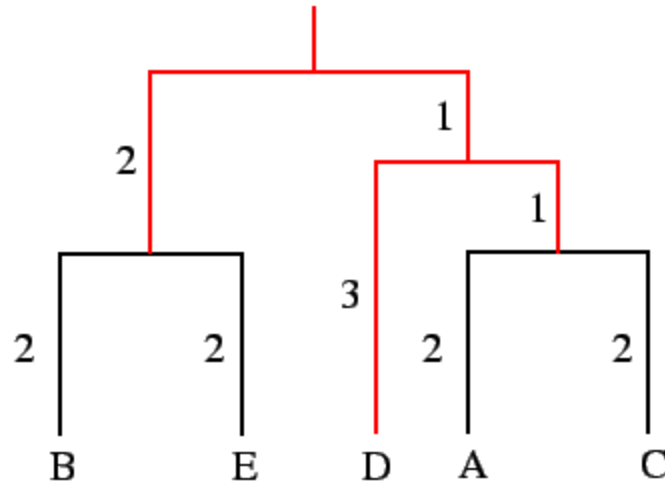
Cladogram A cladogram is a tree that only represents a branching pattern. The edge lengths do not represent anything.

Phylogram A phylogram is a phylogenetic tree where edge lengths represent time or genetic distance.

Formulas:

Number of unrooted trees for n taxa $N_u = (2n-5)!/[2^{n-3}*(n-3)!]$ (N > 2)

Number of rooted trees for n taxa $N_r = (2n-3)!/[2^{n-2}*(n-2)!]$ (N > 1)