Phylogeny & Tree Terminology Part I

Branches – aka edges, pathway or connection between nodes.

Consensus tree – trees that represent the commonality (if any) among a set of trees generated by a phylogenetic analysis, e.g., Strict, Adam's, Majority rule, etc.

Evolutionary Distance – the number of steps or evolutionary changes required to explain the data given a particular tree topology. Obtained by summing the number of character state changes along each branch and internode of the tree.

External Nodes – aka leaves or OTUs, represent sequences or data that exists for extant organisms.

Internal Nodes – these represent hypothetical or inferred ancestors.

Nodes – Can be external or internal. These are the branching points on the tree.

OTUs – Operational Taxonomic Units.

Outgroup – a group used in analysis to establish polarity of characters. Usually a sister group, but may be further out, more than one may be used.

Phylogeny – The true evolutionary tree we are trying to estimate.

Root – Ancestor for the entire tree, when known. Shows direction of change and therefore phylogeny is established.

Taxon – type of organism (ranked in many ways, species, class, subdivision). "Taxa" is plural for taxon.

Tree – graphical representation/mathematical structure used to model or map actual evolutionary history. Comprised of nodes and branches. Must be rooted to show phylogeny.

Phylogeny & Tree Terminology Part II

Homology – Resemblance due to inheritance from common ancestry, i.e., truly linked traits or characteristics pasted down from ancestor to offspring.

Homoplasy – Resemblance due to parallelism and/or convergenence and NOT due to common ancestry, i.e., nature trying to trick you yet again.

Orthologous – Homology that arises by divergence and/or speciation.

Paralogous – Homology that arises from gene duplication.

Cladogram – Dendrogram of branching diagram constructed by cladistic principles and methods (need not be rooted). Neither axis means anything.

Additive tree – Depicts the amount of evolutionary change to have occurred along the different branches. One axis is used to measure evolutionary change.

Ultrametric tree – Depicts the actual times of divergence under a constant clock assumption. One axis is used to measure time.

Ingroup – The group under study (should be monophyletic).

Clade, Lineage, or Cluster – A monophyletic group.

Polytomy – represents either simultaneous divergence of multiple sequences and thereby taxa (i.e., hard polytomy) or more likely the inability to resolve certain branches (bifurcations) due to insufficient or conflicting data (i.e., soft polytomy).

Phylogeny & Tree Terminology Part III

Apomorphy – Derived character state.

Plesiomorphy – Ancestral character state.

Autapomorphy – Derived character state found only in one clade.

Synapomorphy – Shared-derived character state, the heart of cladistic theory.

Monophyletic – A group of organisms that have a common evolutionary ancestry (history). Members share a set of relationships through common ancestry that are not shared with any other taxa outside the group.

Paraphyletic – Groups based on plesiomorpies or shared ancestral characteristics. Exclude taxa with autapomorphies, e.g., reptiles.

Polyphyletic – Groups based erroneously on convergent characters, e.g., vultures or eyes.