Phylogenetic tree

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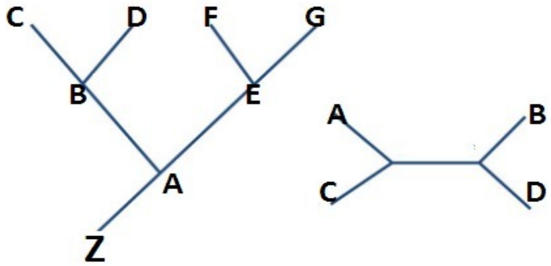
Phylogenetic tree or evolutionary tree is a branching diagram or "tree" showing the evolutionary relationships among various biological species or other entities—their phylogeny based upon similarities and differences in their physical or genetic characteristics. All life on Earth is part of a single phylogenetic tree, indicating common ancestry.

Definition: A diagrammatic representation of the evolutionary history of major groups of organisms is called phyligenetic tree.

Types: There are mainly two types of phylogenetic tree, they are 1) Rooted 2) Unrooted.

Rooted phylogenetic tree: A rooted phylogenetic tree is a directed tree with a unique node — the root — corresponding to the most recent common ancestor of all the entities at the leaves of the tree. The root node does not have a parent node, but serves as the parent of all other nodes in the tree. The root is therefore a node of degree 2 while other internal nodes have a minimum degree of 3 (where "degree" here refers to the total number of incoming and outgoinh edges number of incoming and outgoing edges)



Rooted tree **Unrooted tree.**

Unrooted phylogenetic tree : Unrooted trees illustrate the relatedness of the leaf nodes without making assumptions about ancestry. They do not require the ancestral root to be known or inferred Unrooted trees can always be generated from rooted ones by simply omitting the root. By contrast, inferring the root of an unrooted tree requires some means of identifying ancestry. This is normally done by including an out-group in the input data so that the root is necessarily between the out-group and the rest of the taxa in the tree, or by introducing additional assumptions about the relative rates of evolution on each branch, such as an application of the molecular clock hypothesis.

Special types of phylogenetic tree: There are some special types of phyligenetic trees, they are

Dendrogram

A dendrogram is a general name for a tree, whether phylogenetic or not, and hence also for the diagrammatic representation of a phylogenetic tree.

Cladogram

A cardiogram only represents a branching pattern; i.e., its branch lengths do not represent time or relative amount of character change, and its internal nodes do not represent ancestors.

Phylogram

A phylogram is a phylogenetic tree that has branch lengths proportional to the amount of character change.

Chronogram

A chronogram of Lepidoptera In this phylogenetic tree type, branch lengths are proportional to geological time.

A chronogram is a phylogenetic tree that explicitly represents time through its branch lengths.

Dahlgrenogram

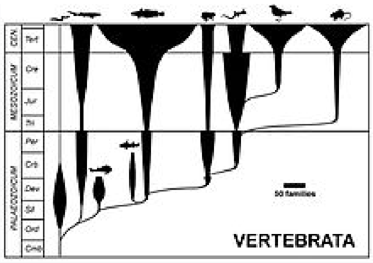
A Dahlgrenogram is a diagram representing a cross section of a phylogenetic tree

A phylogenetic network is not strictly

Phylogenetic network

speaking a tree, but rather a more general graph, or a directed acyclic graph in the case of rooted networks. They are used to overcome some of the limitations inherent to trees.

Spindle diagram



A spindle diagram, showing the evolution of the vertebrates at class level, width of spindles indicating number of families. Spindle diagrams are often used in evolutionary taxonomy.

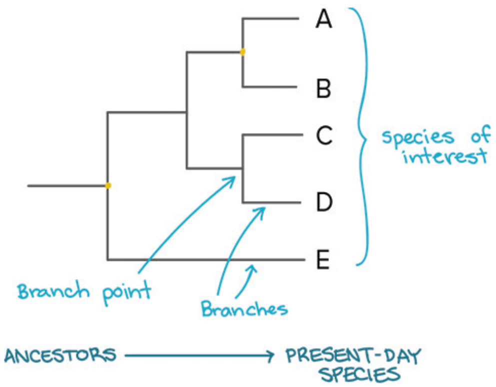
A sspindle diagram, or bubble diagram, is often called a romerogram, after its popularisation by the American palaeontologist Alfred Romer. It represents taxonomic diversity (horizontal width) against geological time (vertical axis) in order to reflect the variation of abundance of various taxa through time. However, a spindle diagram is not an evolutionary tree: [the taxonomic spindles obscure the actual relationships of the parent taxon to the daughter toxin and have the disadvantage of involving the paraphyly of the parental group. This type of diagram is no longer used in the form originally proposed.

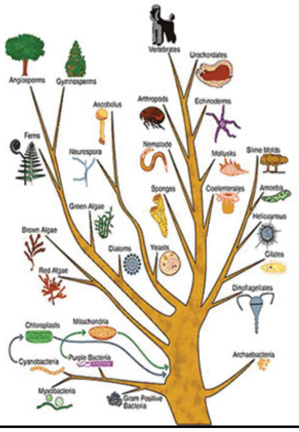
How to construct the phylogenetic tree

Phylogenetic trees composed with a nontrivial number of input sequences are constructed using computational phylogenetics methods. Distance-matrix methods such as neighbor-joining or UPGMA, which calculate genetic distance from multiple sequence alignments, are simplest to implement. Many sequence alignment methods such as ClustalW also create trees by using the simpler algorithms of tree construction. Maximum parsimony is another simple method of estimating phylogenetic trees, but implies an implicit model of evolution (i.e. parsimony). More advanced methods use the optimality criterion of maximum likelihood, often within a Bayesian framework, and apply an explicit model of evolution to phylogenetic tree estimation. Identifying the optimal tree using many of these techniques is NP-hard, so heuristic search and optimization methods are used in combination with tree-scoring functions to identify a reasonably good tree that fits the data.

A phylogenetic tree is a visual representation of the relationship between different organisms, showing the path through evolutionary time from a common ancestor to different descendants.

- Similarities and divergence among related biological sequences revealed by sequence alignment often have to be rationalized and visualized in the context of phylogenetic trees. Thus, molecular phylogenetics is a fundamental aspect of bioinformatics.
- Molecular phylogenetics is the branch of phylogeny that analyzes genetic, hereditary molecular differences, predominately in DNA sequences, to gain information on an organism’s evolutionary relationships.
- The similarity of biological functions and molecular mechanisms in living organisms strongly suggests that species descended from a common ancestor. Molecular phylogenetics uses the structure and function of molecules and how they change over time to infer these evolutionary relationships.
- From these analyses, it is possible to determine the processes by which diversity among species has been achieved. The result of a molecular phylogenetic analysis is expressed in a phylogenetic tree.





Multiple sequence alignment :

Multiple sequence alignments can be used to create a phylogenetic tree. This is made possible by two reasons. The first is because functional domains that are known in annotated sequences can be used for alignment in non-annotated sequences. The other is that conserved regions known to be functionally important can be found. This makes it possible for multiple sequence alignments to be used to analyze and find evolutionary relationships through homology between sequences. Point mutations and insertion or deletion events can be detected.

Multiple sequence alignments can also be used to identify functionally important sites, such as binding sites, active sites, or sites corresponding to other key functions, by locating conserved domains. When looking at multiple sequence alignments, it is useful to consider different aspects of the sequences when comparing sequences. These aspects include identity, similarity, and homology. Identity means that the sequences have identical residues at their respective positions. On the other hand, similarity has to do with the sequences being compared having similar residues quantitatively. For example, in terms of nucleotide sequences, pyrimidines are considered similar to each other, as are purines. Similarity ultimately leads to homology, in that the more similar sequences are, the closer they are to being homologous. This similarity in sequences can then go on to help find common ancestry.

Ref : https://en.wikipedia.org/wiki/Phylogenetic_tree

https://en.wikipedia.org/wiki/Multiple_sequence_alignmenthttps://microbenotes.com/how-to-construct-a-phylogenetic-tree/

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