## branch (of a phylogenetic tree) [includes "branch length"]
Lineages of taxonomic units that link nodes within a phylogenetic tree.

In a rooted tree, branches indicate direct transmission of genetic information from the taxonomic unit located at one end (parent) of the branch to the other (child). To determine the direction of transmission, consider removing the branch of interest from the tree to yield two unconnected subtrees, each of which contains only one of the nodes directly linked by the branch of interest. The subtree containing the root node contains the more ancestral of the two nodes linked by the branch of interest; hence, the direction of transfer of genetic information is from this more ancestral node to the other node linked by the branch of interest. For an unrooted tree, it is unknown which of the subtrees contains the root node, hence in unrooted trees the direction of transmission of genetic information is not specified.

If the branch is part of a scaled phylogenetic tree, then a value is associated with the branch that indicates some measure of the difference between the two taxonomic units directly linked by the branch; this value is often referred to as the "branch length". If the tree is "unscaled", no such value is associated with the branch, that is, no branch length is specified or defined.

A branch that links two internal nodes is known as an internal, inner, or interior branch. Branches linking an internal and an external node are referred to as external branches (also terminal branches).

## branch length
See "branch".

## node (of a phylogenetic tree)
In phylogenetic trees, nodes represent taxonomic units. Nodes between which there is direct transfer of genetic information are linked to each other by branches. Nodes in a phylogenetic tree that are attached to only a single terminal branch are referred to as terminal nodes (also external nodes, leaves, or tips), and represent operational taxonomic units. Nodes attached to more than one branch are referred to as internal (also interior) nodes, and represent hypothetical taxonomic units.

## phylogenetic tree [includes "root"]
A description of a path of transmission of genetic information between a set of operational (and usually also hypothetical, if the tree contains any internal nodes) taxonomic units (see Operational Taxonomic Units (OTUs) and Hypothetical Taxonomic Units (HTUs)). Tree structures, as understood in graph theory, can be used to represent phylogenetic trees. In graph theory, trees are defined as undirected graphs for which exactly one path connects any two nodes (or "vertices"), i.e., a tree is any connected graph that does not contain any cycles. Phylogenetic trees consist of nodes (operational or hypothetical taxonomic units) that are connected via branches.

Phylogenetic trees are described as either "rooted" or "unrooted". In a rooted tree, there is one node (the "root node") that represents the most recent common ancestor of all other taxa in the tree. While it is assumed that such an ancestor also exists for an unrooted tree, i.e., that all the OTUs share a most recent common ancestor, in an unrooted tree no inference is made about where on the tree this HTU might be.
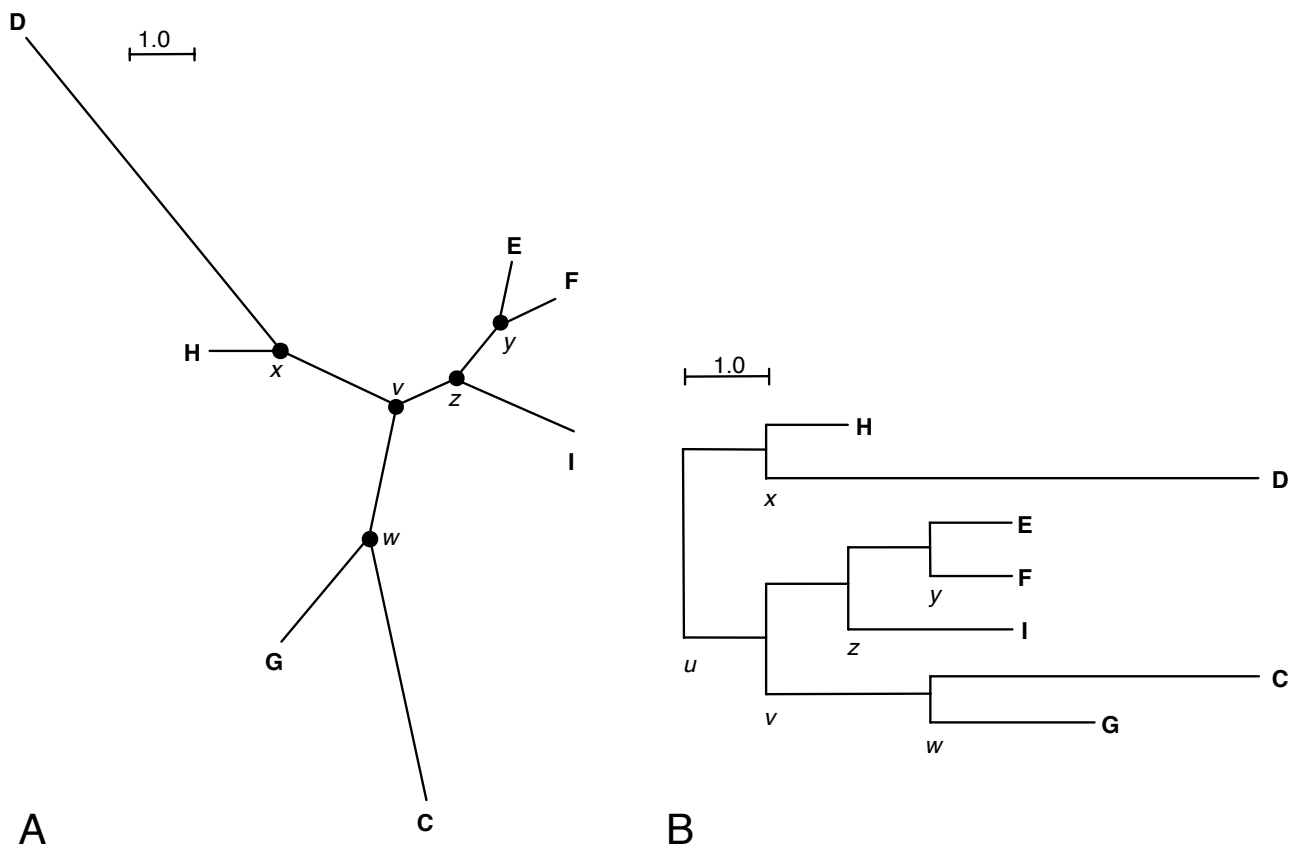
Figure A above shows an unrooted scaled phylogenetic tree in which all terminal nodes (C-H) and all internal nodes (v-z) are labeled. Internal nodes are indicated using solid dots. Figure B above shows a rooted scaled phylogenetic tree that has the same unrooted topology and set of branch lengths as the tree in figure A; the difference between the two trees is that in figure B the position of the root node is specified (half way along the branch linking nodes x and v of the tree in figure A). Thus, the tree in figure B contains an additional internal node (u) which is the root node.

## polytomy

An internal node of a phylogenetic tree is described as a multifurcation if (i) it is in a rooted tree and is linked to three or more daughter subtrees or (ii) it is in an unrooted tree and is attached to four or more branches. A tree that contains any multifurcations can be described as a multifurcating tree.
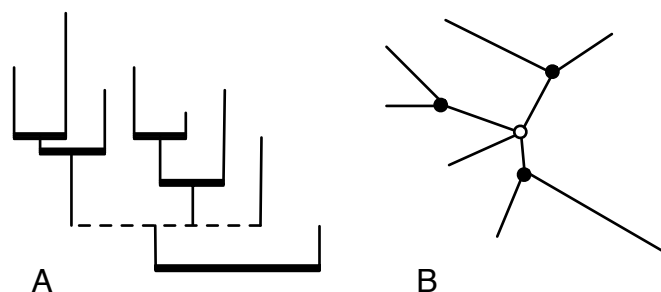


The rooted tree, A, in the figure above, contains five bifurcations (thick horizontal lines) and one multifurcation (dashed horizontal line). The unrooted tree, B, in the figure above, contains 3 bifurcations (solid dots) and one multifurcation (hollow dot).

**root**

See "phylogenetic tree"

**sister group**

In a rooted bifurcating tree, any internal node represents an ancestor of two subtrees. These two subtrees are sometimes referred to as "sister groups" of each other, i.e., subtree A is the sister group of subtree B (and accordingly subtree B is the sister group of subtree A). As this definition depends on knowing the direction of genetic transmission along the branches of the tree (i.e., which nodes/branches are ancestral and which are descendant), it is only possible to identify sister groups in the context of a rooted phylogenetic tree; in unrooted trees the direction of transmission of genetic information is not specified, so it is not possible to identify which of the subtrees linked to an internal node are ancestral and which are descendant. To overcome this problem, the concept of adjacent groups was developed for referring to subtrees linked to the same internal node in unrooted trees.

**subtree**

A tree obtained by detaching a branch from a larger phylogenetic tree.
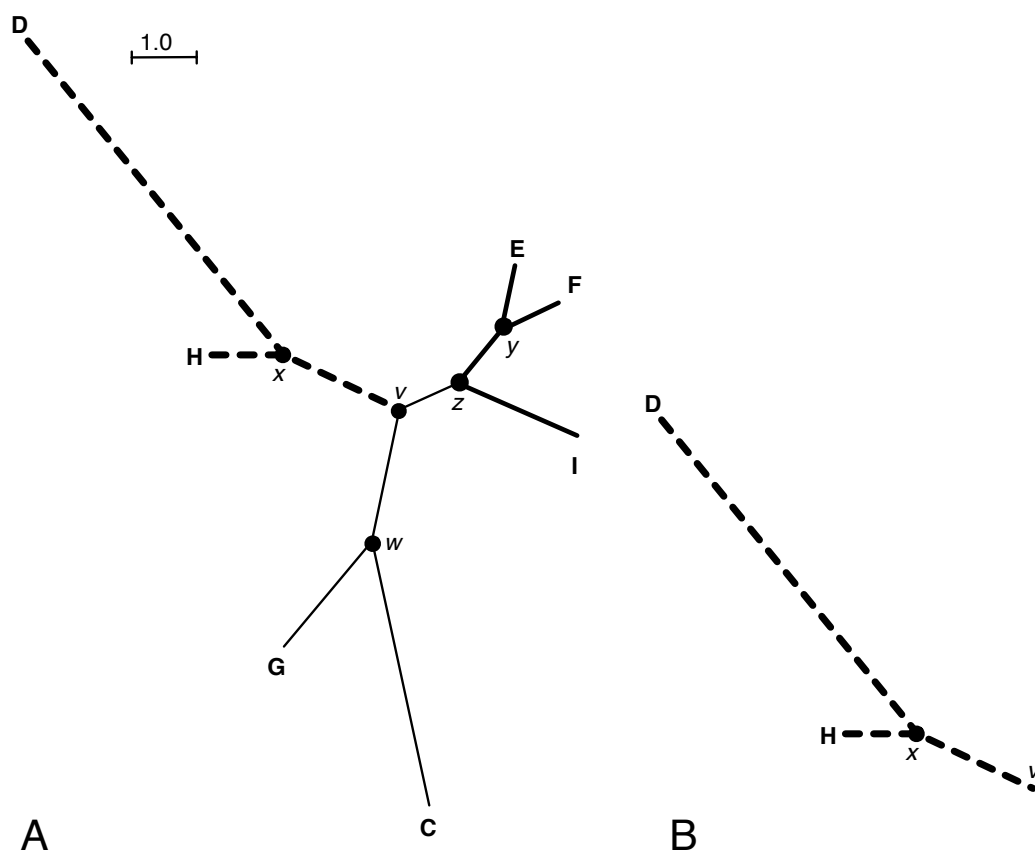


Tree B shown in the figure above is a subtree of tree A, as it can be obtained by detaching the branch that links internal nodes x and v in tree A from the rest of tree A.

## 4taxonomic unit

Phylogenetic trees can be used to describe patterns of genetic transmission between different kinds of entities, for example: different species, different individuals within a population of the same species, different genes within a gene family. The term "taxonomic unit" is used to refer to the entities between which patterns and paths of genetic transfer are described. Thus, for some trees, the taxonomic units will be individuals within a population, in other trees they will be different species.

## topology (of a phylogenetic tree)

The pattern of linkage between the nodes in a tree.

A given tree topology can be represented in many different ways. Consider, for example, the tree topology in which the following list describes all pairs of nodes that are directly linked to each other: AE, ED, DB, EF, and DC. Three different representations of this topology are shown in the figure below.
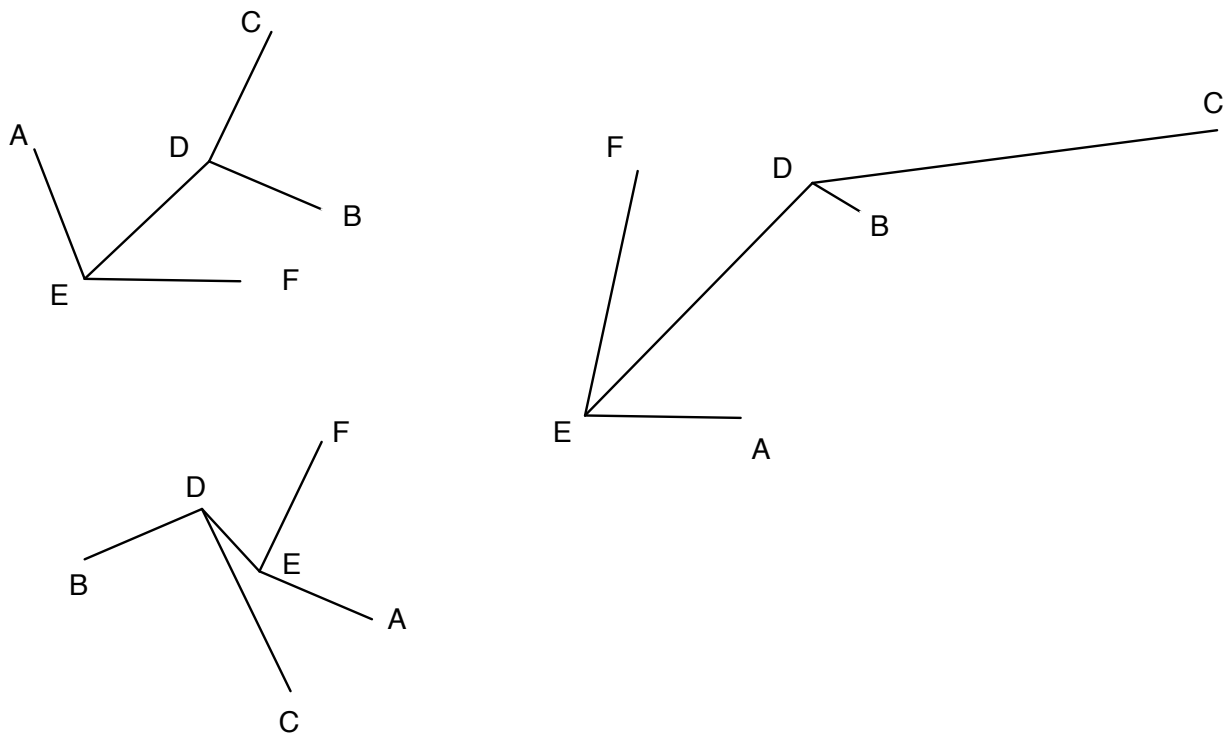


In the figure below, however, the two trees have different topologies i.e. in Tree A the list of nodes directly linked to each other is HD, DE, EF, EC and DG, while for Tree B it is HD, DE, EF, EG, and DC.

A     B
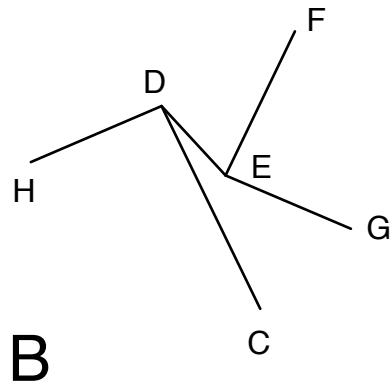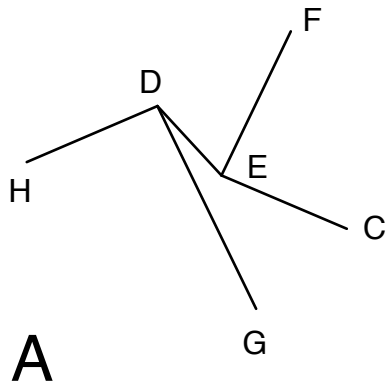
Note that the pattern of links between nodes, and hence the tree topology, is independent of the lengths of the branches.

Definitions taken from entries written by Aidan Budd and Alexandros Stamantakis in the 2nd edition of the "Dictionary of Bioinformatics and Computational Biology" (eds John M. Hancock and Marketa J. Zvelebil)