

Building a Phylogeny Tree

Molecular Phylogenetics

Phylogeny: the evolutionary history of organisms or population.

Phylogenetics: the study of phylogenies-the study of the evolutionary relationships among various species.

Phylogenetic analysis: means of estimating the evolutionary relationships.

The similarity among organisms/groups means they are descent from a common ancestor.

Molecular Phylogenetics: the use of DNA and protein sequence information and their change over evolutionary time infer the evolutionary relationship among a set of homologous genes or proteins.

- The regions of DNA - coding and non-coding regions – evolve at different speeds.
- Coding regions evolve more slowly, because a mutation that cause a change in a protein is generally more costly to the organism- it is less likely to survive and leave offspring.

Phylogenetic Tree

Phylogenetic tree/Evolutionary tree: a diagrammatic representation-branching/tree like diagramme- of the evolutionary relationship among various taxa.

Traditionally, physical differences between organisms were used to deduce evolutionary relationships between them, for example, whether an organism has a backbone, or if it has wings.

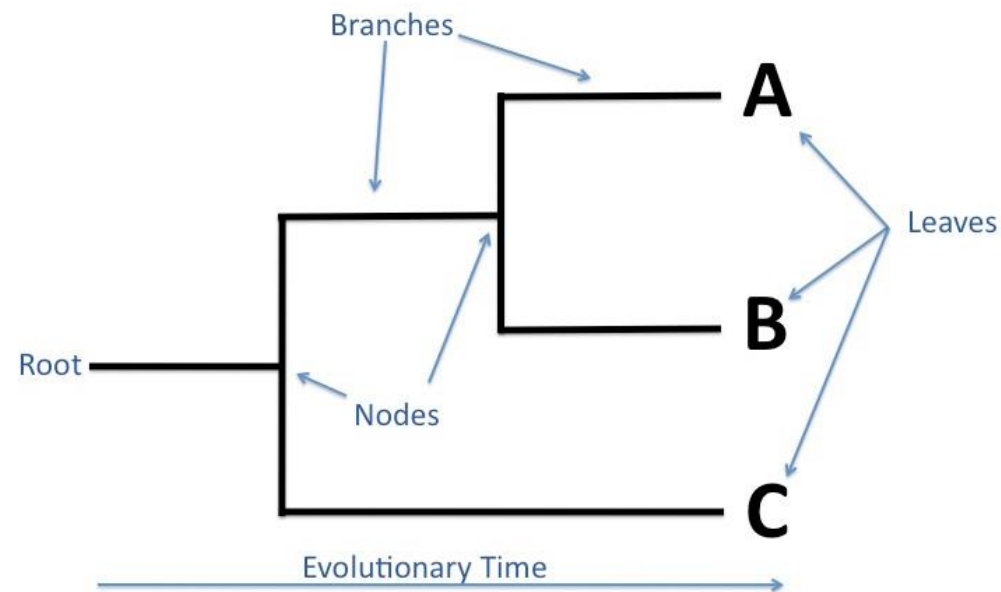
This may cause problems, however.

We know from DNA sequencing studies that DNA mutations occur randomly at a very slow rate and are passed from parents to offspring.

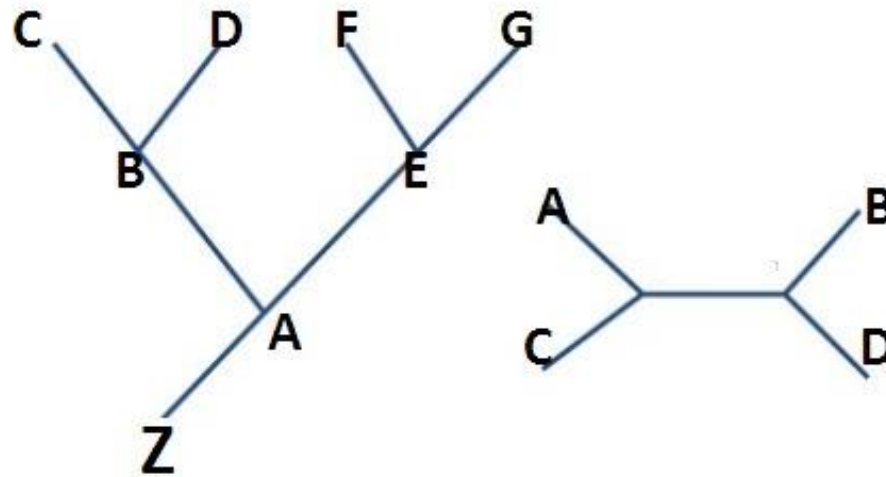
Assuming that all organisms have a common ancestor, differences in *homologous sequences* can be used to measure how long it has been since the organisms diverged.

In other words, the longer the time since two species diverged from a common ancestor, the more different their DNA sequences will be.

- Phylogenetic trees are branching diagrams composed of **nodes** and **branches**.
- The branching pattern of a tree is called the **topology** of the tree.
- **Nodes**; taxonomic units such as species, populations, genes or proteins.
- **Branch**; is called an edge and represents the time estimate of the evolutionary relationships among the taxonomic units.



- Phylogenetic trees can be rooted or unrooted.
- A rooted tree has a node (the root) from which the rest of the trees diverges.



**Rooted
tree**

Unrooted tree

- A **cladogram** is a branching hierarchical tree that shows the relationships between clades; cladograms are unscaled
- The **dendrogram** means a hierarchical cluster arrangement where similar objects are grouped into clusters; a dendrogram shows the relationships among various clusters

Phylogenetic Analysis Tool

- Phylogeny.fr
- One click
- Molecular Evolutionary Genetics Analysis (MEGA)

Construction of a phylogenetic tree involves the following step;

- Selection of the appropriate molecular marker (genes/proteins/mtDNA)
- Multiple Sequence Alignment
- Selection of a model of evolution
- Construction of the phylogenetic tree
- Assessment of the reliability of the tree