

Another Molecular Phylogenetic Analysis Technique

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Abstract

Molecular phylogenetics is that the branch of phylogeny that analyzes genetic, hereditary molecular differences, predominately in DNA sequences, to realize information on an organism's evolutionary relationships. From these analyses, it's possible to work out the processes by which diversity among species has been achieved. The results of a molecular phylogenetic analysis is expressed during a phylogenetic tree. Molecular phylogenetics is one aspect of molecular systematics, a broader term that also includes the utilization of molecular data in taxonomy and biogeography.

Molecular phylogenetics and molecular evolution correlate. Molecular evolution is that the process of selective changes (mutations) at a molecular level (genes, proteins, etc.) throughout various branches within the tree of life (evolution). Molecular phylogenetics makes inferences of the evolutionary relationships that arise thanks to molecular evolution and leads to the development of a phylogenetic tree. The figure displayed on the proper depicts the phylogenetic tree of life together of the primary detailed trees, consistent with information known within the 1870s by Haeckel.

Techniques and Applications

Every living organism contains deoxyribonucleic acid (DNA), Ribonucleic Acid (RNA), and proteins. Generally, closely related organisms have a high degree of similarity within the molecular structure of those substances, while the molecules of organisms distantly related often show a pattern of dissimilarity. Conserved sequences, like mitochondrial DNA, are expected to accumulate mutations over time, and assuming a continuing rate of mutation, provide a molecular clock for dating divergence. Molecular phylogeny uses such data to create a "relationship tree" that shows the probable evolution of varied organisms. With the invention of Sanger sequencing in 1977, it became possible to isolate and identify these molecular structures. High-throughput sequencing can also be used to obtain the transcriptome of an organism, allowing inference of phylogenetic relationships using transcriptomic data.

The most common approach is that the comparison of homologous sequences for genes using sequence alignment techniques to spot similarity. Another application of molecular phylogeny is in DNA barcoding, wherein the species of a private organism is identified using small sections of mitochondrial DNA or chloroplast DNA. Another application of the techniques that make this possible are often seen within the very limited field of human genetics, like the ever-more-popular use of genetic testing to work out a child's paternity, also because the emergence of a replacement branch of criminal forensics focused on evidence referred to as genetic profiling.

Molecular Phylogenetic Analysis

There are several methods available for performing a molecular phylogenetic

analysis. One method, including a comprehensive step-by-step protocol on constructing a phylogenetic tree, including DNA/Amino Acid contiguous sequence assembly, multiple sequence alignment, model-test (testing best-fitting substitution models), and phylogeny reconstruction using Maximum Likelihood and Bayesian Inference, is out there at Nature Protocol.

Another molecular phylogenetic analysis technique has been described by Pevsner and shall be summarized within the sentences to follow (Pevsner, 2015). A phylogenetic analysis typically consists of 5 major steps. The primary stage comprises sequence acquisition. The subsequent step consists of performing a multiple sequence alignment, which is that the fundamental basis of constructing a phylogenetic tree. The third stage includes different models of DNA and aminoalkanoic acid substitution. Several models of substitution exist. A couple of examples include Hamming distance, the Jukes and Cantor one-parameter model, and therefore the Kimura two-parameter model (see Models of DNA evolution). The fourth stage consists of varied methods of tree building, including distance-based and character-based methods. The normalized Hamming distance and therefore the refore the Jukes-Cantor correction formulas provide the degree of divergence and the probability that a nucleotide changes to a different, respectively. Common tree-building methods include unweighted pair group method using first moment (UPGMA) and Neighbour joining, which are distance-based methods, Maximum parsimony, which may be a character-based method, and Maximum likelihood estimation and Bayesian inference, which are character-based/model-based methods. UPGMA may be a simple method; however, it's less accurate than the neighbour-joining approach. Finally, the last step comprises evaluating the trees. This assessment of accuracy consists of consistency, efficiency, and robustness.

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