

New Approach to Construct Phylogenetic Tree

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Abstract : Numerous scientific works present various methods to analyze the data for several domains, specially the comparison of classifications. In our recent work, we presented a new approach to help the user choose the best classification method from the results obtained by every method, by basing itself on the distances between the trees of classification. The result of our approach was in the form of a dendrogram contains methods as a succession of connections. This approach is much needed in phylogeny analysis. This discipline is intended to analyze the sequences of biological macro molecules for information on the evolutionary history of living beings, including their relationship. The product of phylogeny analysis is a phylogenetic tree. In this paper, we recommend the use of a new method of construction the phylogenetic tree based on comparison of different classifications obtained by different molecular genes.

Keywords : hierarchical classification, classification methods, structure of tree, genes, phylogenetic analysis

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