Abstract

PHYLOGENY is the concept of phylogenetic trees which is typically a graphical representation of the evolutionary relationships among three or more genes or organisms. The tree construction can be done through different tree-building methods which include methods based on distances and characters. After a phylogenetic tree is being constructed, it is important to access its accuracy which refers to the degree to which a tree approximates the true tree. The best approach to test the phylogeneies is bootstrap analysis or simply bootstrapping. Bootstrapping is not a technique to check the accuracy of a tree. Instead, it describes the robustness of the tree topology. This paper discusses the searching and analyses of different possible inputs selected on the basis of family of genes or organisms so as to obtain the most optimal result. An algorithm was developed to determine the reliability of an inferred phylogenetic tree.
- Huson, D. H. and Bryan, D. 2006 "Applications of phylogenetic networks in phylogenetic studies;", Center for Bioinformatics (ZBIT), Tu"bingen University, Tu"bingen, Germany; and _Department of Mathematics, Auckland University, Auckland, New Zealand, pp 1-14.
- Torres, M. et al. 2011 "Tool that integrates distance based programs for reconstructing phylogenetic trees;", Univ. Estaudal de Santa Cruz, Ilheus, Brazil, pp 895-901.

**Index Terms**

Computer Science  
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**Keywords**

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