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EVOLUTIONARY ALGORITHMS FOR PHYLOGENETIC TREE RECONSTRUCTION

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Abstract

In this paper we compare and introduce methodologies which can perform a highly accurate phylogenetic analysis. The Multi-Stack algorithm categorically is a distance-based method. Thus it uses only the distance values of the sequences of interest to build a phylogenetic tree. And also we propose a genetic algorithm for maximum parsimony based phylogenetic trees reconstruction.

Key Words and Phrases : *Phylogenetic tree, Tree reconstruction, Distance-based, UPGMA, Neighbor Joining, Maximum parsimony, Genetic Algorithms.*