

Efficient Parallel Algorithm for Constructing Evolutionary Trees of Human Mitochondrial DNA from Distance Matrices

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Abstract

Constructing evolutionary trees for species set is an important problem in biology and in taxonomy to find the relationship among species. There is a category of evolutionary tree called ultrametric tree, in which we assume that the rate of evolution is constant. An ultrametric tree is a rooted and edge weighted binary tree in which every internal node has the same path length to all the leaves in its subtree. Unfortunately, the problem of constructing a minimum ultrametric tree has been shown to be NP-hard. In this paper, we have developed an efficient parallel branch-and-bound algorithm to construct the minimum ultrametric tree from distance matrix. The proposed parallel algorithm is based on the master-slave centralize architecture with efficient load-balancing, bounded, and communication strategies. The experimental results show that our proposed algorithm can find optimal solution for 35 species of Human Mitochondrial DNA within reasonable time by using 16 personal computers, while, to the best of our knowledge, there is no report of algorithms solving the problem even for 25 species. In the future, our goal is to find optimal or approximate solutions for total 136 species of Human Mitochondrial DNA within reasonable time.

Keyword :