A Fast Technique for Constructing Evolutionary Tree with the Application of Compact Sets

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Abstract

Constructing an evolutionary tree has many techniques, and usually biologists use distance matrix on this activity. The evolutionary tree can assist in taxonomy for biologists to analyze the phylogeny. In this paper, we specifically employ the compact sets to convert the original matrix into several small matrices for constructing evolutionary tree in parallel. By the properties of compact sets, we do not spend much time and do keep the correct relations among species. Besides, we adopt both Human Mitochondrial DNAs and randomly generated matrix as input data in the experiments. In comparison with conventional technique, the experimental results show that utilizing compact sets can definitely construct the evolutionary tree in a reasonable time.

Keyword：computational biology, evolutionary tree, compact sets, branch-and-bound.