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A review on Multiple Sequence Alignment from the perspective of Genetic Algorithm

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Abstract

Sequence alignment is an active research area in the field of bioinformatics. It is also a crucial task as it guides many other tasks like phylogenetic analysis, function, and/or structure prediction of biological macromolecules like DNA, RNA, and Protein. Proteins are the building blocks of every living organism. Although protein alignment problem has been studied for several decades, unfortunately, every available method produces alignment results differently for a single alignment problem. Multiple sequence alignment is characterized as a very high computational complex problem. Many stochastic methods, therefore, are considered for improving the accuracy of alignment. Among them, many researchers frequently use Genetic Algorithm. In this study, we have shown different types of the method applied in alignment and the recent trends in the multiobjective genetic algorithm for solving multiple sequence alignment. Many recent studies have demonstrated considerable progress in finding the alignment accuracy.

1. Introduction

In an organism, DNA is the genetic material that acts as a medium to transmit genetic information from one generation to another (Graur and Li 2002). All the living things diverge

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