Abstract

In the last decade, biologists have experienced a fundamental shift away from the traditional empirical research to large-scale, computer-based research. Today bio-informatics is a systematic and predictive discipline which encompasses genomics, informatics, automation, and miniaturization. This fusion of biology and information science is expected to continue and expand for the foreseeable future. DNA Sequence alignment is a commonly observed problem in bio-informatics for establishing similarity and evolutionary relationship between DNA sequences. This paper has presented a DNA multiple sequence alignment technique by a genetic algorithm based on Hidden Markov Model and Fuzzy Levenshtein Distance.

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DNA Multiple Sequence Alignment by a Hidden Markov Model and Fuzzy Levenshtein Distance based Genetic Algorithm

**Index Terms**

Computer Science

Artificial Intelligence

**Keywords**

Genetic Algorithm  Hidden Markov Model  Fuzzy Levenshtein Distance