Abstract

Biological sequence alignment is one of the crucial tasks of computational bioinformatics, and provides base for other tasks of bioinformatics. In this paper, we discuss two different approaches to sequence matching – Boolean algebra and fuzzy logic. First method is a two-valued logic whereas the second is a multi-valued logic. Both the methods perform
sequence matching by direct comparison method using the operations of Boolean algebra and fuzzy logic respectively. To ensure the optimal alignment, dynamic programming is employed to align the sequences progressively. Both the methods are implemented and then tested on few sets of real biological sequences taken from NCBI bank and their performances are compared with the CLUSTALW algorithm.

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Biological Sequence Matching using Boolean algebra vs. Fuzzy Logic


Index Terms

Computer Science

Bioinformatics

Key words

Sequence alignment
Boolean algebra
Fuzzy

Logic

Sequence matching

global alignment

dynamic programming