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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**Index Terms**

Computer Science

Bioinformatics

**Key words**

Sequence alignment  Boolean algebra  Fuzzy Logic

Sequence matching

  global alignment

  dynamic programming