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.

Reference

- Pin-Teng Chang, Lung-Ting Hung, Kuo-Ping Lin, Chih-sheng Lin, Kuo-Chen Hung, “Protein Sequence Alignment Based on Fuzzy Arithmetic and Genetic Algorithm”, 2006 IEEE International Conference on Fuzzy Systems, pp. 1362-1367
- Sara Nasser, Gregory L. Vert, Monica Nicolescu1 and Alison Murray, "Multiple Sequence Alignment using Fuzzy Logic", Proceedings of the 2007 IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology, pp. 304-311
- Farhana Naznin, Ruhul Sarker, and Daryl Essam , “Iterative Progressive Alignment Method (IPAM) for Multiple Sequence Alignment”, Computers & Industrial Engineering, 2009, pp. 536-541
- David W. Mount, “Bioinformatics: Sequence and Genome Analysis”, Cold Spring Harbor Laboratory Press
Biological Sequence Matching using Boolean algebra vs. Fuzzy Logic


Index Terms

Computer Science

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Key words

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