Abstract

Multiple sequence alignment (MSA) is an NP-complete and important problem in bioinformatics. In this paper, we have proposed iterative alignment method using a Genetic Algorithm for Multiple Sequence Alignment, named TSGA-MSA. The steps in this algorithm are discussed in details and its performances on a set of benchmark datasets from the BAliBase 2.0 are analysed. The experimental results, the effects of the initial generation and genetic operators
TSGA-MSA: Trace Sequence Algorithm for Alignment of MSA

on the performance of this algorithm, the parameter settings, and a comparison of results with other well-known algorithm are presented and discussed.

References

- Fernando, J., Juan, M., Juan, A. and Miguel, A. : An Evolutionary Approach for
Performing Multiple Sequence Alignment, IEEE, 2010, pp. 4244-8126

Index Terms
Computer Science
Algorithms

Keywords
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