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
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
Genetic Algorithm Multiple Sequence Alignment Dna Etc.