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

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Performing Multiple Sequence Alignment, IEEE, 2010, pp. 4244-8126

**Index Terms**

Computer Science  
Algorithms

**Keywords**

Genetic Algorithm  
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