

Multiobjective characteristic-based framework for Multiple Sequence Alignment

Abstract:

An alignment of two sequences is determined by inserting spaces in necessary position in such a way that the length of the two final sequences will be the same. Multiple sequence alignment(MSA) is an alignment problem which can align three or more DNA, RNA and protein sequences to understand the evolutionary relationship among species and know the differences among their probable ancestors. It is one of the most challenging problems in computational biology and huge number of researches are already going on to improve the complexity of this NP-hard problem. In this paper, a framework is proposed to find the best configuration of alignment parameters combined with three well known multiobjective evolutionary algorithms: NSGA-II, IBEA and MOEA/D. Three widely used aligners: Kalign, MAFFT and MUSCLE are compared here to measure the performance of the selected parameters.

Team members:

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Selected papers:

1. Multiobjective characteristic-based framework for very-large multiple sequence alignment: Álvaro Rubio-Largo a, Leonardo Vanneschi, Mauro Castelli, Miguel A. Vega-Rodríguez
2. On the Complexity of Multiple Sequence Alignment: Lusheng Wang and Tao Jiang.
3. Computational Complexity of Multiple Sequence Alignment with SP-Score: Winfried Just