



Partitioning Algorithm for Multiple Sequence Alignment

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Abstract

Sequence alignment is an important task in bioinformatics which involves typical database search where data is in the form of DNA, RNA or protein sequence. For alignment various methods have been devised starting from pairwise alignment to multiple sequence alignment (MSA). To perform multiple sequence alignment various methods exist like progressive, iterative and concepts of dynamic programming in which we use Needleman Wunsch and Smith Waterman Algorithm. This paper proposes method based on partitioning algorithm for multiple sequence alignment and its results are also shown. The partitioning approach significantly improves the solution time and quality by utilizing the locality structure of the problem.

Keywords: Multiple sequence alignment, partitioning algorithm

Full text: <https://sites.google.com/a/ijrit.com/papers/home/V1111132.pdf>