Abstract

This paper presents a Modified Dynamic Parallel Algorithm for Sequence Alignment in BioSequences. DNA sequence alignment between two or more bio sequences using algorithms is a complex problem due to its applicability in the field of biology. This algorithm achieves its efficiency in using computational resources by making a $M \times N$ matrix, $M$ represents the length of first sequence and $N$ represents the length of the second sequence. This modified Dynamic algorithm performs calculation to fill the three main diagonal cells without evaluating other cells in the matrix. The proposed model is based on Index Based Pattern Matching using Multithreading [13] to obtain the optimal alignment using Multithreading. The executed results indicate that with the proposed algorithm Memory Efficiency and Fast Execution are achieved over the well-known dynamic programming approach Needleman-Wunsch and Hirschberg approach.

References

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Index Terms

Computer Science

Algorithms

Keywords

DNA operations sequence alignment Multithreading score