A VERSATILE EXACT PATTERN MATCHING ALGORITHM FOR BIOLOGICAL SEQUENCES
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ABSTRACT
Pattern matching is essential for locating nucleotide or amino acid sequence patterns in the biological databases. In this paper, Zhu-Takaoka Fast Search algorithm (ZTFS) algorithms are modified to reduce the computational time complexity and also the number of shifts done while comparing the pattern with the given string. The experimental results on biological sequence of Enterobacteria phage lambda and Measles virus proves that the modified algorithm works faster than other existing algorithms, especially in case of longer patterns of nucleotide sequences. The algorithm has also been extended to classify the input biological sequences into different possible combinations of tricodons and amino acids present in the sequence. Computational complexity calculations and performance analysis for character comparisons are presented to indicate the potential reduction in time complexity of the proposed algorithm.

KEY WORDS: Pattern matching, Amino acids, Character comparisons, Nucleotide sequences, Measles virus