Abstract

Pattern matching, the problem of finding sub-sequences within a long sequence is essential for many applications such as information retrieval, disease analysis, structural and functional analysis, logic programming, theorem-proving, term rewriting and DNA-computing. In computational biology the essential components for DNA applications is the exact string matching algorithms. Many databases like GenBank were built by researchers for DNA and protein sequences; the string matching problem is the core problem for searching these databases. As the size of the database grows, the more important research area is to design an efficient string matching algorithms. This paper proposes a new pattern matching technique called An Index based Pattern matching using Multithreading for DNA sequences. The method specified in this paper performs parallel string searching using multiple threads simultaneously, each thread is responsible for searching one part of the text. The proposed algorithm is an efficient algorithm that can be used to search for exact occurrences of patterns in DNA sequences.
- Raju Bhukya,DVLN Somayajulu,&quot;An Index Based K-Partitions Multiple Pattern matching Algorithm&quot;, Proc. of Int. Conf. on Advances in Computer Science 2010.
- Ziad A. A.  Alqadi, &quot;Multiple Skip Multiple Pattern Matching Algorithm &quot;, IAENG International Journal of Computer Science, 34:2, IJCS_34_2_03, Advance online publication: 17 November 2007.

**Index Terms**

Computer Science  
Pattern Recognition

**Keywords**

Exact String matching algorithms  
pattern matching  
DNA sequence  
Multithreading  
Context Switching
An Index based Pattern Matching using Multithreading