

Performance Evaluation of Various DNA Pattern Matching Algorithms Using Different Genome Datasets

PROJECT TEAM

- 1) HARIPRIYA R - 19PT09
- 2) LIBIKAA K - 19PT12
- 3) KIRUPA S - 19PT24

PROJECT DESCRIPTION

Pattern matching algorithms play a vital role for searching and analyzing patterns in computational biology. The functional and structural relationship among different DNA databases is performed by different algorithms. Matching algorithms is a major research area. This project surveys the performance of Naïve exact matching, and Knuth-Morris-Pratt (KMP) algorithms. The main process of this study is to find the **matched DNA sequence from the database using these pattern matching algorithms**. This study determines a more **efficient pattern matching algorithm** by analyzing the matching result.

ALGORITHM DESIGN TECHNIQUE

STRINGS

A pattern will be a description of a set of strings, each string being a sequence of symbols. We use different pre-procedure and algorithms for matching this pattern of DNA sequence. Our analysis is an effort to explore multiple DNA pattern matching algorithms with different genomes. We are planning to implement the pseudo-code in C++ programming language.

pattern matching : Given a specific sequence of DNA string P generally called pattern searching in large genome sequence T to locate P in T.