

ABSTRACT

There is a need for biological analysis by searching for similarities in biological sequences (RNA, DNA, protein). The search for similarity in a computer science problem is the string-matching problem. String matching for biological analysis needs can be done by comparing pairs of strings or biological sequences (pairwise sequence alignment) or comparing groups of biological sequences (multiple sequence alignment). The main algorithm in pairwise alignment or multiple sequence alignment is Dynamic Programming (DP).

Bit-parallelism or Bit-Vector is one of the algorithms developed from the DP algorithm, which adapts the way words work in computer systems. Word is a unit consisting of a binary data set. Bit parallelism transforms the computational units in the dp matrix into word units.

In this study, two algorithms have been implemented, namely dynamic programming and bit-parallelism to find a match between two input strings and compare the speed and level of complexity between the two algorithms. The results of this study are the two algorithms are influenced by the environment in which the algorithm is run, in this case the author uses Matlab and VS code. In Matlab Environment, Dinamic Programming Matrix has higher speed than Bit-Parallelism because in matlab bit level operation uses libraries that can add time for bit-parallelism. Meanwhile, in the VS code environment, it is shown that bit-parallelism has a faster time than DP Matrix and gets 98% better efficiency.

Keywords: String Matching, Bit-Parallelism, Dynamic Programming Matrix.