Abstract

It is becoming increasingly difficult to ignore the importance of aligning DNA and Protein sequences to infer properties of new sequences from well-known reference sequences established and sorted in genetics databanks. Many studies in recent years have focused on different implementations of Sequences Alignment Problems (SAP). However, researcher confused with the ambiguous classification of the SAP. This paper is set out mainly to review, investigate, and analysis current trends in shared memory and hardware implementation of local SAP using Smith-Waterman algorithm. The literatures are addressing and evaluating in order to highlight their advantages and disadvantages.

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