The topic in this paper is how to improve time in waterman algorithm using OpenMP and SIMD.

The main problem of the paper revolves around high complexity of waterman algorithm and high time consuming

Since those algorithms are important in executing sequence alignment for very large sequences so time consuming has to be reduced by openMP (API) and SIMD.

The sequence alignment is very important in bioinformatics field because it answers an important question for molecular biologists: if two sequences of DNA are related or not?

Smith-waterman algorithm is one of the most important algorithms to align the sequences.

In this paper will use openMP ,SIMD and AVX2 to improve time in the algorithm.

OpenMP is API which stands for application programming interface on a variety of platforms, instruction set architecture (ISA)

OpenMP supports multi platforms shared memory, multiprocessing programming in c++ ,c and fortran.

SIMD stands for single instruction , multiple data.

This is a form of parallel computers according to Flynn's taxonomy

It refers to computers with multiple processing elements that perform the same operation on a large number of data points at the same time.

Advanced Vector Extensions (AVX, also known as Sandy Bridge New Extensions) are extensions to the x86 instruction set architecture introduced by Intel

AVX2 (also known as Haswell New Instructions)

Most integer commands are expanded to 256 bits and fused multiply-accumulate (FMA) operations.

This paper is divided into 3 sections,

First section: software algorithms in sequence alignment and related work

Second section: discussion and results

Third section: conclusion and the references