Abstract

We present a novel implementation of the pairwise DNA sequence alignment problem other than the Dynamic programming solution presented by Smith Waterman Algorithm. The proposed implementation uses CUDA; the parallel computing platform and programming model invented by NVIDIA. The main idea of the proposed implementation is assigning different nucleotide weights then merging the sub-sequences of match using the GPU Architecture according to predefined rules to get the optimum local alignment. We parallelize the whole solution for the pairwise DNA sequence alignment using CUDA and compare the results against a similar semi-parallelized solution and a traditional Smith-Waterman implementation on traditional processors; Experimental results demonstrate a considerable reduction in the running time.
References

- Rafia Inam, 2011. An Introduction to GPGPU Programming - CUDA Architecture, Mälardalen University, Mälardalen Real-Time Research Centre.
Index Terms

Computer Science

Applied Sciences

Keywords

GPU  GPGPU  CUDA  sequence alignment algorithms  molecular biology.