

Biological sequence alignments: A review of hardware accelerators and a new PE computing strategy

Abstract

One of the most challenging tasks in sequence alignment is its repetitive and time-consuming alignment matrix computations. In addition, performing sequence alignment in hardware, i.e. FPGA requires more hardware resources as the number of processing elements is replicated to increase performance throughput. This paper first reviews the existing FPGA-based biological sequence alignment core architectures and then proposed an efficient scheduling strategy, the so-called overlap computation and configuration (OCC) towards realizing optimized biological sequence alignment core architecture targeting for pairwise sequence alignment. In this research work, double buffering-based core architecture have been proposed and implemented on Xilinx Virtex-5 FPGA. Results have shown that this approach gained more than 10K times speed-up as compared to the GPP solution..

Keywords

Component; FPGA; Pairwise sequence alignment and bio-marker; Systolic arrays