

An FPGA-based Multiprocessor System for BLAST Algorithm

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Basic Local Alignment Search Tool or BLAST is an algorithm in the field of bioinformatics for comparing primary biological sequence, such as the amino-acid sequences of different proteins or the nucleotides of DNA sequences. A BLAST search enables a researcher to compare a query sequence with a library or database of sequences, and identify library sequences that resemble the query sequence above a certain threshold.

Due to the high complexity of BLAST algorithm and the large amount of data to be processed, many software and hardware approaches have been introduced with the scope to speed up the execution time of this algorithm. The majority of the approaches that have been introduced take advantage of the high parallelism of the BLAST algorithm.

Recent advantages in Field Programmable Gate Array (FPGA) technologies have made it possible to create soft-core Multiprocessor Embedded Systems (MES), which emphasize in reducing the amount of the dedicated hardware needed to design a system, while increasing the flexibility of the design with the use of software.

In this work we introduce a new approach to the solution of the complex BLAST algorithm with the use of FPGA and soft-core processors. We have created a network of 14 Xilinx Microblaze processors, in which each of them solves the BLAST-n algorithm. All processors at the same time compare the same query with a different part of the database and report the results.

The main goal of this work is to create a system that utilizes the advantages of FPGAs and soft-core processors, and with a proper parallelism of data, to increase the runtime performance and the throughput of the BLAST software.