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RESEARCH ARTICLE

FPGA Implementation of Wu-Manber Algorithm for BLASTN DNA Sequence Matching

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Abstract

BLAST is one of the most popular sequence analysis tools used by molecular biologists. Blast is fast and it is ubiquitous within the genomic community. However, because the size of genomic databases is growing rapidly, the computation time of BLAST, when performing a complete genomic database search, is continuously increasing. In order to overcome this time consuming process, we propose a PPBF architecture, which is used to speed up the BLASTN process more than the NCBI BLASTN software running on a general purpose computer.

Index Terms- Bloom filter, Genomic sequence analysis, hash table.

Full Text: <http://www.ijcsmc.com/docs/papers/March2014/V3I3201451.pdf>