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Burrows-Wheeler Aligner: A Parallel Approach

Abstract

The advent of mainframe computing brought about a fundamentally different way of approaching problems for many branches of science. But none has transformed quite like the science of biology. With genome sequencing now commonplace, an organism may be completely represented as a sequence of numbers. Harnessing the power of computers, sequences of genomes (and thus organisms) may be compared in meaningful ways.

Burrows-Wheeler Aligner (BWA) is one such utility for performing these comparisons. As expected, a sequence of genes may consist of millions of characters; efficient processing might still require days of computing. Due to BWA's prevalence in bioinformatics research, the aim of this project is to reduce the time required to perform alignment utilizing parallel computation strategies. The paper explores two parallel architectures, MPI and CUDA, and the computational advantages of each as applied to the BWA-SW genome sequence alignment algorithm.

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