DOCTORAL THESIS

GPU accelerated sequence alignment

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Abstract

DNA sequence alignment is a fundamental task in gene information processing, which is about searching the location of a string (usually based on newly collected DNA data) in the existing huge DNA sequence databases. Due to the huge amount of newly generated DNA data and the complexity of approximate string match, sequence alignment becomes a time-consuming process. Hence how to reduce the alignment time becomes a significant research problem. Some algorithms of string alignment based on HASH comparison, suffix array and BWT, which have been proposed for DNA sequence alignment. Although these algorithms have reached the speed of O(N), they still cannot meet the increasing demand if they are running on traditional CPUs.

Recently, GPUs have been widely accepted as an efficient accelerator for many scientific and commercial applications. A typical GPU has thousands of processing cores which can speed up repetitive computations significantly as compared to multi-core CPUs. However, sequence alignment is one kind of computation procedure with intensive data access, i.e., it is memory-bounded. The access to GPU memory and IO has more significant influence in performance when compared to the computing capabilities of GPU cores. By analyzing GPU memory and IO characteristics, this thesis produces novel parallel algorithms for DNA sequence alignment applications. This thesis consists of six parts. The first two parts explain some basic knowledge of DNA sequence alignment and GPU computing. The third part investigates the performance of data access on different types of GPU memory. The fourth part describes a parallel method to accelerate short-read sequence alignment based on BWT algorithm. The fifth part proposes the parallel algorithm for accelerating BLASTN, one of the most popular sequence alignment software. It shows how multi-threaded control and multiple GPU cards can accelerate the BLASTN algorithm significantly. The sixth part concludes the whole thesis.

To summarize, through analyzing the layout of GPU memory and comparing data under the mode of multithread access, this thesis analyzes and concludes a perfect optimization method to achieve sequence alignment on GPU. The outcomes can help practitioners in bioinformatics to improve their working efficiency by significantly reducing the sequence alignment time.

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