

## High-Performance Computing on Very Large-Scale Biological Data

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### Editorial

In the past decade, due to the rapid growth of high-throughput instrumentations both of volume and complexity of biomedical data have been increasing dramatically. To process these big size data the high performance computing technologies become very important role. Recently, two interesting computing technologies, cloud computing and GPU computing, have been applied to solve very large-scale problem in bioinformatics. The paper by Hung, et al. entitled "Implementation of a Parallel Protein Structure Alignment Service on Cloud" proposed a protein structure alignment algorithm implemented by Hadoop to efficiently compare a interesting protein structure with a large database. Cloud-based bioinformatics applications can process data that are stored in many places. Therefore, they can make a significant breakthrough to achieve a high quality healthcare.

Recently, the next generation sequencing technologies have been applied in many biological domains. Therefore, huge amount of biological data have been discovered and published. Different to Hadoop, GPU is a hardware device that can launch massive threads to simultaneously execute single instruction to copy with data. The paper by Lin, et al. entitled "GPU-UPGMA: high-performance computing for UPGMA algorithm based on Graphics Processing Units" build a UPGMA phylogenetic tree by using GPU architecture. GPU-UPGMA takes advantage of high performance. It shows that building a large phylogenetic tree can be completed in very short time, and it can be superior to the traditional UPGMA method running on CPU over 10X times. These developments and applications on software framework or hardware devices would facilitate biological research to accelerate computational performance.