Bioinformatics: High Performance Parallel Computer Architectures (Embedded Multi-Core Systems)

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New sequencing technologies have broken many experimental barriers to genome scale sequencing, leading to the extraction of huge quantities of sequence data. This expansion of biological databases established the need for new ways to harness and apply the astounding amount of available genomic information and convert it into substantive biological understanding.

A complilation of recent approaches from prominent researchers, **Bioinformatics: High Performance Parallel Computer Architectures** discusses how to take advantage of bioinformatics applications and algorithms on a variety of modern parallel architectures. Two factors continue to drive the increasing use of modern parallel computer architectures to address problems in computational biology and bioinformatics: high-throughput techniques for DNA sequencing and gene expression analysis—which have led to an exponential growth in the amount of digital biological data—and the multi- and many-core revolution within computer architecture.

Presenting key information about how to make optimal use of parallel architectures, this book:

- Describes algorithms and tools including pairwise sequence alignment, multiple sequence alignment, BLAST, motif finding, pattern matching, sequence assembly, hidden Markov models, proteomics, and evolutionary tree reconstruction

- Addresses GPGPU technology and the associated massively threaded CUDA programming model

- Reviews FPGA architecture and programming

- Presents several parallel algorithms for computing alignments on the Cell/BE architecture, including linear-space pairwise alignment, syntenic alignment, and spliced alignment

- Assesses underlying concepts and advances in orchestrating the phylogenetic likelihood function on parallel computer architectures (ranging from FPGAs upto the IBM BlueGene/L supercomputer)

- Covers several effective techniques to fully exploit the computing capability of many-core CUDA-enabled GPUs to accelerate protein sequence database searching, multiple sequence alignment, and motif finding

- Explains a parallel CUDA-based method for correcting sequencing base-pair errors in HTSR data

Because the amount of publicly available sequence data is growing faster than single processor core performance speed, modern bioinformatics tools need to take advantage of parallel computer architectures. Now that the era of the many-core processor has begun, it is expected that future mainstream processors will be parallel systems. Beneficial to anyone actively involved in research and applications, this book helps you to get the most out of these tools and create optimal HPC solutions for bioinformatics.

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