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A compilation 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 ...

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

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Bioinformatics could greatly benefit from increased computational resources delivered by High Performance Computing. However, the decision-making about which is the best architecture to deliver good performance for a set of Bioinformatics applications is a hard task. The traditional way is finding the architecture with a high theoretical peak of performance, obtained with benchmark tests.

Leveraging High Performance Computing for Bioinformatics ...

Abstract. In the last 10 years, we are witnessing one of the major revolutions in parallel systems. The consolidation of heterogeneous systems at different levels -from desktop computers to large-scale systems such as supercomputers, clusters or grids, through all kinds of low-power devices- is providing a computational power unimaginable just few years ago, trying to follow the wake of Moore ...

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 compilation 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.

Discover how to streamline complex bioinformatics applications with parallel computing This publication enables readers to handle more complex bioinformatics applications and larger and richer data sets. As the editor clearly shows, using powerful parallel computing tools can lead to significant breakthroughs in deciphering genomes, understanding genetic disease, designing customized drug therapies, and understanding evolution. A broad range of bioinformatics applications is covered with demonstrations on how each one can be parallelized to improve performance and gain faster rates of computation. Current parallel computing techniques and technologies are examined, including distributed computing and grid computing. Readers are provided with a mixture of algorithms, experiments, and simulations that provide not only qualitative but also quantitative insights into the dynamic field of bioinformatics. *Parallel Computing for Bioinformatics and Computational Biology* is a contributed work that serves as a repository of case studies, collectively demonstrating how parallel computing streamlines difficult problems in bioinformatics and produces better results. Each of the chapters is authored by an established expert in the field and carefully edited to ensure a consistent approach and high standard throughout the publication. The work is organized into five parts: * Algorithms and models * Sequence analysis and microarrays * Phylogenetics * Protein folding * Platforms and enabling technologies Researchers, educators, and students in the field of bioinformatics will discover how high-performance computing can enable them to handle more complex data sets, gain deeper insights, and make new discoveries.

High-Performance Computing using FPGA covers the area of high performance reconfigurable computing (HPRC). This book provides an overview of architectures, tools and applications for High-Performance Reconfigurable Computing (HPRC). FPGAs offer very high I/O bandwidth and fine-grained, custom and flexible parallelism and with the ever-increasing computational needs coupled with the frequency/power wall, the increasing maturity and capabilities of FPGAs, and the advent of multicore processors which has caused the acceptance of parallel computational models. The Part on architectures will introduce different FPGA-based HPC platforms: attached co-processor HPRC architectures such as the CHREC 's Novo-G and EPCC 's Maxwell systems; tightly coupled HPRC architectures, e.g. the Convey hybrid-core computer; reconfigurably networked HPRC architectures, e.g. the QPACE system, and standalone HPRC architectures such as EPFL 's CONFETTI system. The Part on Tools will focus on high-level programming approaches for HPRC, with chapters on C-to-Gate tools (such as Impulse-

C, AutoESL, Handel-C, MORA-C++); Graphical tools (MATLAB-Simulink, NI LabVIEW); Domain-specific languages, languages for heterogeneous computing(for example OpenCL, Microsoft 's Kiwi and Alchemy projects). The part on Applications will present case from several application domains where HPRC has been used successfully, such as Bioinformatics and Computational Biology; Financial Computing; Stencil computations; Information retrieval; Lattice QCD; Astrophysics simulations; Weather and climate modeling.

The two volume set LNCS 9043 and 9044 constitutes the refereed proceedings of the Third International Conference on Bioinformatics and Biomedical Engineering, IWBBIO 2015, held in Granada, Spain, in April 2015. The 135 papers presented were carefully reviewed and selected from 268 submissions. The scope of the conference spans the following areas: bioinformatics for healthcare and diseases, biomedical engineering, biomedical image analysis, biomedical signal analysis, computational genomics, computational proteomics, computational systems for modelling biological processes, e Health, next generation sequencing and sequence analysis, quantitative and systems pharmacology, Hidden Markov Model (HMM) for biological sequence modeling, advances in computational intelligence for bioinformatics and biomedicine, tools for next generation sequencing data analysis, dynamics networks in system medicine, interdisciplinary puzzles of measurements in biological systems, biological networks, high performance computing in bioinformatics, computational biology and computational chemistry, advances in drug discovery and ambient intelligence for bio emotional computing.

Recent developments in computer science enable algorithms previously perceived as too time-consuming to now be efficiently used for applications in bioinformatics and life sciences. This work focuses on proteins and their structures, protein structure similarity searching at main representation levels and various techniques that can be used to accelerate similarity searches. Divided into four parts, the first part provides a formal model of 3D protein structures for functional genomics, comparative bioinformatics and molecular modeling. The second part focuses on the use of multithreading for efficient approximate searching on protein secondary structures. The third and fourth parts concentrate on finding 3D protein structure similarities with the support of GPUs and cloud computing. Parts three and four both describe the acceleration of different methods. The text will be of interest to researchers and software developers working in the field of structural bioinformatics and biomedical databases.

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

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"This book provides insight into the current trends and emerging issues by investigating grid and cloud evolution, workflow management, and the impact new computing systems have on the education fields as well as the industries"--Provided by publisher.

Powerful, flexible, and easy to use, Python is an ideal language for building software tools and applications for life science research and development. This unique book shows you how to program with Python, using code examples taken directly from bioinformatics. In a short time, you'll be using sophisticated techniques and Python modules that are particularly effective for bioinformatics programming. Bioinformatics Programming Using Python is perfect for anyone involved with bioinformatics -- researchers, support staff, students, and software developers interested in writing bioinformatics applications. You'll find it useful whether you already use Python, write code in another language, or have no programming experience at all. It's an excellent self-instruction tool, as well as a handy reference when facing the challenges of real-life programming tasks. Become familiar with Python's fundamentals, including ways to develop simple applications Learn how to use Python modules for pattern matching, structured text processing, online data retrieval, and database access Discover generalized patterns that cover a large proportion of how Python code is used in bioinformatics Learn how to apply the principles and techniques of object-oriented programming Benefit from the "tips and traps" section in each chapter

This book constitutes the refereed proceedings of the First International Conference on Applied Computing to Support Industry: Innovation and Technology, ACRIT 2019, held in Ramadi, Iraq, in September 2019. The 38 revised full papers and 1 short paper were carefully reviewed and selected from 159 submissions. The papers of this volume are organized in topical sections on theory, methods and tools to support computer science; computer security and cryptography; computer network and communication; real world application in information science and technology.

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