Título: Parallel Computing For Bioinformatics And Computational Biology

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Sinopsis

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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.