Distributed and Sequential Algorithms for Bioinformatics and Computational Biology

Harnessing the Power of Algorithms for Biological Data Analysis and Discovery

In the era of big data and computational biology, efficient algorithms have become indispensable tools for analyzing and interpreting the vast amount of biological data available. Distributed and Sequential Algorithms for Bioinformatics and Computational Biology provides a comprehensive overview of the latest algorithmic techniques specifically designed for bioinformatics and computational biology applications.

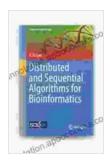
Key Features

- Authoritative Authors: Written by leading experts in the field, this book presents state-of-the-art algorithms and their practical applications in bioinformatics.
- Comprehensive Coverage: Covers a wide range of topics, including sequence alignment, phylogenetics, genome assembly, gene regulation, and protein-protein interactions.
- Practical Applications: Demonstrates how algorithms can be applied to solve real-world problems in bioinformatics and computational biology.
- Real-World Examples: Includes case studies and examples to illustrate the practical implementation of algorithms in biological

research.

 Accessible Presentation: Written in a clear and concise style, making it accessible to both students and researchers.

Chapter Outline



Distributed and Sequential Algorithms for Bioinformatics (Computational Biology Book 23)

by Christoffer Petersen

4.5 out of 5

Language : English

File size : 12730 KB

Text-to-Speech : Enabled

Screen Reader : Supported

Enhanced typesetting : Enabled

Word Wise : Enabled

Print length : 586 pages



Chapter 1: ** to Bioinformatics and Computational Biology**

Overview of the field and its computational challenges

Chapter 2:Sequence Alignment Algorithms

- Dynamic programming algorithms (Smith-Waterman, Needleman-Wunsch)
- Heuristic algorithms (BLAST, FASTA)
- Alignment visualization and statistical significance

Chapter 3:Phylogenetic Tree Construction

- Distance-based methods (NJ, UPGMA, Neighbor-Joining)
- Character-based methods (Parsimony, Maximum Likelihood)
- Phylogenetic tree viewing and editing

Chapter 4:Genome Assembly Algorithms

- De Bruijn graph construction
- Overlap-layout-consensus methods
- Hybrid assembly approaches

Chapter 5: Gene Regulation Algorithms

- RNA-seq data analysis
- ChIP-seq data analysis
- Motif finding and transcription factor binding site prediction

Chapter 6:Protein-Protein Interaction Prediction

- Protein sequence analysis
- Protein structure prediction
- Docking and binding site prediction

Chapter 7:Distributed Algorithms for Bioinformatics

Parallel sequence alignment

- Phylogenetic tree construction
- Genome assembly
- Gene regulation analysis

Chapter 8:Applications and Case Studies

- DNA barcoding for species identification
- Drug discovery using molecular dynamics simulations
- Single-cell RNA sequencing for developmental biology

Distributed and Sequential Algorithms for Bioinformatics and Computational Biology is a valuable resource for graduate students, researchers, and professionals in the fields of bioinformatics, computational biology, and data science. With its comprehensive coverage, practical examples, and accessible presentation, this book provides a solid foundation for understanding and applying algorithms to solve challenging biological problems.

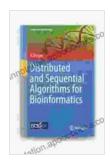
Target Audience

- Graduate students and researchers in bioinformatics and computational biology
- Computational scientists and data analysts interested in biological data

- Biologists and medical professionals seeking to leverage computational tools
- Software developers working on bioinformatics applications

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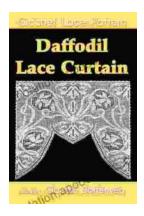
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