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ALGORITHMS IN COMPUTATIONAL MOLECULAR BIOLOGY

Techniques, Approaches and Applications

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Algorithms In Computational Molecular Biology Techniques Approaches And Applications

Yi Pan, Min Li, Jianxin Wang



Algorithms In Computational Molecular Biology Techniques Approaches And Applications:

Algorithms in Computational Molecular Biology Mourad Elloumi, Albert Y. Zomaya, 2011-04-04 This book represents the most comprehensive and up to date collection of information on the topic of computational molecular biology Bringing the most recent research into the forefront of discussion Algorithms in Computational Molecular Biology studies the most important and useful algorithms currently being used in the field and provides related problems It also succeeds where other titles have failed in offering a wide range of information from the introductory fundamentals right up to the latest most advanced levels of study *Computational Methods for Next Generation Sequencing Data Analysis* Ion Mandoiu, Alexander Zelikovskiy, 2016-09-12 Introduces readers to core algorithmic techniques for next generation sequencing NGS data analysis and discusses a wide range of computational techniques and applications This book provides an in depth survey of some of the recent developments in NGS and discusses mathematical and computational challenges in various application areas of NGS technologies The 18 chapters featured in this book have been authored by bioinformatics experts and represent the latest work in leading labs actively contributing to the fast growing field of NGS The book is divided into four parts Part I focuses on computing and experimental infrastructure for NGS analysis including chapters on cloud computing modular pipelines for metabolic pathway reconstruction pooling strategies for massive viral sequencing and high fidelity sequencing protocols Part II concentrates on analysis of DNA sequencing data covering the classic scaffolding problem detection of genomic variants including insertions and deletions and analysis of DNA methylation sequencing data Part III is devoted to analysis of RNA seq data This part discusses algorithms and compares software tools for transcriptome assembly along with methods for detection of alternative splicing and tools for transcriptome quantification and differential expression analysis Part IV explores computational tools for NGS applications in microbiomics including a discussion on error correction of NGS reads from viral populations methods for viral quasispecies reconstruction and a survey of state of the art methods and future trends in microbiome analysis *Computational Methods for Next Generation Sequencing Data Analysis* Reviews computational techniques such as new combinatorial optimization methods data structures high performance computing machine learning and inference algorithms Discusses the mathematical and computational challenges in NGS technologies Covers NGS error correction de novo genome transcriptome assembly variant detection from NGS reads and more This text is a reference for biomedical professionals interested in expanding their knowledge of computational techniques for NGS data analysis The book is also useful for graduate and post graduate students in bioinformatics *Mathematical and Computational Methods in Biomechanics of Human Skeletal Systems* Jiri Nedoma, Jiri Stehlik, Ivan Hlavacek, Josef Danek, Tatjana Dostalova, Petra Preckova, 2011-06-09 Cutting edge solutions to current problems in orthopedics supported by modeling and numerical analysis Despite the current successful methods and achievements of good joint implantations it is essential to further optimize the shape of implants so they may better resist extreme long term mechanical demands This book provides the

orthopedic biomechanical and mathematical basis for the simulation of surgical techniques in orthopedics It focuses on the numerical modeling of total human joint replacements and simulation of their functions along with the rigorous biomechanics of human joints and other skeletal parts The book includes An introduction to the anatomy and biomechanics of the human skeleton biomaterials and problems of alloarthroplasty The definition of selected simulated orthopedic problems Constructions of mathematical model problems of the biomechanics of the human skeleton and its parts Replacement parts of the human skeleton and corresponding mathematical model problems Detailed mathematical analyses of mathematical models based on functional analysis and finite element methods Biomechanical analyses of particular parts of the human skeleton joints and corresponding replacements A discussion of the problems of data processing from nuclear magnetic resonance imaging and computer tomography This timely book offers a wealth of information on the current research in this field The theories presented are applied to specific problems of orthopedics Numerical results are presented and discussed from both biomechanical and orthopedic points of view and treatment methods are also briefly addressed Emphasis is placed on the variational approach to the investigated model problems while preserving the orthopedic nature of the investigated problems The book also presents a study of algorithmic procedures based on these simulation models This is a highly useful tool for designers researchers and manufacturers of joint implants who require the results of suggested experiments to improve existing shapes or to design new shapes It also benefits graduate students in orthopedics biomechanics and applied mathematics

Algorithmic and Artificial Intelligence Methods for Protein Bioinformatics Yi Pan, Min Li, Jianxin Wang, 2013-11-12

Algorithmic and Artificial Intelligence Methods for Protein Bioinformatics An in depth look at the latest research methods and applications in the field of protein bioinformatics This book presents the latest developments in protein bioinformatics introducing for the first time cutting edge research results alongside novel algorithmic and AI methods for the analysis of protein data In one complete self contained volume *Algorithmic and Artificial Intelligence Methods for Protein Bioinformatics* addresses key challenges facing both computer scientists and biologists arming readers with tools and techniques for analyzing and interpreting protein data and solving a variety of biological problems Featuring a collection of authoritative articles by leaders in the field this work focuses on the analysis of protein sequences structures and interaction networks using both traditional algorithms and AI methods It also examines in great detail data preparation simulation experiments evaluation methods and applications *Algorithmic and Artificial Intelligence Methods for Protein Bioinformatics* Highlights protein analysis applications such as protein related drug activity comparison Incorporates salient case studies illustrating how to apply the methods outlined in the book Tackles the complex relationship between proteins from a systems biology point of view Relates the topic to other emerging technologies such as data mining and visualization Includes many tables and illustrations demonstrating concepts and performance figures *Algorithmic and Artificial Intelligence Methods for Protein Bioinformatics* is an essential reference for bioinformatics specialists in research and industry and for anyone wishing

to better understand the rich field of protein bioinformatics Distributed and Sequential Algorithms for Bioinformatics Kayhan Erciyes,2015-10-31 This unique textbook reference presents unified coverage of bioinformatics topics relating to both biological sequences and biological networks providing an in depth analysis of cutting edge distributed algorithms as well as of relevant sequential algorithms In addition to introducing the latest algorithms in this area more than fifteen new distributed algorithms are also proposed Topics and features reviews a range of open challenges in biological sequences and networks describes in detail both sequential and parallel distributed algorithms for each problem suggests approaches for distributed algorithms as possible extensions to sequential algorithms when the distributed algorithms for the topic are scarce proposes a number of new distributed algorithms in each chapter to serve as potential starting points for further research concludes each chapter with self test exercises a summary of the key points a comparison of the algorithms described and a literature review Biological Knowledge Discovery Handbook Mourad Elloumi,Albert Y.

Zomaya,2015-02-04 The first comprehensive overview of preprocessing mining and postprocessing of biological data Molecular biology is undergoing exponential growth in both the volume and complexity of biological data and knowledge discovery offers the capacity to automate complex search and data analysis tasks This book presents a vast overview of the most recent developments on techniques and approaches in the field of biological knowledge discovery and data mining KDD providing in depth fundamental and technical field information on the most important topics encountered Written by top experts Biological Knowledge Discovery Handbook Preprocessing Mining and Postprocessing of Biological Data covers the three main phases of knowledge discovery data preprocessing data processing also known as data mining and data postprocessing and analyzes both verification systems and discovery systems BIOLOGICAL DATA PREPROCESSING Part A Biological Data Management Part B Biological Data Modeling Part C Biological Feature Extraction Part D Biological Feature Selection BIOLOGICAL DATA MINING Part E Regression Analysis of Biological Data Part F Biological Data Clustering Part G Biological Data Classification Part H Association Rules Learning from Biological Data Part I Text Mining and Application to Biological Data Part J High Performance Computing for Biological Data Mining Combining sound theory with practical applications in molecular biology Biological Knowledge Discovery Handbook is ideal for courses in bioinformatics and biological KDD as well as for practitioners and professional researchers in computer science life science and mathematics

Computational Biology and Bioinformatics Ka-Chun Wong,2016-04-27 The advances in biotechnology such as the next generation sequencing technologies are occurring at breathtaking speed Advances and breakthroughs give competitive advantages to those who are prepared However the driving force behind the positive competition is not only limited to the technological advancement but also to the companion data analy Multiple Biological Sequence Alignment Ken Nguyen,Xuan Guo,Yi Pan,2016-07-18 Covers the fundamentals and techniques of multiple biological sequence alignment and analysis and shows readers how to choose the appropriate sequence analysis tools for their tasks This book describes the

traditional and modern approaches in biological sequence alignment and homology search This book contains 11 chapters with Chapter 1 providing basic information on biological sequences Next Chapter 2 contains fundamentals in pair wise sequence alignment while Chapters 3 and 4 examine popular existing quantitative models and practical clustering techniques that have been used in multiple sequence alignment Chapter 5 describes characterizes and relates many multiple sequence alignment models Chapter 6 describes how traditionally phylogenetic trees have been constructed and available sequence knowledge bases can be used to improve the accuracy of reconstructing phylogeny trees Chapter 7 covers the latest methods developed to improve the run time efficiency of multiple sequence alignment Next Chapter 8 covers several popular existing multiple sequence alignment server and services and Chapter 9 examines several multiple sequence alignment techniques that have been developed to handle short sequences reads produced by the Next Generation Sequencing technique NSG Chapter 10 describes a Bioinformatics application using multiple sequence alignment of short reads or whole genomes as input Lastly Chapter 11 provides a review of RNA and protein secondary structure prediction using the evolution information inferred from multiple sequence alignments Covers the full spectrum of the field from alignment algorithms to scoring methods practical techniques and alignment tools and their evaluations Describes theories and developments of scoring functions and scoring matrices Examines phylogeny estimation and large scale homology search Multiple Biological Sequence Alignment Scoring Functions Algorithms and Applications is a reference for researchers engineers graduate and post graduate students in bioinformatics and system biology and molecular biologists Ken Nguyen PhD is an associate professor at Clayton State University GA USA He received his PhD MSc and BSc degrees in computer science all from Georgia State University His research interests are in databases parallel and distribute computing and bioinformatics He was a Molecular Basis of Disease fellow at Georgia State and is the recipient of the highest graduate honor at Georgia State the William M Suttles Graduate Fellowship Xuan Guo PhD is a postdoctoral associate at Oak Ridge National Lab USA He received his PhD degree in computer science from Georgia State University in 2015 His research interests are in bioinformatics machine leaning and cloud computing He is an editorial assistant of International Journal of Bioinformatics Research and Applications Yi Pan PhD is a Regents Professor of Computer Science and an Interim Associate Dean and Chair of Biology at Georgia State University He received his BE and ME in computer engineering from Tsinghua University in China and his PhD in computer science from the University of Pittsburgh Dr Pan s research interests include parallel and distributed computing optical networks wireless networks and bioinformatics He has published more than 180 journal papers with about 60 papers published in various IEEE ACM journals He is co editor along with Albert Y Zomaya of the Wiley Series in Bioinformatics

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