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Yi Pan and Albert Y. Zomaya, Series Editors

Computational Methods for Next Generation Sequencing Data Analysis



EDITED BY
Ion I. Măndoiu • Alexander Zelikovskiy



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Computational Methods for Next Generation Sequencing Data Analysis Ion Mandoiu, Alexander Zelikovsky, 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 quasiespecies 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

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Encyclopedia of Bioinformatics and Computational Biology

,2018-08-21 Encyclopedia of Bioinformatics and Computational Biology ABC of Bioinformatics Three Volume Set combines elements of computer science information technology mathematics statistics and biotechnology providing the methodology and in silico solutions to mine biological data and processes The book covers Theory Topics and Applications with a special focus on Integrative omics and Systems Biology The theoretical methodological underpinnings of BCB including phylogeny are covered as are more current areas of focus such as translational bioinformatics cheminformatics and environmental informatics Finally Applications provide guidance for commonly asked questions This major reference work spans basic and cutting edge methodologies authored by leaders in the field providing an invaluable resource for students scientists professionals in research institutes and a broad swath of researchers in biotechnology and the biomedical and pharmaceutical industries Brings together information from computer science information technology mathematics statistics and biotechnology Written and reviewed by leading experts in the field providing a unique and authoritative resource Focuses on the main theoretical and methodological concepts before expanding on specific topics and applications Includes interactive images multimedia tools and crosslinking to further resources and databases

Precision Molecular

Pathology of Aggressive B-Cell Lymphomas Genevieve M. Crane,Sanam Loghavi,2024-02-14 Written by experts in the field Precision Molecular Pathology of Aggressive B Cell Lymphomas contains the most recent revisions from the 5th Edition WHO and 2022 International Consensus Classification diagnostic categories and serves as an important resource for trainees pathologists haematologist oncologists other clinicians involved in lymphoma care and lymphoma researchers It provides a comprehensive yet concise synthesis of emerging molecular advances that inform patient care and improve understanding of disease mechanisms In addition it provides the necessary background to how molecular techniques are performed to enable the reader to better interpret and critically evaluate relevant and emerging data As part of the Molecular Pathology Library

series this book focuses specifically on aggressive B cell lymphomas given the increasing relevance of molecular data for diagnosis and treatment of these disorders This evidence based text contains 25 chapters and is divided into 5 parts Part 1 provides a brief history and background of aggressive B cell lymphomas Landmark events in their classification and treatment are given in order to place the substantial advances in the field in context Part 2 reviews molecular pathology methods including the increasing use of next generation sequencing techniques in clinical practice Parts 3 and 4 focus on individual subtypes of aggressive B cell lymphoma including a summary of the diagnostic criteria and key pathologic and clinical features for each entity Finally Part 5 focuses on emerging molecular technologies that may significantly impact clinical practice

Comparative Genomics Mathieu Blanchette,Aïda Ouangraoua,2018-10-04 This book constitutes the proceedings of the 16th International Conference on Comparative Genomics RECOMB CG 2018 held in Magog Orford QC Canada in October 2018 The 18 full papers presented were carefully reviewed and selected from 29 submissions The papers cover topics such as genome rearrangements genome sequencing applied comparative genomics reconciliation and coalescence and phylogenetics

Computational methods for microbiome analysis, volume 2 Setubal,Nikos Kyrpides,2023-01-04

An Introduction to Molecular Biotechnology Michael Wink,2020-12-03 Die Neuauflage dieses heraus renommierten Lehrbuchs wurde als Antwort auf die rasanten Fortschritte in dem Fachgebiet vollst ndig aktualisiert und pr sentiert neue leistungsstarke Methoden und Konzepte in der Biotechnologie u a Genome Editing reprogrammierte Stammzellen und personalisierte Medizin Auf eine Einf hrung in die Grundlagen der Molekular und Zellbiologie folgt eine Beschreibung der Standardverfahren darunter Aufreinigung und Analyse von Biomolek len Verfahren der Klonierung Gen Expressionssysteme Methoden des Genome Editing Protein Labeling und In situ Verfahren Standard und hochaufl sende Mikroskopie Der dritte Teil legt den Schwerpunkt auf wichtige Forschungs und Anwendungsgebiete von der funktionalen Genomik Proteomik und Bioinformatik bis hin zu Drug Targeting rekombinante Antik rper und Systembiologie Der letzte Teil wirft einen Blick auf Unternehmen der Biotechnologie und untersucht Fragestellungen des geistigen Eigentums den Rechtsrahmen f r pharmazeutische Produkte und das Zusammenspiel von Startup und gr eren Unternehmen Die Inhalte sind durchg ngig heraus ansprechend illustriert mit Hunderten von farbigen Diagrammen und Fotos Dieses Lehrbuch vermittelt Studenten und Berufspraktikern der Biowissenschaften Pharmazie und Biochemie alles Wissenswerte rund um die molekulare Biotechnologie

Multiple Biological Sequence Alignment Ken Nguyen,Xuan Guo,Yi Pan,2016-06-10 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 learning 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

Biomolecular Interactions Part B
,2022-05-25 Biomolecular Interactions Part A Volume 169 the latest release in the Methods in Cell Biology series highlights new advances in the field with this new volume presenting interesting chapters on a variety of timely topics including Emerging Mechanisms of Targeted Protein Degradation by Molecular Glues Design and use of programmable DNA Hydrogels Oligomerization of membrane receptors Approaches to measure in live cells Interactions of alpha synuclein with biomolecules Gel electrophoresis based method for biomolecular interaction Recombinant centrosome expression in bacterial system Reconstituting CCL5 CCR5 complex for structural and mechanistic analysis Protein engineering and design in ion

channel receptors and much more Provides the authority and expertise of leading contributors from an international board of authors Presents the latest release in the Methods in Cell Biology series Updated release includes the latest information on biomolecular interactions instead of protein protein interactions

Artificial Intelligence and Machine Learning in Drug Design and Development Abhirup Khanna, May El Barachi, Sapna Jain, Manoj Kumar, Anand Nayyar, 2024-06-21 The book is a comprehensive guide that explores the use of artificial intelligence and machine learning in drug discovery and development covering a range of topics including the use of molecular modeling docking identifying targets selecting compounds and optimizing drugs The intersection of Artificial Intelligence AI and Machine Learning ML within the field of drug design and development represents a pivotal moment in the history of healthcare and pharmaceuticals The remarkable synergy between cutting edge technology and the life sciences has ushered in a new era of possibilities offering unprecedented opportunities formidable challenges and a tantalizing glimpse into the future of medicine AI can be applied to all the key areas of the pharmaceutical industry such as drug discovery and development drug repurposing and improving productivity within a short period Contemporary methods have shown promising results in facilitating the discovery of drugs to target different diseases Moreover AI helps in predicting the efficacy and safety of molecules and gives researchers a much broader chemical pallet for the selection of the best molecules for drug testing and delivery In this context drug repurposing is another important topic where AI can have a substantial impact With the vast amount of clinical and pharmaceutical data available to date AI algorithms find suitable drugs that can be repurposed for alternative use in medicine This book is a comprehensive exploration of this dynamic and rapidly evolving field In an era where precision and efficiency are paramount in drug discovery AI and ML have emerged as transformative tools reshaping the way we identify design and develop pharmaceuticals This book is a testament to the profound impact these technologies have had and will continue to have on the pharmaceutical industry healthcare and ultimately patient well being The editors of this volume have assembled a distinguished group of experts researchers and thought leaders from both the AI ML and pharmaceutical domains Their collective knowledge and insights illuminate the multifaceted landscape of AI and ML in drug design and development offering a roadmap for navigating its complexities and harnessing its potential In each section readers will find a rich tapestry of knowledge case studies and expert opinions providing a 360 degree view of AI and ML s role in drug design and development Whether you are a researcher scientist industry professional policymaker or simply curious about the future of medicine this book offers 19 state of the art chapters providing valuable insights and a compass to navigate the exciting journey ahead Audience The book is a valuable resource for a wide range of professionals in the pharmaceutical and allied industries including researchers scientists engineers and laboratory workers in the field of drug discovery and development who want to learn about the latest techniques in machine learning and AI as well as information technology professionals who are interested in the application of machine learning and artificial intelligence in drug development

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Table of Contents Computational Methods For Next Generation Sequencing Data Analysis Wiley Series In Bioinformatics

1. Understanding the eBook Computational Methods For Next Generation Sequencing Data Analysis Wiley Series In Bioinformatics
 - The Rise of Digital Reading Computational Methods For Next Generation Sequencing Data Analysis Wiley Series In Bioinformatics
 - Advantages of eBooks Over Traditional Books
2. Identifying Computational Methods For Next Generation Sequencing Data Analysis Wiley Series In Bioinformatics
 - Exploring Different Genres
 - Considering Fiction vs. Non-Fiction
 - Determining Your Reading Goals
3. Choosing the Right eBook Platform
 - Popular eBook Platforms
 - Features to Look for in an Computational Methods For Next Generation Sequencing Data Analysis Wiley Series In Bioinformatics

- User-Friendly Interface
- 4. Exploring eBook Recommendations from Computational Methods For Next Generation Sequencing Data Analysis Wiley Series In Bioinformatics
 - Personalized Recommendations
 - Computational Methods For Next Generation Sequencing Data Analysis Wiley Series In Bioinformatics User Reviews and Ratings
 - Computational Methods For Next Generation Sequencing Data Analysis Wiley Series In Bioinformatics and Bestseller Lists
- 5. Accessing Computational Methods For Next Generation Sequencing Data Analysis Wiley Series In Bioinformatics Free and Paid eBooks
 - Computational Methods For Next Generation Sequencing Data Analysis Wiley Series In Bioinformatics Public Domain eBooks
 - Computational Methods For Next Generation Sequencing Data Analysis Wiley Series In Bioinformatics eBook Subscription Services
 - Computational Methods For Next Generation Sequencing Data Analysis Wiley Series In Bioinformatics Budget-Friendly Options
- 6. Navigating Computational Methods For Next Generation Sequencing Data Analysis Wiley Series In Bioinformatics eBook Formats
 - ePub, PDF, MOBI, and More
 - Computational Methods For Next Generation Sequencing Data Analysis Wiley Series In Bioinformatics Compatibility with Devices
 - Computational Methods For Next Generation Sequencing Data Analysis Wiley Series In Bioinformatics Enhanced eBook Features
- 7. Enhancing Your Reading Experience
 - Adjustable Fonts and Text Sizes of Computational Methods For Next Generation Sequencing Data Analysis Wiley Series In Bioinformatics
 - Highlighting and Note-Taking Computational Methods For Next Generation Sequencing Data Analysis Wiley Series In Bioinformatics
 - Interactive Elements Computational Methods For Next Generation Sequencing Data Analysis Wiley Series In Bioinformatics

8. Staying Engaged with Computational Methods For Next Generation Sequencing Data Analysis Wiley Series In Bioinformatics
 - Joining Online Reading Communities
 - Participating in Virtual Book Clubs
 - Following Authors and Publishers Computational Methods For Next Generation Sequencing Data Analysis Wiley Series In Bioinformatics
9. Balancing eBooks and Physical Books Computational Methods For Next Generation Sequencing Data Analysis Wiley Series In Bioinformatics
 - Benefits of a Digital Library
 - Creating a Diverse Reading Collection Computational Methods For Next Generation Sequencing Data Analysis Wiley Series In Bioinformatics
10. Overcoming Reading Challenges
 - Dealing with Digital Eye Strain
 - Minimizing Distractions
 - Managing Screen Time
11. Cultivating a Reading Routine Computational Methods For Next Generation Sequencing Data Analysis Wiley Series In Bioinformatics
 - Setting Reading Goals Computational Methods For Next Generation Sequencing Data Analysis Wiley Series In Bioinformatics
 - Carving Out Dedicated Reading Time
12. Sourcing Reliable Information of Computational Methods For Next Generation Sequencing Data Analysis Wiley Series In Bioinformatics
 - Fact-Checking eBook Content of Computational Methods For Next Generation Sequencing Data Analysis Wiley Series In Bioinformatics
 - Distinguishing Credible Sources
13. Promoting Lifelong Learning
 - Utilizing eBooks for Skill Development
 - Exploring Educational eBooks
14. Embracing eBook Trends
 - Integration of Multimedia Elements

- Interactive and Gamified eBooks

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