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BIOMOLECULAR NETWORKS

Methods and Applications in Systems Biology

LUONAN CHEN
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Biomolecular Networks Methods And Applications In Systems Biology Wiley Series In Bioinformatics

Ion Mandoiu, Alexander Zelikovsky



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Biomolecular Networks Luonan Chen,Rui-Sheng Wang,Xiang-Sun Zhang,2009-06-29 Alternative techniques and tools for analyzing biomolecular networks With the recent rapid advances in molecular biology high throughput experimental methods have resulted in enormous amounts of data that can be used to study biomolecular networks in living organisms With this development has come recognition of the fact that a complicated living organism cannot be fully understood by merely analyzing individual components Rather it is the interactions of components or biomolecular networks that are ultimately responsible for an organism s form and function This book addresses the important need for a new set of computational tools to reveal essential biological mechanisms from a systems biology approach Readers will get comprehensive coverage of analyzing biomolecular networks in cellular systems based on available experimental data with an emphasis on the aspects of network system integration and engineering Each topic is treated in depth with specific biological problems and novel computational methods GENE NETWORKS Transcriptional regulation reconstruction of gene regulatory networks and inference of transcriptional regulatory networks PROTEIN INTERACTION NETWORKS Prediction of protein protein interactions topological structure of biomolecular networks alignment of biomolecular networks and network based prediction of protein function METABOLIC NETWORKS AND SIGNALING NETWORKS Analysis reconstruction and applications of metabolic networks modeling and inference of signaling networks and other topics and new trends In addition to theoretical results and methods many computational software tools are referenced and available from the authors Web sites *Biomolecular Networks* is an indispensable reference for researchers and graduate students in bioinformatics computational biology systems biology computer science and applied mathematics

Computational Methods for Next Generation Sequencing Data Analysis Ion Mandoiu,Alexander Zelikovsky,2016-10-03 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 Pattern Recognition in Computational Molecular Biology Mourad Elloumi,Costas Iliopoulos,Jason T. L. Wang,Albert Y. Zomaya,2015-11-30 A comprehensive overview of high performance pattern recognition techniques and approaches to Computational Molecular Biology This book surveys the developments of techniques and approaches on pattern recognition related to Computational Molecular Biology Providing a broad coverage of the field the authors cover fundamental and technical information on these techniques and approaches as well as discussing their related problems The text consists of twenty nine chapters organized into seven parts Pattern Recognition in Sequences Pattern Recognition in Secondary Structures Pattern Recognition in Tertiary Structures Pattern Recognition in Quaternary Structures Pattern Recognition in Microarrays Pattern Recognition in Phylogenetic Trees and Pattern Recognition in Biological Networks Surveys the development of techniques and approaches on pattern recognition in biomolecular data Discusses pattern recognition in primary secondary tertiary and quaternary structures as well as microarrays phylogenetic trees and biological networks Includes case studies and examples to further illustrate the concepts discussed in the book Pattern Recognition in Computational Molecular Biology Techniques and Approaches is a reference for practitioners and professional researches in Computer Science Life Science and Mathematics This book also serves as a supplementary reading for graduate students and young researches interested in Computational Molecular Biology *Evolutionary Computation in Gene Regulatory Network Research* Hitoshi Iba,Nasimul Noman,2016-01-20 Introducing a handbook for gene regulatory network research using evolutionary computation with applications for computer scientists computational and system biologists This book is a step by step guideline for research in gene regulatory networks GRN using evolutionary computation EC The book is organized into four parts that deliver materials in a way equally attractive for a reader with training in computation or biology Each of these sections authored by well known researchers and experienced practitioners provides the relevant materials for the interested readers The first part of this book contains an introductory background to the field The second part presents the EC approaches for analysis and reconstruction of GRN from gene expression data The third part of this book covers the contemporary advancements in the automatic construction of gene regulatory and reaction networks and gives direction and guidelines for future research Finally the last part of this book focuses on applications of

GRNs with EC in other fields such as design engineering and robotics Provides a reference for current and future research in gene regulatory networks GRN using evolutionary computation EC Covers sub domains of GRN research using EC such as expression profile analysis reverse engineering GRN evolution applications Contains useful contents for courses in gene regulatory networks systems biology computational biology and synthetic biology Delivers state of the art research in genetic algorithms genetic programming and swarm intelligence Evolutionary Computation in Gene Regulatory Network Research is a reference for researchers and professionals in computer science systems biology and bioinformatics as well as upper undergraduate graduate and postgraduate students Hitoshi Iba is a Professor in the Department of Information and Communication Engineering Graduate School of Information Science and Technology at the University of Tokyo Tokyo Japan He is an Associate Editor of the IEEE Transactions on Evolutionary Computation and the journal of Genetic Programming and Evolvable Machines Nasimul Noman is a lecturer in the School of Electrical Engineering and Computer Science at the University of Newcastle NSW Australia From 2002 to 2012 he was a faculty member at the University of Dhaka Bangladesh Noman is an Editor of the BioMed Research International journal His research interests include computational biology synthetic biology and bioinformatics **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

Algorithmic and Artificial Intelligence Methods for Protein Bioinformatics Yi Pan,Min Li,Jianxin Wang,2013-10-07 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

Classification Analysis of DNA Microarrays Leif E.

Peterson, 2013-06-24 Wiley Series in Bioinformatics Computational Techniques and Engineering Yi Pan and Albert Y Zomaya Series Editors Wide coverage of traditional unsupervised and supervised methods and newer contemporary approaches that help researchers handle the rapid growth of classification methods in DNA microarray studies Proliferating classification methods in DNA microarray studies have resulted in a body of information scattered throughout literature conference proceedings and elsewhere This book unites many of these classification methods in a single volume In addition to traditional statistical methods it covers newer machine learning approaches such as fuzzy methods artificial neural networks evolutionary based genetic algorithms support vector machines swarm intelligence involving particle swarm optimization and more Classification Analysis of DNA Microarrays provides highly detailed pseudo code and rich graphical programming features plus ready to run source code Along with primary methods that include traditional and contemporary classification it offers supplementary tools and data preparation routines for standardization and fuzzification dimensional reduction via crisp and fuzzy c means PCA and non linear manifold learning and computational linguistics via text analytics and n gram analysis recursive feature extraction during ANN kernel based methods ensemble classifier fusion This powerful new resource Provides information on the use of classification analysis for DNA microarrays used for large scale high throughput transcriptional studies Serves as a historical repository of general use supervised classification methods as well as newer contemporary methods Brings the reader quickly up to speed on the various classification methods by implementing the programming pseudo code and source code provided in the book Describes implementation methods that help shorten discovery times Classification Analysis of DNA Microarrays is useful for professionals and graduate students in computer

science bioinformatics biostatistics systems biology and many related fields

Data Management of Protein Interaction Networks Mario Cannataro, Pietro H. Guzzi, 2012-02-03 Current PPI databases do not offer sophisticated querying interfaces and especially do not integrate existing information about proteins Current algorithms for PIN analysis use only topological information while emerging approaches attempt to exploit the biological knowledge related to proteins and kinds of interaction e g protein function localization structure described in Gene Ontology or PDB The book discusses technologies standards and databases for respectively generating representing and storing PPI data It also describes main algorithms and tools for the analysis comparison and knowledge extraction from PINs Moreover some case studies and applications of PINs are also discussed

Biological Individuality Scott Lidgard, Lynn K Nyhart, 2017-05-24 Individuals are things that everybody knows or thinks they do Yet even scholars who practice or analyze the biological sciences often cannot agree on what an individual is and why One reason for this disagreement is that the many important biological individuality concepts serve very different purposes defining classifying or explaining living structure function interaction persistence or evolution Indeed as the contributors to Biological Individuality reveal nature is too messy for simple definitions of this concept organisms too quirky in the diverse ways they reproduce function and interact and human ideas about individuality too fraught with philosophical and historical meaning Bringing together biologists historians and philosophers this book provides a multifaceted exploration of biological individuality that identifies leading and less familiar perceptions of individuality both past and present what they are good for and in what contexts Biological practice and theory recognize individuals at myriad levels of organization from genes to organisms to symbiotic systems We depend on these notions of individuality to address theoretical questions about multilevel natural selection and Darwinian fitness to illuminate empirical questions about development function and ecology to ground philosophical questions about the nature of organisms and causation and to probe historical and cultural circumstances that resonate with parallel questions about the nature of society Charting an interdisciplinary research agenda that broadens the frameworks in which biological individuality is discussed this book makes clear that in the realm of the individual there is not and should not be a direct path from biological paradigms based on model organisms through to philosophical generalization and historical reification

Introduction to Protein Structure Prediction Huzefa Rangwala, George Karypis, 2011-03-16 A look at the methods and algorithms used to predict protein structure A thorough knowledge of the function and structure of proteins is critical for the advancement of biology and the life sciences as well as the development of better drugs higher yield crops and even synthetic bio fuels To that end this reference sheds light on the methods used for protein structure prediction and reveals the key applications of modeled structures This indispensable book covers the applications of modeled protein structures and unravels the relationship between pure sequence information and three dimensional structure which continues to be one of the greatest challenges in molecular biology With this resource readers will find an all encompassing examination of the problems methods tools

servers databases and applications of protein structure prediction and they will acquire unique insight into the future applications of the modeled protein structures The book begins with a thorough introduction to the protein structure prediction problem and is divided into four themes a background on structure prediction the prediction of structural elements tertiary structure prediction and functional insights Within those four sections the following topics are covered Databases and resources that are commonly used for protein structure prediction The structure prediction flagship assessment CASP and the protein structure initiative PSI Definitions of recurring substructures and the computational approaches used for solving sequence problems Difficulties with contact map prediction and how sophisticated machine learning methods can solve those problems Structure prediction methods that rely on homology modeling threading and fragment assembly Hybrid methods that achieve high resolution protein structures Parts of the protein structure that may be conserved and used to interact with other biomolecules How the loop prediction problem can be used for refinement of the modeled structures The computational model that detects the differences between protein structure and its modeled mutant Whether working in the field of bioinformatics or molecular biology research or taking courses in protein modeling readers will find the content in this book invaluable

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