

Knowledge Discovery in Bioinformatics

Techniques, Methods, and Applications



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Knowledge Discovery In Bioinformatics Techniques Methods And Applications

Mourad Elloumi, Albert Y. Zomaya



Knowledge Discovery In Bioinformatics Techniques Methods And Applications:

Knowledge Discovery in Bioinformatics Xiaohua Hu, Yi Pan, 2007-06-11 The purpose of this edited book is to bring together the ideas and findings of data mining researchers and bioinformaticians by discussing cutting edge research topics such as gene expressions protein RNA structure prediction phylogenetics sequence and structural motifs genomics and proteomics gene findings drug design RNAi and microRNA analysis text mining in bioinformatics modelling of biochemical pathways biomedical ontologies system biology and pathways and biological database management *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 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

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

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 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

Mathematical Methods for Knowledge Discovery and Data Mining Felici, Giovanni, Vercellis, Carlo, 2007-10-31 This book focuses on the mathematical models and methods that support most data mining applications and solution techniques covering such topics as association rules Bayesian methods data visualization kernel methods neural networks text speech and image recognition an invaluable resource for scholars and practitioners in the fields of biomedicine engineering finance manufacturing marketing performance measurement and telecommunications Provided by publisher

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 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

Analysis of Biological Networks Björn H. Junker,Falk Schreiber,2011-09-20 An introduction to biological networks and methods for their analysis Analysis of Biological Networks is the first book of its kind to provide readers with a comprehensive introduction to the structural analysis of biological networks at the interface of biology and computer science The book begins with a brief overview of biological networks and graph theory graph algorithms and goes on to explore global network properties network centralities network motifs network clustering Petri nets signal transduction and gene regulation networks protein interaction networks metabolic networks phylogenetic networks ecological networks and correlation networks Analysis of Biological Networks is a self contained introduction to this important research topic assumes no expert knowledge in computer science or biology and is accessible to professionals and students alike Each chapter concludes with a summary of main points and with exercises for readers to test their understanding of the material presented Additionally an FTP site with links to author provided data for the book is available for deeper study This book is suitable as a resource for researchers in computer science biology bioinformatics advanced biochemistry and the life sciences and also serves as an ideal reference text for graduate level courses in bioinformatics and biological research

Computational Intelligence and Pattern Analysis in Biology Informatics Ujjwal Maulik,Sanghamitra Bandyopadhyay,Jason T. Wang,2011-03-21 An invaluable tool in Bioinformatics this unique volume provides both theoretical and experimental results and describes basic principles of computational intelligence and pattern analysis while deepening the reader s understanding of the ways in which these principles can be used for analyzing biological data in an efficient manner This book synthesizes current research in the integration of computational intelligence and pattern analysis techniques either individually or in a hybridized manner The purpose is to analyze biological data and enable extraction of more meaningful information and insight from it Biological data for analysis

include sequence data secondary and tertiary structure data and microarray data These data types are complex and advanced methods are required including the use of domain specific knowledge for reducing search space dealing with uncertainty partial truth and imprecision efficient linear and or sub linear scalability incremental approaches to knowledge discovery and increased level and intelligence of interactivity with human experts and decision makers Chapters authored by leading researchers in CI in biology informatics Covers highly relevant topics rational drug design analysis of microRNAs and their involvement in human diseases Supplementary material included program code and relevant data sets correspond to chapters

Protein Interaction Networks Aidong Zhang, 2009-04-06 The analysis of protein protein interactions is fundamental to the understanding of cellular organization processes and functions Proteins seldom act as single isolated species rather proteins involved in the same cellular processes often interact with each other Functions of uncharacterized proteins can be predicted through comparison with the interactions of similar known proteins Recent large scale investigations of protein protein interactions using such techniques as two hybrid systems mass spectrometry and protein microarrays have enriched the available protein interaction data and facilitated the construction of integrated protein protein interaction networks The resulting large volume of protein protein interaction data has posed a challenge to experimental investigation This book provides a comprehensive understanding of the computational methods available for the analysis of protein protein interaction networks It offers an in depth survey of a range of approaches including statistical topological data mining and ontology based methods The author discusses the fundamental principles underlying each of these approaches and their respective benefits and drawbacks and she offers suggestions for future research

Research Anthology on Machine Learning Techniques, Methods, and Applications Management Association, Information Resources, 2022-05-13 Machine learning continues to have myriad applications across industries and fields To ensure this technology is utilized appropriately and to its full potential organizations must better understand exactly how and where it can be adapted Further study on the applications of machine learning is required to discover its best practices challenges and strategies The Research Anthology on Machine Learning Techniques Methods and Applications provides a thorough consideration of the innovative and emerging research within the area of machine learning The book discusses how the technology has been used in the past as well as potential ways it can be used in the future to ensure industries continue to develop and grow Covering a range of topics such as artificial intelligence deep learning cybersecurity and robotics this major reference work is ideal for computer scientists managers researchers scholars practitioners academicians instructors and students

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 *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 *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

Elements of Computational Systems Biology Huma M. Lodhi, Stephen H. Muggleton, 2010-03-25 Groundbreaking long ranging research in this emergent field that enables solutions to complex biological problems Computational systems biology is an emerging discipline that is evolving quickly due to recent advances in biology such as genome sequencing high throughput technologies and the recent development of sophisticated computational methodologies Elements of Computational Systems Biology is a comprehensive reference covering the computational frameworks and techniques needed to help research scientists and professionals in computer science biology chemistry pharmaceutical science and physics solve complex biological problems Written by leading experts in the field this practical resource gives detailed descriptions of core subjects including biological network modeling analysis and inference presents a measured introduction to foundational topics like genomics and describes state of the art software tools for systems biology Offers a coordinated integrated systems view of defining and applying computational and mathematical tools and methods to solving problems in systems biology Chapters provide a multidisciplinary approach and range from analysis modeling prediction reasoning inference and exploration of biological systems to the implications of computational systems biology on drug design and medicine Helps reduce the gap between mathematics and biology by presenting chapters on mathematical models of biological systems Establishes solutions in computer science biology chemistry and physics by presenting an in depth description of computational methodologies for systems biology Elements of Computational Systems Biology is intended for academic industry researchers and scientists in computer science biology mathematics chemistry physics biotechnology and pharmaceutical science It is also accessible to undergraduate and graduate students in machine learning data mining bioinformatics computational biology and systems biology courses

Statistical Modelling and Machine Learning Principles for Bioinformatics Techniques, Tools, and Applications K. G. Srinivasa, G. M. Siddesh, S. R. Manisekhar, 2020-01-30 This book discusses topics related to bioinformatics statistics and machine learning presenting the latest research in various areas of bioinformatics It also highlights the role of computing and machine learning in knowledge extraction from biological data and how this knowledge can be applied in fields such as drug design health supplements gene therapy proteomics and agriculture

Biological Data Mining in

Protein Interaction Networks Li, Xiao-Li,Ng, See-Kiong,2009-05-31 The goal of this book is to disseminate research results and best practices from cross disciplinary researchers and practitioners interested in and working on bioinformatics data mining and proteomics Provided by publisher *Principles of Big Graph: In-depth Insight* ,2023-01-24 Principles of Big Graph In depth Insight Volume 128 in the Advances in Computer series highlights new advances in the field with this new volume presenting interesting chapters on a variety of topics including CESDAM Centered subgraph data matrix for large graph representation Bivariate cluster and suitability analysis of NoSQL Solutions for big graph applications An empirical investigation on Big Graph using deep learning Analyzing correlation between quality and accuracy of graph clustering geneBF Filtering protein coded gene graph data using bloom filter Processing large graphs with an alternative representation MapReduce based convolutional graph neural networks A comprehensive review Fast exact triangle counting in large graphs using SIMD acceleration A comprehensive investigation on attack graphs Qubit representation of a binary tree and its operations in quantum computation Modified ML KNN Role of similarity measures and nearest neighbor configuration in multi label text classification on big social network graph data Big graph based online learning through social networks Community detection in large scale real world networks Power rank An interactive web page ranking algorithm GA based energy efficient modelling of a wireless sensor network The major challenges of big graph and their solutions A review and An investigation on socio cyber crime graph Provides an update on the issues and challenges faced by current researchers Updates on future research agendas Includes advanced topics for intensive research for researchers

Trends and Applications in Knowledge Discovery and Data Mining Shuhan Yuan,Fragkiskos Malliaros,Xin Zheng,2025-07-23 This book constitutes the refereed proceedings of five workshops that were held in conjunction with the 29th Pacific Asia Conference on Knowledge Discovery and Data Mining PAKDD 2025 held in Sydney New South Wales Australia during June 10 13 2025 The 31 papers presented in here were carefully reviewed and selected from 54 submissions This volume includes the proceedings from the following Workshops Workshop on Advanced Data Driven Techniques for Urban Resilience ADUR 2025 Workshop of Foundational AI for Pervasive Computing FairPC 2025 Workshop on Graph Learning with Foundation Models GLFM 2025 Workshop on Pattern Mining and Machine Learning for Bioinformatics PM4B 2025 Workshop on Research and Applications of Foundation Models for Data Mining and Affective Computing RAFDA 2025

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