

Protein Networks and Pathway Analysis

Edited by

Yuri Nikolsky
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 Humana Press

Protein Networks And Pathway Analysis Methods In Molecular Biology

Yuri Nikolsky, Julie Bryant



Protein Networks And Pathway Analysis Methods In Molecular Biology:

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Biological Networks and Pathway Analysis Tatiana V. Tatarinova, Yuri Nikolsky, 2018-08-03 In this volume expert practitioners present a compilation of methods of functional data analysis often referred to as systems biology and its applications in drug discovery medicine and basic disease research It covers such important issues as the elucidation of protein compound and gene interactions as well as analytical tools including networks interactome and ontologies and clinical applications of functional analysis As a volume in the highly successful Methods in Molecular Biology series this work provides detailed description and hands on implementation advice Reputable comprehensive and cutting edge Biological Networks and Pathway Analysis presents both wet lab experimental methods and computational tools in order to cover a broad spectrum of issues in this fascinating new field

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Recent Advances in Biological Network Analysis Byung-Jun Yoon,Xiaoning Qian,2021-01-13 This book reviews recent advances in the emerging field of computational network biology with special emphasis on comparative network analysis and network module detection The chapters in this volume are contributed by leading international researchers in computational network biology and offer in depth insight on the latest techniques in network alignment network clustering and network module detection Chapters discuss the advantages of the respective techniques and present the current challenges and open problems in the field Recent Advances in Biological Network Analysis Comparative Network Analysis and Network Module Detection will serve as

a great resource for graduate students academics and researchers who are currently working in areas relevant to computational network biology or wish to learn more about the field Data scientists whose work involves the analysis of graphs networks and other types of data with topological structure or relations can also benefit from the book s insights

Systems Biology in Drug Discovery and Development Daniel L. Young, Seth Michelson, 2011-10-18 The first book to focus on comprehensive systems biology as applied to drug discovery and development Drawing on real life examples Systems Biology in Drug Discovery and Development presents practical applications of systems biology to the multiple phases of drug discovery and development This book explains how the integration of knowledge from multiple sources and the models that best represent that integration inform the drug research processes that are most relevant to the pharmaceutical and biotechnology industries The first book to focus on comprehensive systems biology and its applications in drug discovery and development it offers comprehensive and multidisciplinary coverage of all phases of discovery and design including target identification and validation lead identification and optimization and clinical trial design and execution as well as the complementary systems approaches that make these processes more efficient It also provides models for applying systems biology to pharmacokinetics pharmacodynamics and candidate biomarker identification Introducing and explaining key methods and technical approaches to the use of comprehensive systems biology on drug development the book addresses the challenges currently facing the pharmaceutical industry As a result it is essential reading for pharmaceutical and biotech scientists pharmacologists computational modelers bioinformaticians and graduate students in systems biology pharmaceutical science and other related fields

Emerging Bioinformatic Tools in Toxicogenomics Danyel Jennen, Paul Jennings, 2020-02-27 Toxicogenomics was established as a merger of toxicology with genomics approaches and methodologies more than 15 years ago and considered of major value for studying toxic mechanisms of action in greater depth and for classification of toxic agents for predicting adverse human health risks While the original focus was on technological validation of in particular microarray based whole genome expression analysis transcriptomics mainly through cross comparing different platforms for data generation MAQC I it was soon appreciated that actually the wide variety of data analysis approaches represents the major source of inter study variation This led to early attempts towards harmonizing data analysis protocols focusing on microarray based models for predicting toxicological and clinical end points and on different methods for GWAS data MAQC II Simultaneously further technological developments geared by increasing insights into the complexity of cellular regulation enabled analyzing molecular perturbations across multiple genomics scales epigenomics and microRNAs metabolomics While these were initially still based on microarray technology this is currently being phased out and replaced by a variety of next generation sequencing based methods enabling exploration of genomic responses to toxicants at even greater depth SEQC I This raises the demand for reliable and robust data analysis approaches ranging from harmonized bioinformatics concepts for preprocessing raw data to non supervised and supervised methods for

capturing and integrating the dynamic perturbations of cell function across dose and time and thus retrieving mechanistic insights across multiple regulation scales Traditional toxicology focused on dose dependently determining apical endpoints of toxicity With the advent of toxicogenomics efforts towards better understanding underlying molecular mechanisms has led to the development of the concept of Adverse Outcome Pathways which are basically presented as a structural network of linearly related gene gene interactions regulating key events for inducing apical toxic endpoints of interest Impulse challenges from exposure of biological systems to toxic agents will however induce a cascade type of events presenting both adverse and adaptive processes thus requiring bioinformatics approaches and methods for complex dynamic data generated not only across dose but clearly also across time Currently time resolved toxicogenomics data sets are increasingly being assembled in the course of large scaled research projects for instance devoted towards developing toxicogenomics based predictive assays for evaluating chemical safety which are no longer animal based

Applying Machine Learning Techniques to Bioinformatics: Few-Shot and Zero-Shot Methods Lilhore, Umesh Kumar, Kumar, Abhishek, Simaiya, Sarita, Vyas, Narayan, Dutt, Vishal, 2024-03-22 Why are cutting edge data science techniques such as bioinformatics few shot learning and zero shot learning underutilized in the world of biological sciences In a rapidly advancing field the failure to harness the full potential of these disciplines limits scientists ability to unlock critical insights into biological systems personalized medicine and biomarker identification This untapped potential hinders progress and limits our capacity to tackle complex biological challenges The solution to this issue lies within the pages of Applying Machine Learning Techniques to Bioinformatics This book serves as a powerful resource offering a comprehensive analysis of how these emerging disciplines can be effectively applied to the realm of biological research By addressing these challenges and providing in depth case studies and practical implementations the book equips researchers scientists and curious minds with the knowledge and techniques needed to navigate the ever changing landscape of bioinformatics and machine learning within the biological sciences

Bioinformatics in Rice Research Manoj Kumar Gupta, Lambodar Behera, 2021-09-24 This book provides an up to date review of classic and advanced bioinformatics approaches and their utility in rice research It summarizes databases and tools for analyzing DNA proteins and gene expression profiles mapping genetic variations annotation of protein and RNA molecules phylogenetic analysis and pathway enrichment In addition it presents high throughput technologies that are widely used to provide deep insights into the genetic architecture of important traits in the rice genome The book subsequently discusses techniques for identifying RNA protein DNA protein interactions and molecular markers including SNP and microsatellites in the contexts of rice breeding and genetics Lastly it explores various tools that are used to identify and characterize non coding RNA in rice and their potential role in rice research

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