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Functional Coherence of Molecular Networks in Bioinformatics

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Functional Coherence Of Molecular Networks In Bioinformatics:

Functional Coherence of Molecular Networks in Bioinformatics Mehmet Koyutürk, Shankar Subramaniam, Ananth Grama, 2011-09-22 Molecular networks provide descriptions of the organization of various biological processes including cellular signaling metabolism and genetic regulation Knowledge on molecular networks is commonly used for systems level analysis of biological function research and method development in this area has grown tremendously in the past few years This book will provide a detailed review of existing knowledge on the functional characterization of biological networks In 15 chapters authored by an international group of prolific systems biology and bioinformatics researchers it will organize conceptualize and summarize the existing core of research results and computational methods on understanding biological function from a network perspective

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Computational Network Analysis with R Matthias Dehmer, Yongtang Shi, Frank Emmert-Streib, 2016-07-22 This new title in the well established Quantitative Network Biology series includes innovative and existing methods for analyzing network data in such areas as network biology and chemoinformatics With its easy to follow introduction to the theoretical background and application oriented chapters the book demonstrates that R is a powerful language for statistically analyzing networks and for solving such large scale phenomena as network sampling and bootstrapping Written by editors and authors with an excellent track record in the field this is the ultimate reference for R in Network Analysis

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Maoguo Gong, Qing Cai, Lijia Ma, Shanfeng Wang, Yu Lei, 2017-09-19 This book presents the latest research advances in complex network structure analytics based on computational intelligence CI approaches particularly evolutionary optimization Most if not all network issues are actually optimization problems which are mostly NP hard and challenge conventional optimization techniques To effectively and efficiently solve these hard optimization problems CI based network structure analytics offer significant advantages over conventional network analytics techniques Meanwhile using CI techniques may facilitate smart decision making by providing multiple options to choose from while conventional methods can only offer a decision maker a single suggestion In addition CI based network structure analytics can greatly facilitate network modeling and analysis And employing CI techniques to resolve network issues is likely to inspire other fields of study such as recommender systems system biology etc which will in turn expand CI s scope and applications As a comprehensive text the book covers a range of key topics including network community discovery evolutionary optimization network structure balance analytics network robustness analytics community based personalized recommendation influence maximization and biological network alignment Offering a rich blend of theory and practice the book is suitable for students researchers and practitioners interested in network analytics and computational intelligence both as a textbook and as a reference work

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Bioinformatics and Biomedical Engineering Ignacio Rojas,Francisco Ortuño,2017-03-30 This two volume set LNBI 10208 and LNBI 10209 constitutes the proceedings of the 5th International Work Conference on Bioinformatics and Biomedical Engineering IWBBIO 2017 held in Granada Spain in April 2017 The 122 papers presented were carefully reviewed and selected from 309 submissions The scope of the conference spans the following areas advances in computational intelligence for critical care bioinformatics for healthcare and diseases biomedical engineering biomedical image analysis biomedical signal analysis biomedicine challenges representing large scale biological data computational genomics computational proteomics computational systems for modeling biological processes data driven biology new tools techniques and resources eHealth high throughput bioinformatic tools for genomics oncological big data and new mathematical tools smart sensor and sensor network architectures time lapse experiments and multivariate biostatistics

Protein Function Prediction for Omics Era Daisuke Kihara,2011-04-19 Gene function annotation has been a central question in molecular biology The importance of computational function prediction is increasing because more and more large scale biological data including genome sequences protein structures protein protein interaction data microarray expression data and mass spectrometry data are awaiting biological interpretation Traditionally when a genome is sequenced function annotation of genes is done by homology search methods such as BLAST or FASTA However since these methods are developed before the genomics era conventional use of them is not necessarily most suitable for analyzing a large scale data Therefore we observe emerging development of computational gene function prediction methods which are targeted to analyze large scale data and also those which use such omics data as additional source of function prediction In this book we overview this emerging exciting field The authors have been selected from 1 those who develop novel purely computational methods 2 those who develop function prediction methods which use omics data 3 those who maintain and update data base of function annotation of particular model organisms E coli which are frequently referred

Research in Computational Molecular Biology Martin Vingron,Limsoon Wong,2008-03-14 This book constitutes the refereed proceedings of the 12th Annual International Conference on Research in Computational Molecular Biology RECOMB 2008 It presents current issues in algorithmic theoretical and experimental bioinformatics

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