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Elements of Computational Systems Biology

John Wiley & Sons 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.

Biomolecular Networks

Methods and Applications in Systems Biology

John Wiley & Sons 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.

Chemoinformatics and Advanced Machine Learning Perspectives: Complex Computational Methods and Collaborative Techniques

Complex Computational Methods and Collaborative Techniques

IGI Global "This book is a timely compendium of key elements that are crucial for the study of machine learning in chemoinformatics, giving an overview of current research in machine learning and their applications to chemoinformatics tasks"--Provided by publisher.

Systems Biology in Practice

Concepts, Implementation and Application

John Wiley & Sons Presenting the main concepts, this book leads students as well as advanced researchers from different disciplines to an understanding of current ideas in the complex field of comprehensive experimental investigation of biological objects, analysis of data, development of models, simulation, and hypothesis generation. It provides readers with guidance on how a specific complex biological question may be tackled: - How to formulate questions that can be answered - Which experiments to perform - Where to find information in databases and on the Internet - What kinds of models are appropriate - How to use simulation tools - What can be learned from the comparison of experimental data and modeling results - How to make testable predictions. The authors demonstrate how mathematical concepts can illuminate the principles underlying biology at a genetic, molecular, cellular and even organism level, and how to use mathematical tools for analysis and prediction.

Algorithms for Computational Biology

First International Conference, AlCoB 2014, Tarragona, Spain, July 1-3, 2014, Proceedings

Springer This book constitutes the refereed proceedings of the First International Conference, AlCoB 2014, held in July 2014 in Tarragona, Spain. The 20 revised full papers were carefully reviewed and selected from 39 submissions. The scope of AlCoB includes topics of either theoretical or applied interest, namely: exact sequence analysis, approximate sequence analysis, pairwise sequence alignment, multiple sequence alignment, sequence assembly, genome rearrangement, regulatory motif finding, phylogeny reconstruction, phylogeny comparison, structure prediction, proteomics: molecular pathways, interaction networks, transcriptomics: splicing variants, isoform inference and quantification, differential analysis, next-generation sequencing: population genomics, metagenomics, metatranscriptomics, microbiome analysis, systems biology.

Transactions on Computational Systems Biology XIV

Special Issue on Computational Models for Cell Processes

Springer The LNCS journal Transactions on Computational Systems Biology is devoted to inter- and multidisciplinary research in the fields of computer science and life sciences and supports a paradigmatic shift in the techniques from computer and information science to cope with the new challenges arising from the systems oriented point of view of biological phenomena. This, the 14th Transactions on Computational Systems Biology volume, guest edited by Ion Petre and Erik de Vink, focuses on Computational Models for Cell Processes and features a number of carefully selected and enhanced contributions, initially presented at the CompMod workshop, which took place in Aachen, Germany, in September 2011. The papers, written from different points of view and following various approaches, cover a wide range of topics within the field of modeling and analysis of biological systems. In addition, two regular submissions deal with models of self-assembling systems and metabolic constraints on the evolution of genetic codes.

A Systems Theoretic Approach to Systems and Synthetic Biology II: Analysis and Design of Cellular Systems

Springer The complexity of biological systems has intrigued scientists from many disciplines and has given birth to the highly influential field of systems biology wherein a wide array of mathematical techniques, such as flux balance analysis, and technology platforms, such as next generation sequencing, is used to understand, elucidate, and predict the functions of complex biological systems. More recently, the field of synthetic biology, i.e., de novo engineering of biological systems, has emerged. Scientists from various fields are focusing on how to render this engineering process more predictable, reliable, scalable, affordable, and easy. Systems and control theory is a branch of engineering and applied sciences that rigorously deals with the complexities and uncertainties of interconnected systems with the objective of characterising fundamental systemic properties such as stability, robustness, communication capacity, and other performance metrics. Systems and control theory also strives to offer concepts and methods that facilitate the design of systems with rigorous guarantees on these properties. Over the last 100 years, it has made stellar theoretical and technological contributions in diverse fields such as aerospace, telecommunication, storage, automotive, power systems, and others. Can it have, or evolve to have, a similar impact in biology? The chapters in this book demonstrate that, indeed, systems and control theoretic concepts and techniques can have a significant impact in systems and synthetic biology. Volume II contains chapters contributed by leading researchers in the field of systems and synthetic biology that concern modeling physiological processes and bottom-up constructions of scalable biological systems. The modeling problems include characterisation and synthesis of memory, understanding how homoeostasis is maintained in the face of shocks and relatively gradual perturbations, understanding the functioning and robustness of biological clocks such as those at the core of circadian rhythms, and understanding how the cell cycles can be regulated, among others. Some of the bottom-up construction problems investigated in Volume II are as follows: How should biomacromolecules, platforms, and scalable architectures be chosen and synthesised in order to build programmable de novo biological systems? What are the types of constrained optimisation problems encountered in this process and how can these be solved efficiently? As the eminent computer scientist Donald Knuth put it, "biology easily has 500 years of exciting problems to work on". This edited book presents but a small fraction of those for the benefit of (1) systems and control theorists interested in molecular and cellular biology and (2) biologists interested in rigorous modelling, analysis and control of biological systems.

Evolutionary Computation in Gene Regulatory Network Research

John Wiley & Sons 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, Toyko, 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.

Bioinformatics Algorithms

Techniques and Applications

John Wiley & Sons Presents algorithmic techniques for solving problems in bioinformatics, including applications that shed new light on molecular biology This book introduces algorithmic techniques in bioinformatics, emphasizing their application to solving novel problems in post-genomic molecular biology. Beginning with a thought-provoking discussion on the role of algorithms in twenty-first-century bioinformatics education, Bioinformatics Algorithms covers: General algorithmic techniques, including dynamic programming, graph-theoretical methods, hidden Markov models, the fast Fourier transform, seeding, and approximation algorithms Algorithms and tools for genome and sequence analysis, including formal and approximate models for gene clusters, advanced algorithms for non-overlapping local alignments and genome tilings, multiplex PCR primer set selection, and sequence/network motif finding Microarray design and analysis, including algorithms for microarray physical design, missing value imputation, and meta-analysis of gene expression data Algorithmic issues arising in the analysis of genetic variation across human population, including computational inference of haplotypes from genotype data and disease association search in case/control epidemiologic studies Algorithmic approaches in structural and systems biology, including topological and structural classification in biochemistry, and prediction of protein-protein and domain-domain interactions Each chapter begins with a self-contained introduction to a computational problem; continues with a brief review of the existing literature on the subject and an in-depth description of recent algorithmic and methodological developments; and concludes with a brief experimental study and a discussion of open research challenges. This clear and approachable presentation makes the book appropriate for researchers, practitioners, and graduate students alike.

Discovery Science

14th International Conference, DS 2011, Espoo, Finland, October 5-7, Proceedings

Springer This book constitutes the refereed proceedings of the 14th International Conference on Discovery Science, DS 2011, held in Espoo, Finland, in October 2011 - co-located with ALT 2011, the 22nd International Conference on Algorithmic Learning Theory. The 24 revised full papers presented together with 5 invited lectures were carefully revised and selected from 56 submissions. The papers cover a wide range including the development and analysis of methods for automatic scientific knowledge discovery, machine learning, intelligent data analysis, theory of learning, as well as their application to knowledge discovery.

Agent and Multi-Agent Systems: Technologies and Applications

9th KES International Conference, KES-AMSTA 2015 Sorrento, Italy, June 2015, Proceedings

Springer Agents and multi-agent systems are related to a modern software paradigm which has long been recognized as a promising technology for constructing autonomous, complex and intelligent systems. The topics covered in this volume include agent-oriented software engineering, agent co-operation, co-ordination, negotiation, organization and communication, distributed problem solving, specification of agent communication languages, agent privacy, safety and security, formalization of ontologies and conversational agents. The volume highlights new trends and challenges in agent and multi-agent research and includes 38 papers classified in the following specific topics: learning paradigms, agent-based modeling and simulation, business model innovation and disruptive technologies, anthropic-oriented computing, serious games and business intelligence, design and implementation of intelligent agents and multi-agent systems, digital economy, and advances in networked virtual enterprises. Published papers have been presented at the 9th KES Conference on Agent and Multi-Agent Systems – Technologies and Applications (KES-AMSTA 2015) held in Sorrento, Italy. Presented results should be of value to the research community working in the fields of artificial intelligence, collective computational intelligence, robotics, dialogue systems and, in particular, agent and multi-agent systems, technologies, tools and applications.

Complexity and Dynamics

PediaPress

Machine Learning in Bioinformatics

John Wiley & Sons An introduction to machine learning methods and their applications to problems in bioinformatics Machine learning techniques are increasingly being used to address problems in computational biology and bioinformatics. Novel computational techniques to analyze high throughput data in the form of sequences, gene and protein expressions, pathways, and images are becoming vital for understanding diseases and future drug discovery. Machine learning techniques such as Markov models, support vector machines, neural networks, and graphical models have been successful in analyzing life science data because of their capabilities in handling randomness and uncertainty of data noise and in generalization. From an internationally recognized panel of prominent researchers in the field, Machine Learning in Bioinformatics compiles recent approaches in machine learning methods and their applications in addressing contemporary problems in bioinformatics. Coverage includes: feature selection for genomic and proteomic data mining; comparing variable selection methods in gene selection and classification of microarray data; fuzzy gene mining; sequence-based prediction of residue-level properties in proteins; probabilistic methods for long-range features in biosequences; and much more. Machine Learning in Bioinformatics is an indispensable resource for computer scientists, engineers, biologists, mathematicians, researchers, clinicians, physicians, and medical informaticists. It is also a valuable reference text for computer science, engineering, and biology courses at the upper undergraduate and graduate levels.

The Mathematical Legacy of Leon Ehrenpreis

Springer Science & Business Media Leon Ehrenpreis has been one of the leading mathematicians in the twentieth century. His contributions to the theory of partial differential equations were part of the golden era of PDEs, and led him to what is maybe his most important contribution, the Fundamental Principle, which he announced in 1960, and fully demonstrated in 1970. His most recent work, on the other hand, focused on a novel and far reaching understanding of the Radon transform, and offered new insights in integral geometry. Leon Ehrenpreis died in 2010, and this volume collects writings in his honor by a cadre of distinguished mathematicians, many of which were his collaborators.

Principles of Computational Cell Biology

From Protein Complexes to Cellular Networks

John Wiley & Sons Computational cell biology courses are increasingly obligatory for biology students around the world but of course also a must for mathematics and informatics students specializing in bioinformatics. This book, now in its second edition is geared towards both audiences. The author, Volkhard Helms, has, in addition to extensive teaching experience, a strong background in biology and informatics and knows exactly what the key points are in making the book accessible for students while still conveying in depth knowledge of the subject.About 50% of new content has been added for the new edition. Much more room is now given to statistical methods, and several new chapters address protein-DNA interactions, epigenetic modifications, and microRNAs.

Bioinformatics

A Practical Guide to the Analysis of Genes and Proteins

John Wiley & Sons "In this book, Andy Baxevanis and Francis Ouellette . . . haveundertaken the difficult task of organizing the knowledge in thisfield in a logical progression and presenting it in a digestibleform. And they have done an excellent job. This fine text will makea major impact on biological research and, in turn, on progress inbiomedicine. We are all in their debt." —Eric Lander from the Foreword Reviews from the First Edition "...provides a broad overview of the basic tools for sequenceanalysis ... For biologists approaching this subject for the firsttime, it will be a very useful handbook to keep on the shelf afterthe first reading, close to the computer." —Nature Structural Biology "...should be in the personal library of any biologist who usesthe Internet for the analysis of DNA and protein sequencedata." —Science "...a wonderful primer designed to navigate the novice throughthe intricacies of in scripto analysis ... The accomplished genesearcher will also find this book a useful addition to theirlibrary ... an excellent reference to the principles ofbioinformatics." —Trends in Biochemical Sciences This new edition of the highly successful Bioinformatics:A Practical Guide to the Analysis of Genes and Proteinsprovides a sound foundation of basic concepts, with practicaldiscussions and comparisons of both computational tools anddatabases relevant to biological research. Equipping biologists with the modern tools necessary to solvepractical problems in sequence data analysis, the Second Editioncovers the broad spectrum of topics in bioinformatics, ranging fromInternet concepts to predictive algorithms used on sequence,structure, and expression data. With chapters written by experts inthe field, this up-to-date reference thoroughly covers vitalconcepts and is appropriate for both the novice and the experiencedpractitioner. Written in clear, simple language, the book isaccessible to users without an advanced mathematical or computerscience background. This new edition includes: All new end-of-chapter Web resources, bibliographies, andproblem sets Accompanying Web site containing the answers to the problems,as well as links to relevant Web resources New coverage of comparative genomics, large-scale genomeanalysis, sequence assembly, and expressed sequence tags A glossary of commonly used terms in bioinformatics andgenomics Bioinformatics: A Practical Guide to the Analysis of Genesand Proteins, Second Edition is essential reading forresearchers, instructors, and students of all levels in molecularbiology and bioinformatics, as well as for investigators involvedin genomics, positional cloning, clinical research, andcomputational biology.

CONCUR 2013 -- Concurrency Theory

24th International Conference, CONCUR 2013, Buenos Aires, Argentina, August 27-30,

2013, Proceedings

Springer This book constitutes the thoroughly refereed proceedings of the 24th International Conference on Concurrency Theory, CONCUR 2013, held in Buenos Aires, Argentina, August 27-30, 2013. The 34 revised full papers presented together with 4 invited talks were carefully reviewed and selected from 115 submissions. The papers are organized in topics such as process semantics and modal transition systems, VAS and pushdown systems, Pi calculus and interaction nets, linearizability and verification of concurrent programs, verification of infinite models, model measure and reversibility, stochastic models, message-based interaction processes, principles of automatic verification, and games and control synthesis.

Philosophy of Systems Biology

Perspectives from Scientists and Philosophers

Springer The emergence of systems biology raises many fascinating questions: What does it mean to take a systems approach to problems in biology? To what extent is the use of mathematical and computational modelling changing the life sciences? How does the availability of big data influence research practices? What are the major challenges for biomedical research in the years to come? This book addresses such questions of relevance not only to philosophers and biologists but also to readers interested in the broader implications of systems biology for science and society. The book features reflections and original work by experts from across the disciplines including systems biologists, philosophers, and interdisciplinary scholars investigating the social and educational aspects of systems biology. In response to the same set of questions, the experts develop and defend their personal perspectives on the distinctive character of systems biology and the challenges that lie ahead. Readers are invited to engage with different views on the questions addressed, and may explore numerous themes relating to the philosophy of systems biology. This edited work will appeal to scholars and all levels, from undergraduates to researchers, and to those interested in a variety of scholarly approaches such as systems biology, mathematical and computational modelling, cell and molecular biology, genomics, systems theory, and of course, philosophy of biology.

Computational Intelligence and Pattern Analysis in Biology Informatics

John Wiley & Sons 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.

Applications of Membrane Computing in Systems and Synthetic Biology

Springer Science & Business Media Membrane Computing was introduced as a computational paradigm in Natural Computing. The models introduced, called Membrane (or P) Systems, provide a coherent platform to describe and study living cells as computational systems. Membrane Systems have been investigated for their computational aspects and employed to model problems in other fields, like: Computer Science, Linguistics, Biology, Economy, Computer Graphics, Robotics, etc. Their inherent parallelism, heterogeneity and intrinsic versatility allow them to model a broad range of processes and phenomena, being also an efficient means to solve and analyze problems in a novel way. Membrane Computing has been used to model biological systems, becoming with time a thorough modeling paradigm comparable, in its modeling and predicting capabilities, to more

established models in this area. This book is the result of the need to collect, in an organic way, different facets of this paradigm. The chapters of this book, together with the web pages accompanying them, present different applications of Membrane Systems to Biology. Deterministic, non-deterministic and stochastic systems paired with different algorithms and methodologies show the full potential of this framework. The book is addressed to researchers interested in applications of discrete biological models and the interplay between Membrane Systems and other approaches to analyze complex systems.

Explanation in Biology

An Enquiry into the Diversity of Explanatory Patterns in the Life Sciences

Springer Patterns of explanation in biology have long been recognized as different from those deployed in other scientific disciplines, especially that of physics. Celebrating the diversity of interpretative models found in biology, this volume details their varying types as well as explaining their relationships to one another. It covers the key differentials with other sciences in the nature of explanation, such as the existence in biology of varieties unheard of in the physical sciences, such as teleological, evolutionary and even functional explanations. Offering a wealth of fresh analysis of the phenomenon, chapters examine aspects ranging from the role of mathematics in explaining cell development to the complexities thrown up by evolutionary-developmental biology, where explanation is altered by multidisciplinarity itself. They cover major domains such as ecology and systems biology, as well as contemporary trends, such as the mechanistic explanations spawned by progress in molecular biology. With contributions from researchers of many different nationalities, the book provides a many-angled perspective on a revealing feature of the discipline of biology.

Evolutionary Genomics and Systems Biology

John Wiley & Sons A comprehensive, authoritative look at an emergent area in post-genomic science, Evolutionary genomics is an up-and-coming, complex field that attempts to explain the biocomplexity of the living world. Evolutionary Genomics and Systems Biology is the first full-length book to blend established and emerging concepts in bioinformatics, evolution, genomics, and structural biology, with the integrative views of network and systems biology. Three key aspects of evolutionary genomics and systems biology are covered in clear detail: the study of genomic history, i.e., understanding organismal evolution at the genomic level; the study of macromolecular complements, which encompasses the evolution of the protein and RNA machinery that propels life; and the evolutionary and dynamic study of wiring diagrams—macromolecular components in interaction—in the context of genomic complements. The book also features: A solid, comprehensive treatment of phylogenomics, the evolution of genomes, and the evolution of biological networks, within the framework of systems biology A special section on RNA biology—translation, evolution of structure, and micro RNA and regulation of gene expression Chapters on the mapping of genotypes to phenotypes, the role of information in biology, protein architecture and biological function, chromosomal rearrangements, and biological networks and disease Contributions by leading authorities on each topic Evolutionary Genomics and Systems Biology is an ideal book for students and professionals in genomics, bioinformatics, evolution, structural biology, complexity, origins of life, systematic biology, and organismal diversity, as well as those individuals interested in aspects of biological sciences as they interface with chemistry, physics, and computer science and engineering.

Systems Biology in Drug Discovery and Development

John Wiley & Sons 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.

Algorithmic and Artificial Intelligence Methods for Protein Bioinformatics

John Wiley & Sons 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.

Analysis of Biological Networks

John Wiley & Sons An introduction to biological networks and methods for theiranalysis Analysis of Biological Networks is the first book of itskind to provide readers with a comprehensive introduction to thestructural analysis of biological networks at the interface ofbiology and computer science. The book begins with a brief overviewof biological networks and graph theory/graph algorithms and goeson to explore: global network properties, network centralities,network motifs, network clustering, Petri nets, signal transductionand gene regulation networks, protein interaction networks,metabolic networks, phylogenetic networks, ecological networks, andcorrelation networks. Analysis of Biological Networks is a self-containedintroduction to this important research topic, assumes no expertknowledge in computer science or biology, and is accessible toprofessionals and students alike. Each chapter concludes with asummary of main points and with exercises for readers to test theirunderstanding of the material presented. Additionally, an FTP sitewith links to author-provided data for the book is available fordeeper study. This book is suitable as a resource for researchers in computerscience, biology, bioinformatics, advanced biochemistry, and thelife sciences, and also serves as an ideal reference text forgraduate-level courses in bioinformatics and biologicalresearch.

Computational Biology

A Hypertextbook

John Wiley & Sons An introduction to the world of bioinformatics Massive increases in computing power and the ability to routinely sequence whole genomes of living organisms have begun to fundamentally alter our understanding of biology, medicine, and agriculture. At the intersection of the growing information and genomics revolutions sits bioinformatics, which uses modern computational power to reveal patterns in biological data sets, especially DNA, RNA, and protein sequences. Computational Biology: A Hypertextbook, by Scott Kelley and Dennis Didulo, provides a wonderful introduction for anyone who wants to learn the basics of bioinformatics. This book is more than a textbook because of the wealth of online ancillary materials and how the print and electronic components are integrated to form a complete educational resource. Aspects that make Computational Biology: A Hypertextbook a unique and valuable tool for teaching and learning bioinformatics include Clear explanations of the basic biology of DNA, RNA, and proteins and how the related bioinformatics algorithms work Extensive exercises that enable students to practice with the same bioinformatics applications that are used by scientists worldwide Tutorials, sample data sets, and interactive learning tools developed with teachers in mind and field-tested by hundreds of students Online tutorials and curated web links that are accurate (instead of frustrating!) and won't lead to dead ends Online resources that work on multiple platforms and electronic devices Computational Biology: A Hypertextbook is written in an accessible voice, punctuated with humor, and designed to significantly increase computational competencies. Biology and computer

science undergraduate and graduate students will thoroughly enjoy learning from this unique hypertextbook, as will anyone with an interest in exploring this burgeoning topic.

Modeling in Systems Biology

The Petri Net Approach

Springer Science & Business Media The emerging, multi-disciplinary field of systems biology is devoted to the study of the relationships between various parts of a biological system, and computer modeling plays a vital role in the drive to understand the processes of life from an holistic viewpoint. Advancements in experimental technologies in biology and medicine have generated an enormous amount of biological data on the dependencies and interactions of many different molecular cell processes, fueling the development of numerous computational methods for exploring this data. The mathematical formalism of Petri net theory is able to encompass many of these techniques. This essential text/reference presents a comprehensive overview of cutting-edge research in applications of Petri nets in systems biology, with contributions from an international selection of experts. Those unfamiliar with the field are also provided with a general introduction to systems biology, the foundations of biochemistry, and the basics of Petri net theory. Further chapters address Petri net modeling techniques for building and analyzing biological models, as well as network prediction approaches, before reviewing the applications to networks of different biological classification. Topics and features: investigates the modular, qualitative modeling of regulatory networks using Petri nets, and examines an Hybrid Functional Petri net simulation case study; contains a glossary of the concepts and notation used in the book, in addition to exercises at the end of each chapter; covers the topological analysis of metabolic and regulatory networks, the analysis of models of signaling networks, and the prediction of network structure; provides a biological case study on the conversion of logical networks into Petri nets; discusses discrete modeling, stochastic modeling, fuzzy modeling, dynamic pathway modeling, genetic regulatory network modeling, and quantitative analysis techniques; includes a Foreword by Professor Jens Reich, Professor of Bioinformatics at Humboldt University and Max Delbrück Center for Molecular Medicine in Berlin. This unique guide to the modeling of biochemical systems using Petri net concepts will be of real utility to researchers and students of computational biology, systems biology, bioinformatics, computer science, and biochemistry.

Computational Protein Science

Methods in Structural Bioinformatics

Wiley-Interscience Computational Protein Science: Methods in Structural Bioinformatics provides understanding about the scope and power of current techniques in protein sequence-structure-function analysis and prediction, and gives insight into the intellectual achievements in protein bioinformatics. It covers sequence-to-sequence and sequence-to-structure comparison techniques, as well as algorithms for the prediction of protein structural topology and domain structure. An important focus will be discussing integrative approaches that tie various methods and data sets together. In addition to a rigorous overview, the book will emphasize the artistic elements in the analysis and prediction algorithms, and discuss their significance for addressing the outstanding problems in protein computational biology.

Introduction to Synthetic Biology

About Modeling, Computation, and Circuit Design

Springer The textbook is based on the lectures of the course "Synthetic Biology" for Master's students in biology and biotechnology at the Harbin Institute of Technology. The goal of the textbook is to explain how to make mathematical models of synthetic gene circuits that will, later on, drive the circuit implementation in the lab. Concepts such as kinetics, circuit dynamics and equilibria, stochastic and deterministic simulations, parameter analysis and optimization are presented. At the end of the textbook, a chapter contains a description of structural motifs (e.g. positive and negative feedback loops, Boolean gates) that carry out specific functions and can be combined into larger networks. Moreover,

several chapters show how to build up (an analyse, where possible) models for synthetic gene circuits with four different open-source software i.e. COPASI, XPPAUT, BioNetGeN, and Parts & Pools-ProMoT.

Computational Systems Biology in Medicine and Biotechnology

Methods and Protocols

Springer Nature This volume addresses the latest state-of-the-art systems biology-oriented approaches that--driven by big data and bioinformatics--are utilized by Computational Systems Biology, an interdisciplinary field that bridges experimental tools with computational tools to tackle complex questions at the frontiers of knowledge in medicine and biotechnology. The chapters in this book are organized into six parts: systems biology of the genome, epigenome, and redox proteome; metabolic networks; aging and longevity; systems biology of diseases; spatiotemporal patterns of rhythms, morphogenesis, and complex dynamics; and genome scale metabolic modeling in biotechnology. In every chapter, readers will find varied methodological approaches applied at different levels, from molecular, cellular, organ to organisms, genome to phenome, and health and disease. Written in the highly successful Methods in Molecular Biology series format, chapters include introductions to their respective topics; criteria utilized for applying specific methodologies; lists of the necessary materials, reagents, software, databases, algorithms, mathematical models, and dedicated analytical procedures; step-by-step, readily reproducible laboratory, bioinformatics, and computational protocols all delivered in didactic and clear style and abundantly illustrated with express case studies and tutorials; and tips on troubleshooting and advice for achieving reproducibility while avoiding mistakes and misinterpretations. The overarching goal driving this volume is to excite the expert and stimulate the newcomer to the field of Computational Systems Biology. Cutting-edge and authoritative, Computational Systems Biology in Medicine and Biotechnology: Methods and Protocols is a valuable resource for pre- and post-graduate students in medicine and biotechnology, and in diverse areas ranging from microbiology to cellular and organismal biology, as well as computational and experimental biologists, and researchers interested in utilizing comprehensive systems biology oriented methods. .

Formal Methods for Dynamical Systems

13th International School on Formal Methods for the Design of Computer, Communication, and Software Systems, SFM 2013, Bertinoro, Italy, June 17-22, 2013. Advanced Lectures

Springer This book presents 5 tutorial lectures given by leading researchers at the 13th edition of the International School on Formal Methods for the Design of Computer, Communication and Software Systems, SFM 2013, held in Bertinoro, Italy, in June 2013. SFM 2013 was devoted to dynamical systems and covered several topics including chaotic dynamics; information theory; systems biology; hybrid systems; quantum computing; and automata-based models and model checking.

Computational Systems Biology

From Molecular Mechanisms to Disease

Academic Press This comprehensively revised second edition of Computational Systems Biology discusses the experimental and theoretical foundations of the function of biological systems at the molecular, cellular or organismal level over temporal and spatial scales, as systems biology advances to provide clinical solutions to complex medical problems. In

particular the work focuses on the engineering of biological systems and network modeling. Logical information flow aids understanding of basic building blocks of life through disease phenotypes Evolved principles gives insight into underlying organizational principles of biological organizations, and systems processes, governing functions such as adaptation or response patterns Coverage of technical tools and systems helps researchers to understand and resolve specific systems biology problems using advanced computation Multi-scale modeling on disparate scales aids researchers understanding of dependencies and constraints of spatio-temporal relationships fundamental to biological organization and function.

Systems Biology

John Wiley & Sons Systems biology is a relatively new biological study field that focuses on the systematic study of complex interactions in biological systems, thus using a new perspective (integration instead of reduction) to study them. Particularly from year 2000 onwards, the term is used widely in the biosciences, and in a variety of contexts. Systems biology is the study of the interconnected aspect of molecular, cellular, tissue, whole animal and ecological processes, and comprises mathematical and mechanistic studies of dynamical, mesoscopic, open, spatiotemporally defined, nonlinear, complex systems that are far from thermodynamic equilibrium.

Grid Computing for Bioinformatics and Computational Biology

John Wiley & Sons The only single, up-to-date source for Grid issues in bioinformatics and biology Bioinformatics is fast emerging as an important discipline for academic research and industrial applications, creating a need for the use of Grid computing techniques for large-scale distributed applications. This book successfully presents Grid algorithms and their real-world applications, provides details on modern and ongoing research, and explores software frameworks that integrate bioinformatics and computational biology. Additional coverage includes: * Bio-ontology and data mining * Data visualization * DNA assembly, clustering, and mapping * Molecular evolution and phylogeny * Gene expression and micro-arrays * Molecular modeling and simulation * Sequence search and alignment * Protein structure prediction * Grid infrastructure, middleware, and tools for bio data Grid Computing for Bioinformatics and Computational Biology is an indispensable resource for professionals in several research and development communities including bioinformatics, computational biology, Grid computing, data mining, and more. It also serves as an ideal textbook for undergraduate- and graduate-level courses in bioinformatics and Grid computing.

Structural Bioinformatics

John Wiley & Sons Structural Bioinformatics was the first major effort to showthe application of the principles and basic knowledge of the largerfield of bioinformatics to questions focusing on macromolecularstructure, such as the prediction of protein structure and howproteins carry out cellular functions, and how the application ofbioinformatics to these life science issues can improve healthcareby accelerating drug discovery and development. Designed primarilyas a reference, the first edition nevertheless saw widespread useas a textbook in graduate and undergraduate university coursesdealing with the theories and associated algorithms, resources, andtools used in the analysis, prediction, and theoreticalunderpinnings of DNA, RNA, and proteins. This new edition contains not only thorough updates of theadvances in structural bioinformatics since publication of thefirst edition, but also features eleven new chapters dealing withfrontier areas of high scientific impact, including: sampling andsearch techniques; use of mass spectrometry; genome functionalannotation; and much more. Offering detailed coverage for practitioners while remainingaccessible to the novice, Structural Bioinformatics, SecondEdition is a valuable resource and an excellent textbook for arange of readers in the bioinformatics and advanced biologyfields. Praise for the previous edition: "This book is a gold mine of fundamental and practicalinformation in an area not previously well represented in bookform." —Biochemistry and Molecular Education "... destined to become a classic reference work for workers atall levels in structural bioinformatics...recommended with greatenthusiasm for educators, researchers, and graduatestudents." —BAMBED "...a useful and timely summary of a rapidly expandingfield." —Nature Structural Biology "...a terrific job in this timely creation of a compilation ofarticles that appropriately addresses this issue." —Briefings in Bioinformatics

Systems Biology

A Textbook

John Wiley & Sons This advanced textbook is tailored for an introductory course in Systems Biology and is well-suited for biologists as well as engineers and computer scientists. It comes with student-friendly reading lists and a companion website featuring a short exam prep version of the book and educational modeling programs. The text is written in an easily accessible style and includes numerous worked examples and study questions in each chapter. For this edition, a section on medical systems biology has been included.

Handbook of Research on Systems Biology Applications in Medicine

IGI Global "This book highlights the use of systems approaches including genomic, cellular, proteomic, metabolomic, bioinformatics, molecular, and biochemical, to address fundamental questions in complex diseases like cancer diabetes but also in ageing"--Provided by publisher.

Parallel Computing for Bioinformatics and Computational Biology

Models, Enabling Technologies, and Case Studies

John Wiley & Sons Discover how to streamline complex bioinformatics applications withparallel computing This publication enables readers to handle more complexbioinformatics applications and larger and richer data sets. As theeditor clearly shows, using powerful parallel computing tools canlead to significant breakthroughs in deciphering genomes,understanding genetic disease, designing customized drug therapies,and understanding evolution. A broad range of bioinformatics applications is covered withdemonstrations on how each one can be parallelized to improveperformance and gain faster rates of computation. Current parallelcomputing techniques and technologies are examined, includingdistributed computing and grid computing. Readers are provided witha mixture of algorithms, experiments, and simulations that providenot only qualitative but also quantitative insights into thedynamic field of bioinformatics. Parallel Computing for Bioinformatics and Computational Biology isa contributed work that serves as a repository of case studies,collectively demonstrating how parallel computing streamlinesdifficult problems in bioinformatics and produces better results.Each of the chapters is authored by an established expert in thefield and carefully edited to ensure a consistent approach and highstandard throughout the publication. The work is organized into five parts: * Algorithms and models * Sequence analysis and microarrays * Phylogenetics * Protein folding * Platforms and enabling technologies Researchers, educators, and students in the field of bioinformaticswill discover how high-performance computing can enable them tohandle more complex data sets, gain deeper insights, and make newdiscoveries.

Systems Biology and Synthetic Biology

John Wiley & Sons The genomic revolution has opened up systematic investigations and engineering designs for various life forms. Systems biology and synthetic biology are emerging as two complementary approaches, which embody the breakthrough in biology and invite application of engineering principles. Systems Biology and Synthetic Biology emphasizes the similarity between biology and engineering at the system level, which is important for applying systems and engineering theories to biology problems. This book demonstrates to students, researchers, and industry that systems biology relies on synthetic biology technologies to study biological systems, while synthetic biology depends on knowledge obtained from systems biology approaches.

Pathway Analysis for Drug Discovery

Computational Infrastructure and Applications

John Wiley & Sons This book introduces drug researchers to the novel computational approaches of pathway analysis and explains the existing applications that can save time and money in the drug discovery process. It covers traditional computational methods and software for pathway analysis microarray, proteomics, and metabolomics. It explains pathway reconstruction of diseases and toxic states, pathway analysis in various phases, dynamic modeling of drug responses, and more. This is a core resource for drug discovery and pharmaceutical industry researchers, chemists, and biologists and for professionals in related fields.