Contact Map

H. Anandakumar, R. Arulmurugan, Chow Chee Onn

Making Contact Glenn Burger,2003-02-26 When civilizations first encounter each other a cascade of change is triggered that both challenges and reinforces the identities of all parties. Making Contact revisits key encounters between cultures in the medieval and early modern world. Contributors cross disciplinary boundaries to explore the implications of contact. Scott D. Westrem examines the imagined Africa depicted in the Bell Mappamundi. Day-to-day accommodations between the religious identities of Vilnius, in the Polish-Lithuanian Commonwealth, are explored by David Frick. Steven F. Kruger argues that medieval Christian identity was destabilized by the living Talmudic tradition. Individual Jesuits who were critical to the success of contact in Japan are evaluated by Nakai Ayako. Linda Woodbridge argues that Elizabethan attitudes towards aboriginals paralleled their attitudes towards English vagrants. Despite a nod to Arcadian conventions, travel narratives of Virginia were preoccupied with finding wealth, according to Paul W. DePasquale's research. Rick H. Lee examines the conflicting loyalties of Pierre Raddisson in the New World. Richard A. Young demonstrates that the Florida shipwreck narratives of Cabeza de Vaca were groomed for intended audiences, past and present. This rich interdisciplinary collaboration contributes to the debate on boundaries between disciplines, as well as boundaries between the Middle Ages and the early modern period, and also between historical and theoretical perspectives. Making Contact draws our attention to the important ways in which historic encounters with contrasting 'others' have shaped the identities of both individual and corporate 'selves' over a span of five centuries.

Computational Intelligence Methods for Bioinformatics and Biostatistics Francesco Masulli, Roberto Tagliaferri, Gennady M. Verkhivker, 2009-06-23 This book constitutes the thoroughly refereed post-conference proceedings of the Fifth International Meeting on Computational Intelligence Methods for Bioinformatics and Biostatistics, CIBB 2008, held in Vietri sul Mare, Italy, in October 2008. The 23 revised full papers presented together with 3 invited lectures were carefully reviewed and selected from 69 submissions. The main goal of the CIBB meetings is to provide a forum open to researchers from different disciplines to present and discuss problems concerning computational techniques in bioinformatics, systems biology and medical informatics with a particular focus on neural networks, machine learning, fuzzy logic, and evolutionary computation methods.

Adaptive and Natural Computing Algorithms Bartlomiej Beliczynski, Andrzej Dzielinski, Marcin Iwanowski, Bernadete Ribeiro, 2007-07-03 This two volume set constitutes the refereed proceedings of the 8th International Conference on Adaptive and Natural Computing Algorithms, ICANNGA 2007, held in Warsaw, Poland, in April 2007. Coverage in the first volume includes evolutionary computation, genetic algorithms, and particle swarm optimization. The second volume covers neural networks, support vector machines, biomedical signal and image processing, biometrics, computer vision.

Algorithms in Bioinformatics Raffaele Giancarlo, Sridhar Hannenhalli, 2007-08-24 The refereed proceedings from the 7th International Workshop on Algorithms in Bioinformatics are provided in this volume. Papers address current issues in algorithms in bioinformatics, ranging from mathematical tools to experimental studies of approximation algorithms to significant computational analyses. Biological problems examined include genetic mapping, sequence alignment and analysis, phylogeny, comparative genomics, and protein structure.

Introduction to Protein Structure Prediction Huzefa Rangwala, George Karypis, 2011-03-16 A look at the methods and algorithms used to predict proteinstructure A thorough knowledge of the function and structure of proteinsis critical for the advancement of biology and the life sciences aswell as the development of better drugs, higher-yield crops, andeven synthetic bio-fuels. To that end, this reference sheds lighton the methods used for protein structure prediction and revealsthe key applications of modeled structures. This indispensable bookcovers the applications of modeled protein structures and unravelsthe relationship between pure sequence information andthree-dimensional structure, which continues to be one of thegreatest 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 willacquire unique insight into the future applications of the modeledprotein structures. The book begins with a thorough introduction to the protein structure prediction problem and is divided into fourthemes: a background on structure prediction, the prediction of structural elements, tertiary structure prediction, and functionalinsights. Within those four sections, the following topics are covered: Databases and resources that are commonly used for proteinstructure 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 proteinstructures 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 bloody research or taking courses in protein modeling, readers will find the content in this book invaluable.

Homology Modeling Sławomir Filipek, 2023-03-23 This detailed volume provides state-of-the-art methodologies and reviews of important topics in the field of homology modeling. From homology modeling in the twilight zone and improving accuracy through sequence space analysis to approaches to construct multi-protein complex models, the book explores a wide variety of uses and applications of this valuable technique. Written for the highly successful Methods in Molecular Biology series, the chapters include introductions to their respective topics, lists of the necessary programs, webservers, and databases, step-by-step and readily reproducible protocols, as well as tips on troubleshooting and avoiding known pitfalls. Authoritative and practical, Homology Modeling: Methods and Protocols serves as an ideal guide to recent homology modeling procedures, assumptions made, and model quality assessment that will illuminate the black box of homology modeling for novice readers and broaden the knowledge of this methodology for professionals.

Advances in Research and Applications Gerald Litwack, 2000-01-27 Under the capable and qualified editorial leadership of Dr. Gerald Litwack, Vitamins and Hormones continues to publish cutting-edge reviews of interest to endocrinologists, biochemists, nutritionists, pharmacologists, cell biologists, and molecular biologists. First published in 1943, Vitamins and Hormones is the longest-running serial published by Academic Press. In the early days of the Serial, the subjects of vitamins and hormones were quite distinct. Now, new discoveries have proved that several of the vitamins function as hormones and many of the substances inferred by the title of the serial function in signal transduction processes. Accordingly, the Editor-in-Chief has expanded the scope of the serial to reflect this newer understanding of function-structure relationships in cellular communication. The Editorial Board now reflects expertise in the field of hormone action, vitamin action, X-ray crystal structure, physiology, and enzyme mechanisms.

Computational Intelligence and Sustainable Systems H. Anandakumar, R. Arulmurugan, Chow Chee Onn, 2018-12-14 This book features research related to computational intelligence and energy and thermal aware management of computing resources. The authors publish original and timely research in current areas of power, energy, temperature, and environmental engineering as and advances in computational intelligence that are benefiting the fields. Topics include signal processing architectures, algorithms, and applications; biomedical informatics and computation; artificial intelligence and machine learning; green technologies in information; and more. The book includes contributions from a wide range of researchers, academicians, and industry professionals. The book is made up both of extended papers presented at the International Conference on Intelligent Computing and Sustainable System (ICICSS 2018), September 20-21, 2018, and other accepted papers on R&D and original research work related to the practice and theory of technologies to enable and support Intelligent Computing applications.

Mathematical Methods for Protein Structure Analysis and Design Concettina Guerra, Sorin Istrail, 2003-06-25 The papers collected in this volume

reproduce contributions by leading sch- arstoaninternationalschoolandworkshopwhichwasorganizedandheldwith thegoaloftakinga snapshotofadiscipline undertumultuous growth. Indeed, the area of protein folding, docking and alignment is developing in response to needs for a mix of heterogeneous expertise spanning biology, chemistry, mathematics, computer science, and statistics, among others. Some of the problems encountered in this area are not only important for the scienti?c challenges they pose, but also for the opportunities they disclose intermsofmedicalandindustrialexploitation. Atypicalexampleiso?eredby protein-drug interaction (docking), a problem posing daunting computational problems at the crossroads of geometry, physics and chemistry, and, at the same time, a problem with unimaginable implications for the pharmacopoeia of the future. The schoolfocused on problems posed by the study of the mechanisms - hind protein folding, and explored di?erent ways of attacking these problems under objective evaluations of the methods. Together with a relatively small core of consolidated knowledge and tools, important re?ections were brought to this e?ort by studies in a multitude of directions and approaches. It is obviously impossible to predict which, if any, among these techniques will prove completely successful, but it is precisely the implicit dialectic among them that best conveys the current ?avor of the ?eld. Such unique diversity and richness inspired the format of the meeting, and also explains the slight departure of the present volume from the typical format in this series: the exposition of the current sediment is complemented here by a selection of quali?ed specialized contributions.

Bioinformatics Research and Applications Ion Mandoiu, Alexander Zelikovsky, 2007-08-06 This book constitutes the refereed proceedings of the Third International Symposium on Bioinformatics Research and Applications, ISBRA 2007, held in Atlanta, GA, USA in May 2007. The 55 revised full papers presented together with three invited talks cover a wide range of topics, including clustering and classification, gene expression analysis, gene networks, genome analysis, motif finding, pathways, protein structure prediction, protein domain interactions, phylogenetics, and software tools.

Information and Communication Technology Durgesh Kumar Mishra, Ahmad Taher Azar, Amit Joshi, 2017-10-12 This book volume contains 31 papers presented at ICICT 2016: Second International Congress on Information and Communication Technology. The conference was held during 12-13 December 2016, Bangkok, Thailand and organized communally by G R Foundation, and Computer Society of India Division IV – Communication and Division V – Education and Research. This volume contains papers mainly focused on ICT for computation, algorithms and data analytics, and IT security.

Machine Learning for Peptide Structure, Function, and Design Ruiquan Ge, Chuan Dong, Juexin Wang, Yanjie Wei, 2022-11-07
Advances in Cardiac Mapping and Catheter Ablation: Part II, An Issue of Cardiac Electrophysiology Clinics Mohammad Shenasa, Amin Al-Ahmad, 2019-11-21 This issue of Cardiac Electrophysiology Clinics, guest edited by Mohammad Shenasa and Amin Al-Ahmad, is the second part of our Advances in Cardiac Mapping and Catheter Ablation issue. Article topics will include, but are not limited to, New Findings in Atrial Fibrillation Mechanisms; Mapping and Ablation of Neuraxial in Patients with Ventricular Arrhythmias; How to Map and Ablate Rotors in Atrial Fibrillation; Postablation Atrial Arrhythmias; Substrate Mapping in Ventricular Arrhythmias; Challenges in Ablation of Complex Congenital Heart Disease; Mapping and Ablation of Ventricular Arrhythmias from the RV and LV Outflow Tract; Novel Insights on Idiopathic VF and Early Repolarization; Novel Observations in Mapping and Ablation in Brugada Syndrome; Ablations of Ventricular Arrhythmias; Mapping and Ablation of Arrhythmias from uncommon sites; Mapping and Ablation of VT in Patients with HF and Cardiomyopathies; Mapping and Ablation of Unmappable VT, VT Storm, and Those in Acute Myocardial Infarction; Mapping and Ablation of Ventricle Arrhythmia in patients of LVAD; Fluoroless Catheter Ablation of Cardiac Arrhythmias; Toward a Uniform Ablation Protocol for Paroxysmal; Persistent and Permanent AF; and The Ideal Mapping System.

<u>Systems Biology Modelling and Analysis</u> Elisabetta De Maria,2022-11-18 Systems Biology Modelling and Analysis Describes important modelling and computational methods for systems biology research to enable practitioners to select and use the most suitable technique Systems Biology

Modelling and Analysis provides an overview of state-of-the-art techniques and introduces related tools and practices to formalize models and automate reasoning for systems biology. The authors present and compare the main formal methods used in systems biology for modelling biological networks, including discussion of their advantages, drawbacks, and main applications. Each chapter includes an intuitive presentation of the specific formalism, a brief history of the formalism and of its applications in systems biology, a formal description of the formalism and its variants, at least one realistic case study, some applications of formal techniques to validate and make deep analysis of models encoded with the formalism, and a discussion on the kind of biological systems for which the formalism is suited, along with concrete ideas on its possible evolution. Edited by a highly qualified expert with significant experience in the field, some of the methods and techniques covered in Systems Biology Modelling and Analysis include: Petri nets, an important tool for studying different aspects of biological systems, ranging from simple signaling pathways to metabolic networks and beyond Pathway Logic, a formal, rule-based system and interactive viewer for developing executable models of cellular processes Boolean networks, a mathematical model which has been widely used for decades in the context of biological regulation networks Answer Set Programming (ASP), which has proven to be a strong logic programming paradigm to deal with the inherent complexity of biological models For systems biologists, biochemists, bioinformaticians, molecular biologists, pharmacologists, and computer scientists, Systems Biology Modelling and Analysis is a comprehensive all-in-one resource to understand and harness the field's current models and techniques while also preparing for their potential developments in coming years with the help of the author's expert insight.

Integer Linear Programming in Computational and Systems Biology Dan Gusfield, 2019-06-13 Integer linear programming (ILP) is a versatile modeling and optimization technique that is increasingly used in non-traditional ways in biology, with the potential to transform biological computation. However, few biologists know about it. This how-to and why-do text introduces ILP through the lens of computational and systems biology. It uses indepth examples from genomics, phylogenetics, RNA, protein folding, network analysis, cancer, ecology, co-evolution, DNA sequencing, sequence analysis, pedigree and sibling inference, haplotyping, and more, to establish the power of ILP. This book aims to teach the logic of modeling and solving problems with ILP, and to teach the practical 'work flow' involved in using ILP in biology. Written for a wide audience, with no biological or computational prerequisites, this book is appropriate for entry-level and advanced courses aimed at biological and computational students, and as a source for specialists. Numerous exercises and accompanying software (in Python and Perl) demonstrate the concepts.

Computational Modeling of Biological Systems Nikolay V Dokholyan,2012-02-12 Computational modeling is emerging as a powerful new approach to study and manipulate biological systems. Multiple methods have been developed to model, visualize, and rationally alter systems at various length scales, starting from molecular modeling and design at atomic resolution to cellular pathways modeling and analysis. Higher time and length scale processes, such as molecular evolution, have also greatly benefited from new breeds of computational approaches. This book provides an overview of the established computational methods used for modeling biologically and medically relevant systems.

Prediction of Contact Maps Using Support Vector Machines ,2002 Contact map prediction is of great interests for its application in fold recognition and protein 3D structure determination. In particular, we focusd on predicting non-local interactions in this paper. We employed Support Vector Machines (SVMs) as the machine learning tool and incorporated AAindex to extract correlated mutation analysis (CMA) and sequence profile (SP) features. In addition, we evaluated the effectiveness of different features for various fold classes. On average, our predictor achieved an prediction accuracy of 0.2238 with an improvement over a randompredictor of a factor 11.7, which is better than reported studies. Our study showed that predicted secondary structure features play an important roles for the proteins containing beta structures. Models based on secondary structure features and CMA features produce different sets of predictions. Our study also suggests that models learned separately for different protein fold

families may achieve better performance than a unified model.

Symbolic Approaches to Modeling and Analysis of Biological Systems Cedric Lhoussaine, Elisabeth Remy, 2023-08-29

Handbook of Research on Computational Grid Technologies for Life Sciences, Biomedicine, and Healthcare Cannataro, Mario, 2009-05-31 This book provides methodologies and developments of grid technologies applied in different fields of life sciences--Provided by publisher.

Advanced Data Mining and Applications Changjie Tang,2008-09-29 This book constitutes the refereed proceedings of the 4th International Conference on Advanced Data Mining and Applications, ADMA 2008, held in Chengdu, China, in October 2008. The 35 revised full papers and 43 revised short papers presented together with the abstract of 2 keynote lectures were carefully reviewed and selected from 304 submissions. The papers focus on advancements in data mining and peculiarities and challenges of real world applications using data mining and feature original research results in data mining, spanning applications, algorithms, software and systems, and different applied disciplines with potential in data mining.

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