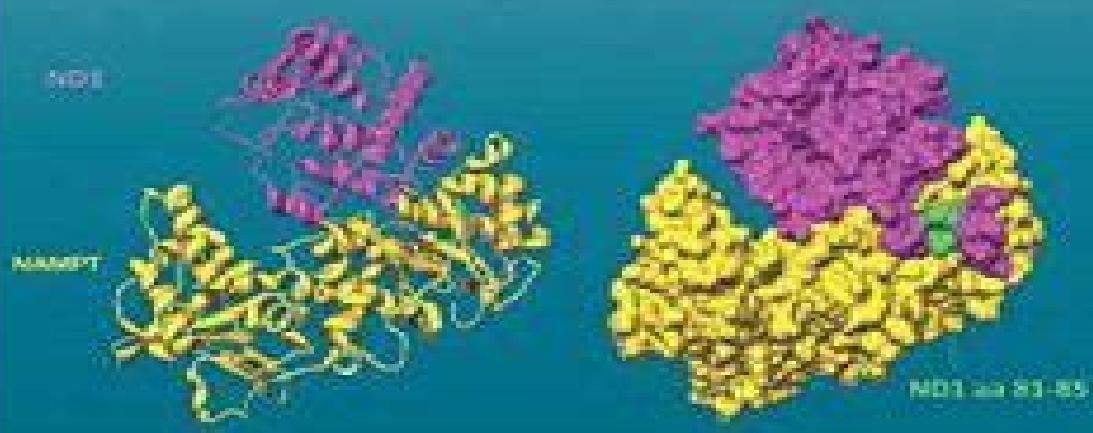


Big Data Analysis for Bioinformatics and Biomedical Discoveries



Edited by

Shui Qing Ye



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A CHAPMAN & HALL BOOK

Bioinformatics Biomedical Discoveries Mathematical Computational

Frédéric Cazals, Pierre Kornprobst

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Big Data Analysis for Bioinformatics and Biomedical Discoveries Shui Qing Ye,2016-01-13 Demystifies Biomedical and Biological Big Data AnalysesBig Data Analysis for Bioinformatics and Biomedical Discoveries provides a practical guide to the nuts and bolts of Big Data enabling you to quickly and effectively harness the power of Big Data to make groundbreaking biological discoveries carry out translational medical research and implem Computational Immunology Shyamasree Ghosh,2020-01-31 Computational Immunology Applications focuses on different mathematical models statistical tools techniques and computational modelling that helps in understanding complex phenomena of the immune system and its biological functions The book also focuses on the latest developments in computational biology in designing of drugs targets biomarkers for early detection and prognosis of a disease It highlights the applications of computational methods in deciphering the complex processes of the immune system and its role in health and disease This book discusses the most essential topics including Next generation sequencing NGS and computational immunology Computational modelling and biology of diseases Drug designing Computation and identification of biomarkers Application in organ transplantation Application in disease detection and therapy Computational methods and applications in understanding of the invertebrate immune system S Ghosh is MSc PhD PGDHE PGDBI is PhD from IICB CSIR Kolkata awarded the prestigious National Scholarship from the Government of India She has worked and published extensively in glycobiology sialic acids immunology stem cells and nanotechnology She has authored several publications that include books and encyclopedia chapters in reputed journals and books

Phytochemicals as Lead Compounds for New Drug Discovery Chukwuebuka Egbuna,Shashank Kumar,Jonathan C. Ifemeje,Shahira M. Ezzat,Saravanan Kaliyaperumal,2019-09-07 Phytochemicals as Lead Compounds for New Drug Discovery presents complete coverage of the recent advances in the discovery of phytochemicals from medicinal plants as models to the development of new drugs and chemical entities Functional bioactive compounds of plant origin have been an invaluable source for many human therapeutic drugs and have played a major role in the treatment of diseases around the world These compounds possess enormous structural and chemical diversity and have led to many important discoveries This book presents fundament concepts and factors affecting the choice for plant based products as well as recent advances in computer aided drug discovery and FDA drug candidacy acceptance criteria It also details the various bioactive lead compounds and molecular targets for a range of life threatening diseases including cancer diabetes and neurodegenerative diseases Written by a global team of experts Phytochemicals as Lead Compounds for New Drug Discovery is an ideal resource for drug developers phytochemists plant biochemists food and medicinal chemists nutritionists and toxicologists chemical ecologists taxonomists analytical chemists and other researchers in those fields It will also be very valuable to professors students and researchers in this domain Presents fundamental concepts and factors affecting choice for plant based products Details the FDA drug candidacy acceptance criteria including bottlenecks and way

forward Highlights recent advances in computational based drug discovery Focuses on the discovery of new drugs and potential druggable targets for the treatment of chronic diseases of world importance **Computational Exome and Genome Analysis** Peter N. Robinson, Rosario Michael Piro, Marten Jager, 2017-09-13 Exome and genome sequencing are revolutionizing medical research and diagnostics but the computational analysis of the data has become an extremely heterogeneous and often challenging area of bioinformatics Computational Exome and Genome Analysis provides a practical introduction to all of the major areas in the field enabling readers to develop a comprehensive understanding of the sequencing process and the entire computational analysis pipeline

Modeling in Computational Biology and Biomedicine Frédéric Cazals, Pierre Kornprobst, 2012-11-06 Computational biology mathematical biology biology and biomedicine are currently undergoing spectacular progresses due to a synergy between technological advances and inputs from physics chemistry mathematics statistics and computer science The goal of this book is to evidence this synergy by describing selected developments in the following fields bioinformatics biomedicine and neuroscience This work is unique in two respects first by the variety and scales of systems studied and second by its presentation Each chapter provides the biological or medical context follows up with mathematical or algorithmic developments triggered by a specific problem and concludes with one or two success stories namely new insights gained thanks to these methodological developments It also highlights some unsolved and outstanding theoretical questions with a potentially high impact on these disciplines Two communities will be particularly interested in this book The first one is the vast community of applied mathematicians and computer scientists whose interests should be captured by the added value generated by the application of advanced concepts and algorithms to challenging biological or medical problems The second is the equally vast community of biologists Whether scientists or engineers they will find in this book a clear and self contained account of concepts and techniques from mathematics and computer science together with success stories on their favorite systems The variety of systems described represents a panoply of complementary conceptual tools On a practical level the resources listed at the end of each chapter databases software offer invaluable support for getting started on a specific topic in the fields of biomedicine bioinformatics and neuroscience

Handbook of Research on Systems Biology Applications in Medicine Daskalaki, Andriani, 2008-11-30 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 **Informatics for Health Professionals** Kathleen Mastrian, Dee McGonigle, 2019-12-19 Informatics for Health Professionals is an excellent resource to provide healthcare students and professionals with the foundational knowledge to integrate informatics principles into practice **Statistical Bioinformatics** Jae K. Lee, 2011-09-20 This book provides an essential understanding of statistical concepts necessary for the analysis of genomic and proteomic data using computational techniques The author presents both basic and advanced topics focusing on those that are relevant to the

computational analysis of large data sets in biology Chapters begin with a description of a statistical concept and a current example from biomedical research followed by more detailed presentation discussion of limitations and problems The book starts with an introduction to probability and statistics for genome wide data and moves into topics such as clustering classification multi dimensional visualization experimental design statistical resampling and statistical network analysis Clearly explains the use of bioinformatics tools in life sciences research without requiring an advanced background in math statistics Enables biomedical and life sciences researchers to successfully evaluate the validity of their results and make inferences Enables statistical and quantitative researchers to rapidly learn novel statistical concepts and techniques appropriate for large biological data analysis Carefully revisits frequently used statistical approaches and highlights their limitations in large biological data analysis Offers programming examples and datasets Includes chapter problem sets a glossary a list of statistical notations and appendices with references to background mathematical and technical material Features supplementary materials including datasets links and a statistical package available online Statistical Bioinformatics is an ideal textbook for students in medicine life sciences and bioengineering aimed at researchers who utilize computational tools for the analysis of genomic proteomic and many other emerging high throughput molecular data It may also serve as a rapid introduction to the bioinformatics science for statistical and computational students and audiences who have not experienced such analysis tasks before *Nursing Informatics and the Foundation of Knowledge* Dee McGonigle,Kathleen Mastrian,2014-03-06 Explains how nursing informatics relates to knowledge acquisition knowledge processing knowledge generation and knowledge dissemination and feedback all of which build the science of nursing

General Catalog -- University of California, Santa Cruz University of California, Santa Cruz,2008 **Genome Research**,2009 **Government Research Directory** Cengage Gale,2008-12 *Fuzzy Systems in Bioinformatics and Computational Biology* Yaochu Jin,Lipo Wang,2008-12-28 Biological systems are inherently stochastic and uncertain Thus research in bioinformatics biomedical engineering and computational biology has to deal with a large amount of uncertainties Fuzzy logic has shown to be a powerful tool in capturing different uncertainties in engineering systems In recent years fuzzy logic based modeling and analysis approaches are also becoming popular in analyzing biological data and modeling biological systems Numerous research and application results have been reported that demonstrated the effectiveness of fuzzy logic in solving a wide range of biological problems found in bioinformatics biomedical engineering and computational biology Contributed by leading experts world wide this edited book contains 16 chapters presenting representative research results on the application of fuzzy systems to genome sequence assembly gene expression analysis promoter analysis cis regulation logic analysis and synthesis reconstruction of genetic and cellular networks as well as biomedical problems such as medical image processing electrocardiogram data classification and anesthesia monitoring and control This volume is a valuable reference for researchers practitioners as well as graduate students working in the field of bioinformatics biomedical engineering and

computational biology [Computational Modeling in Bioengineering and Bioinformatics](#) Nenad Filipovic,2019-10-09

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