

## Book review

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### Review of "Computational Modeling of Genetic and Biochemical Networks" edited by James M. Bower and Hamid Bolouri Werner Dubitzky\*

Address: School of Biomedical Sciences, University of Ulster, Coleraine, Co. Londonderry, BT52 1SA, UK

Email: Werner Dubitzky\* - [w.dubitzky@ulster.ac.uk](mailto:w.dubitzky@ulster.ac.uk)

\* Corresponding author

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#### Book details

Bower JM, Bolouri H, (editors): *Computational Modeling of Genetic and Biochemical Networks* Cambridge, Massachusetts: London, England: The MIT Press; 2001. 390 pages, ISBN Number: 0262024810, \$35

Since the coming-of-age of the scientific discipline called *bioinformatics* it has become increasingly clear that computers in biology will be important not only for managing and analyzing biological and biomedical data but also for modeling and simulation of life processes and systems. The field concerned with this aspect of computers in biology has become known as *computational biology*. *Computational Modeling of Genetic and Biochemical Networks*, edited by James M. Bower and Hamid Bolouri, is a text that deals exclusively with computational biology concepts and applications. The book can be seen as an advocate of this increasingly important discipline as it presents a range of problems and methodologies that demonstrate that biology can be approached systematically and systematically by fully characterizing – through a combination of theory, simulation and experiment – entire biological systems such as metabolism, signal transduction and gene regulation, their interacting biochemical networks, or even higher levels of biological organization. The book is organized into two parts: Part I. Modeling Genetic Networks and Part II. Modeling Biochemical Networks.

The first part of the book is concerned with models of gene regulation, including protein-DNA and DNA-DNA interactions. Five chapters are devoted to this topic, by reviewing several tools and methods that are currently available for unraveling genetic regulatory networks at

various levels of resolution and abstraction. They include logical and probabilistic approaches, which are applied to problems including prokaryotic and eukaryotic systems. Chapter 1 provides an excellent introduction into the basics of gene regulation and reviews a range of methods and tools that have been used to model gene-regulatory mechanisms and systems. Against this background, Chapters 2 to 5 discuss different studies and methodologies in detail.

The second part of the book tackles protein interactions produced by gene regulation. It first considers interactions among few molecules and then goes on to present models aimed at understanding reactions and diffusion by large numbers of molecules. This part has six chapters. Although an overview chapter, like Chapter 1 in Part I is missing, collectively, the introductions of the six chapters provide an interesting and comprehensive overview of the different biological systems and their background and the relevant modeling methodologies and tools. The biological systems considered in this part include cell cycle regulation, signaling pathways, and excitable membranes and synaptic interactions.

Overall, the volume provides an excellent and broad overview of computational biology and the methodologies and tools needed to model and simulate complex biological systems. One message the book conveys is that tackling computational biology problems requires significant effort and considerable knowledge of mathematics, information technology (IT) and biology. While a great effort is made to cover the relevant background in biology, theory and IT, it could nevertheless be difficult to follow

# Computational Modeling Of Genetic And Biochemical Networks Computational Molecular Biology

**Mahmood A. Mahdavi**



## **Computational Modeling Of Genetic And Biochemical Networks Computational Molecular Biology:**

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**Computational Modeling Of Gene Regulatory Networks - A Primer** Hamid Bolouri, 2008-08-13 This book serves as an introduction to the myriad computational approaches to gene regulatory modeling and analysis and is written specifically with experimental biologists in mind Mathematical jargon is avoided and explanations are given in intuitive terms In cases where equations are unavoidable they are derived from first principles or at the very least an intuitive description is provided Extensive examples and a large number of model descriptions are provided for use in both classroom exercises as well as self guided exploration and learning As such the book is ideal for self learning and also as the basis of a semester long course for undergraduate and graduate students in molecular biology bioengineering genome sciences or systems biology a

**Computation in Cells and Tissues** R. Paton, Hamid Bolouri, W. Michael L. Holcombe, J. Howard Parish, Richard Tateson, 2013-03-14 The field of biologically inspired computation has coexisted with mainstream computing since the 1930s and the pioneers in this area include Warren McCulloch Walter Pitts Robert Rosen Otto Schmitt Alan Turing John von Neumann and Norbert Wiener Ideas arising out of studies of biology have permeated algorithmics automata theory artificial intelligence graphics information systems and software design Within this context the biomolecular cellular and tissue levels of biological organisation have had a considerable inspirational impact on the development of computational ideas Such innovations include neural computing systolic arrays genetic and immune algorithms cellular automata artificial tissues DNA computing and protein memories With the rapid growth in biological knowledge there remains a vast source of ideas yet to be tapped This includes developments associated with biomolecular genomic enzymic metabolic signalling and developmental systems and the various impacts on distributed adaptive hybrid and emergent computation This multidisciplinary book brings together a collection of chapters by biologists computer scientists engineers and mathematicians who were drawn together to examine the ways in which the interdisciplinary displacement of concepts and ideas could develop new insights into emerging computing paradigms Funded by the UK Engineering and Physical Sciences Research Council EPSRC the CytoCom Network formally met on five occasions to examine and discuss common issues in biology and computing that could be exploited to develop emerging models of computation

**Mathematical Analysis of Evolution, Information, and Complexity** Wolfgang Arendt, Wolfgang P. Schleich, 2009-07-10 Mathematical Analysis of Evolution Information and Complexity deals with the analysis of evolution information and complexity The time evolution of systems or processes is a central question in science this text covers a broad range of problems including diffusion processes neuronal networks quantum theory and cosmology Bringing together a

wide collection of research in mathematics information theory physics and other scientific and technical areas this new title offers elementary and thus easily accessible introductions to the various fields of research addressed in the book

**Artificial Intelligence: Theories, Models and Applications** John Darzentas, 2008-09-19 This book constitutes the refereed proceedings of the 5th Hellenic Conference on Artificial Intelligence SETN 2008 held at Syros Greece in October 2008 The 27 revised full papers together with 17 revised short papers were carefully reviewed and selected from 76 submissions The papers address any area of artificial intelligence particular fields of interest include Adaptive Systems AI and Creativity AI architectures Artificial Life Autonomous Systems Data Mining and Knowledge Discovery Hybrid Intelligent Systems Methods Intelligent Agents Multi agent Systems Intelligent Distributed Systems Intelligent Information Retrieval Intelligent Natural Interactivity Intelligent Virtual Environments Knowledge Representation and Reasoning Logic Programming Knowledge Based Systems Machine Learning Neural Nets Genetic Algorithms Natural Language Processing Planning and Scheduling Problem Solving Constraint Satisfaction Robotics Machine Vision Machine Sensing

**Computational Methods in Systems Biology** Corrado Priami, 2006-10-11 This book constitutes the refereed proceedings of the International Conference on Computational Methods in Systems Biology CMSB 2006 held in Trento Italy in October 2006 The 22 fully revised papers presented together with 2 invited talks were carefully reviewed and selected from 68 submissions The papers present a variety of techniques from computer sciences such as language design concurrency theory software engineering and formal methods

Mammalian Genomics Anatoly Ruvinsky, Jennifer A. Marshall Graves, 2005 Genomics has experienced a dramatic development during the last 15 20 years Data from mammalian genomes such as the human mouse and rat have already been published while others such as the dog cattle and chimpanzee will soon follow This book summarizes the current knowledge of mammalian genomics and offers a comparative analysis of genomes known today This analysis includes farm companion and lab animals Topics covered include structural and functional aspects of the mammalian genome mechanisms of genomic changes at the molecular level evolution of DNA sequences comparative chromosome mapping and painting genome databases gene prediction and the use of genomic information to understand inherited diseases Contributors include leading researchers from Europe USA Australia and Japan

*Bioinformatics* Mahmood A. Mahdavi, 2011-11-02 Bioinformatics Trends and Methodologies is a collection of different views on most recent topics and basic concepts in bioinformatics This book suits young researchers who seek basic fundamentals of bioinformatic skills such as data mining data integration sequence analysis and gene expression analysis as well as scientists who are interested in current research in computational biology and bioinformatics including next generation sequencing transcriptional analysis and drug design Because of the rapid development of new technologies in molecular biology new bioinformatic techniques emerge accordingly to keep the pace of in silico development of life science This book focuses partly on such new techniques and their applications in biomedical science These techniques maybe useful

in identification of some diseases and cellular disorders and narrow down the number of experiments required for medical diagnostic

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