

Natural Computing Series

Nataša Jonoska
Masahico Saito *Editors*

Discrete and Topological Models in Molecular Biology

 Springer

Discrete And Topological Models In Molecular Biology

Natural Computing Series

University of Michigan--Dearborn



Discrete And Topological Models In Molecular Biology Natural Computing Series:

Discrete and Topological Models in Molecular Biology Nataša Jonoska, Masahico Saito, 2013-12-23 Theoretical tools and insights from discrete mathematics theoretical computer science and topology now play essential roles in our understanding of vital biomolecular processes The related methods are now employed in various fields of mathematical biology as instruments to zoom in on processes at a molecular level This book contains expository chapters on how contemporary models from discrete mathematics in domains such as algebra combinatorics and graph and knot theories can provide perspective on biomolecular problems ranging from data analysis molecular and gene arrangements and structures and knotted DNA embeddings via spatial graph models to the dynamics and kinetics of molecular interactions The contributing authors are among the leading scientists in this field and the book is a reference for researchers in mathematics and theoretical computer science who are engaged with modeling molecular and biological phenomena using discrete methods It may also serve as a guide and supplement for graduate courses in mathematical biology or bioinformatics introducing nontraditional aspects of mathematical biology

Algebraic and Combinatorial Computational Biology Raina Robeva, Matthew Macauley, 2018-10-08 Algebraic and Combinatorial Computational Biology introduces students and researchers to a panorama of powerful and current methods for mathematical problem solving in modern computational biology Presented in a modular format each topic introduces the biological foundations of the field covers specialized mathematical theory and concludes by highlighting connections with ongoing research particularly open questions The work addresses problems from gene regulation neuroscience phylogenetics molecular networks assembly and folding of biomolecular structures and the use of clustering methods in biology A number of these chapters are surveys of new topics that have not been previously compiled into one unified source These topics were selected because they highlight the use of technique from algebra and combinatorics that are becoming mainstream in the life sciences Integrates a comprehensive selection of tools from computational biology into educational or research programs Emphasizes practical problem solving through multiple exercises projects and spinoff computational simulations Contains scalable material for use in undergraduate and graduate level classes and research projects Introduces the reader to freely available professional software Supported by illustrative datasets and adaptable computer code

ReCombinatorics Dan Gusfield, 2014-07-11 Combinatorial structure and algorithms for deducing genetic recombination history represented by ancestral recombination graphs and other networks and their role in the emerging field of phylogenetic networks In this book Dan Gusfield examines combinatorial algorithms to construct genealogical and exact phylogenetic networks particularly ancestral recombination graphs ARGs The algorithms produce networks or information about networks that serve as hypotheses about the true genealogical history of observed biological sequences and can be applied to practical biological problems Phylogenetic trees have been the traditional means to represent evolutionary history but there is a growing realization that networks rather

than trees are often needed most notably for recent human history This has led to the development of ARGs in population genetics and more broadly to phylogenetic networks ReCombinatorics offers an in depth rigorous examination of current research on the combinatorial graph theoretic structure of ARGs and explicit phylogenetic networks and algorithms to reconstruct or deduce information about those networks ReCombinatorics a groundbreaking contribution to the emerging field of phylogenetic networks connects and unifies topics in population genetics and phylogenetics that have traditionally been discussed separately and considered to be unrelated It covers the necessary combinatorial and algorithmic background material the various biological phenomena the mathematical population genetic and phylogenetic models that capture the essential elements of these phenomena the combinatorial and algorithmic problems that derive from these models the theoretical results that have been obtained related software that has been developed and some empirical testing of the software on simulated and real biological data

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 in depth 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

Big Data and Differential Privacy Nii O. Attoh-Okine, 2017-05-12 A comprehensive introduction to the theory and practice of contemporary data science analysis for railway track engineering Featuring a practical introduction to state of the art data analysis for railway track engineering Big Data and Differential Privacy Analysis Strategies for Railway Track Engineering addresses common issues with the implementation of big data applications while exploring the limitations advantages and disadvantages of more conventional methods In addition the book provides a unifying approach to analyzing large volumes of data in railway track engineering using an array of proven methods and software technologies Dr Attoh Okine considers some of today s most notable applications and implementations and highlights when a particular method or algorithm is most appropriate Throughout the book presents numerous real world examples to illustrate the latest railway engineering big data applications of predictive analytics such as the Union Pacific Railroad s use of big data to reduce train derailments increase the velocity of shipments and reduce emissions In addition to providing an overview of the latest software tools used to analyze the large amount of data obtained by railways Big Data and Differential Privacy Analysis Strategies for Railway Track Engineering Features a

unified framework for handling large volumes of data in railway track engineering using predictive analytics machine learning and data mining Explores issues of big data and differential privacy and discusses the various advantages and disadvantages of more conventional data analysis techniques Implements big data applications while addressing common issues in railway track maintenance Explores the advantages and pitfalls of data analysis software such as R and Spark as well as the Apache™ Hadoop data collection database and its popular implementation MapReduce Big Data and Differential Privacy is a valuable resource for researchers and professionals in transportation science railway track engineering design engineering operations research and railway planning and management The book is also appropriate for graduate courses on data analysis and data mining transportation science operations research and infrastructure management

NII ATTOH OKINE PhD PE is Professor in the Department of Civil and Environmental Engineering at the University of Delaware The author of over 70 journal articles his main areas of research include big data and data science computational intelligence graphical models and belief functions civil infrastructure systems image and signal processing resilience engineering and railway track analysis Dr Attoh Okine has edited five books in the areas of computational intelligence infrastructure systems and has served as an Associate Editor of various ASCE and IEEE journals

Language, Life, Limits Arnold Beckmann, Ersébet Csuhaj-Varjú, Klaus Meer, 2014-06-05 This book constitutes the refereed proceedings of the 10th Conference on Computability in Europe CiE 2014 held in Budapest Hungary in June 2014 The 42 revised papers presented were carefully reviewed and selected from 78 submissions and included together with 15 invited papers in this proceedings The conference had six special sessions computational linguistics bio inspired computation history and philosophy of computing computability theory online algorithms and complexity in automata theory

Unconventional Computation and Natural Computation Daniela Genova, Jarkko Kari, 2023-05-31 This book constitutes the proceedings of the 20th International Conference on Unconventional Computation and Natural Computation UCNC 2023 held in Jacksonville FL USA in March 13 17 2023 The UCNC conference series covers fundamental research on computation beyond the standard Turing model including computational models and methods inspired by nature and the computational properties of natural processes

Logical Modeling of Cellular Processes: From Software Development to Network Dynamics Matteo Barberis, Tomáš Helikar, 2019-08-16 Mathematical models have become invaluable tools for understanding the intricate dynamic behavior of complex biochemical and biological systems Among computational strategies logical modeling has been recently gaining interest as an alternative approach to address network dynamics Due to its advantages including scalability and independence of kinetic parameters the logical modeling framework is becoming increasingly popular to study the dynamics of highly interconnected systems such as cell cycle progression T cell differentiation and gene regulation Novel tools and standards have been developed to increase the interoperability of logical models which can now be employed to respond a variety of biological questions This Research Topic brings together the most recent and cutting edge approaches in the area

of logical modeling including among others novel biological applications software development and model analysis techniques

Infobiotics Vincenzo Manca, 2013-03-12 The book presents topics in discrete biomathematics Mathematics has been widely used in modeling biological phenomena However the molecular and discrete nature of basic life processes suggests that their logic follow principles that are intrinsically based on discrete and informational mechanisms The ultimate reason of polymers as key element of life is directly based on the computational power of strings and the intrinsic necessity of metabolism is related to the mathematical notion of multiset The switch of the two roots of bioinformatics suggests a change of perspective In bioinformatics the biologists ask computer scientists to assist them in processing biological data Conversely in infobiotics mathematicians and computer scientists investigate principles and theories yielding new interpretation keys of biological phenomena Life is too important to be investigated by biologists alone and though computers are essential to process data from biological laboratories many fundamental questions about life can be appropriately answered by a perspicacious intervention of mathematicians computer scientists and physicists who will complement the work of chemists biochemists biologists and medical investigators The volume is organized in seven chapters The first part is devoted to research topics Discrete information and life Strings and genomes Algorithms and Biorhythms Life Strategies the second one to mathematical backgrounds Numbers and Measures Languages and Grammars Combinations and Chances

Computational Matter Susan Stepney, Steen Rasmussen, Martyn Amos, 2018-07-20 This book is concerned with computing in materio that is unconventional computing performed by directly harnessing the physical properties of materials It offers an overview of the field covering four main areas of interest theory practice applications and implications Each chapter synthesizes current understanding by deliberately bringing together researchers across a collection of related research projects The book is useful for graduate students researchers in the field and the general scientific reader who is interested in inherently interdisciplinary research at the intersections of computer science biology chemistry physics engineering and mathematics

Applications of Membrane Computing Gabriel Ciobanu, Mario J. Pérez-Jiménez, Gheorghe

Păun, 2007-08-06 Membrane computing is a branch of natural computing which investigates computing models abstracted from the structure and functioning of living cells and from their interactions in tissues or higher order biological structures The models considered called membrane systems P systems are parallel distributed computing models processing multisets of symbols in cell like compartmental architectures In many applications membrane systems have considerable advantages among these are their inherently discrete nature parallelism transparency scalability and nondeterminism In dedicated chapters leading experts explain most of the applications of membrane computing reported so far in biology computer science computer graphics and linguistics The book also contains detailed reviews of the software tools used to simulate P systems

Springer Handbook of Model-Based Science Lorenzo Magnani, Tommaso Bertolotti, 2017-05-22 This handbook offers the first comprehensive reference guide to the interdisciplinary field of model based reasoning It highlights the role of

models as mediators between theory and experimentation and as educational devices as well as their relevance in testing hypotheses and explanatory functions The Springer Handbook merges philosophical cognitive and epistemological perspectives on models with the more practical needs related to the application of this tool across various disciplines and practices The result is a unique reliable source of information that guides readers toward an understanding of different aspects of model based science such as the theoretical and cognitive nature of models as well as their practical and logical aspects The inferential role of models in hypothetical reasoning abduction and creativity once they are constructed adopted and manipulated for different scientific and technological purposes is also discussed Written by a group of internationally renowned experts in philosophy the history of science general epistemology mathematics cognitive and computer science physics and life sciences as well as engineering architecture and economics this Handbook uses numerous diagrams schemes and other visual representations to promote a better understanding of the concepts This also makes it highly accessible to an audience of scholars and students with different scientific backgrounds All in all the Springer Handbook of Model Based Science represents the definitive application oriented reference guide to the interdisciplinary field of model based reasoning

Mathematical Reviews ,2004 **Topological Data Analysis for Genomics and Evolution** Raul Rabadan,Andrew J. Blumberg,2019-12-19 An introduction to geometric and topological methods to analyze large scale biological data includes statistics and genomic applications *Government Reports Announcements & Index* ,1993 **Index Medicus** ,2003 Vols for 1963 include as pt 2 of the Jan issue Medical subject headings **Abstracts of Papers Presented to the American Mathematical Society** American Mathematical Society,2003 *Dissertation Abstracts International* ,1996
Undergraduate Announcement University of Michigan--Dearborn,1987 **Annales zoologici Fennici** ,2008

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