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KEY=GENE - MARQUIS EDWARDS

Simple Mathematical Models of Gene Regulatory Dynamics

Springer **This is a short and self-contained introduction to the field of mathematical modeling of gene-networks in bacteria. As an entry point to the field, we focus on the analysis of simple gene-network dynamics. The notes commence with an introduction to the deterministic modeling of gene-networks, with extensive reference to applicable results coming from dynamical systems theory. The second part of the notes treats extensively several approaches to the study of gene-network dynamics in the presence of noise—either arising from low numbers of molecules involved, or due to noise external to the regulatory process. The third and final part of the notes gives a detailed treatment of three well studied and concrete examples of gene-network dynamics by considering the lactose operon, the tryptophan operon, and the lysis-lysogeny switch. The notes contain an index for easy location of particular topics as well as an extensive bibliography of the current literature. The target audience of these notes are mainly graduates students and young researchers with a solid mathematical background (calculus, ordinary differential equations, and probability theory at a minimum), as well as with basic notions of biochemistry, cell biology, and molecular biology. They are meant to serve as a readable and brief entry point into a field that is currently highly active, and will allow the reader to grasp the current state of research and so prepare them for defining and tackling new research problems.**

Mathematical Modelling & Computing in Biology and Medicine

5th ESMTB Conference 2002

Società Editrice Esculapio

Topology and Dynamics of an Artificial Genetic Regulatory Network Model

Handbook of Research on Computational Methodologies in Gene Regulatory Networks

IGI Global **"This book focuses on methods widely used in modeling gene networks including structure discovery, learning, and optimization"--Provided by publisher.**

Probabilistic Boolean Networks

The Modeling and Control of Gene Regulatory Networks

SIAM **The first comprehensive treatment of probabilistic Boolean networks, unifying different strands of current research and addressing emerging issues.**

Computer Methods

Academic Press **The combination of faster, more advanced computers and more quantitatively oriented biomedical researchers has recently yielded new and more precise methods for the analysis of biomedical data. These better analyses have enhanced the conclusions that can be drawn from biomedical data, and they have changed the way that experiments are designed and performed. This volume, along with previous and forthcoming Computer Methods volumes for the Methods in Enzymology serial, aims to inform biomedical researchers about recent applications of modern data analysis and simulation methods as applied to biomedical research. * Presents step-by-step computer methods and discusses the techniques in detail to enable their implementation in solving a wide range of problems * Informs biomedical researchers of the modern data analysis methods that have developed alongside computer hardware *Presents methods at the "nuts and bolts" level to identify and resolve a problem and analyze what the results mean**

Systems Biology

Modeling, Analysis, and Simulation

Springer Nature **This book discusses the mathematical simulation of biological systems, with a focus on the modeling of gene expression, gene regulatory networks and stem cell regeneration. The diffusion of morphogens is addressed by introducing various reaction-diffusion equations based on different hypotheses concerning the process of morphogen gradient formation. The robustness of steady-state gradients is also covered through boundary value problems. The introduction gives an overview of the relevant biological concepts (cells, DNA, organism development) and provides the requisite mathematical preliminaries on continuous dynamics and stochastic modeling. A basic understanding of calculus is assumed. The techniques described in this book encompass a wide range of mechanisms, from molecular behavior to population dynamics, and the inclusion of recent developments in the literature together with first-hand results make it an ideal reference for both new students and experienced researchers in the field of systems biology and**

applied mathematics.

Computational Methods in Systems Biology

20th International Conference, CMSB 2022, Bucharest, Romania, September 14–16, 2022, Proceedings

<u>Springer Nature</u> **This book constitutes the refereed proceedings of the 20th International Conference on Computational Methods in Systems Biology, CMSB 2022, held in Bucharest, Romania, in September 2022. The 13 full papers and 4 tool papers were carefully reviewed and selected from 43 submissions. CMSB focuses on modeling, simulation, analysis, design and control of biological systems. The papers are arranged thematically as follows: Chemical reaction networks; Boolean networks; continuous and hybrid models; machine learning; software.**

Frontiers in Biophysics, Vol. 6

<u>Allied Publishers</u>

Modeling with Nonsmooth Dynamics

<u>Springer Nature</u> **This volume looks at the study of dynamical systems with discontinuities. Discontinuities arise when systems are subject to switches, decisions, or other abrupt changes in their underlying properties that require a 'non-smooth' definition. A review of current ideas and introduction to key methods is given, with a view to opening discussion of a major open problem in our fundamental understanding of what nonsmooth models are. What does a nonsmooth model represent: an approximation, a toy model, a sophisticated qualitative capturing of empirical law, or a mere abstraction? Tackling this question means confronting rarely discussed indeterminacies and ambiguities in how we define, simulate, and solve nonsmooth models. The author illustrates these with simple examples based on genetic regulation and investment games, and proposes precise mathematical tools to tackle them. The volume is aimed at students and researchers who have some experience of dynamical systems, whether as a modelling tool or studying theoretically. Pointing to a range of theoretical and applied literature, the author introduces the key ideas needed to tackle nonsmooth models, but also shows the gaps in understanding that all researchers should be bearing in mind. Mike Jeffrey is a researcher and lecturer at the University of Bristol with a background in mathematical physics, specializing in dynamics, singularities, and asymptotics.**

Handbook of Swarm Intelligence

Concepts, Principles and Applications

<u>Springer Science & Business Media</u> **From nature, we observe swarming behavior in the form of ant colonies, bird flocking, animal herding, honey bees, swarming of bacteria, and many more. It is only in recent years that researchers have taken notice of such natural swarming systems as culmination of some form of innate collective intelligence, albeit swarm intelligence (SI) - a metaphor that inspires a myriad of computational problem-solving techniques. In computational intelligence, swarm-like algorithms have been successfully applied to solve many real-world problems in engineering and sciences. This handbook volume serves as a useful foundational as well as consolidatory state-of-art collection of articles in the field from various researchers around the globe. It has a rich collection of contributions pertaining to the theoretical and empirical study of single and multi-objective variants of swarm intelligence based algorithms like particle swarm optimization (PSO), ant colony optimization (ACO), bacterial foraging optimization algorithm (BFOA), honey bee social foraging algorithms, and harmony search (HS). With chapters describing various applications of SI techniques in real-world engineering problems, this handbook can be a valuable resource for researchers and practitioners, giving an in-depth flavor of what SI is capable of achieving.**

Applied Biological Engineering

Principles and Practice

<u>BoD – Books on Demand</u> **Biological engineering is a field of engineering in which the emphasis is on life and life-sustaining systems. Biological engineering is an emerging discipline that encompasses engineering theory and practice connected to and derived from the science of biology. The most important trend in biological engineering is the dynamic range of scales at which biotechnology is now able to integrate with biological processes. An explosion in micro/nanoscale technology is allowing the manufacture of nanoparticles for drug delivery into cells, miniaturized implantable microsensors for medical diagnostics, and micro-engineered robots for on-board tissue repairs. This book aims to provide an updated overview of the recent developments in biological engineering from diverse aspects and various applications in clinical and experimental research.**

Dynamics of Mathematical Models in Biology

Bringing Mathematics to Life

<u>Springer</u> **This volume focuses on contributions from both the mathematics and life science community surrounding the concepts of time and dynamicity of nature, two significant elements which are often overlooked in modeling process to avoid exponential computations. The book is divided into three distinct parts: dynamics of genomes and genetic variation, dynamics of motifs, and dynamics of biological networks. Chapters included in dynamics of genomes and genetic variation analyze the molecular mechanisms and evolutionary processes that shape the structure and function of genomes and those that govern genome dynamics. The dynamics of motifs portion of the volume provides an overview of current methods for motif searching in DNA, RNA and proteins, a key process to discover emergent properties of cells, tissues, and organisms. The part devoted to the dynamics of biological networks covers networks aptly discusses networks in complex biological functions and activities that interpret processes in cells. Moreover, chapters in this section examine several mathematical models and algorithms available for integration, analysis, and characterization. Once life scientists began to produce experimental data at an unprecedented pace, it become clear that mathematical models were necessary to interpret data, to structure information with the aim to unveil biological mechanisms, discover results, and make predictions. The second annual "Bringing Maths to Life" workshop held in Naples, Italy October 2015, enabled a bi-directional flow of ideas from and international group of mathematicians and biologists. The venue allowed mathematicians to introduce novel algorithms, methods, and software that may be useful to model aspects of life science, and life scientists posed new challenges for mathematicians.**

Mathematical Modeling in Systems Biology

An Introduction

<u>MIT Press</u> An introduction to the mathematical concepts and techniques needed for the construction and analysis of models in molecular systems biology. Systems techniques are integral to current research in molecular cell biology, and system-level investigations are often accompanied by mathematical models. These models serve as working hypotheses: they help us to understand and predict the behavior of complex systems. This book offers an introduction to mathematical concepts and techniques needed for the construction and interpretation of models in molecular systems biology. It is accessible to upper-level undergraduate or graduate students in life science or engineering who have some familiarity with calculus, and will be a useful reference for researchers at all levels. The first four chapters cover the basics of mathematical modeling in molecular systems biology. The last four chapters address specific biological domains, treating modeling of metabolic networks, of signal transduction pathways, of gene regulatory networks, and of electrophysiology and neuronal action potentials. Chapters 3-8 end with optional sections that address more specialized modeling topics. Exercises, solvable with pen-and-paper calculations, appear throughout the text to encourage interaction with the mathematical techniques. More involved end-of-chapter problem sets require computational software. Appendixes provide a review of basic concepts of molecular biology, additional mathematical background material, and tutorials for two computational software packages (XPPAUT and MATLAB) that can be used for model simulation and analysis.

Delay and Uncertainty in Human Balancing Tasks

<u>Springer Nature</u> This book demonstrates how delay differential equations (DDEs) can be used to compliment the laboratory investigation of human balancing tasks. This approach is made accessible to non-specialists by comparing mathematical predictions and experimental observations. For example, the observation that a longer pole is easier to balance on a fingertip than a shorter one demonstrates the essential role played by a time delay in the balance control mechanism. Another balancing task considered is postural sway during quiet standing. With the inverted pendulum as the driver and the feedback control depending on state variables or on an internal model, the feedback can be identified by determining a critical pendulum length and/or a critical delay. This approach is used to identify the nature of the feedback for the pole balancing and postural sway examples. Motivated by the question of how the nervous system deals with these feedback control challenges, there is a discussion of ''microchaotic'' fluctuations in balance control and how robust control can be achieved in the face of uncertainties in the estimation of control parameters. The final chapter suggests some topics for future research. Each chapter includes an abstract and a point-by-point summary of the main concepts that have been established. A particularly useful numerical integration method for the DDEs that arise in balance control is semi-discretization. This method is described and a MATLAB template is provided. This book will be a useful source for anyone studying balance in humans, other bipedal organisms and humanoid robots. Much of the material has been used by the authors to teach senior undergraduates in computational neuroscience and students in bio-systems, biomedical, mechanical and neural engineering.

Modeling and Analysis of Bio-molecular Networks

<u>Springer Nature</u> This book addresses a number of questions from the perspective of complex systems: How can we quantitatively understand the life phenomena? How can we model life systems as complex bio-molecular networks? Are there any methods to clarify the relationships among the structures, dynamics and functions of bio-molecular networks? How can we statistically analyse large-scale bio-molecular networks? Focusing on the modeling and analysis of bio-molecular networks, the book presents various sophisticated mathematical and statistical approaches. The life system can be described using various levels of bio-molecular networks, including gene regulatory networks, and protein-protein interaction networks. It first provides an overview of approaches to reconstruct various bio-molecular networks, and then discusses the modeling and dynamical analysis of simple genetic circuits, coupled genetic circuits, middle-sized and large-scale biological networks, clarifying the relationships between the structures, dynamics and functions of the networks covered. In the context of large-scale bio-molecular networks, it introduces a number of statistical methods for exploring important bioinformatics applications, including the identification of significant bio-molecules for network medicine and genetic engineering. Lastly, the book describes various state-of-art statistical methods for analysing omics data generated by high-throughput sequencing. This book is a valuable resource for readers interested in applying systems biology, dynamical systems or complex networks to explore the truth of nature.

MicroRNA Regulatory Network: Structure and Function

<u>Springer</u> This book discusses topics related to the topological structure and biological function of gene networks regulated by microRNAs. It focuses on analyzing the relation between topological structure and biological function, applying these theoretical results to gene networks involving microRNA, illustrating their biological mechanisms, and identifying the roles of microRNA in controlling various phenomena emerging from the networks. In addition, the book explains how to control the complex biological phenomena using mathematical tools and offers a new perspective on studying microRNA. It is a useful resource for graduate students and researchers who are working on or interested in microRNAs and gene network.

Dynamics of Coupled Map Lattices and of Related Spatially Extended Systems

<u>Springer Science & Business Media</u> This book is about the dynamics of coupled map lattices (CML) and of related spatially extended systems. It will be useful to post-graduate students and researchers seeking an overview of the state-of-the-art and of open problems in this area of nonlinear dynamics. The special feature of this book is that it describes the (mathematical) theory of CML and some related systems and their phenomenology, with some examples of CML modeling of concrete systems (from physics and biology). More precisely, the book deals with statistical properties of (weakly) coupled chaotic maps, geometric aspects of (chaotic) CML, monotonic spatially extended systems, and dynamical models of specific biological systems.

Structures and Boolean Dynamics in Gene Regulatory Networks

Handbook of Research on Systems Biology Applications in Medicine

<u>IGI Global</u> "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.

Analysis of Deterministic Cyclic Gene Regulatory Network Models with Delays

<u>Birkhäuser</u> This brief examines a deterministic, ODE-based model for gene regulatory networks (GRN) that incorporates nonlinearities and time-delayed feedback. An introductory chapter provides some insights into molecular biology and GRNs. The mathematical tools necessary for studying the GRN model are then reviewed, in particular Hill functions and Schwarzian derivatives. One chapter is devoted to the analysis of GRNs under negative feedback with time delays and a special case of a homogenous GRN is considered. Asymptotic stability analysis of GRNs under positive feedback is then considered in a separate chapter, in which conditions leading to bi-stability are derived. Graduate and advanced undergraduate students and researchers in control engineering, applied mathematics, systems biology and synthetic biology will find this brief to be a clear and concise introduction to the modeling and analysis of GRNs.

Geometrical Dynamics of Complex Systems

A Unified Modelling Approach to Physics, Control, Biomechanics, Neurodynamics and Psycho-Socio-Economical Dynamics

<u>Springer Science & Business Media</u> **Geometrical Dynamics of Complex Systems is a graduate?level monographic textbook. Itrepresentsacomprehensiveintroductionintorigorousgeometrical dynamicsofcomplexsystemsofvariousnatures. By?complexsystems?,inthis book are meant high?dimensional nonlinear systems, which can be (but not necessarily are) adaptive. This monograph proposes a uni?ed geometrical - proachtodynamicsofcomplexsystemsofvariouskinds:engineering,physical, biophysical, psychophysical, sociophysical, econophysical, etc. As their names suggest, all these multi?input multi?output (MIMO) systems have something in common: the underlying physics. However, instead of dealing with the pop- 1 ular ?soft complexity philosophy?, we rather propose a rigorous geometrical and topological approach. We believe that our rigorous approach has much greater predictive power than the soft one. We argue that science and te- nology is all about prediction and control. Observation, understanding and explanation are important in education at undergraduate level, but after that it should be all prediction and control. The main objective of this book is to show that high?dimensional nonlinear systems and processes of ?real life? can be modelled and analyzed using rigorous mathematics, which enables their complete predictability and controllability, as if they were linear systems. It is well?known that linear systems, which are completely predictable and controllable by de?nition ? live only in Euclidean spaces (of various - mensions). They are as simple as possible, mathematically elegant and fully elaborated from either scienti?c or engineering side. However, in nature, no- ing is linear. In reality, everything has a certain degree of nonlinearity, which means: unpredictability, with subsequent uncontrollability.**

Tools and Techniques in Biomolecular Science

<u>Oxford University Press</u> **This book reviews the theoretical concepts and experimental details underpinning the broad range of modern technologies that are currently being used to advance our understanding of the biomolecular sciences.**

Mathematical Models in the Biosciences II

<u>Yale University Press</u> **Volume Two of an award-winning professor's introduction to essential concepts of calculus and mathematical modeling for students in the biosciences This is the second of a two-part series exploring essential concepts of calculus in the context of biological systems. Building on the essential ideas and theories of basic calculus taught in Mathematical Models in the Biosciences I, this book focuses on epidemiological models, mathematical foundations of virus and antiviral dynamics, ion channel models and cardiac arrhythmias, vector calculus and applications, and evolutionary models of disease. It also develops differential equations and stochastic models of many biomedical processes, as well as virus dynamics, the Clancy-Rudy model to determine the genetic basis of cardiac arrhythmias, and a sketch of some systems biology. Based on the author's calculus class at Yale, the book makes concepts of calculus less abstract and more relatable for science majors and premedical students.**

Mathematics as a Tool

Tracing New Roles of Mathematics in the Sciences

<u>Springer</u> **This book puts forward a new role for mathematics in the natural sciences. In the traditional understanding, a strong viewpoint is advocated, on the one hand, according to which mathematics is used for truthfully expressing laws of nature and thus for rendering the rational structure of the world. In a weaker understanding, many deny that these fundamental laws are of an essentially mathematical character, and suggest that mathematics is merely a convenient tool for systematizing observational knowledge. The position developed in this volume combines features of both the strong and the weak viewpoint. In accordance with the former, mathematics is assigned an active and even shaping role in the sciences, but at the same time, employing mathematics as a tool is taken to be independent from the possible mathematical structure of the objects under consideration. Hence the tool perspective is contextual rather than ontological. Furthermore, tool-use has to respect conditions like suitability, efficacy, optimality, and others. There is a spectrum of means that will normally differ in how well they serve particular purposes. The tool perspective underlines the inevitably provisional validity of mathematics: any tool can be adjusted, improved, or lose its adequacy upon changing practical conditions.**

Computational Methods in Systems Biology

International Conference, CMSB 2006, Trento, Italy, October 18-19, 2006, Proceedings

<u>Springer</u> **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.**

Evolutionary Computation in Gene Regulatory Network Research

<u>John Wiley & Sons</u> **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.**

BIOMAT 2005

Proceedings of the International Symposium on Mathematical and Computational Biology, Rio de Janeiro, Brazil, 3-8 December 2005

World Scientific **This volume contains the contributions of the keynote speakers to the BIOMAT 2005 symposium, as well as a collection of selected papers by pioneering researchers. It provides a comprehensive review of the mathematical modeling of cancer development, Alzheimer''s disease, malaria, and aneurysm development. Various models for the immune system and epidemiological issues are analyzed and reviewed. The book also explores protein structure prediction by optimization and combinatorial techniques (Steiner trees). The coverage includes bioinformatics issues, regulation of gene expression, evolution, development, DNA and array modeling, and small world networks. Sample Chapter(s). Chapter 1: Modelling Aspects of Vascular Cancer Development (581 KB). Contents: Biological Modeling: A Mathematical Analysis of Cylindrical Shaped Aneurysms (T A Kwembe & S N Jones); On the Origin of Metazoans (F W Cummings); Optimal Control of Distributed Systems Applied to the Problems of Ambient Pollution (S F Arantes & J E M Rivera); Epidemiology and Immunology: Modeling the in Vivo Dynamics of Viral Infections (R M Ribeiro); The Basic Reproductive Rate in the Malaria Model (A P Wyse et al.); Epidemiological Model with Fast Dispersion (M R Ricard et al.); Protein Structure: Structure Prediction of Alpha-Helical Proteins (S R McAllister & C A Floudas); Steiner Minimal Trees, Twist Angles, and the Protein Folding Problem (J M Smith); Steiner Trees as Intramolecular Networks of the Biomacromolecular Structures (R P Mondaini); Bioinformatics: Optimization of Between Group Analysis of Gene Expression Disease Class Prediction (F Baty et al.); On Biclustering with Features Selection for Microarray Data Sets (P M Pardalos et al.); Simple and Effective Classifiers to Model Biological Data (R L Salvini et al.); and other papers. Readership: Graduate students and researchers in biology, mathematics and physics."**

The Princeton Guide to Evolution

Princeton University Press **The Princeton Guide to Evolution is a comprehensive, concise, and authoritative reference to the major subjects and key concepts in evolutionary biology, from genes to mass extinctions. Edited by a distinguished team of evolutionary biologists, with contributions from leading researchers, the guide contains some 100 clear, accurate, and up-to-date articles on the most important topics in seven major areas: phylogenetics and the history of life; selection and adaptation; evolutionary processes; genes, genomes, and phenotypes; speciation and macroevolution; evolution of behavior, society, and humans; and evolution and modern society. Complete with more than 100 illustrations (including eight pages in color), glossaries of key terms, suggestions for further reading on each topic, and an index, this is an essential volume for undergraduate and graduate students, scientists in related fields, and anyone else with a serious interest in evolution. Explains key topics in some 100 concise and authoritative articles written by a team of leading evolutionary biologists Contains more than 100 illustrations, including eight pages in color Each article includes an outline, glossary, bibliography, and cross-references Covers phylogenetics and the history of life; selection and adaptation; evolutionary processes; genes, genomes, and phenotypes; speciation and macroevolution; evolution of behavior, society, and humans; and evolution and modern society**

Animal Biotechnology

Models in Discovery and Translation

Academic Press **Animal Biotechnology: Models in Discovery and Translation, Second Edition, provides a helpful guide to anyone seeking a thorough review of animal biotechnology and its application to human disease and welfare. This updated edition covers vital fundamentals, including animal cell cultures, genome sequencing analysis, epigenetics and animal models, gene expression, and ethics and safety concerns, along with in-depth examples of implications for human health and prospects for the future. New chapters cover animal biotechnology as applied to various disease types and research areas, including in vitro fertilization, human embryonic stem cell research, biosensors, enteric diseases, biopharming, organ transplantation, tuberculosis, neurodegenerative disorders, and more. Highlights the latest biomedical applications of genetically modified and cloned animals, with a focus on cancer and infectious diseases Offers first-hand accounts of the use of biotechnology tools, including molecular markers, stem cells, animal cultures, tissue engineering, ADME and CAM Assay Includes case studies that illustrate safety assessment issues, ethical considerations, and intellectual property rights associated with the translation of animal biotechnology studies**

Models of Life

Cambridge University Press **An overview of current models of biological systems, reflecting the major advances that have been made over the past decade.**

Information Processing and Biological Systems

Springer Science & Business Media **Living beings require constant information processing for survival. In cells, information is being processed and propagated at various levels, from the gene regulatory network to chemical pathways, to the interaction with the environment. How this is achieved and how information is coded is still poorly understood. For example, what a cell interprets as information in the temporal level of an mRNA and what is interpreted as noise remains an open question. Recently, information theoretical methods and other tools, developed in the context of engineering and natural sciences, have been applied to study diverse biological processes. This book covers the latest findings on how information is processed in various biological processes, ranging from information processing and propagation in gene regulatory networks to information processing in natural language. An overview is presented of the state-of-the-art in information processing in biological systems and the opinion of current leaders in this research field on future research directions.**

Modular Studies of Gene Networks

In Numero Predictions, in Vivo Dynamics

Abstract: The deduction of phenotypic cellular responses from the structure and behavior of complex gene regulatory networks is one of the defining challenges of systems biology. This goal will require a detailed understanding of the modular components that constitute whole-genome regulation. This thesis explores computational and experimental techniques for studying the expression dynamics of gene regulatory networks. We first pursued an integrated approach, combining experimental work with a quantitative theoretical model, to analyze and describe the dynamics of a simple, isolated genetic module, an in vivo autocatalytic single-gene network. The network exhibited bistable expression states, which validated predictions arising from a system-specific mathematical description of the underlying biochemistry. Since the experiments revealed large fluctuations in the expression states, we augmented the model with noise terms and obtained striking agreement between model and experimental results. This work demonstrates that isolated gene networks, coupled with quantitative models which account for the stochastic nature of gene expression, can elucidate key properties of functional genetic modules. Next, we turned to the design of artificial genetic networks. Cellular AND/OR logic gates were constructed from well-characterized components that uniquely respond to applied stimuli. In contrast to the autocatalytic gene network study, logic gates were constructed to achieve simple, predetermined function setting the stage for detailed characterization.

Finally, we designed and utilized artificial RNA control modules as regulatory components of gene networks. These systems functioned as catalytic activators and repressors to regulate post-transcriptional gene expression. This universal type of switching strategy can target the expression of any prokaryotic gene and may be extended as a post-transcriptional regulator in eukaryotes. These simple networks represent a first step towards constructing a framework of logical cellular control, whereby biological processes can be controlled or monitored at the protein, DNA and RNA levels. Such a framework can lead to the modular dissection of whole cell regulatory networks.

Undergraduate Mathematics for the Life Sciences

Models, Processes, and Directions

MAA

A Variational Approach to Nonsmooth Dynamics

Applications in Unilateral Mechanics and Electronics

Springer This brief examines mathematical models in nonsmooth mechanics and nonregular electrical circuits, including evolution variational inequalities, complementarity systems, differential inclusions, second-order dynamics, Lur'e systems and Moreau's sweeping process. The field of nonsmooth dynamics is of great interest to mathematicians, mechanicians, automatic controllers and engineers. The present volume acknowledges this transversality and provides a multidisciplinary view as it outlines fundamental results in nonsmooth dynamics and explains how to use them to study various problems in engineering. In particular, the author explores the question of how to redefine the notion of dynamical systems in light of modern variational and nonsmooth analysis. With the aim of bridging between the communities of applied mathematicians, engineers and researchers in control theory and nonlinear systems, this brief outlines both relevant mathematical proofs and models in unilateral mechanics and electronics.

Multiple Aspects of DNA and RNA: from Biophysics to Bioinformatics

Lecture Notes of the Les Houches Summer School 2004

Elsevier This book is dedicated to the multiple aspects, that is, biological, physical and computational of DNA and RNA molecules. These molecules, central to vital processes, have been experimentally studied by molecular biologists for five decades since the discovery of the structure of DNA by Watson and Crick in 1953. Recent progresses (e.g. use of DNA chips, manipulations at the single molecule level, availability of huge genomic databases...) have revealed an imperious need for theoretical modelling. Further progresses will clearly not be possible without an integrated understanding of all DNA and RNA aspects and studies. The book is intended to be a desktop reference for advanced graduate students or young researchers willing to acquire a broad interdisciplinary understanding of the multiple aspects of DNA and RNA. It is divided in three main sections: The first section comprises an introduction to biochemistry and biology of nucleic acids. The structure and function of DNA are reviewed in R. Lavery's chapter. The next contribution, by V. Fritsch and E. Westhof, concentrates on the folding properties of RNA molecules. The cellular processes involving these molecules are reviewed by J. Kadonaga, with special emphasis on the regulation of transcription. These chapters does not require any preliminary knowledge in the field (except that of elementary biology and chemistry). The second section covers the biophysics of DNA and RNA, starting with basics in polymer physics in the contribution by R. Khokhlov. A large space is then devoted to the presentation of recent experimental and theoretical progresses in the field of single molecule studies. T. Strick's contribution presents a detailed description of the various micro-manipulation techniques, and reviews recent experiments on the interactions between DNA and proteins (helicases, topoisomerases, ...). The theoretical modeling of single molecules is presented by J. Marko, with a special attention paid to the elastic and topological properties of DNA. Finally, advances in the understanding of electrophoresis, a technique of crucial importance in everyday molecular biology, are exposed in T. Duke's contribution. The third section presents provides an overview of the main computational approaches to integrate, analyse and simulate molecular and genetic networks. First, J. van Helden introduces a series of statistical and computational methods allowing the identification of short nucleic fragments putatively involved in the regulation of gene expression from sets of promoter sequences controlling co-expressed genes. Next, the chapter by Samsonova et al. connects this issue of transcriptional regulation with that of the control of cell differentiation and pattern formation during embryonic development. Finally, H. de Jong and D. Thieffry review a series of mathematical approaches to model the dynamical behaviour of complex genetic regulatory networks. This contribution includes brief descriptions and references to successful applications of these approaches, including the work of B. Novak, on the dynamical modelling of cell cycle in different model organisms, from yeast to mammals. . Provides a comprehensive overview of the structure and function of DNA and RNA at the interface between physics, biology and information science.

Origination of Organismal Form

Beyond the Gene in Developmental and Evolutionary Biology

MIT Press A more comprehensive version of evolutionary theory that focuses as much on the origin of biological form as on its diversification. The field of evolutionary biology arose from the desire to understand the origin and diversity of biological forms. In recent years, however, evolutionary genetics, with its focus on the modification and inheritance of presumed genetic programs, has all but overwhelmed other aspects of evolutionary biology. This has led to the neglect of the study of the generative origins of biological form. Drawing on work from developmental biology, paleontology, developmental and population genetics, cancer research, physics, and theoretical biology, this book explores the multiple factors responsible for the origination of biological form. It examines the essential problems of morphological evolution—why, for example, the basic body plans of nearly all metazoans arose within a relatively short time span, why similar morphological design motifs appear in phylogenetically independent lineages, and how new structural elements are added to the body plan of a given phylogenetic lineage. It also examines discordances between genetic and phenotypic change, the physical determinants of morphogenesis, and the role of epigenetic processes in evolution. The book discusses these and other topics within the framework of evolutionary developmental biology, a new research agenda that concerns the interaction of development and evolution in the generation of biological form. By placing epigenetic processes, rather than gene sequence and gene expression changes, at the center of morphological origination, this book points the way to a more comprehensive theory of evolution.

Dynamical Models of Biology and Medicine

MDPI Mathematical and computational modeling approaches in biological and medical research are experiencing rapid growth globally. This Special Issue Book intends to scratch the surface of this exciting phenomenon. The subject areas covered involve general mathematical methods and their applications in biology and medicine, with an emphasis on work related to mathematical and computational modeling of the complex dynamics observed in biological and medical research. Fourteen rigorously reviewed papers were included in this Special Issue. These papers cover several timely topics relating to classical population biology, fundamental biology, and modern medicine. While the authors of these papers dealt with very different modeling questions, they were all motivated by specific applications in biology and medicine and employed innovative mathematical and computational methods to study the complex dynamics of their models. We hope that these papers detail case studies that will inspire many additional mathematical modeling efforts in biology and medicine

Mathematical Models of Cancer and Different Therapies

Unified Framework

<u>Springer Nature</u> **This book provides a unified framework for various currently available mathematical models that are used to analyze progression and regression in cancer development, and to predict its dynamics with respect to therapeutic interventions. Accurate and reliable model representations of cancer dynamics are milestones in the field of cancer research. Mathematical modeling approaches are becoming increasingly common in cancer research, as these quantitative approaches can help to validate hypotheses concerning cancer dynamics and thus elucidate the complexly interlaced mechanisms involved. Even though the related conceptual and technical information is growing at an exponential rate, the application of said information and realization of useful healthcare devices are lagging behind. In order to remedy this discrepancy, more interdisciplinary research works and course curricula need to be introduced in academic, industrial, and clinical organizations alike. To that end, this book reformulates most of the existing mathematical models as special cases of a general model, allowing readers to easily get an overall idea of cancer dynamics and its modeling. Moreover, the book will help bridge the gap between biologists and engineers, as it brings together cancer dynamics, the main steps involved in mathematical modeling, and control strategies developed for cancer management. This also allows readers in both medical and engineering fields to compare and contrast all the therapy-based models developed to date using a single source, and to identify unexplored research directions.**

Intermediate Physics for Medicine and Biology

<u>Springer</u> **This classic text has been used in over 20 countries by advanced undergraduate and beginning graduate students in biophysics, physiology, medical physics, neuroscience, and biomedical engineering. It bridges the gap between an introductory physics course and the application of physics to the life and biomedical sciences. Extensively revised and updated, the fifth edition incorporates new developments at the interface between physics and biomedicine. New coverage includes cyclotrons, photodynamic therapy, color vision, x-ray crystallography, the electron microscope, cochlear implants, deep brain stimulation, nanomedicine, and other topics highlighted in the National Research Council report BIO2010. As with the previous edition, the first half of the text is primarily biological physics, emphasizing the use of ideas from physics to understand biology and physiology, and the second half is primarily medical physics, describing the use of physics in medicine for diagnosis (mainly imaging) and therapy. Prior courses in physics and in calculus are assumed. Intermediate Physics for Medicine and Biology is also ideal for self study and as a reference for workers in medical and biological research. Over 850 problems test and enhance the student's understanding and provide additional biological examples. A solutions manual is available to instructors. Each chapter has an extensive list of references.**