Dynamic Models In Biology

This book and CD-ROM package integrates the use of STELLA software into the teaching of health, nutrition and physiology, and may be used on its own in nutrition and physiology courses, or can serve as a supplement to introduce the role that simulation modelling can play. The author presents key subjects ranging from the theory of metabolic control, through weight regulation to bone metabolism, and gives readers the tools to simulate these using the STELLA software. Topics include methods for simulation of gene expression, a multi-stage model of tumour development, theories of ageing, circadian rhythms and physiological time, as well as a model for managing weight loss and preventing obesity.

This book describes a powerful and flexible technique for the modeling of behavior, based on evolutionary principles. The technique employs stochastic dynamic programming and permits the analysis of behavioral adaptations wherein organisms respond to changes in their environment and in their own current physiological state. Models can be constructed to reflect sequential decisions concerned simultaneously with foraging, reproduction, predator avoidance, and other activities. The authors show how to construct and use dynamic behavioral models. Part I covers the mathematical background and computer programming, and then uses a paradigm of foraging under risk of predation to exemplify the general modeling technique. Part II consists of five "applied" chapters illustrating the scope of the dynamic modeling approach. They treat hunting behavior in lions, reproduction in insects, migrations of aquatic organisms, clutch size and parental care in birds, and movement of spiders and raptors. Advanced topics, including the study of dynamic evolutionarily stable strategies, are discussed in Part III.

Why do organisms become extremely abundant one year and then seem to disappear a few years later? Why do population outbreaks in particular species happen more or less regularly in certain locations, but only irregularly (or never at all) in other locations? Complex population dynamics have fascinated biologists for decades. By bringing together mathematical models, statistical analyses, and field experiments, this book offers a comprehensive new synthesis of the theory of population oscillations. Peter Turchin first reviews the conceptual tools that ecologists use to investigate population oscillations, introducing population modeling and the statistical analysis of time series data. He then provides an in-depth discussion of several case studies--including the larch budmoth, southern pine beetle, red grouse, voles and lemmings, snowshoe hare, and ungulates--to develop a new analysis of the mechanisms that drive population oscillations in nature. Through such work, the author argues, ecologists can develop general laws of population dynamics that will help turn ecology into a truly quantitative and predictive science. Complex Population Dynamics integrates theoretical and empirical studies into a major new synthesis of current knowledge about population dynamics. It is also a pioneering work that sets the course for ecology's future as a predictive science.

Dynamic Models in Biology offers an introduction to modern mathematical biology. This book provides a short introduction to modern mathematical methods in modeling dynamical phenomena and treats the broad topics of population dynamics, epidemiology, evolution, immunology, morphogenesis, and pattern formation. Primarily employing differential equations, the author presents accessible descriptions of difficult mathematical models. Recent mathematical results are included, but the author's presentation gives intuitive meaning to all the main formulae. Besides mathematicians who want to get acquainted with this relatively new field of applications, this book is useful for physicians, biologists, agricultural engineers, and environmentalists. Key Topics Include: Chaotic dynamics of populations The spread of sexually transmitted diseases Problems of the origin of life Models of immunology Formation of animal hide patterns The intuitive meaning of mathematical formulae explained with many figures Applying new mathematical results in modeling biological phenomena Miklos Farkas is a professor at Budapest University of Technology where he has researched and instructed mathematics for over thirty years. He has taught at universities in the former Soviet Union, Canada, Australia, Venezuela, Nigeria, India, and Columbia. Prof. Farkas received the 1999 Bolyai Award of the Hungarian Academy of Science and the 2001 Albert Szentgyorgyi Award of the Hungarian Ministry of Education. A 'down-to-earth' introduction to the growing field of modern mathematical biology Also includes appendices which provide background material that goes beyond advanced calculus and linear algebra

A Primer in Mathematical Models in Biology

An Introduction

Dynamic Models and Control of Biological Systems

Dynamical Systems in Population Biology

The Importance of Species

Covering the major topics of evolutionary game theory, Game-Theoretical Models in Biology presents both abstract and practical mathematical models of real biological situations. It discusses the static aspects of game theory in a mathematically rigorous way that is appealing to mathematicians. In addition, the authors explore many applications of game theory to biology, making the text useful to biologists as well. The book describes a wide range of topics in evolutionary games, including matrix games, replicator dynamics, the hawk-dove game, and the prisoner's dilemma. It covers the evolutionarily stable strategy, a key concept in biological games, and offers in-depth details of the mathematical models. Most chapters illustrate how to use MATLAB® to solve various games. Important biological phenomena, such as the sex ratio of so many species being close to a half, the evolution of cooperative behavior, and the existence of adornments (for example, the peacock's tail), have been explained using ideas underpinned by game theoretical modeling. Suitable for readers studying and working at the interface of mathematics and the life sciences, this book shows how evolutionary game theory is used in the modeling of these diverse biological phenomena.

Mathematical Biology has grown at an astonishing rate and has established itself as a distinct discipline. Mathematical modeling is now being applied in every major discipline in the biological sciences. Though the field has become increasingly large and specialized, this book remains important as a text that introduces some of the exciting problems which arise in the biological sciences and gives some indication of the wide spectrum of questions that modeling can address.

This book is intended as a text for a first course on creating and analyzing computer simulation models of biological systems. The expected audience for this book are students wishing to use dynamic models to interpret real data mueh as they would use standard statistical techniques. It is meant to provide both the essential principles as well as the details and equa tions applicable to a few particular systems and subdisciplines. Biological systems, however, encompass a vast, diverse array of topics and problems. This book discusses only a select number of these that I have found to be useful and interesting to biologists just beginning their appreciation of computer simulation. The examples chosen span classical mathematical models of well-studied systems to state-of-the-art topics such as cellular automata and artificial life. I have stressed the relationship between the models and the biology over mathematical analysis in order to give the reader a sense that mathematical models really are useful to biologists. In this light, I have sought examples that address fundamental and, I think, interesting biological questions. Almost all of the models are directly COIIl pared to quantitative data to provide at least a partial demonstration that some biological models can accurately predict.

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.

Systems Biology

Dynamical Systems for Biological Modeling

Mathematical Modeling in Systems Biology

An Introduction to Computational Systems Biology

Mathematical Biology II

Modeling Biological Systems

This comprehensively revised second edition of Computational Systems Biology discusses the experimental and theoretical foundations of the function of biological systems at the molecular, cellular or organismal level over temporal and spatial scales, as systems biology advances to provide clinical solutions to complex medical problems. In particular the work focuses on the engineering of biological systems and network modeling. Logical information flow aids understanding of basic building blocks of life through disease phenotypes Evolved principles gives insight into underlying organizational principles of biological organizations, and systems processes, governing functions such as adaptation or response patterns Coverage of technical tools and systems helps researchers to understand and resolve specific systems biology problems using advanced computation Multi-scale modeling on disparate scales aids researchers understanding of dependencies and constraints of spatio-temporal relationships fundamental to biological organization and function.

Dynamical Systems for Biological Modeling: An Introduction prepares both biology and mathematics students with the understanding and techniques necessary to undertake basic modeling of biological systems. It achieves this through the development and analysis of dynamical systems. The approach emphasizes qualitative ideas rather than explicit computations. Some technical details are necessary, but a qualitative approach emphasizing ideas is essential for understanding. The modeling approach helps students focus on essentials rather than extensive mathematical details, which is helpful for students whose primary interests are in sciences other than mathematics need or want. The book discusses a variety of biological modeling topics, including population biology, epidemiology, immunology, intraspecies competition, harvesting, predator-prey systems, structured populations, and more. The authors also include examples of problems with solutions and some exercises which follow the examples quite closely. In addition, problems are included which go beyond the examples, both in mathematical analysis and in the development of mathematical models for biological problems, in order to encourage deeper understanding and an eagerness to use mathematics in learning about biology.

This book provides an introduction to the analysis of stochastic dynamic models in biology and medicine. The main aim is to offer a coherent set of probabilistic techniques and mathematical tools which can be used for the simulation and analysis of various biological phenomena. These tools are illustrated on a number of examples. For each example, the biological background is described, and mathematical models are developed following a unified set of principles. These models are then analyzed and, finally, the biological implications of the mathematical results are interpreted. The biological topics covered include gene expression, biochemistry, cellular regulation, and cancer biology. The book will be accessible to graduate students who have a strong background in differential equations, the theory of nonlinear dynamical systems, Markovian stochastic processes, and both discrete and continuous state spaces, and who are familiar with the basic concepts of probability theory.

Many biologists and ecologists have developed models that find widespread use in theoretical investigations and in applications to organism behavior, disease control, population and metapopulation theory, ecosystem dynamics, and environmental management. This book captures and extends the process of model development by concentrating on the dynamic aspects of these processes and by providing the tools such that virtually anyone with basic knowledge in the Life Sciences can develop meaningful dynamic models. Examples of the systems modeled in the book range from models of cell development, the beating heart, the growth and spread of insects, spatial competition and extinction, to the spread and control of epidemics, including the conditions for the development of chaos. Key features: - easy-to-learn and easy-to-use software - examples from many subdisciplines of biology, covering models of cells, organisms, populations, and metapopulations - no prior computer or programming experience required Key benefits: - learn how to develop modeling skills and system thinking on your own rather than use models developed by others - be able to easily run models under alternative assumptions and investigate the implications of these assumptions for the dynamics of the biological system being modeled - develop skills to assess the dynamics of biological systems

Complex Population Dynamics

Nonlinear Dynamics, Mathematical Biology, And Social Science

Perspectives on Expendability and Triage

Wise Use Of Alternative Therapies

Modeling Dynamic Phenomena in Molecular and Cellular Biology

Modeling Dynamic Biological Systems

Population dynamics is an important subject in mathematical biology. A cen tral problem is to study the long-term behavior of modeling systems. Most of these systems are governed by various evolutionary equations such as difference, ordinary, functional, and partial differential equations (see, e. g. , [165, 142, 218, 119, 55]). As we know, interactive populations often live in a fluctuating environment

example, physical environmental conditions such as temperature and humidity and the availability of food, water, and other resources u
vary in time with seasonal or daily variations. Therefore, more realistic models should be nonautonomous systems. In particular, if the d
a model are periodic functions of time with commensurate period, a periodic system arises; if these periodic functions have different (n
periods, we get an almost periodic system. The existing reference books, from the dynamical systems point of view, mainly focus on
autonomous biological systems. The book of Hess [106J is an excellent reference for periodic parabolic boundary value problems with
applications to population dynamics. Since the publication of this book there have been extensive investigations on periodic, asymptotic
periodic, almost periodic, and even general nonautonomous biological systems, which in turn have motivated further development of the
theory of dynamical systems. In order to explain the dynamical systems approach to periodic population problems, let us consider, as a
illustration, two species periodic competitive systems dUI dt = !I(t,UI,U2), (O.

These lectures develop simple models of complex social processes using nonlinear dynamics and mathematical biology. Dynamical
analogies between seemingly disparate social and biological phenomena,revolutions and epidemics, arms races, and ecosystem
dynamics,are revealed and exploited. Nonlinear Dynamics, Mathematical Biology, and Social Science invites social scientists to relax,in so
cases abandon,the predominant assumption of perfectly informed utility maximization and explore social dynamics from such perspectiv
epidemiology and predator-prey theory. The volume includes a concentrated course on nonlinear dynamical systems.

Designed to explore the applications of mathematical techniques and methods related to biology, this text explores five areas: cell grow
enzymatic reactions, physiological tracers, biological fluid dynamics and diffusion. Topics essentially follow a course in elementary differe
equations — some linear algebra and graph theory; requires only a knowledge of elementary calculus.

Dynamic Systems Biology Modeling and Simuation consolidates and unifies classical and contemporary multiscale methodologies for
mathematical modeling and computer simulation of dynamic biological systems – from molecular/cellular, organ-system, on up to popula
levels. The book pedagogy is developed as a well-annotated, systematic tutorial – with clearly spelled-out and unified nomenclature – de
from the author's own modeling efforts, publications and teaching over half a century. Ambiguities in some concepts and tools are clari
and others are rendered more accessible and practical. The latter include novel qualitative theory and methodologies for recognizing
dynamical signatures in data using structural (multicompartmental and network) models and graph theory; and analyzing structural and
measurement (data) models for quantification feasibility. The level is basic-to-intermediate, with much emphasis on biomodeling from re
biodata, for use in real applications. Introductory coverage of core mathematical concepts such as linear and nonlinear differential and
difference equations, Laplace transforms, linear algebra, probability, statistics and stochastics topics; PLUS ……. The pertinent biology,
biochemistry, biophysics or pharmacology for modeling are provided, to support understanding the amalgam of "math modeling" with lif
sciences. Strong emphasis on quantifying as well as building and analyzing biomodels: includes methodology and computational tools for
parameter identifiability and sensitivity analysis; parameter estimation from real data; model distinguishability and simplification; and pra
bioexperiment design and optimization. Companion website provides solutions and program code for examples and exercises using Matla
Simulink, VisSim, SimBiology, SAAMII, AMIGO, Copasi and SBML-coded models. A full set of PowerPoint slides are available from the
author for teaching from his textbook. He uses them to teach a 10 week quarter upper division course at UCLA, which meets twice a v
there are 20 lectures. They can easily be augmented or stretched for a 15 week semester course. Importantly, the slides are editable, s
can be readily adapted to a lecturer's personal style and course content needs. The lectures are based on excerpts from 12 of the first
chapters of DSBMS. They are designed to highlight the key course material, as a study guide and structure for students following the f
content. The complete PowerPoint slide package (~25 MB) can be obtained by instructors (or prospective instructors) by emailing the
directly, at: joed@cs.ucla.edu

Exploring the Equations of Life

Dynamic Systems Biology Modeling and Simulation

Dynamic Modeling in Behavioral Ecology

A Primer on the Computational Biology of Excitable Cells

Dynamic Modeling in the Health Sciences

Dynamic Models in Biology

The emerging, multi-disciplinary field of systems biology is devoted to the study of the relationships between various parts of a biological system, and computer modeling plays a vital role in the drive to understand the processes of life from an holistic viewpoint. Advancements in experimental technologies in biology and medicine have generated an enormous amount of biological data on the dependencies and interactions of many different molecular cell processes, fueling the development of numerous computational methods for exploring this data. The mathematical formalism of Petri net theory is able to encompass many of these techniques. This essential text/reference presents a comprehensive overview of cutting-edge research in applications of Petri nets in systems biology, with contributions from an international selection of experts. Those unfamiliar with the field are also provided with a general introduction to systems biology, the foundations of biochemistry, and the basics of Petri net theory. Further chapters address Petri net modeling techniques for building and analyzing biological models, as well as network prediction approaches, before reviewing the applications to networks of different biological classification. Topics and features: investigates the modular, qualitative modeling of regulatory networks using Petri nets, and examines an Hybrid Functional Petri net simulation case study; contains a glossary of the concepts and notation used in the book, in addition to exercises at the end of each chapter; covers the topological analysis of metabolic and regulatory networks, the analysis of models of signaling networks, and the prediction of network structure; provides a biological case study on the conversion of logical networks into Petri nets; discusses discrete modeling, stochastic modeling, fuzzy modeling, dynamic pathway modeling, genetic regulatory network modeling, and quantitative analysis techniques; includes a Foreword by Professor Jens Reich, Professor of Bioinformatics at Humboldt University and Max Delbrück Center for Molecular Medicine in Berlin. This unique guide to the modeling of biochemical systems using Petri net concepts will be of real utility to researchers and students of computational biology, systems biology, bioinformatics, computer science, and biochemistry.

Linear and non-linear models of populations, molecular evolution, phylogenetic tree construction, genetics, and infectious diseases are presented with minimal prerequisites.

This textbook provides an introduction to dynamic modeling in molecular cell biology, taking a computational and intuitive approach. Detailed illustrations, examples, and exercises are included throughout the text. Appendices containing mathematical and computational techniques are provided as a reference tool.

From the spontaneous rapid firing of cortical neurons to the spatial diffusion of disease epidemics, biological systems exhibit rich dynamic behaviour over a vast range of time and space scales. Unifying many of these diverse phenomena, Dynamics of Biological Systems provides the computational and mathematical platform from which to understand the underlying processes of the phenomena. Through an extensive tour of various biological systems, the text introduces computational methods for simulating spatial diffusion processes in excitable media, such as the human heart, as well as mathematical tools for dealing with systems of nonlinear ordinary and partial differential equations, such as neuronal activation and disease diffusion. The mathematical models and computer simulations offer insight into the dynamics of temporal and spatial biological systems, including cardiac pacemakers, artificial electrical defibrillation, pandemics, pattern formation, flocking behaviour, the interaction of autonomous agents, and hierarchical and structured network topologies. Tools from complex systems and complex networks are also presented for dealing with real phenomenological systems. With exercises and projects in each chapter, this classroom-tested text shows students how to apply a variety of mathematical and computational techniques to model and analyze the temporal and spatial phenomena of biological systems. MATLAB® implementations of algorithms and case studies are available on the author's website.

A Theoretical/Empirical Synthesis (MPB-35)

This richly illustrated third edition provides a thorough training in practical mathematical biology and shows how exciting mathematical challenges can arise from a genuinely interdisciplinary involvement with the biosciences. It has been extensively updated and extended to cover much of the growth of mathematical biology. From the reviews: ""This book, a classical text in mathematical biology, cleverly combines mathematical tools with subject area sciences."--SHORT BOOK REVIEWS

Since the first edition of Stochastic Modelling for Systems Biology, there have been many interesting developments in the use of "likelihood-free" methods of Bayesian inference for complex stochastic models. Having been thoroughly updated to reflect this, this third edition covers everything necessary for a good appreciation of stochastic kinetic modelling of biological networks in the systems biology context. New methods and applications are included in the book, and the use of R for practical illustration of the algorithms has been greatly extended. There is a brand new chapter on spatially extended systems, and the statistical inference chapter has also been extended with new methods, including approximate Bayesian computation (ABC). Stochastic Modelling for Systems Biology, Third Edition is now supplemented by an additional software library, written in Scala, described in a new appendix to the book. New in the Third Edition New chapter on spatially extended systems, covering the spatial Gillespie algorithm for reaction diffusion master equation models in 1- and 2-d, along with fast approximations based on the spatial chemical Langevin equation Significantly expanded chapter on inference for stochastic kinetic models from data, covering ABC, including ABC-SMC Updated R package, including code relating to all of the new material New R package for parsing SBML models into simulatable stochastic Petri net models New open-source software library, written in Scala, replicating most of the functionality of the R packages in a fast, compiled, strongly typed, functional language Keeping with the spirit of earlier editions, all of the new theory is presented in a very informal and intuitive manner, keeping the text as accessible as possible to the widest possible readership. An effective introduction to the area of stochastic modelling in computational systems biology, this new edition adds additional detail and computational methods that will provide a stronger foundation for the development of more advanced courses in stochastic biological modelling. This book delivers a comprehensive and insightful account of applying mathematical modelling approaches to very large biological systems and networks—a fundamental aspect of computational systems biology. The book covers key modelling paradigms in detail, while at the same time retaining a simplicity that will appeal to those from less quantitative fields. Key Features: A hands-on approach to modelling Covers a broad spectrum of modelling, from static networks to dynamic models and constraint-based models Thoughtful exercises to test and enable understanding of concepts State-of-the-art chapters on exciting new developments, like community modelling and biological circuit design Emphasis on coding and software tools for systems biology Companion website featuring lecture videos, figure slides, codes, supplementary exercises, further reading, and appendices: https://ramanlab.github.io/SysBioBook/ An Introduction to Computational Systems Biology: Systems-Level Modelling of Cellular Networks is highly multi-disciplinary and will appeal to biologists, engineers, computer scientists, mathematicians and others.

Drawing on the latest research in the field, Systems Biology: Mathematical Modeling and Model Analysis presents many methods for modeling and analyzing biological systems, in particular cellular systems. It shows how to use predictive mathematical models to acquire and analyze knowledge about cellular systems. It also explores how the models are systematically applied in biotechnology. The first part of the book introduces biological basics, such as metabolism, signaling, gene expression, and control as well as mathematical modeling fundamentals, including deterministic models and thermodynamics. The text also discusses linear regression methods, explains the differences between linear and nonlinear regression, and illustrates how to determine input variables to improve estimation accuracy during experimental design. The second part covers intracellular processes, including enzymatic reactions, polymerization processes, and signal transduction. The author highlights the process–function–behavior sequence in cells and shows how modeling and analysis of signal transduction units play a mediating role between process and function. The third part presents theoretical methods that address the dynamics of subsystems and the behavior near a steady state. It covers techniques for determining different time scales, sensitivity analysis, structural kinetic modeling, and theoretical control engineering aspects, including a method

for robust control. It also explores frequent patterns (motifs) in biochemical networks, such as the feed-forward loop in the transcriptional network of E. coli. Moving on to models that describe a large number of individual reactions, the last part looks at how these cellular models are used in biotechnology. The book also explains how graphs can illustrate the link between two components in large networks with several interactions.

Dynamics of Biological Systems
Dynamical Models in Biology
Modeling in Systems Biology
Computational Cell Biology
Cellular Biophysics and Modeling
Systems Biology: Simulation of Dynamic Network States

The dynamic development of various processes is a central problem of biology and indeed of all the sciences. The mathematics describing that development is, in general, complicated, because the models that are realistic are usually nonlinear. Consequently many biologists may not notice a possible application of theory. They may be unable to decide whether a particular model captures the essence of a system, or to appreciate that analysis of a model can reveal important aspects of biological problems and may even describe in detail how a system works. The aim of this textbook is to remedy the situation by adopting a general approach to model analysis and applying it several times to problems (drawn primarily from molecular and cellular biology) of gradually increasing biological and mathematical complexity. Although material of considerable sophistication is included, little mathematical background is required – only some exposure to elementary calculus; appendixes supply the necessary mathematics and the author concentrates on concepts rather than techniques. He also emphasizes the role of computers in giving a full picture of model behavior and complementing more qualitative analysis. Some problems suitable for computer analysis are also included. This is a class-tested textbook suitable for a one-semester course for advanced undergraduate and beginning graduate students in biology or applied mathematics. It can also be used as a source book for teachers and a reference for specialists. Dynamic Systems Biology Modeling and Simuation consolidates and unifies classical and contemporary multiscale methodologies for mathematical modeling and computer simulation of dynamic biological systems – from molecular/cellular, organ-system, on up to population levels. The book pedagogy is developed as a well-annotated, systematic tutorial – with clearly spelled-out and unified nomenclature – derived from the author's own modeling efforts, publications and teaching over half a century. Ambiguities in some concepts and tools are clarified and others are rendered more accessible and practical. The latter include novel qualitative theory and methodologies for recognizing dynamical signatures in data using structural (multicompartmental and network) models and graph theory; and analyzing structural and measurement (data) models for quantification feasibility. The level is basic-to-intermediate, with much emphasis on biomodeling from real biodata, for use in real applications. Introductory coverage of core mathematical concepts such as linear and nonlinear differential and difference equations, Laplace transforms, linear algebra, probability, statistics and stochastic topics; PLUS ... The pertinent biology, biochemistry, biophysics or pharmacology for modeling are provided, to support understanding the amalgam of "math modeling" with life sciences. Strong emphasis on quantifying as well as building and analyzing biomodels: includes methodology and computational tools for parameter identifiability and sensitivity analysis; parameter estimation from real data; model distinguishability and simplification; and practical bioexperiment design and optimization. Companion website provides solutions and program code for examples and exercises using Matlab, Simulink, VisSim, SimBiology, SAAMII, AMIGO, Copasi and SBML-coded models.

At a time of unprecedented expansion in the life sciences, evolution is the one theory that transcends all of biology. Any observation of a living system must ultimately be interpreted in the context of its evolution. Evolutionary change is the consequence of mutation and natural selection, which are two concepts that can be described by mathematical equations. Evolutionary Dynamics is concerned with these equations of life. In this book, Martin A. Nowak draws on the languages of biology and mathematics to outline the mathematical principles according to which life evolves. His work introduces readers to the powerful yet simple laws that govern the evolution of living systems, no matter how complicated they might seem. Evolution has become a mathematical theory, Nowak suggests, and any idea of an evolutionary process or mechanism should be studied in the context of the mathematical equations of evolutionary dynamics. His book presents a range of analytical tools that can be used to this end: fitness landscapes, mutation matrices, genomic sequence space, random drift, quasispecies, replicators, the Prisoner's Dilemma, games in finite and infinite populations, evolutionary graph theory, games on grids, evolutionary kaleidoscopes, fractals, and spatial chaos. Nowak then shows how evolutionary dynamics applies to critical real-world problems, including the progression of viral diseases such as AIDS, the virulence of infectious agents, the unpredictable mutations that lead to cancer, the evolution of altruism, and even the evolution of human language. His book makes a clear and compelling case for understanding every living system—and everything that arises as a consequence of living systems—in terms of evolutionary dynamics.

This self-contained introduction to the fast-growing field of Mathematical Biology is written for students with a mathematical background. It sets the subject in a historical context and guides the reader towards questions of current research interest. A broad range of topics is covered including: Population dynamics, Infectious diseases, Population genetics and evolution, Dispersal, Molecular and cellular biology, Pattern formation, and Cancer modelling. Particular attention is paid to situations where the simple assumptions of homogenity made in early models break down and the process of mathematical modelling is seen in action.

A Primer on Modeling Infrastructure

Kinetic Modelling in Systems Biology
Essential Mathematical Biology
Systems-Level Modelling of Cellular Networks
Principles and Applications
A Biologist's Guide to Mathematical Modeling in Ecology and Evolution
This volume highlights problems from a range of biological and medical applications that can be interpreted as questions about system behavior or control. Topics include drug resistance in cancer and malaria, biological fluid dynamics, auto-regulation in the kidney, anti-coagulation therapy, evolutionary diversification and photo-transduction. Mathematical techniques used to describe and investigate these biological and medical problems include ordinary, partial and stochastic differentiation equations, hybrid discrete-continuous approaches, as well as 2 and 3D numerical simulation.
With more and more interest in how components of biological systems interact, it is important to understand the various aspects of systems biology. Kinetic Modelling in Systems Biology focuses on one of the main pillars in the future development of systems biology. It explores both the methods and applications of kinetic modeling in this emerging f
A textbook on mathematical modelling techniques with powerful applications to biology, combining theoretical exposition with exercises and examples.
Thirty years ago, biologists could get by with a rudimentary grasp of mathematics and modeling. Not so today. In seeking to answer fundamental questions about how biological systems function and change over time, the modern biologist is as likely to rely on sophisticated mathematical and computer-based models as traditional fieldwork. In this book, Sarah Otto and Troy Day provide biology students with the tools necessary to both interpret models and to build their own. The book starts at an elementary level of mathematical modeling, assuming that the reader has had high school mathematics and first-year calculus. Otto and Day then gradually build in depth and complexity, from classic models in ecology and evolution to more intricate class-structured and probabilistic models. The authors provide primers with instructive exercises to introduce readers to the more advanced subjects of linear algebra and probability theory. Through examples, they describe how models have been used to understand such topics as the spread of HIV, chaos, the age structure of a country, speciation, and extinction. Ecologists and evolutionary biologists today need enough mathematical training to be able to assess the power and limits of biological models and to develop theories and models themselves. This innovative book will be an indispensable guide to the world of mathematical models for the next generation of biologists. A how-to guide for developing new mathematical models in biology Provides step-by-step recipes for constructing and analyzing models Interesting biological applications Explores classical models in ecology and evolution Questions at the end of every chapter Primers cover important mathematical topics Exercises with answers Appendixes summarize useful rules Labs and advanced material available
From Molecular Mechanisms to Disease
Collective Behavior In Systems Biology
Spatial Models and Biomedical Applications
Mathematics in Population Biology
The Petri Net Approach
Mathematical Models in Biology

From controlling disease outbreaks to predicting heart attacks, dynamic models are increasingly crucial for understanding biological processes. Many universities are starting undergraduate programs in computational biology to introduce students to this rapidly growing field. In Dynamic Models in Biology, the first text on dynamic models specifically written for undergraduate students in the biological sciences, ecologist Stephen Ellner and mathematician John Guckenheimer teach students how to understand, build, and use dynamic models in biology. Developed from a course taught by Ellner and Guckenheimer at Cornell University, the book is organized around biological applications, with mathematics and computing developed through case studies at the molecular, cellular, and population levels. The authors cover both simple analytic models--the sort usually found in mathematical biology texts--and the complex computational models now used by both biologists and mathematicians. Linked to a Web site with computer-lab materials and exercises, Dynamic Models in Biology is a major new introduction to dynamic models for students in the biological sciences, mathematics, and engineering.
Collective Behavior In Systems Biology: A Primer on Modeling Infrastructure offers a survey of established and emerging methods for quantifying process behavior in cellular systems. It introduces and applies mathematics and related abstract methods to processes in biological systems - why they are used, how they work, and what they mean. Emphasizing differential equations in an interdisciplinary approach, this book discusses infrastructure for kinetic modeling, technological system and control theories, optimization, and process behavior in cellular networks. The knowledge that the reader gains will be valuable for entering and keeping up with a rapidly developing discipline. Introduces basics of mathematical and

abstract methods for understanding, predicting, and modifying collective behavior in cellular systems Targets biomedical professionals as well as computational specialists who are willing to take advantage of novel high-throughput data acquisition technologies

Biophysical models have been used in biology for decades, but they have been limited in scope and size. In this book, Bernhard Ø. Palsson shows how network reconstructions that are based on genomic and bibliomic data, and take the form of established stoichiometric matrices, can be converted into dynamic models using metabolomic and fluxomic data. The Mass Action Stoichiometric Simulation (MASS) procedure can be used for any cellular process for which data is available and allows a scalable step-by-step approach to the practical construction of network models. Specifically, it can treat integrated processes that need explicit accounting of small molecules and protein, which allows simulation at the molecular level. The material has been class-tested by the author at both the undergraduate and graduate level. All computations in the text are available online in MATLAB and MATHEMATICA® workbooks, allowing hands-on practice with the material.

Mathematical Models in Biology is an introductory book for readers interested in biological applications of mathematics and modeling in biology. A favorite in the mathematical biology community, it shows how relatively simple mathematics can be applied to a variety of models to draw interesting conclusions. Connections are made between diverse biological examples linked by common mathematical themes. A variety of discrete and continuous ordinary and partial differential equation models are explored. Although great advances have taken place in many of the topics covered, the simple lessons contained in this book are still important and informative. Audience: the book does not assume too much background knowledge--essentially some calculus and high-school algebra. It was originally written with third- and fourth-year undergraduate mathematical-biology majors in mind; however, it was picked up by beginning graduate students as well as researchers in math (and some in biology) who wanted to learn about this field.

Stochastic Modelling for Systems Biology, Third Edition

Evolutionary Dynamics

Computational Systems Biology

What every neuroscientist should know about the mathematical modeling of excitable cells, presented at an introductory level. A great many species are threatened by the expanding human population. Though the public generally favors environmental protection, conservation does not come without sacrifice and cost. Many decision makers wonder if every species is worth the trouble. Of what consequence would the extinction of, say, spotted owls or snail darters be? Are some species expendable? Given the reality of limited money for conservation efforts, there is a compelling need for scientists to help conservation practitioners set priorities and identify species most in need of urgent attention. Ecology should be capable of providing guidance that goes beyond the obvious impulse to protect economically valuable species (salmon) or aesthetically appealing ones (snow leopards). Although some recent books have considered the ecosystem services provided by biodiversity as an aggregate property, this is the first to focus on the value of particular species. It provides the scientific approaches and analyses available for asking what we can expect from losing (or gaining) species. The contributors are outstanding ecologists, theoreticians, and evolutionary biologists who gathered for a symposium honoring Robert T. Paine, the community ecologist who experimentally demonstrated that a single predator species can act as a keystone species whose removal dramatically alters entire ecosystem communities. They build on Paine's work here by exploring whether we can identify species that play key roles in ecosystems before they are lost forever. These are some of our finest ecologists asking some of our hardest questions. They are, in addition to the editors, S.E.B. Abella, G. C. Chang, D. Doak, A. L. Downing, W. T. Edmondson, A. S. Flecker, M. J. Ford, C.D.G. Harley, E. G. Leigh Jr., S. Lubetkin, S. M. Louda, M. Marvier, P. McElhany, B. A. Menge, W. F. Morris, S. Naeem, S. R. Palumbi, A. G. Power, T. A. Rand, R. B. Root, M. Ruckelshaus, J. Ruesink, D. E. Schindler, T. W. Schoener, D. Simberloff, D. A. Spiller, M. J. Wonham, and J. T. Wootton.