Mathematical Models In Biology

Dynamic Models in BiologyStochastic Models in BiologyMathematical Models in BiologyModels in BiologyA Primer in Mathematical Models in BiologyMathematical Models in BiologyLinear Models in BiologyTheoretical Models in BiologySingle-Cell-Based Models in Biology and MedicineNeutral Models in BiologyMathematical Models for Society and BiologyDynamical Models in BiologyModelling, Analysis and Optimization of BiosystemsModeling Biological Systems:Systems BiologyMathematical Modeling in Systems BiologyModel-Based Hypothesis Testing in BiomedicineTheoretical Models in BiologyModeling Dynamic Phenomena in Molecular and Cellular BiologyA Biologist's Guide to Mathematical Modeling in Ecology and Evolution Stephen P. Ellner Narendra S. Goel Elizabeth Spencer Allman David Brown Lee A. Segel Valeria Zazzu Michael R. Cullen Glenn W. Rowe Alexander Anderson Matthew H. Nitecki Edward Beltrami Miklós Farkas Werner Krabs James W. Haefner Andreas Kremling Brian P. Ingalls Rikard Johansson Glenn W. Rowe Lee A. Segel Sarah P. Otto

Dynamic Models in Biology Stochastic Models in Biology Mathematical Models in Biology Models in Biology A Primer in Mathematical Models in Biology Mathematical Models in Biology Linear Models in Biology Theoretical Models in Biology Single-Cell-Based Models in Biology and Medicine Neutral Models in Biology Mathematical Models for Society and Biology Dynamical Models in Biology Modelling, Analysis and Optimization of Biosystems Modeling Biological Systems: Systems Biology Mathematical Modeling in Systems Biology Model-Based Hypothesis Testing in Biomedicine Theoretical Models in Biology Modeling Dynamic Phenomena in Molecular and Cellular Biology A Biologist's Guide to Mathematical Modeling in Ecology and Evolution *Stephen P. Ellner Narendra S. Goel Elizabeth Spencer Allman David Brown Lee A. Segel Valeria Zazzu Michael R. Cullen Glenn W. Rowe Alexander Anderson Matthew H. Nitecki Edward Beltrami Miklós Farkas Werner Krabs James W. Haefner Andreas Kremling Brian P. Ingalls Rikard Johansson Glenn W. Rowe Lee A. Segel Sarah P. Otto*

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 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

stochastic models in biology describes the usefulness of the theory of stochastic process in studying biological phenomena the book describes analysis of biological systems and experiments though probabilistic models rather than deterministic methods the text reviews the mathematical analyses for modeling different biological systems such as the random processes continuous in time and discrete in state space the book also discusses population growth and extinction through malthus law and the work of macarthur and wilson the text then explains the dynamics of a population of interacting species the book also addresses population genetics under systematic evolutionary pressures known as deterministic equations and genetic changes in a finite population known as stochastic equations the text then turns to stochastic modeling of biological systems at the molecular level particularly the kinetics of biochemical reactions the book also presents various useful equations such as the differential equation for generating functions for birth and death processes the text can prove valuable for biochemists cellular biologists and researchers in the medical and chemical field who are tasked to perform data analysis

this introductory textbook on mathematical biology focuses on discrete models across a variety of biological subdisciplines biological topics treated include linear and non linear models of populations markov models of molecular evolution phylogenetic tree construction genetics and infectious disease models the coverage of models of molecular evolution and phylogenetic tree construction from dna sequence data is unique among books at this level computer investigations with matlab are incorporated throughout in both exercises and more extensive projects to give readers hands on experience with the mathematical models developed matlab programs accompany the text mathematical tools such as matrix algebra eigenvector analysis and basic probability are motivated by biological models and given self contained developments so that mathematical prerequisites are minimal

this text provides an introduction to the use of mathematical models in biology the statistical techniques for fitting and testing them and associated computing methods the properties of models and methods of fitting and testing are demonstrated by computer simulation illustrations

this textbook introduces differential equations biological applications and simulations and emphasizes molecular events biochemistry and enzyme kinetics excitable systems neural signals and small protein and genetic circuits a primer on mathematical models in biology will appeal to readers because it grew out of a course that the popular and highly respected applied mathematician lee segel taught at the weizmann institute and it represents his unique perspective combines clear and useful mathematical methods with applications that illustrate the power of such tools and includes many exercises in reasoning modeling and simulations

this book presents an exciting collection of contributions based on the workshop bringing maths to life held october 27 29 2014 in naples italy the state of the art research in biology and the statistical and analytical challenges facing huge masses of data collection are treated in this work specific topics explored in depth surround the sessions and special invited sessions of the workshop and include genetic variability via differential expression molecular dynamics and

modeling complex biological systems viewed from quantitative models and microscopy images processing to name several in depth discussions of the mathematical analysis required to extract insights from complex bodies of biological datasets to aid development in the field novel algorithms methods and software tools for genetic variability molecular dynamics and complex biological systems are presented in this book researchers and graduate students in biology life science and mathematics statistics will find the content useful as it addresses existing challenges in identifying the gaps between mathematical modeling and biological research the shared solutions will aid and promote further collaboration between life sciences and mathematics

this book surveys theoretical models in three broad areas of biology the origin of life the immune system and memory in the brain introducing mathematical and mainly computational models that have been used to construct simulations most current books on theoretical biology fall into one of two categories a books that specialize in one area of biology and treat theoretical models in considerable depth and b books that concentrate on purely mathematical models with computers used only to find numerical solutions to differential equations for example although some mathmatical models are considered in this book the main emphasis is on stochastic computer modles of biological systems such techniques have a much greater potential for producting detailed realistic models of individual systems and are likely to be the preferred modelling methods of the future by considering three different areas in biology the book shows how several of these modelling techniques have been successfully applied in diverse areas put simply this book is important becuase it shows how the power of modern computers is allowing researchers in theoretical biology to break free of the constraints on modelling that were imposed by the traditional differential equation approach anyone who is interested in the theoretical models of complicated living systems should have this in his or her library g b ermentrout bulletin of mathematical biology

many different single cell based models have been developed and applied to biological and medical problems computational approaches used are monte carlo simulations energy minimisation techniques volume conservation laws solutions of the equations of motion for each individual cell or for each point on the cell membrane they differ in the level of detail that defines the cell structure and subsequently in the number of individual cells that the model can incorporate this volume presents a collection of mathematical and computational single cell based models and their application the main sections cover four general model groupings hybrid cellular automata cellular potts lattice free cells and viscoelastic cells each section is introduced by a discussion of the applicability of the particular modelling approach and its advantages and disadvantages which will make the book suitable for students starting research in mathematical biology as well as scientists modelling multicellular processes

neutral models are constructed to help scientists understand complex patterns of form structure or behavior that may not be observed directly in this unique volume eight distinguished scientists present a comprehensive study of the use of neutral models in testing biological theories they describe the principles of model testing and explore how they are applied to

research in molecular biology genetics ecology evolution and paleontology in addition to the editors the contributors include stephen stigler david raup paul harvey l b slobodkin stuart kauffman william wimsatt and james crow

mathematical modeling for society and biology engagingly relates mathematics to compelling real life problems in biology and contemporary society it shows how mathematical tools can be used to gain insight into these modern common problems to provide effective real solutions beltrami s creative non threatening approach draws on a wealth of interesting examples pertaining to current social and biological issues central ideas appear again in different contexts throughout the book showing the general unity of the modeling process the models are strikingly novel and based on issues of real concern most have never appeared in book form through the relevance of these models mathematics becomes not just figures and numbers but a means to a more refined understanding of the world

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

mathematical models in biology and medicine cannot be based on natural laws as it is the case with physics and chemistry this is due to the fact that biological and medical processes are concerned with living organisms mathematical models however can be used as a language by which certain aspects of biological or medical processes can be expressed in general several mathematical models can be designed in order to describe a biological or medical process and there is no unique criterion which model gives the best description this book presents several of these models and shows applications of them to different biological and medical problems the book shows that operations research expertise is necessary in respect to modeling analysis and optimization of biosystems

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 sy

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

the utilization of mathematical tools within biology and medicine has traditionally been less widespread compared to other hard sciences such as physics and chemistry however an increased need for tools such as data processing bioinformatics statistics and mathematical

modeling have emerged due to advancements during the last decades these advancements are partly due to the development of high throughput experimental procedures and techniques which produce ever increasing amounts of data for all aspects of biology and medicine these data reveal a high level of inter connectivity between components which operate on many levels of control and with multiple feedbacks both between and within each level of control however the availability of these large scale data is not synonymous to a detailed mechanistic understanding of the underlying system rather a mechanistic understanding is gained first when we construct a hypothesis and test its predictions experimentally identifying interesting predictions that are quantitative in nature generally requires mathematical modeling this in turn requires that the studied system can be formulated into a mathematical model such as a series of ordinary differential equations where different hypotheses can be expressed as precise mathematical expressions that influence the output of the model within specific sub domains of biology the utilization of mathematical models have had a long tradition such as the modeling done on electrophysiology by hodgkin and huxley in the 1950s however it is only in recent years with the arrival of the field known as systems biology that mathematical modeling has become more commonplace the somewhat slow adaptation of mathematical modeling in biology is partly due to historical differences in training and terminology as well as in a lack of awareness of showcases illustrating how modeling can make a difference or even be required for a correct analysis of the experimental data in this work i provide such showcases by demonstrating the universality and applicability of mathematical modeling and hypothesis testing in three disparate biological systems in paper ii we demonstrate how mathematical modeling is necessary for the correct interpretation and analysis of dominant negative inhibition data in insulin signaling in primary human adipocytes in paper iii we use modeling to determine transport rates across the nuclear membrane in yeast cells and we show how this technique is superior to traditional curve fitting methods we also demonstrate the issue of population heterogeneity and the need to account for individual differences between cells and the population at large in paper iv we use mathematical modeling to reject three hypotheses concerning the phenomenon of facilitation in pyramidal nerve cells in rats and mice we also show how one surviving hypothesis can explain all data and adequately describe independent validation data finally in paper i we develop a method for model selection and discrimination using parametric bootstrapping and the combination of several different empirical distributions of traditional statistical tests we show how the empirical log likelihood ratio test is the best combination of two tests and how this can be used not only for model selection but also for model discrimination in conclusion mathematical modeling is a valuable tool for analyzing data and testing biological hypotheses regardless of the underlying biological system further development of modeling methods and applications are therefore important since these will in all likelihood play a crucial role in all future aspects of biology and medicine especially in dealing with the burden of increasing amounts of data that is made available with new experimental techniques användandet av matematiska verktyg har inom biologi och medicin traditionellt sett varit mindre utbredd jämfört med andra ämnen inom naturvetenskapen såsom fysik och kemi ett ökat behov av verktyg som databehandling bioinformatik statistik och matematisk modellering har trätt fram tack vare framsteg under de senaste decennierna dessa framsteg är delvis ett resultat av utvecklingen av storskaliga datainsamlingstekniker inom alla områden av

biologi och medicin så har dessa data avslöjat en hög nivå av interkonnektivitet mellan komponenter verksamma på många kontrollnivåer och med flera återkopplingar både mellan och inom varje nivå av kontroll tillgång till storskaliga data är emellertid inte synonymt med en detaljerad mekanistisk förståelse för det underliggande systemet snarare uppnås en mekanisk förståelse först när vi bygger en hypotes vars prediktioner vi kan testa experimentellt att identifiera intressanta prediktioner som är av kvantitativ natur kräver generellt sett matematisk modellering detta kräver i sin tur att det studerade systemet kan formuleras till en matematisk modell såsom en serie ordinära differentialekvationer där olika hypoteser kan uttryckas som precisa matematiska uttryck som påverkar modellens output inom vissa delområden av biologin har utnyttjandet av matematiska modeller haft en lång tradition såsom den modellering gjord inom elektrofysiologi av hodgkin och huxley på 1950 talet det är emellertid just på senare år med ankomsten av fältet systembiologi som matematisk modellering har blivit ett vanligt inslag den något långsamma adapteringen av matematisk modellering inom biologi är bl a grundad i historiska skillnader i träning och terminologi samt brist på medvetenhet om exempel som illustrerar hur modellering kan göra skillnad och faktiskt ofta är ett krav för en korrekt analys av experimentella data i detta arbete tillhandahåller jag sådana exempel och demonstrerar den matematiska modelleringens och hypotestestningens allmängiltighet och tillämpbarhet i tre olika biologiska system i arbete ii visar vi hur matematisk modellering är nödvändig för en korrekt tolkning och analys av dominant negativ inhiberingsdata vid insulinsignalering i primära humana adipocyter i arbete iii använder vi modellering för att bestämma transporthastigheter över cellkärnmembranet i jästceller och vi visar hur denna teknik är överlägsen traditionella kurvpassningsmetoder vi demonstrerar också frågan om populationsheterogenitet och behovet av att ta hänsyn till individuella skillnader mellan celler och befolkningen som helhet i arbete iv använder vi matematisk modellering för att förkasta tre hypoteser om hur fenomenet facilitering uppstår i pyramidala nervceller hos råttor och möss vi visar också hur en överlevande hypotes kan beskriva all data inklusive oberoende valideringsdata slutligen utvecklar vi i arbete i en metod för modellselektion och modelldiskriminering med hjälp av parametrisk bootstrapping samt kombinationen av olika empiriska fördelningar av traditionella statistiska tester vi visar hur det empiriska log likelihood ratio testet är den bästa kombinationen av två tester och hur testet är applicerbart inte bara för modellselektion utan också för modelldiskriminering sammanfattningsvis är matematisk modellering ett värdefullt verktyg för att analysera data och testa biologiska hypoteser oavsett underliggande biologiskt system vidare utveckling av modelleringsmetoder och tillämpningar är därför viktigt eftersom dessa sannolikt kommer att spela en avgörande roll i framtiden för biologi och medicin särskilt när det gäller att hantera belastningen från ökande datamängder som blir tillgänglig med nya experimentella tekniker

this book surveys theoretical models in three broad areas of biology the origin of life the immune system and memory in the brain introducing mathematical and mainly computational methods that have been used to construct simulations most current books on theoretical biology fall into one of two categories a books that specialize in one area of biology and treat theoretical models in considerable depth and b books that concentrate on purely mathematical models with computers used only to find numerical solutions to differential equations for example although some mathematical models are considered in this book the main emphasis is

on stochastic computer models of biological systems such techniques have a much greater potential for producing detailed realistic models of individual systems and are likely to be the preferred modelling methods of the future by considering three different areas in biology the book shows how several of these modelling techniques have been successfully applied in diverse areas put simply this book is important because it shows how the power of modern computers is allowing researchers in theoretical biology to break free of the constraints modelling that were imposed by the traditional differential equation approach

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

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

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