

Mathematical Models In Biology

Models in Biology Dynamic Models in Biology Stochastic Models in Biology Mathematical Models in Biology Mathematical Models in Biology A Primer in Mathematical Models in Biology Linear Models in Biology Mathematical Models for Society and Biology Mathematical Models in Biology and Medicine Mathematical Modeling in Systems Biology Neutral Models in Biology Theoretical Models in Biology Modeling Biological Systems: Dynamical Models in Biology Single-Cell-Based Models in Biology and Medicine Model-Based Hypothesis Testing in Biomedicine A Biologist's Guide to Mathematical Modeling in Ecology and Evolution Theoretical Models in Biology David Brown Stephen P. Ellner Narendra S. Goel Valeria Zazu Elizabeth Spencer Allman Manfred Dietrich Laubichler Elisabeth S. Allman Lee A. Segel Michael R. Cullen Edward Beltrami IFIP-TC4 Working Conference on Mathematical Models in Biology and Medicine \$ (1972 : Varna, Bulgarie) Brian P. Ingalls Matthew H. Nitecki Glenn W. Rowe James W. Haefner Miklós Farkas Alexander Anderson Rikard Johansson Sarah P. Otto Glenn W. Rowe Models in Biology Dynamic Models in Biology Stochastic Models in Biology Mathematical Models in Biology Mathematical Models in Biology Modeling Biology Mathematical Models in Biology A Primer in Mathematical Models in Biology Linear Models in Biology Mathematical Models for Society and Biology Mathematical Models in Biology and Medicine Mathematical Modeling in Systems Biology Neutral Models in Biology Theoretical Models in Biology Modeling Biological Systems: Dynamical Models in Biology Single-Cell-Based Models in Biology and Medicine Model-Based Hypothesis Testing in Biomedicine A Biologist's Guide to Mathematical Modeling in Ecology and Evolution Theoretical Models in Biology David Brown Stephen P. Ellner Narendra S. Goel Valeria Zazu Elizabeth Spencer Allman Manfred Dietrich Laubichler Elisabeth S. Allman Lee A. Segel Michael R. Cullen Edward Beltrami IFIP-TC4 Working Conference on Mathematical Models in Biology and Medicine \$ (1972 : Varna, Bulgarie) Brian P. Ingalls Matthew H. Nitecki Glenn W. Rowe James W. Haefner Miklós Farkas Alexander Anderson Rikard Johansson Sarah P. Otto Glenn W. Rowe

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

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 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

experts examine new modeling strategies for the interpretation of biological data and their integration into the conceptual framework of theoretical biology detailing approaches that focus on morphology development behavior or evolution abstract and conceptual models have become an indispensable tool for analyzing the flood of highly detailed empirical data generated in recent years by advanced techniques in the biosciences scientists are developing new modeling strategies for analyzing data

integrating results into the conceptual framework of theoretical biology and formulating new hypotheses in modeling biology leading scholars investigate new modeling strategies in the domains of morphology development behavior and evolution the emphasis on models in the biological sciences has been accompanied by a new focus on conceptual issues and a more complex understanding of epistemological concepts contributors to modeling biology discuss models and modeling strategies from the perspectives of philosophy history and applied mathematics individual chapters discuss specific approaches to modeling in such domains as biological form development and behavior finally the book addresses the modeling of these properties in the context of evolution with a particular emphasis on the emerging field of evolutionary developmental biology or evo devo contributors giorgio a ascoli chandrajit bajaj james p collins luciano da fontoura costa kerstin dautenhahn nigel r franks scott gilbert marta ibañes miguel juan carlos izpisúa belmonte alexander s klyubin thomas j koehnle manfred d laubichler sabina leonelli james a r marshall george r mcghee jr gerd b müller christopher l nehaniv karl j niklas lars olsson eiríkur palsson daniel polani diego rasskin gutman hans jörg rheinberger alexei v samsonovich jeffrey c schank harry b m uylings jaap van pelt iain werry

a textbook on mathematical modelling techniques with powerful applications to biology combining theoretical exposition with exercises and examples

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

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

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

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 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 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

i principles 1 1 models of systems 3 1 1 systems models and modeling 3 1 2 uses of scientific models 4 1 3 example island biogeography 6 1 4 classifications of models 10 1 5 constraints on model structure 12 1 6 some terminology 12 1 7 misuses of models the dark side 13 1 8 exercises 15 2 the modeling process 17 2 1 models are problems 17 2 2 two alternative approaches 18 2 3 an example population doubling time 24 2 4 model objectives 28 2 5 exercises 30 3 qualitative model formulation 32 3 1 how to eat an elephant 32 3 2 forrester diagrams 33 3 3 examples 36 3 4 errors in forrester diagrams 44 3 5 advantages and disadvantages of forrester diagrams 44 3 6 principles of qualitative formulation 45 3 7 model simplification 47 3 8 other modeling problems 49 viii contents 3 9 exercises 53 4 quantitative model formulation i 4 1 from qualitative to quantitative finite difference equations and differential equations 4 2 4 3 biological feedback in quantitative models 4 4 example model 4 5 exercises 5 quantitative model formulation i1 8 1 5 1 physical processes 8 1 5 2 using the toolbox of biological processes 89 5 3 useful functions 96 5 4 examples 102 5 5 exercises 104 6 numerical techniques 107 6 1 mistakes computers make 107 6 2 numerical integration 110 6 3 numerical instability and stiff equations 115

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

aimed at postgraduate students in a variety of biology related disciplines 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

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 modellerings 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

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

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

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