Lecture Notes in Biomathematics

13

Mathematical Models
in Biological Discovery

Mathematical Models In Biological Discovery

N. MacDonald

Mathematical Models In Biological Discovery:

Mathematical Models in biological discovery ,1975 *Mathematical Models in Biological Discovery* Daniel L. Solomon,Charles F Walter,1977 **CONTRIBUTIONS OF MATHEMATICAL MODELS TO BIOLOGICAL DISCOVERY-SYMPOSIUM- 141ST ANNUAL MEETING- PAPERS- AAAS.** , *Mathematical Models in Biological Discovery* ,1977

Dynamics of Mathematical Models in Biology Alessandra Rogato,Valeria Zazzu,Mario Guarracino,2016-11-03 This volume focuses on contributions from both the mathematics and life science community surrounding the concepts of time and dynamicity of nature two significant elements which are often overlooked in modeling process to avoid exponential computations The book is divided into three distinct parts dynamics of genomes and genetic variation dynamics of motifs and dynamics of biological networks Chapters included in dynamics of genomes and genetic variation analyze the molecular mechanisms and evolutionary processes that shape the structure and function of genomes and those that govern genome dynamics The dynamics of motifs portion of the volume provides an overview of current methods for motif searching in DNA RNA and proteins a key process to discover emergent properties of cells tissues and organisms The part devoted to the dynamics of biological networks covers networks aptly discusses networks in complex biological functions and activities that interpret processes in cells Moreover chapters in this section examine several mathematical models and algorithms available for integration analysis and characterization Once life scientists began to produce experimental data at an unprecedented pace it become clear that mathematical models were necessary to interpret data to structure information with the aim to unveil biological mechanisms discover results and make predictions The second annual Bringing Maths to Life workshop held in Naples Italy October 2015 enabled a bi directional flow of ideas from and international group of mathematicians and biologists The venue allowed mathematicians to introduce novel algorithms methods and software that may be useful to model aspects of life science and life scientists posed new challenges for mathematicians **Math and Bio 2010** Lynn Arthur Steen,2005 Math and bio 2010 grew out of Meeting the Challenges Education across the Biological Mathematical and Computer Sciences a joint project of the Mathematical Association of America MAA the National Science Foundation Division of Undergraduate Education NSF DUE the National Institute of General Medical Sciences NIGMS the American Association for the Advancement of Science AAAS and the American Society for Microbiology ASM Foreword p vi Stochastic Methods in Biology Motoo Kimura,Gopinath Kallianpur,Takeyuki Hida,2013-03-13 The use of probabilistic methods in the biological sciences has been so well established by now that mathematical biology is regarded by many as a distinct dis cipline with its own repertoire of techniques The purpose of the Workshop on sto chastic methods in biology held at Nagoya University during the week of July 8 12 1985 was to enable biologists and probabilists from Japan and the U S to discuss the latest developments in their respective fields and to exchange ideas on the ap plicability of the more recent developments in stochastic process theory to problems in biology Eighteen papers were presented at the Workshop and have been grouped

under the following headings I Population genetics five papers II Measure valued diffusion processes related to population genetics three papers III Neurophysiology two papers IV Fluctuation in living cells two papers V Mathematical methods related to other problems in biology epidemiology population dynamics etc six papers An important feature of the Workshop and one of the reasons for organizing it has been the fact that the theory of stochastic differential equations SDE s has found a rich source of new problems in the fields of population genetics and neuro biology This is especially so for the relatively new and growing area of infinite dimensional i e measure valued or distribution valued SDE s The papers in II and III and some of the papers in the remaining categories represent these areas   Mathematical Modelling and Computers in Endocrinology Rosalind McIntosh,2012-12-06 The building of conceptual models is an inherent part of our interaction with the world and the foundation of scientific investigation Scientists often perform the processes of modelling subconsciously unaware of the scope and significance of this activity and the techniques available to assist in the description and testing of their ideas Mathematics has three important contributions to make in biological modelling 1 it provides unambiguous languages for expressing relationships at both qualitative and quantitative levels of observation 2 it allows effective analysis and prediction of model behaviour and can thereby organize experimental effort productively 3 it offers rigorous methods of testing hypotheses by comparing models with experimental data by providing a means of objectively excluding unsuitable concepts the development of ideas is given a sound experimental basis Many modern mathematical techniques can be exploited only with the aid of computers These machines not only provide increased speed and accuracy in determining the consequences of model assumptions but also greatly extend the range of problems which can be explored The impact of computers in the biological sciences has been widespread and revolutionary and will continue to be so   Current Catalog National Library of Medicine (U.S.), First multi year cumulation covers six years 1965 70   **Rhythms in Biology and Other Fields of Application** Société mathématique de France,Société mathématique de France. Journées,1983-06 This volume contains most of the talks presented at the Journ es de la Soci t Math ma ique de France entitled Rhythms in Biology and other fields of application Determi nistic and Stochastic Approaches held in Luminy from the 14th th to the 18 of September 1981 The aim of our meeting was to bring together scien tists from different disciplines to discuss a common topic and to stimulate exchanges between participants We hope that this goal was reached This volume is divided into four chapters In each one the papers are arranged in alphabetical order by first author Chapters one and two contain papers devoted to descrip tion or modelling of rhythmic biolog ical phenomena Chapters three and four deal with models for the study of rhythms invol ving the use of deterministic or stochastic tools capable of fruitful transfer to Biology We are pleased that these Proceedings appear in a series which constitutes an interface between Biologists and Mathema ticians We are indebted to all who provided us with their help particularly the Centre International de Rencontres Math matiques C I R M at Luminy the Soci t Mathematique de France S M F the Delegation aux Relations Universitaires Internationales D R U I and

the Laboratoire d Informatique et de Math matiques Appliquees de Grenoble I M A G Special thanks are due to Mrs A Litman for her dedi cation and her efficiency throughout the organization of this meeting G enobie Vecembe 1982 *Systems Biology in Cancer Research and Drug Discovery* Asfar S Azmi,2012-09-29 Systems Biology in Cancer Research and Drug Discovery provides a unique collection of chapters by world class researchers describing the use of integrated systems biology and network modeling in the cancer field where traditional tools have failed to deliver expected promise This book touches four applications aspects of systems biology i in understanding aberrant signaling in cancer ii in identifying biomarkers and prognostic markers especially focused on angiogenesis pathways iii in unwinding microRNAs complexity and iv in anticancer drug discovery and in clinical trial design This book reviews the state of the art knowledge and touches upon cutting edge newer and improved applications especially in the area of network modeling It is aimed at an audience ranging from students academics basic researcher and clinicians in cancer research This book is expected to benefit the field of translational cancer medicine by bridging the gap between basic researchers computational biologists and clinicians who have one ultimate goal and that is to defeat cancer **Intrinsic Geometry of Biological Surface Growth** Philip H. Todd,1986-05 1 1 General Introduction The work which comprises this essay formed part of a multidiscip linary project investigating the folding of the developing cerebral cortex in the ferret The project as a whole combined a study at the histological level of the cytoarchitectural development concom itant with folding and a mathematical study of folding viewed from the perspective of differential geometry We here concentrate on the differential geometry of brain folding Histological results which have some significance to the geometry of the cortex are re ferred to but are not discussed in any depth As with any truly multidisciplinary work this essay has objectives which lie in each of its constituent disciplines From a neuroana tomical point of view the work explores the use of the surface geo metry of the developing cortex as a parameter for the underlying growth process Geometrical parameters of particular interest and theoretical importance are surface curvatures Our experimental portion reports the measurement of the surface curvature of the ferret brain during the early stages of folding The use of sur face curvatures and other parameters of differential geometry in the formulation of theoretical models of cortical folding is dis cussed **Mathematics in Biology and Medicine** Vincenzo Capasso,Enea Grosso,Stefano L. Paveri-Fontana,1985-03 These Proceedings contain a large part of the papers presented at the International Conference Mathematics in Biology and Medicine organized by the Dipartimento di Matematica and the Istituto di Igiene at the University of Bari Italy July 18 22 1983 The main objective of the Conference was to bring together scientists in pure and applied mathematics and scientists in biology and medicine The purpose was to exchange ideas and discuss the common problems encoun red in the formulation ana lysis and numerical treatment of mathematical models in the biomedical sciences Si mulation methods and problems of validation of models vs experimental data were al so treated SUrveys on recent mathematical results motivated by biological questioffi were given Altogether we think that a balance between mathematical

and biomedical aspects was maintained The Scientific Committee consisted of E Biondi Milano P Colli Franzone Udine I Galligani Bologna M Iannelli Trento G Koch Roma E Marubini Milano C Matessi Pavia M Primicerio Firenze L M Ricciardi Napoli R Rinaldi Milano A Zampieri Roma and the European Liaison Committee consisted of R M Anderson United Kingdom N T J Bailey Switzerland O Diekmann The Netherlands K Dietz F R Germany K P Hadeler F R Germany J P Kernevez France

Revue Roumaine de Mathématiques Pures Et Appliquées ,1981 **Temporal-Pattern Learning in Neural Models** Carme Torras i Genis,1985-12 While the ability of animals to learn rhythms is an unquestionable fact the underlying neurophysiological mechanisms are still no more than conjectures This monograph explores the requirements of such mechanisms reviews those previously proposed and postulates a new one based on a direct electric coding of stimulation frequencies Experi mental support for the option taken is provided both at the single neuron and neural network levels More specifically the material presented divides naturally into four parts a description of the experimental and theoretical framework where this work becomes meaningful Chapter 2 a detailed specifica tion of the pacemaker neuron model proposed together with its valida tion through simulation Chapter 3 an analytic study of the behavior of this model when submitted to rhythmic stimulation Chapter 4 and a description of the neural network model proposed for learning together with an analysis of the simulation results obtained when varying seve ral factors related to the connectivity the intraneuronal parameters the initial state and the stimulation conditions Chapter 5 This work was initiated at the Computer and Information Science Depart ment of the University of Massachusetts Amherst and completed at the Institut de c Lber n e t Lca of the Universitat Politecnica de Catalunya Barcelona Computers at the latter place have adopted Catalan as their mother tongue and thus some computer made figures in this monograph specially those in Chapter 5 appear labeled in that tongue **Time Lags in Biological Models** N. MacDonald,1978-11-05 In many biological models it is necessary to allow the rates of change of the variables to depend on the past history rather than only the current values of the variables The models may require discrete lags with the use of delay differential equations or distributed lags with the use of integro differential equations In these lecture notes I discuss the reasons for including lags especially distributed lags in biological models These reasons may be inherent in the system studied or may be the result of simplifying assumptions made in the model used I examine some of the techniques available for studying the solution of the equations A large proportion of the material presented relates to a special method that can be applied to a particular class of distributed lags This method uses an extended set of ordinary differential equations I examine the local stability of equilibrium points and the existence and frequency of periodic solutions I discuss the qualitative effects of lags and how these differ according to the choice of discrete or distributed lag The models studied are drawn from the population dynamiCS of single species logistic growth the chemostat and of interacting pairs of species predation mutualism from cell population dynamiCS haemopoiesis and from biochemical kinetics the Goodwin oscillator The last chapter is devoted to a population model employing difference equations

All these models include non linear terms   Cell Kinetic Modelling and the Chemotherapy of Cancer Helmut Knolle,1988 This monograph establishes a necessary link between experimental cancer research and mathematical modelling of cell population and presents a new approach to the old problem of building a rational basis for the design of radio and chemotherapy of cancer Rather than embark straightaway on model building the author gives priority to the determination of action parameters of cytotoxic drugs A survey of autoradiographic experiments and evaluation methods in cell kinetics is given and classical formulae in this field are improved or generalized The cell cycle retarding effect of certain drugs which in the past raised some controversy is described in a concise quantitative frame work Finally a mathematical model of cell populations under treatment is tested against data from experiments with cell cycle phase specific drugs and is applied to the problem of choosing optimal time schedules of chemotherapy The book will serve as a guide to mathematical cell kinetics for biologists as well as an introduction to the biomedical environment of the field for mathematicians A knowledge of matrix algebra calculus and ordinary differential equations is expected of the reader but is not essential for using the results in the design and evaluation of cell kinetic experiments   **Fundamentals of Ordinary Differential Equations** Mohit Chatterjee,2025-02-20 Fundamentals of Ordinary Differential Equations is a comprehensive guide designed for students researchers and professionals to master ODE theory and applications We cover essential principles advanced techniques and practical applications providing a well rounded resource for understanding differential equations and their real world impact The book offers a multifaceted approach from basic principles to advanced concepts catering to fields like physics engineering biology and economics Mathematical ideas are broken down with step by step explanations examples and illustrations making complex concepts accessible Real world examples throughout each chapter show how ODEs model and analyze systems in diverse disciplines We also explain numerical methods such as Euler s method Runge Kutta and finite differences equipping readers with computational tools for solving ODEs Advanced topics include bifurcation chaos theory Hamiltonian systems and singular perturbations providing an in depth grasp of ODE topics With chapter summaries exercises glossaries and additional resources Fundamentals of Ordinary Differential Equations is an essential reference for students professionals and practitioners across science and engineering fields   **Subject Catalog, 1977** Library of Congress,1977
     Applications of Control Theory in Ecology Yosef Cohen,1987-08-26 This volume forms a collection of papers dealing with 1 applications of the Markov decision process to the optimal clutch size layed by insects 2 optimal life history strategies of annual plants using optimal control theory 3 optimal foraging in a patchy environment using impulse control theory 4 extinction of fur seal using differential games and 5 evolutionary stable strategies using a newly developed mathematical theory based on differential games Readers both applied mathematicians and ecologists interested in mathematical applications in biology and ecology will find fresh approaches to some fundamental questions in ecology and evolution Basic mathematical skills are required yet the applications are rather sophisticated

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