Network Models In Population Biology

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Ivet Bahar, 2.11.20- Network models in biology Population Ecology Population Dynamics

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Inheritance of social status, and its associated costs and benefits, is well demonstrated in humans. Whether such an intergenerational system occurs in other species is harder to demonstrate. Ilany et ...

Rank-dependent social inheritance determines social network structure in spotted hyenas
3 Center for Complex Network Research, Department of Physics, Biology and Computer Science ... is crucial to understanding a large variety of complex processes from population dynamics to disease ...

A network framework of cultural history
Mathematical biology is expanding ... membranes. These models help researchers explore how neurons process different types of inputs. They also provide the basis for detailed models involving networks ...

Mathematical Biology
Scientists from the European Molecular Biology Laboratory and the German Cancer Research Center have presented a new method for generating metabolic profiles of individual cells.

A new method for generating metabolic profiles of single cells
These innovations are needed because of the urgency and enormity of challenges facing global agriculture, including the need to feed a rapidly growing population ... and synthetic biology core to ...

REU: Systems Biology of Plant and Microbiome
PLoS Computational Biology 4: e1000110. Volz, E., L.A. Meyers (2008) Static network approximations and ... Theoretical Population Biolgy, 58: 307-319. Ancel, L.W. (1999) A quantitative model of the ...

Lauren Ancel Meyers
Phelps got his PhD in Integrative Biology from the University ... and information theory, neural network models, the evolution of gene regulation, epigenetics and transcription, sexual selection, ...

Steven M Phelps
Akoya Biosciences Inc., The Spatial Biology Company, has announced partnerships with microscope providers Nikon, CrestOptics and Andor to enable the development of new spatial biology applications, ...

Business Digest: Akoya forms partnerships on spatial biology
Liver steatosis, popularly known as fatty liver, is characterized by an excess of fat in the liver, an organ responsible mainly for the metabolism of nutrients. According to the Brazilian Society of ...

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IAEA experts have contributed to important ecological research — understanding the relationship between living organisms and their physical environment — by using isotopes to study butterfly and bird ...

IAEA and Austrian Research Centre Team-Up to Advance Ecological Research
In addition to serving as models ... population of mouse cells: the progenitor cells that form nephrons, which are the filtering units of the kidney. The team observed the growth of an extensive ...

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Vyant Bio Announces Issuance of Key Patent for High-Throughput Optical Assay of Human Mixed ...
Scientists have presented a new method for generating metabolic profiles of individual cells. The method, which combines fluorescence microscopy and a specific form of mass spectroscopy, can analyze ...

High-throughput metabolic profiling of single cells
2 Royal Museum for Central Africa, Service of Wood Biology, Tervuren ... we compared the observed SPD with four different models of hypothetical population growth drawn from our dataset of screened ...

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Stem cell researchers find key building block to make mini-kidneys
and of stem cell biology and regenerative medicine. The first authors of the study, PhD student Zipeng Zeng and postdoc Biao Huang, and the team started with a population of what are known as ureteric ...

This book is an outgrowth of one phase of an upper-division course on quantitative ecology, given each year for the past eight at Berkeley. I am most grateful to the students in that course and to many graduate students in the Berkeley Department of Zoology and Colleges of Engineering and Natural Resources whose spirited discussions inspired much of the book's content. I also am deeply grateful to those faculty colleagues with whom, at one time or another, I have shared courses or seminars in ecology or population biology, D.M. Auslander, L. Demetrius, G. Oster, O.H. Paris, F.A. Pitelka, A.M. Schultz, Y. Takahashi, D.B. Tyler, and P. Vogelhut, all of whom contributed substantially to the development of my thinking in those fields, to my Depart mental colleagues E. Polak and A.J. Thomasian, who guided me into the litera ture on numerical methods and stochastic processes, and to the graduate students who at one time or another have worked with me on population-biology projects, L.M. Brodnax, S-P. Chan, A. Elterman, G.C. Ferrell, D. Green, C. Hayashi, K-L. Lee, W.F. Martin Jr., D. May, J. Stamnes, G.E. Swanson, and I. Weeks, who, together, undoubtedly provided me with the greatest inspiration. I am indebted to the copy-editing and production staff of Springer-Verlag, especially to Ms. M. Muzeniek, for their diligence and skill, and to Mrs. Alice Peters, biomathematics editor, for her patience.

Integrated Population Biology and Modeling: Part A offers very complex and precise realities of quantifying modern and traditional methods of understanding populations and population dynamics. Chapters cover emerging topics of note, including Longevity dynamics, Modeling human-environment interactions, Survival Probabilities from 5-Year Cumulative Life Table Survival Ratios (Tx+5/Tx): Some Innovative Methodological Investigations, Cell migration Models, Evolutionary Dynamics of Cancer Cells, an Integrated approach for modeling of coastal lagoons: A case for Chilka Lake, India, Population and metapopulation dynamics, Mortality analysis: measures and models, Stationary Population Models, Are there biological and social limits to human longevity?, Probability models in biology, Stochastic Models in Population Biology, and more. Covers emerging topics of note in the subject matter Presents chapters on Longevity dynamics, Modeling human-environment interactions, Survival Probabilities from 5-Year Cumulative Life Table Survival Ratios (Tx+5/Tx), and more

The goal of this book is to search for a balance between simple and analyzable models and unsolvable models which are capable of addressing important questions on population biology. Part I focusses on single species simple models including those which have been used to predict the growth of human and animal population in the past. Single population models are, in some sense, the building blocks of more realistic models -- the subject of Part II. Their role is fundamental to the study of ecological and demographic processes including the role of population structure and spatial heterogeneity -- the subject of Part III. This book, which will include both examples and exercises, is of use to practitioners, graduate students, and scientists working in the field.

The purpose of this book is to show how mathematics can be applied to improve cancer chemotherapy. Unfortunately, most drugs used in treating cancer kill both normal and abnormal cells. However, more cancer cells than normal cells can be destroyed by the drug because tumor cells usually exhibit different growth kinetics than normal cells. To capitalize on this last fact, cell kinetics must be studied by formulating mathematical models of normal and abnormal cell growth. These models allow the therapeutic and harmful effects of cancer drugs to be simulated quantitatively. The combined cell and drug models can be used to study the effects of different methods of administering drugs. The least harmful method of drug administration, according to a given criterion, can be found by applying optimal control theory. The prerequisites for reading this book are an elementary knowledge of ordinary differential equations, probability, statistics, and linear algebra. In order to make this book self-contained, a chapter on cell biology and a chapter on control theory have been included. Those readers who have had some exposure to biology may prefer to omit Chapter I (Cell Biology) and only use it as a reference when required. However, few biologists have been exposed to control theory. Chapter 7 provides a short, coherent and comprehensible presentation of this subject. The concepts of control theory are necessary for a full understanding of Chapters 8 and 9.

"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

Mathematical Demography, the study of population and its analysis through mathematical models, has received increased interest in the mathematical com munity in recent years. It was not until the twentieth century, however, that the study of population, predominantly human population, achieved its math ematical character. The subject of mathematical demography can be viewed from either a deterministic viewpoint or from a stochastic viewpoint. For the sake of brevity, stochastic models are not included in this work. It is, therefore, my intention to consider only established deterministic models in this discussion, starting with the life table as the earliest model, to a generalized matrix model which is developed in this treatise. These deterministic models provide sufficient de velopment and conclusions to formulate sound mathematical population analy sis and estimates of population projections. It should be noted that although the subject of mathematical demography focuses on human populations, the development and results may be applied to any population as long as the preconditions that make the model valid are maintained. Information concerning mathematical demography is at best fragmented.

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.

Progress in Theoretical Biology, Volume 6 covers the theoretical analysis of biological phenomena. The book discusses the potentials in chemical systems far from thermodynamic equilibrium, particularly the reduction of reaction-diffusion systems to catastrophe theory; and a form of logic suited for biology. The text describes the order-disorder transitions in polyelectrolytes and the chaos in systems in population biology. An artificial cognitive-plus-motivational system and pattern generation in networks are also encompassed. Biophysicists and physiologists will find the book invaluable.

It is the task of computational biology to help elucidate the unique characteristics of biological systems. This process has barely begun, and many researchers are testing computational tools that have been used successfully in other fields. Mathematical and statistical network modeling is an important step toward uncovering the organizational principles and dynamic behavior of biological networks. Undoubtedly, new mathematical tools will be needed, however, to meet this challenge. The workhorse of this effort at present comprises the standard tools from applied mathematics, which have proven to be successful for many problems. But new areas of mathematics not traditionally considered applicable are contributing other powerful tools. This volume is intended to introduce this topic to a broad mathematical audience. The aim is to explain some of the biology and the computational and mathematical challenges we are facing. The different chapters provide examples of how these challenges are met, with particular emphasis on nontraditional mathematical approaches.The volume features a broad spectrum of networks across scales, ranging from biochemical networks within a single cell to epidemiological networks encompassing whole cities. Chapter topics include phylogenetics and gene finding using tools from statistics and algebraic geometry, biochemical network inference using tools from computational algebra, control-theoretic approaches to drug delivery using differential equations, and interaction-based modeling and discrete mathematics applied to problems in population dynamics and epidemiology.