

Stochastic Population And Epidemic Models Persistence And Extinction Mathematical Biosciences Institute Lecture Series

Focussing on stochastic models for the spread of infectious diseases in a human population, this book is the outcome of a two-week ICPAM/CIMPA school on "Stochastic models of epidemics" which took place in Ziguinchor, Senegal, December 5-16, 2015. The text is divided into four parts, each based on one of the courses given at the school: homogeneous models (Tom Britton and Etienne Pardoux), two-level mixing models (David Sirl and Frank Ball), epidemics on graphs (Viet Chi Tran), and statistics for epidemic models (Catherine Larédo). The CIMPA school was aimed at PhD students and Post Docs in the mathematical sciences. Parts (or all) of this book can be used as the basis for traditional or individual reading courses on the topic. For this reason, examples and exercises (some with solutions) are provided throughout.

Mathematical and Statistical Estimation Approaches in Epidemiology compiles theoretical and practical contributions of experts in the analysis of infectious disease epidemics in a single volume. Recent collections have focused in the analyses and simulation of deterministic and stochastic models whose aim is to identify and rank epidemiological and social mechanisms responsible for disease transmission. The contributions in this volume focus on the connections between models and disease data with emphasis on the application of mathematical and statistical approaches that quantify model and data uncertainty. The book is aimed at public health experts, applied mathematicians and scientists in the life and social sciences, particularly graduate or advanced undergraduate students, who are interested not only in building and connecting models to data but also in applying and developing methods that quantify uncertainty in the context of infectious diseases. Chowell and Brauer open this volume with an overview of the classical disease transmission models of Kermack-McKendrick including extensions that account for increased levels of epidemiological heterogeneity. Their theoretical tour is followed by the introduction of a simple methodology for the estimation of, the basic reproduction number, R_0 . The use of this methodology is illustrated, using regional data for 1918-1919 and 1968 in uenza pandemics.

This monograph provides a summary of the basic theory of branching processes for single-type and multi-type processes. Classic examples of population and epidemic models illustrate the probability of population or epidemic extinction obtained from the theory of branching processes. The first chapter develops the branching process theory, while in the second chapter two applications to population and epidemic processes of single-type branching process theory are explored. The last two chapters present multi-type branching process applications to epidemic models, and then continuous-time and continuous-state branching processes with applications. In addition, several MATLAB programs for simulating stochastic sample paths are provided in an Appendix. These notes originated as part of a lecture series on Stochastics in Biological Systems at the Mathematical Biosciences Institute in Ohio, USA. Professor Linda Allen is a Paul Whitfield Horn Professor of Mathematics in the Department of Mathematics and Statistics at Texas Tech University, USA.

In this thesis, three stochastic epidemic models for intervention for emerging diseases are considered. The models are variants of real-time, responsive intervention, based upon observing diagnosed cases and targeting intervention

towards individuals they have infected or are likely to have infected, be they housemates or named contacts. These models are: (i) a local tracing model for a disease spreading amongst a community of households, wherein intervention (vaccination and/or isolation) is directed towards housemates of diagnosed individuals, (ii) a contact tracing model for a disease spreading amongst a homogeneously-mixing population, with isolation of traced contacts of a diagnosed individual, (iii) a local tracing and contact tracing model for a disease spreading amongst a community of households, with intervention directed towards housemates of both diagnosed and traced individuals. These are quantified by deriving threshold parameters that determine whether the disease will infect a few individuals or a sizeable proportion of the population, as well as probabilities for such events occurring.

mathematical population dynamics

Stochastic Processes in Epidemiology

Stochastic Modeling of AIDS Epidemiology and HIV Pathogenesis

Applied Mathematical Ecology

Stochastic Epidemic Models and Their Statistical Analysis

Stochastic Modeling of Network-Centric Epidemiological Processes

This text deals with the mathematical and statistical techniques underlying the models used to understand the population dynamics of not only HIV/AIDS, but also of other infectious diseases. Attention is given to the development of strategies for the prevention and control of the international epidemic within the frameworks of the models. The text incorporates stochastic and deterministic formulations within a unifying conceptual framework.

In this thesis several problems concerning the stochastic modelling of emerging infections are considered. Mathematical modelling is often the only available method of predicting the extent of an emerging disease and assessing proposed control measures, as there may be little or no available data on previous outbreaks. Only stochastic models capture the inherent randomness in disease transmission observed in real-life outbreaks, which can strongly influence the outcome of an emerging epidemic because case numbers will initially be small compared with the population size. Chapter 2 considers a model for diseases in which some of the cases exhibit no symptoms and are therefore difficult to observe. Examples of such diseases include influenza, mumps and polio. This chapter investigates the problem of determining whether or not the epidemic has died out if a period containing no symptomatic individuals is observed. When modelling interventions, it is realistic to include a delay between observing the presence of infection and the implementation of control measures. Chapter 3 quantifies the effect that the length of such a delay has on an epidemic amongst a population divided into households. As well as a constant delay, an exponentially distributed delay is also considered. Chapter 4 develops a model for the spread of an emerging strain of influenza in humans. By considering the probability that an outbreak will be contained within a region in which an intervention strategy is active, it becomes possible to quantify and therefore compare the effectiveness of intervention strategies.

Stochastic Population and Epidemic Models Persistence and Extinction Springer
Chapter 1 establishes a mathematical result that can be used to find the numerical solution of the time to extinction of birth-death continuous time Markov chains, as well as the expected value of the integral under the stochastic path. Examples of applications to classical birth-death processes and to the Susceptible- Infected- Susceptible stochastic epidemic models are discussed.

An Introduction

Theory, Models, and Applications to Finance, Biology, and Medicine

The Effect of Population Heterogeneity

Epidemic Models

An Introduction to Stochastic Processes with Applications to Biology

Epidemic Dynamics of Metapopulation Models

This book discusses systematically treatment on the development of stochastic, statistical and state space models of the HIV epidemic and of HIV pathogenesis in HIV-infected individuals, and presents the applications of these models. The book is unique in several ways: (1) it uses stochastic difference and differential equations to present the stochastic models of the HIV epidemic and HIV pathogenesis; in this sense, the deterministic models are considered as special cases when the numbers of different type of people or cells are very large (2) it provides, a critical analysis of deterministic and statistical models in the literature; (3) it develops state space models by combining stochastic models and statistical models; and (4) it provides a detailed discussion on the pros and cons of the different modeling approaches. This book is the first to introduce state space models for the HIV epidemic. It is also the first to develop stochastic models and state space models for the HIV pathogenesis in HIV-infected individuals.

Mathematical modeling is an important tools to analyze and control the spread of infection disease in a society. One of the fundamental questions of mathematical epidemiology is to find threshold conditions that determine whether an infectious disease will spread in a susceptible population when the disease is introduced into the population. The threshold conditions are characterized by the so-called reproductive number, the reproduction number, the reproductive ratio, basic reproductive value, basic reproductive rate, or contact number. This book present the deterministic and stochastic epidemic models for HIV and study of reproductive numbers. The homotopy perturbation method and homotopy analysis method which was used to solve the linear and nonlinear differential equations. Also, the generation of stochastic models in the epidemic disease has been studied.

This is a general introduction to the mathematical modelling of diseases.

The Second Autumn Course on Mathematical Ecology was held at the International Centre for Theoretical Physics in Trieste, Italy in November and December of 1986. During the four year period that had elapsed since the First Autumn Course on Mathematical Ecology, sufficient progress had been made in applied mathematical ecology to merit tilting the balance maintained between theoretical aspects and applications in the 1982 Course toward applications. The course format, while similar to that of the first Autumn Course on Mathematical Ecology, consequently focused upon applications of mathematical ecology. Current areas of application are almost as diverse as the spectrum covered by ecology. The topics of this book reflect this diversity and were chosen because of perceived interest and utility to developing countries. Topical lectures began with foundational material mostly derived from Math

Mathematical Ecology: An Introduction (a compilation of the lectures of the 1982 course published by Springer-Verlag in this series, Volume 17) and, when possible, progressed to the frontiers of research. In addition to the course lectures, workshops were arranged for small groups to supplement and enhance the learning experience. Other perspectives were provided through presentations by course participants and speakers at the associated Research Conference. Many of the research papers are in a companion volume, *Mathematical Ecology: Proceedings Trieste 1986*, published by World Scientific Press in 1988. This book is structured primarily by application area. Part II provides an introduction to mathematical and statistical applications in resource management.

Variation, Growth, and Extinction of Populations

Stochastic Epidemic Models for Emerging Diseases Incorporating Household Structure and Contact Tracing

Limit Theorems for Some Stochastic Epidemic Models

A Hybrid System Approach

Their Structure and Relation to Data

Mathematical Epidemiology of Infectious Diseases Model Building, Analysis and Interpretation O. Diekmann University of Utrecht, The Netherlands J. A. P. Heesterbeek Centre for Biometry Wageningen, The Netherlands The mathematical modelling of epidemics in populations is a vast and important area of study. It is about translating biological assumptions into mathematics, about mathematical analysis aided by interpretation and about obtaining insight into epidemic phenomena when translating mathematical results back into population biology. Model assumptions are formulated in terms of, usually stochastic, behaviour of individuals and then the resulting phenomena, at the population level, are unravelled. Conceptual clarity is attained, assumptions are stated clearly, hidden working hypotheses are attained and mechanistic links between different observables are exposed. Features: * Model construction, analysis and interpretation receive detailed attention * Uniquely covers both deterministic and stochastic viewpoints * Examples of applications given throughout * Extensive coverage of the latest research into the mathematical modelling of epidemics of infectious diseases * Provides a solid foundation of modelling skills The reader will learn to translate, model, analyse and interpret, with the help of the numerous exercises. In literally working through this text, the reader acquires modelling skills that are also valuable outside of epidemiology, certainly within population dynamics, but even beyond that. In addition, the reader receives training in mathematical argumentation. The text is aimed at applied mathematicians with an interest in population biology and epidemiology, at theoretical biologists and epidemiologists. Previous exposure to epidemic concepts is not required, as all background information is given. The book is primarily aimed at self-study and ideally suited for small discussion groups, or for use as a course text.

Based on lecture notes of two summer schools with a mixed audience from mathematical sciences, epidemiology and public health, this volume offers a comprehensive introduction to basic ideas and techniques in modeling infectious diseases, for the comparison of strategies to plan for an anticipated epidemic or pandemic, and to deal with a disease outbreak in real time. It covers detailed case studies for diseases including

pandemic influenza, West Nile virus, and childhood diseases. Models for other diseases including Severe Acute Respiratory Syndrome, fox rabies, and sexually transmitted infections are included as applications. Its chapters are coherent and complementary independent units. In order to accustom students to look at the current literature and to experience different perspectives, no attempt has been made to achieve united writing style or unified notation. Notes on some mathematical background (calculus, matrix algebra, differential equations, and probability) have been prepared and may be downloaded at the web site of the Centre for Disease Modeling (www.cdm.yorku.ca). The technological changes and educational expansion have created the heterogeneity in the human species. Clearly, this heterogeneity generates a structure in the population dynamics, namely: citizen, permanent resident, visitor, and etc. Furthermore, as the heterogeneity in the population increases, the human mobility between meta-populations patches also increases. Depending on spatial scales, a meta-population patch can be decomposed into sub-patches, for examples: homes, neighborhoods, towns, etc. The dynamics of human mobility in a heterogeneous and scaled structured population is still its infancy level. We develop and investigate (1) an algorithmic two scale human mobility dynamic model for a meta-population. Moreover, the two scale human mobility dynamic model can be extended to multi-scales by applying the algorithm. The subregions and regions are interlinked via intra-and inter regional transport network systems. Under various types of growth order assumptions on the intra and interregional residence times of the residents of a sub region, different patterns of static behavior of the mobility process are studied. Furthermore, the human mobility dynamic model is applied to a two-scale population dynamic exhibiting a special real life human transportation network pattern. The static evolution of all categories of residents of a given site (homesite, visiting sites within the region, and visiting sites in other regions) over continuous changes in the intra and inter-regional visiting times is also analyzed. The development of the two scale human mobility dynamic model provides a suitable approach to undertake the study of the non-uniform global spread of emergent infectious diseases of humans in a systematic and unified way. In view of this, we derive (2) a SIRS stochastic epidemic dynamic process in a two scale structured population.

An Introduction to Stochastic Processes with Applications to Biology, Second Edition presents the basic theory of stochastic processes necessary in understanding and applying stochastic methods to biological problems in areas such as population growth and extinction, drug kinetics, two-species competition and predation, the spread of epidemics, and the genetics of inbreeding. Because of their rich structure, the text focuses on discrete and continuous time Markov chains and continuous time and state Markov processes. New to the Second Edition A new chapter on stochastic differential equations that extends the basic theory to multivariate processes, including multivariate forward and backward Kolmogorov differential equations and the multivariate Itô's formula The inclusion of examples and exercises from cellular and molecular biology Double the number of exercises and MATLAB® programs at the end of each chapter Answers and hints to selected exercises in the appendix Additional references from the literature This edition continues to provide an excellent introduction to the fundamental theory of

stochastic processes, along with a wide range of applications from the biological sciences. To better visualize the dynamics of stochastic processes, MATLAB programs are provided in the chapter appendices.

Stochastic Processes in Epidemic Theory

Mathematical Epidemiology

Deterministic and Stochastic Models of AIDS Epidemics and HIV Infections with Intervention

Model Building, Analysis and Interpretation

Epidemics with Heterogeneous Mixing

Stochastic Epidemic Models for Endemic Diseases

This volume presents infectious diseases modeled mathematically, taking seasonality and changes in population behavior into account, using a switched and hybrid systems framework. The scope of coverage includes background on mathematical epidemiology, including classical formulations and results; a motivation for seasonal effects and changes in population behavior, an investigation into term-time forced epidemic models with switching parameters, and a detailed account of several different control strategies. The main goal is to study these models theoretically and to establish conditions under which eradication or persistence of the disease is guaranteed. In doing so, the long-term behavior of the models is determined through mathematical techniques from switched systems theory. Numerical simulations are also given to augment and illustrate the theoretical results and to help study the efficacy of the control schemes.

Traditional infectious disease epidemiology focuses on fitting deterministic and stochastic epidemics models to surveillance case count data. Recently, researchers began to make use of infectious disease agent genetic data to complement statistical analyses of case count data. Such genetic analyses rely on the field of phylodynamics --- a set of population genetics tools that aim at reconstructing demographic history of a population based on molecular sequences of individuals sampled from the population of interest. In this thesis, we aim at designing a general framework that can fit stochastic epidemic models to surveillance count data and to genetic data separately, or to use both sources of information at the same time. Firstly, we propose a Bayesian model that combines phylodynamic inference and stochastic epidemic models. We bypass the current computationally intensive particle Markov chain Monte Carlo (MCMC) methods and achieve computational tractability by using a linear noise approximation (LNA) --- a technique that allows us to approximate probability densities of stochastic epidemic model trajectories. LNA opens the door for using modern MCMC tools to approximate the joint posterior distribution of the disease transmission parameters and of high dimensional vectors describing unobserved changes in the stochastic epidemic model compartment sizes (e.g., numbers of infectious and susceptible individuals). Next, we propose a joint model that allows us to integrate incidence data and genetic data. Finally, we consider the dependency of genetic sequence sampling times on

the latent prevalence of the infectious disease and propose a preferential sampling phylodynamics model that improves performance of phylodynamic inference. In a series of simulation studies, we show that all our proposed estimation methods can successfully recover parameters of stochastic epidemic models. Moreover, we demonstrate that combining multiple data types helps resolve identifiability issues and improves estimation precision. Throughout the dissertation, we use the incidence and genetic data from the 2014 Ebola epidemic in Sierra Leone and Liberia to illustrate our methodological developments.

Mathematical modeling is critical to our understanding of how infectious diseases spread at the individual and population levels. This book gives readers the necessary skills to correctly formulate and analyze mathematical models in infectious disease epidemiology, and is the first treatment of the subject to integrate deterministic and stochastic models and methods. *Mathematical Tools for Understanding Infectious Disease Dynamics* fully explains how to translate biological assumptions into mathematics to construct useful and consistent models, and how to use the biological interpretation and mathematical reasoning to analyze these models. It shows how to relate models to data through statistical inference, and how to gain important insights into infectious disease dynamics by translating mathematical results back to biology. This comprehensive and accessible book also features numerous detailed exercises throughout; full elaborations to all exercises are provided. Covers the latest research in mathematical modeling of infectious disease epidemiology Integrates deterministic and stochastic approaches Teaches skills in model construction, analysis, inference, and interpretation Features numerous exercises and their detailed elaborations Motivated by real-world applications throughout

The present lecture notes describe stochastic epidemic models and methods for their statistical analysis. Our aim is to present ideas for such models, and methods for their analysis; along the way we make practical use of several probabilistic and statistical techniques. This will be done without focusing on any specific disease, and instead rigorously analyzing rather simple models. The reader of these lecture notes could thus have a two-fold purpose in mind: to learn about epidemic models and their statistical analysis, and/or to learn and apply techniques in probability and statistics. The lecture notes require an early graduate level knowledge of probability and They introduce several techniques which might be new to students, but our statistics. intention is to present these keeping the technical level at a minimum. Techniques that are explained and applied in the lecture notes are, for example: coupling, diffusion approximation, random graphs, likelihood theory for counting processes, martingales, the EM-algorithm and MCMC methods. The aim is to introduce and apply these techniques, thus hopefully motivating their further theoretical treatment. A few sections, mainly in Chapter 5, assume some knowledge of weak convergence; we hope that readers not familiar with this theory can understand the these parts at a

heuristic level. The text is divided into two distinct but related parts: modelling and estimation.

Stochastic Population and Epidemic Models

Proceedings of the Second International Conference

Mathematical Modeling of Random and Deterministic Phenomena

Stochastic epidemic models for emerging diseases

Infectious Disease Modeling

Mathematical and Statistical Estimation Approaches in Epidemiology

In this thesis, I looked at an extension of the Reed-Frost epidemic model which had two-sub-populations. By setting up a Markov chain to model the epidemic and finding the transition probabilities of that chain, MATLAB could be used to solve for the expected number of susceptibles and the expected duration. I simulated the model with more than two sub-populations to find the average number of susceptibles and reviewed previously solved stochastic spatial models to understand how to solve the multiple-population Reed-Frost model on a network.

All populations fluctuate stochastically, creating a risk of extinction that does not exist in deterministic models, with fundamental consequences for both pure and applied ecology. This book provides the most comprehensive introduction to stochastic population dynamics, combining classical background material with a variety of modern approaches, including new and previously unpublished results by the authors, illustrated with examples from bird and mammal populations, and insect communities. Demographic and environmental stochasticity are introduced with statistical methods for estimating them from field data. The long-run growth rate of a population is explained and extended to include age structure with both demographic and environmental stochasticity.

Diffusion approximations facilitate the analysis of extinction dynamics and the duration of the final decline. Methods are developed for estimating delayed density dependence from population time series using life history data. Metapopulation viability and the spatial scale of population fluctuations and extinction risk are analyzed. Stochastic dynamics and statistical uncertainty in population parameters are incorporated in Population Viability Analysis and strategies for sustainable harvesting. Statistics of species diversity measures and species abundance distributions are described, with implications for rapid assessments of biodiversity, and methods are developed for partitioning species diversity into additive components. Analysis of the stochastic dynamics of a tropical butterfly community in space and time indicates that most of the variance in the species abundance distribution is due to ecological heterogeneity among species, so that real communities are far from neutral.

This book highlights mathematical research interests that appear in real

life, such as the study and modeling of random and deterministic phenomena. As such, it provides current research in mathematics, with applications in biological and environmental sciences, ecology, epidemiology and social perspectives. The chapters can be read independently of each other, with dedicated references specific to each chapter. The book is organized in two main parts. The first is devoted to some advanced mathematical problems regarding epidemic models; predictions of biomass; space-time modeling of extreme rainfall; modeling with the piecewise deterministic Markov process; optimal control problems; evolution equations in a periodic environment; and the analysis of the heat equation. The second is devoted to a modelization with interdisciplinarity in ecological, socio-economic, epistemological, demographic and social problems. Mathematical Modeling of Random and Deterministic Phenomena is aimed at expert readers, young researchers, plus graduate and advanced undergraduate students who are interested in probability, statistics, modeling and mathematical analysis.

This book is an outcome of the Second International Conference on Mathematical Population Dynamics. It is intended for mathematicians, statisticians, biologists, and medical researchers who are interested in recent advances in analyzing changes in populations of genes, cells, and tumors.

Stochastic Models for Epidemics on Networks

Fitting Stochastic Epidemic Models to Multiple Data Types

Stochastic Population Theories

Study of Stability and Un-stability of Epidemic Disease for Deterministic and Stochastic Models

Mathematical Epidemiology of Infectious Diseases

An Introduction to Continuous-Time Stochastic Processes

Surveys the state of epidemic modelling, resulting from the NATO Advanced Workshop at the Newton Institute in 1993.

Focussing on stochastic models for the spread of infectious diseases in a human population, this book is the outcome of a two-week ICPAM/CIMPA school on "Stochastic models of epidemics" which took place in Ziguinchor, Senegal, December 5-16, 2015. The text is divided into four parts, each based on one of the courses given at the school: homogeneous models (Tom Britton and Etienne Pardoux), two-level mixing models (David Sirl and Frank Ball), epidemics on graphs (Viet Chi Tran), and statistics for epidemic models (Catherine Larédo). The CIMPA school was aimed at PhD students and Post Docs in the mathematical sciences. Parts (or all) of this book can be used as the basis for traditional or individual reading courses on the topic. For this reason, examples and exercises (some with solutions) are provided throughout.

- Only book on extensive, deterministic models, statistic models, stochastic models and state space models and statistical methods for

HIV epidemic involving IV drug usage and HIV epidemic in homosexual populations. - Provides most recent biological insights into HIV pathogenesis and HIV kinetics at the cellular level, and illustrates how to build up mathematical models based on these biological insights. - Only publication that provides in-depth analysis of HAART treatment protocols and discusses possible improvements to the HAART protocol. The book also provides connection between pharmacokinetics with treatment in HIV-infected individuals.

This textbook, now in its fourth edition, offers a rigorous and self-contained introduction to the theory of continuous-time stochastic processes, stochastic integrals, and stochastic differential equations. Expertly balancing theory and applications, it features concrete examples of modeling real-world problems from biology, medicine, finance, and insurance using stochastic methods. No previous knowledge of stochastic processes is required. Unlike other books on stochastic methods that specialize in a specific field of applications, this volume examines the ways in which similar stochastic methods can be applied across different fields. Beginning with the fundamentals of probability, the authors go on to introduce the theory of stochastic processes, the Itô Integral, and stochastic differential equations. The following chapters then explore stability, stationarity, and ergodicity. The second half of the book is dedicated to applications to a variety of fields, including finance, biology, and medicine. Some highlights of this fourth edition include a more rigorous introduction to Gaussian white noise, additional material on the stability of stochastic semigroups used in models of population dynamics and epidemic systems, and the expansion of methods of analysis of one-dimensional stochastic differential equations. An Introduction to Continuous-Time Stochastic Processes, Fourth Edition is intended for graduate students taking an introductory course on stochastic processes, applied probability, stochastic calculus, mathematical finance, or mathematical biology. Prerequisites include knowledge of calculus and some analysis; exposure to probability would be helpful but not required since the necessary fundamentals of measure and integration are provided. Researchers and practitioners in mathematical finance, biomathematics, biotechnology, and engineering will also find this volume to be of interest, particularly the applications explored in the second half of the book.

Stochastic Models in Biology

Stochastic Population Models in Ecology and Epidemiology

Approximation of Population Processes

Mathematical Tools for Understanding Infectious Disease Dynamics

Problems in the Theory and Application of Models of Infectious Diseases

HIV/AIDS, Other Infectious Diseases, and Computers

These notes serve as an introduction to stochastic theories which are useful in population biology; they are based on a course given at the Courant Institute, New York, in the Spring of 1974. In order to make the material accessible to a wide audience, it is assumed that the reader has only a slight acquaintance with

probability theory and differential equations. The more sophisticated topics, such as the qualitative behavior of nonlinear models, are approached through a succession of simpler problems. Emphasis is placed upon intuitive interpretations, rather than upon formal proofs. In most cases, the reader is referred elsewhere for a rigorous development. On the other hand, an attempt has been made to treat simple, useful models in some detail. Thus these notes complement the existing mathematical literature, and there appears to be little duplication of existing works. The authors are indebted to Miss Jeanette Figueroa for her beautiful and speedy typing of this work. The research was supported by the National Science Foundation under Grant No. GP-32996X3. CONTENTS I.

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Time

This collection of papers gives a representative cross-sectional view of recent developments in the field. After a survey paper by C. Lefèvre, 17 other research papers look at stochastic modeling of epidemics, both from a theoretical and a statistical point of view. Some look more specifically at a particular disease such as AIDS, malaria, schistosomiasis and diabetes.

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 through 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.

As Eugene Wigner stressed, mathematics has proven unreasonably effective in the physical sciences and their technological applications. The role of mathematics in the biological, medical and social sciences has been much more modest but has recently grown thanks to the simulation capacity offered by

modern computers. This book traces the history of population dynamics---a theoretical subject closely connected to genetics, ecology, epidemiology and demography---where mathematics has brought significant insights. It presents an overview of the genesis of several important themes: exponential growth, from Euler and Malthus to the Chinese one-child policy; the development of stochastic models, from Mendel's laws and the question of extinction of family names to percolation theory for the spread of epidemics, and chaotic populations, where determinism and randomness intertwine. The reader of this book will see, from a different perspective, the problems that scientists face when governments ask for reliable predictions to help control epidemics (AIDS, SARS, swine flu), manage renewable resources (fishing quotas, spread of genetically modified organisms) or anticipate demographic evolutions such as aging.

Branching Processes

A Short History of Mathematical Population Dynamics

Analysis of Three Stochastic Models for Discrete Populations

Proceedings of a Conference held in Luminy, France, October 23–29, 1988

Stochastic Models and Statistical Tests

Deterministic and Stochastic Models for HIV

Population processes are stochastic models for systems involving a number of similar particles. Examples include models for chemical reactions and for epidemics. The model may involve a finite number of attributes, or even a continuum. This monograph considers approximations that are possible when the number of particles is large. The models considered will involve a finite number of different types of particles.

Mathematical modeling of infectious diseases can help public health officials to make decisions related to the mitigation of epidemic outbreaks. However, over or under estimations of the morbidity of any infectious disease can be problematic. Therefore, public health officials can always make use of better models to study the potential implication of their decisions and strategies prior to their implementation. Previous work focuses on the mechanisms underlying the different epidemic waves observed in Mexico during the novel swine origin influenza H1N1 pandemic of 2009 and showed extensions of classical models in epidemiology by adding temporal variations in different parameters that are likely to change during the time course of an epidemic, such as, the influence of media, social distancing, school closures, and how vaccination policies may affect different aspects of the dynamics of an epidemic. This current work further examines the influence of different factors considering the randomness of events by adding stochastic processes to meta-population models. I present three different approaches to compare different stochastic methods by considering discrete and continuous time. For the continuous time stochastic modeling approach I consider the continuous-time Markov chain process using forward Kolmogorov equations, for the discrete time stochastic modeling I consider stochastic differential equations using Wiener's increment and Poisson point increments, and also I consider the discrete-time Markov chain process. These first two stochastic modeling approaches will be presented in a one city and two city epidemic models using, as a base, our deterministic model. The last one will be discussed briefly on a one city SIS and SIR-type model.

This book covers the mathematical idea of branching processes, and tailors it for a

biological audience.

Stochastic Population Dynamics in Ecology and Conservation

Stochastic Epidemic Models with Inference

An Introduction to the Stochastic Theory of Epidemics and Some Related Statistical Problems

Epidemic Modelling

Persistence and Extinction