

## Infectious Diseases Of Humans Dynamics And Control Oxford Science Publications

Hardly a day goes by without news headlines concerning infectious disease threats. Currently the spectre of a pandemic of influenza A|H1N1 is raising its head, and heated debates are taking place about the pro's and con's of vaccinating young girls against human papilloma virus. For an evidence-based and responsible communication of infectious disease topics to avoid misunderstandings and overreaction of the public, we need solid scientific knowledge and an understanding of all aspects of infectious diseases and their control. The aim of our book is to present the reader with the general picture and the main ideas of the subject. The book introduces the reader to methodological aspects of epidemiology that are specific for infectious diseases and provides insight into the epidemiology of some classes of infectious diseases characterized by their main modes of transmission. This choice of topics bridges the gap between scientific research on the clinical, biological, mathematical, social and economic aspects of infectious diseases and their applications in public health. The book will help the reader to understand the impact of infectious diseases on modern society and the instruments that policy makers have at their disposal to deal with these challenges. It is written for students of the health sciences, both of curative medicine and public health, and for experts that are active in these and related domains, and it may be of interest for the educated layman since the technical level is kept relatively low.

Since the beginning of this century there has been a growing interest in the study of the epidemiology and population dynamics of infectious disease agents. Mathematical and statistical methods have played an important role in the development of this field and a large, and sophisticated, literature exists which is concerned with the theory of epidemiological processes in populations and the dynamics of epidemic and endemic disease phenomena. Much of this literature is, however, rather formal and abstract in character, and the field has tended to become rather detached from its empirical base. Relatively little of the literature, for example, deals with the practical issues which are of major concern to public health workers. Encouragingly, in recent years there are signs of an increased awareness amongst theoreticians of the need to confront predictions with observed epidemiological trends, and to pay close attention to the biological details of the interaction between host and disease agent. This trend has in part been stimulated by the early work of Ross and Macdonald, on the transmission dynamics of tropical parasitic infections, but a further impetus has been the recent advances made by ecologists in blending theory and observation in the study of plant and animal populations.

This book provides an introduction to the computational and complex systems modeling of the global spreading of infectious diseases. The latest developments in the area of contagion processes modeling are discussed, and readers are exposed to real world examples of data-model integration impacting the decision-making process. Recent advances in computational science and the increasing availability of real-world data are making it possible to develop realistic scenarios and real-time forecasts of the global spreading of emerging health threats. The first part of the book guides the reader through sophisticated complex systems modeling techniques with a non-technical and visual approach, explaining and illustrating the construction of the modern framework used to project the spread of pandemics and epidemics. Models can be used to transform data to knowledge that is intuitively communicated by powerful infographics and for this reason, the second part of the book focuses on a set of charts that illustrate possible scenarios of future pandemics. The visual atlas contained allows the reader to identify commonalities and patterns in emerging health threats, as well as explore the wide range of models and data that can be used by policy makers to anticipate trends, evaluate risks and eventually manage future events. Charting the Next Pandemic puts the reader in the position to explore different pandemic scenarios and to understand the potential impact of available containment and prevention strategies. This book emphasizes the importance of a global perspective in the assessment of emerging health threats and captures the possible evolution of the next pandemic, while at the same time providing the intelligence needed to fight it. The text will appeal to a wide range of audiences with diverse technical backgrounds.

As doctors and biologists have learned, to their dismay, infectious disease is a moving target: new diseases emerge every year, old diseases evolve into new forms, and ecological and socioeconomic upheavals change the transmission pathways by which disease spread. By taking an approach focused on the general evolutionary and ecological dynamics of disease, this Very Short Introduction provides a general conceptual framework for thinking about disease. Ecology and evolution provide the keys to answering the 'where', 'why', 'how', and 'what' questions about any particular infectious disease: where did it come from? How is it transmitted from one person to another, and why are some individuals more susceptible than others? What biochemical, ecological, and evolutionary strategies can be used to combat the disease? Is it more effective to block transmission at the population level, or to block infection at the individual level? Through a series of case studies, Benjamin Bolker and Marta L. Wayne introduce the major ideas of infectious disease in a clear and thoughtful way, emphasizing the general principles of infection, the management of outbreaks, and the evolutionary and ecological approaches that are now central to much research about infectious disease. ABOUT THE SERIES: The Very Short Introductions series from Oxford University Press contains hundreds of titles in almost every subject area. These pocket-sized books are the perfect way to get ahead in a new subject quickly. Our expert authors combine facts, analysis, perspective, new ideas, and enthusiasm to make interesting and challenging topics highly readable.

Extraordinary medical advances have led to significant reductions in the burden of infectious diseases in humans. However, infectious diseases still account for more than 13 million annual deaths. This large burden is partly due to some pathogens having found suitable conditions to emerge and spread in denser and more connected host populations, and others having evolved to escape the pressures imposed by the rampant use of antimicrobials. It is then critical to improve our understanding of how diseases spread in these modern landscapes, characterized by new host population structures and socio-economic environments, as well as containment measures such as the deployment of drugs. Thus, the motivation of this dissertation is two-fold. First, we study, using both data-driven and modeling approaches, the spread of infectious diseases in urban areas. As a case study, we use confirmed-cases data on sexually transmitted diseases (STDs) in the United States to assess the conduciveness of population size of urban areas and their socio-economic characteristics as predictors of STD incidence. We find that the scaling of STD incidence in cities is superlinear, and that the percent of African-Americans residing in cities largely determines these statistical patterns. Since disparities in access to health care are often exacerbated in urban areas, within this project we also develop two modeling frameworks to study the effect of health care disparities on epidemic outcomes. Discrepant results between the two approaches indicate that knowledge of the shape of the recovery period distribution, not just its mean and variance, is key for assessing the epidemiological impact of inequalities. The second project proposes to study, from a modeling perspective, the spread of drug resistance in human populations featuring vital dynamics, stochasticity and contact structure. We derive effective treatment regimes that minimize both the overall disease burden and the spread of resistance. Additionally, targeted treatment in structured host populations may lead to higher levels of drug resistance, and if drug-resistant strains are compensated, they can spread widely even when the wild-type strain is below its epidemic threshold.

Despite great advances in public health worldwide, insect vector-borne infectious diseases remain a leading cause of morbidity and mortality. Diseases that are transmitted by arthropods such as mosquitoes, sand flies, fleas, and ticks affect hundreds of millions of people and account for nearly three million deaths all over the world. In the past there was very little hope of controlling the epidemics caused by these diseases, but modern advancements in science and technology are providing a variety of ways in which these diseases can be handled. Clearly, the process of transmission of an infectious disease is a nonlinear (not necessarily linear) dynamic process which can be understood only by appropriately quantifying the vital parameters that govern these dynamics.

When deadly illness spreads through a population at a rapid pace, time may be of the essence in order to save lives. Using mathematics as a language to interpret assumptions concerning the biological and population mechanics, one can make predictions by analyzing actual epidemiological data using mathematical tests and results. Mathematical models can help us understand the right disease status and predict the effects of the disease on populations, which can help limit the spread and devastation of the illness. *Mathematical Models of Infectious Diseases and Social Issues* is a collection of innovative research that examines the dynamics of diseases and their effect on populations. Featuring coverage of a broad range of topics including deterministic models, environmental pollution, and social issues, this book is ideally designed for diagnosticians, clinicians, healthcare providers, pharmacists, government health officials, policymakers, academicians, researchers, and students.

Surveillance for wildlife diseases is critical to our understanding of the emergence, transmission, persistence and control of infectious diseases at the interface of humans, domestic animals, and wildlife populations. *Neospora caninum* is a protozoan parasite capable of infecting a wide range of canid and ungulate species. The importance of the disease relates to economic losses, mainly derived from endemic or epidemic abortions in cattle. In the United States, coyotes and dogs are believed to be the main definitive hosts and white-tailed deer and cows are the main intermediate hosts. Our overall aim was to better understand the wildlife-livestock interface of *N. caninum* in natural settings. First, we estimated the true prevalence of *N. caninum* in three ruminant species by using Bayesian inference. We identified and discussed differences between apparent and true prevalence (TP). Differences in TP for some species suggest differences in the epidemiology of *N. caninum* for these co-located populations. Second, we evaluated the environmental phase of *N. caninum* shed in wild canid scats. Results suggested that the role of this environmental phase in the transmission to ruminants is likely minor. Finally, we evaluated the role of host species heterogeneity in the epidemiology of *N. caninum* circulating in a community. We identified differences in the patterns of immunity, age structure, and maternal and/or fetal antibody duration in three intermediate (ruminant) host species. Also, we estimated the species-specific contributions to the persistence of this pathogen in a community. This research was approached from the One Health perspective and provided a better understanding of *N. caninum* dynamics at the wildlife-livestock interface in an ecosystem.

This book is designed to be a practical study in infectious disease dynamics. The book offers an easy to follow implementation and analysis of mathematical epidemiology. The book focuses on recent case studies in order to explore various conceptual, mathematical, and statistical issues. The dynamics of infectious diseases shows a wide diversity of pattern. Some have locally persistent chains-of-transmission, others persist spatially in 'consumer-resource metapopulations'. Some infections are prevalent among the young, some among the old and some are age-invariant. Temporally, some diseases have little variation in prevalence, some have predictable seasonal shifts and others exhibit violent epidemics that may be regular or irregular in their timing. Models and 'models-with-data' have proved invaluable for understanding and predicting this diversity, and thence help improve intervention and control. Using mathematical models to understand infectious disease dynamics has a very rich history in epidemiology. The field has seen broad expansions of theories as well as a surge in real-life application of mathematics to dynamics and control of infectious disease. The chapters of *Epidemics: Models and Data using R* have been organized in a reasonably logical way: Chapters 1-10 is a mix and match of models, data and statistics pertaining to local disease dynamics; Chapters 11-13 pertains to spatial and spatiotemporal dynamics; Chapter 14 highlights similarities between the dynamics of infectious disease and parasitoid-host dynamics; Finally, Chapters 15 and 16 overview additional statistical methodology useful in studies of infectious disease dynamics. This book can be used as a guide for working with data, models and 'models-and-data' to understand epidemics and infectious disease dynamics in space and time.

News headlines are forever reporting diseases that take huge tolls on humans, wildlife, domestic animals, and both cultivated and native plants worldwide. These diseases can also completely transform the ecosystems that feed us and provide us with other critical benefits, from flood control to water purification. And yet diseases sometimes serve to maintain the structure and function of the ecosystems on which humans depend. Gathering thirteen essays by forty leading experts who convened at the Cary Conference at the Institute of Ecosystem Studies in 2005, this book develops an integrated framework for understanding where these diseases come from, what ecological factors influence their impacts, and how they in turn influence ecosystem dynamics. It marks the first comprehensive and in-depth exploration of the rich and complex linkages between ecology and disease, and provides conceptual underpinnings to understand and ameliorate epidemics. It also sheds light on the roles that diseases play in ecosystems, bringing vital new insights to landscape management issues in particular. While the ecological context is a key piece of the puzzle, effective control and understanding of diseases requires the interaction of professionals in medicine, epidemiology, veterinary medicine, forestry, agriculture, and ecology. The essential resource on the subject, *Infectious Disease Ecology* seeks to bridge these fields with an ecological approach that focuses on systems thinking and complex interactions.

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Initially stimulated by a scholarly workshop convened in Singapore in late 2004, and written over the subsequent 18 months, this volume considers the potentially lethal pattern of infectious disease emergence in Asia. It studies linkages to changes in patterns of human activity, including but not limited to shifts in the distribution and concentration of human settlements and the patterns of movement within and between them. It explores the causes and consequences of infectious agents in the region historically and examines such newly emergent natural biological threats as SARS and avian influenza. Drawing on a range of disciplinary perspectives, the book contains analyses rooted in the social, physical and biological sciences as well as works which span these fields. Among the issues considered are the ways in which changes in our natural and built environment, social and economic pressures, shifting policies and patterns of collaboration in responding to disease impact upon our approach to and success in containing serious threats. Infection control has moved beyond the province of clinical experts, epidemiologists and microbiologists, into the mathematics of epidemic prevention and control, as well as the overall physical and human ecology and historical contexts of emerging infections. Not only does such a broad approach enable appreciation of complex forces driving growing epidemic risks in Asia today, it also reveals the importance and relevance of population dynamics, as well as the global urgency of alleviating unsatisfactory health conditions in Asia. The topic and the broad approach has international appeal beyond the region as many of these forces operate throughout the world.

This volume summarizes the state-of-the-art in the fast growing research area of modeling the influence of information-driven human behavior on the spread and control of infectious diseases. In particular, it features the two main and inter-related "core" topics: behavioral changes in response to global threats, for example, pandemic influenza, and the pseudo-rational opposition to vaccines. In order to make realistic predictions, modelers need to go beyond classical mathematical epidemiology to take these dynamic effects into account. With contributions from experts in this field, the book fills a void in the literature. It goes beyond classical texts, yet preserves the rationale of many of them by sticking to the underlying biology without compromising on scientific

rigor. Epidemiologists, theoretical biologists, biophysicists, applied mathematicians, and PhD students will benefit from this book. However, it is also written for Public Health professionals interested in understanding models, and to advanced undergraduate students, since it only requires a working knowledge of mathematical epidemiology.

This book deals with infectious diseases -- viral, bacterial, protozoan and helminth -- in terms of the dynamics of their interaction with host populations. The book combines mathematical models with extensive use of epidemiological and other data. This analytic framework is highly useful for the evaluation of public health strategies aimed at controlling or eradicating particular infections. Such a framework is increasingly important in light of the widespread concern for primary health care programs aimed at such diseases as measles, malaria, river blindness, sleeping sickness, and schistosomiasis, and the advent of AIDS/HIV and other emerging viruses. Throughout the book, the mathematics is used as a tool for thinking clearly about fundamental and applied problems having to do with infectious diseases. The book is divided into two parts, one dealing with microparasites (viruses, bacteria and protozoans) and the other with macroparasites (helminths and parasitic arthropods). Each part begins with simple models, developed in a biologically intuitive way, and then goes on to develop more complicated and realistic models as tools for public health planning. The book synthesizes previous work in this rapidly growing field (much of which is scattered between the ecological and the medical literature) with a good deal of new material.

This is the first comprehensive text on the methodological issues in epidemiologic research on infectious diseases. It will be an invaluable resource both to students of epidemiology and to established researchers. The authors address such questions as: What needs to be considered when enrolling participants in a study of sexually transmitted diseases? What are common sources of measurement error in population-based studies of respiratory infections? What are some sources of existing data for epidemiologic studies of infectious diseases? Answers to these and many other related questions can be found in this well-organized, comprehensive and authoritative volume - the first to thoroughly address the methodologic issues in conducting epidemiologic research on infectious diseases. The book will be an ideal complement to texts on general epidemiology and infectious disease. An introductory section will make it accessible to a wide variety of disciplines by providing an overview of topics that are foundational to understanding infectious disease epidemiology, such as the immunology of infections, the biology of infectious diseases, and concepts of causation, transmission, and dynamics. The rest of the book is structured around sections on data sources and measurement; methods by transmission type; outbreak investigation and evaluation research; and special topics such as HIV/AIDS research, infections in the elderly, and research collaborations in developing countries.

Vital resource in infectious diseases, will especially appeal to workers in epidemiology, public health and biology.

Though great advances in public health are witnessed world over in recent years, infectious diseases, besides insect vector-borne infectious diseases remain a leading cause of morbidity and mortality. Control of the epidemics caused by the non-vector borne diseases such as tuberculosis, avian influenza (H5N1) and cryptococcus gattii, have left a very little hope in the past. The advancement of research in science and technology has paved way for the development of new tools and methodologies to fight against these diseases. In particular, intelligent technology and machine-learning based methodologies have rendered useful in developing more accurate predictive tools for the early diagnosis of these diseases. In all these endeavors the main focus is the understanding that the process of transmission of an infectious disease is nonlinear (not necessarily linear) and dynamical in character. This concept compels the appropriate quantification of the vital parameters that govern these dynamics. This book is ideal for a general science and engineering audience requiring an in-depth exposure to current issues, ideas, methods, and models. The topics discussed serve as a useful reference to clinical experts, health scientists, public health administrators, medical practitioners, and senior undergraduate and graduate students in applied mathematics, biology, bioinformatics, and epidemiology, medicine and health sciences.

The twentieth century witnessed an era of unprecedented, large-scale, anthropogenic changes to the natural environment. Understanding how environmental factors directly and indirectly affect the emergence and spread of infectious disease has assumed global importance for life on this planet. While the causal links between environmental change and disease emergence are complex, progress in understanding these links, as well as how their impacts may vary across space and time, will require transdisciplinary, transnational, collaborative research. This research may draw upon the expertise, tools, and approaches from a variety of disciplines. Such research may inform improvements in global readiness and capacity for surveillance, detection, and response to emerging microbial threats to plant, animal, and human health. The Influence of Global Environmental Change on Infectious Disease Dynamics is the summary of a workshop hosted by the Institute of Medicine Forum on Microbial Threats in September 2013 to explore the scientific and policy implications of the impacts of global environmental change on infectious disease emergence, establishment, and spread. This report examines the observed and potential influence of environmental factors, acting both individually and in synergy, on infectious disease dynamics. The report considers a range of approaches to improve global readiness and capacity for surveillance, detection, and response to emerging microbial threats to plant, animal, and human health in the face of ongoing global environmental change.

The 1918-19 influenza epidemic killed more than fifty million people worldwide. The SARS epidemic of 2002-3, by comparison, killed fewer than a thousand. The success in containing the spread of SARS was due largely to the rapid global response of public health authorities, which was aided by insights resulting from mathematical models. Models enabled authorities to better understand how the disease spread and to assess the relative effectiveness of different control strategies. In this book, Lisa Sattenspiel and Alun Lloyd provide a comprehensive introduction to mathematical models in epidemiology and show how they can be used to predict and control the geographic spread of major infectious diseases. Key concepts in infectious disease modeling are explained, readers are guided from simple mathematical models to more complex ones, and the strengths and weaknesses of these models are explored. The book highlights the breadth of techniques available to modelers today, such as population-based and individual-based

models, and covers specific applications as well. Sattenspiel and Lloyd examine the powerful mathematical models that health authorities have developed to understand the spatial distribution and geographic spread of influenza, measles, foot-and-mouth disease, and SARS. Analytic methods geographers use to study human infectious diseases and the dynamics of epidemics are also discussed. A must-read for students, researchers, and practitioners, no other book provides such an accessible introduction to this exciting and fast-evolving field.

This book deals with how we construct and use deterministic mathematical models of the transmission of infectious diseases in domestic and wild animals. It is a manual, drawing on examples from the world of veterinary medicine, but will appeal to the interested reader from any background. Mathematical models of infectious disease transmission dynamics are increasingly used to inform population-based disease control strategies. Such strategies are typically implemented by clinicians (in both human and animal medicine), policy makers, and career civil servants. This book will be of value to all such parties.

Zoonotic diseases, which are caused by pathogens that transmit from animals into humans, are responsible for numerous ongoing public health burdens, such as leptospirosis, rabies, and West Nile virus infections, and are also considered a probable source of future epidemics in humans. Describing and quantifying the transmission dynamics of these pathogens is vital if we wish to assess which of the many known zoonotic pathogens pose a threat to humans and which management strategies would be most effective at minimizing that threat. To conduct these assessments, it is necessary to consider the ecological dynamics and interactions driving zoonotic disease transmission. A zoonotic pathogen's impact on humans depends not only on transmission dynamics within the human population, including heterogeneities in human contacts and interactions with endemic human pathogens, but also on disease dynamics within the reservoir and at the human-reservoir interface. Because of the complex ecological interactions driving the spread of zoonotic pathogens, qualitatively and quantitatively characterizing their spread and devising rational management strategies requires combining insights from community ecology, invasion biology, and classical single-host disease ecology with system-specific information about the pathways of transmission within the reservoir, within humans, and between the two. Bringing together these complementary perspectives can shed light on the key processes driving transmission, which is essential for predicting how changes, both purposeful interventions and natural shifts, may alter the system's behavior. In this dissertation, I present three studies that use diverse methods to explore different aspects of zoonotic pathogens' disease dynamics. In chapter 1, I use a theoretical approach to explore the effects of competition between a zoonotic pathogen and a human-endemic pathogen in the context of a disease eradication program. I use a deterministic compartmental model that tracks spillover and transmission of a zoonotic disease in humans as well as transmission of a partially cross-protective endemic human pathogen to examine how the presence of the zoonotic pathogen can reduce the vaccination coverage necessary to eradicate the human pathogen and how the zoonotic pathogen's prevalence is expected to change during and following a successful eradication campaign. I then use the smallpox-monkeypox system as a case study to assess how the theoretical findings apply in a real-world context. In chapter 2, I move from theoretical explorations of disease dynamics to using real-world datasets to inform mechanistic models. Zoonotic disease surveillance datasets are valuable sources of information about disease dynamics, but are generally difficult and expensive to obtain and are associated with a variety of data limitations. This chapter develops methods to extract as much information as possible from these valuable information sources. I develop a model-based inference method that addresses a number of data challenges, including unobserved sources of transmission (both human and zoonotic), limited spatial information, and unknown scope of surveillance, using a spatial model with two levels of mixing. After demonstrating the robustness of the method using simulation studies, I apply the new method to a dataset of human monkeypox cases detected during an active surveillance program from 1982-1986 in the Democratic Republic of the Congo. The results provide estimates of the reproductive number and spillover rate of monkeypox during this surveillance period and suggest that most human-to-human transmission events occur over distances of 30 km or less. Taking advantage of contact-tracing data available for a subset of monkeypox cases, I find that around 80% of contact-traced links could be correctly recovered from transmission trees inferred using only date and location. The results highlight the importance of identifying the appropriate spatial scale of transmission, and show how even imperfect spatiotemporal data can be incorporated into models of zoonotic pathogens to obtain reliable estimates of transmission patterns. Chapter 3 shifts from examining the dynamics of zoonotic pathogens after they have already spilled into humans to evaluating how interventions in the zoonotic reservoir could help reduce the risk of spillover occurring in the first place. This chapter focuses on evaluating interventions to minimize the risk of spillover of swine-origin influenza A viruses (IAV-S) into humans in the United States. In the past decade, the majority of reported human infections with IAV-S in the United States have been associated with individuals exposed to exhibition swine while attending agricultural shows. Because these exhibition swine make up a largely distinct population within the US swine herd, there is great potential to implement control practices within exhibition swine that could substantially reduce risk of spillover into humans. To understand the factors that drive influenza prevalence and persistence in US exhibition swine and to evaluate the impact of potential interventions, I develop a network model that characterizes disease spread into and among exhibition swine. The model incorporates key structural information about the system and is informed by a unique surveillance dataset collected from shows in Ohio, Michigan, and Indiana, including IAV-S genomes from more than one hundred infected swine. I use several different approaches based on both epidemiological and sequence data to estimate parameters describing transmission and to evaluate the expected impact of a set of thirty potential interventions on the risk of spillover into humans. Across all approaches, several interventions consistently are found to perform best at reducing projected spillover risk, including requiring participants to take one or two weeks off between shows and implementing strategies to reduce transmission probabilities among swine at shows. While the

studies presented in these chapters range from theoretical explorations of simplified systems to direct comparisons of intervention impacts incorporating messy real-world data and complex system structure, they all pursue the common goal of providing insights relevant for conceptualizing the prominent forces in a system and for using that understanding to inform decisions on control measures in a real-world context.

This accessible textbook focuses on the dynamics of infectious diseases for wild avian hosts across every level of ecological hierarchy. Although the topics and principles discussed in this book relate to birds, they have a far wider relevance and can also be applied to non-avian, wildlife host-pathogen systems.

The book discusses different therapeutic approaches based on different mathematical models to control the HIV/AIDS disease transmission. It uses clinical data, collected from different cited sources, to formulate the deterministic as well as stochastic mathematical models of HIV/AIDS. It provides complementary approaches, from deterministic and stochastic points of view, to optimal control strategy with perfect drug adherence and also tries to seek viewpoints of the same issue from different angles with various mathematical models to computer simulations. The book presents essential methods and techniques for students who are interested in designing epidemiological models on HIV/AIDS. It also guides research scientists, working in the periphery of mathematical modeling, and helps them to explore a hypothetical method by examining its consequences in the form of a mathematical modelling and making some scientific predictions. The model equations, mathematical analysis and several numerical simulations that are presented in the book would serve to reveal the consequences of the logical structure of the disease transmission, quantitatively as well as qualitatively. One of the chapters introduces the optimal control approach towards the mathematical models, describing the optimal drug dosage process that is discussed with the basic deterministic models dealing with stability analysis. Another one chapter deals with the mathematical analysis for the perfect drug adherence for different drug dynamics during the treatment management. The last chapter of the book consists the stochastic approach to the disease dynamics on HIV/AIDS. This method helps to move the disease HIV/AIDS to extinction as the time to increase. This book will appeal to undergraduate and postgraduate students, as well as researchers, who are studying and working in the field of bio-mathematical modelling on infectious diseases, applied mathematics, health informatics, applied statistics and qualitative public health, etc. Social workers, who are working in the field of HIV, will also find the book useful for complements.

An integrated study of the evolutionary ecology of infectious diseases and the management of virulent pathogens.

For epidemiologists, evolutionary biologists, and health-care professionals, real-time and predictive modeling of infectious disease is of growing importance. This book provides a timely and comprehensive introduction to the modeling of infectious diseases in humans and animals, focusing on recent developments as well as more traditional approaches. Matt Keeling and Pejman Rohani move from modeling with simple differential equations to more recent, complex models, where spatial structure, seasonal "forcing," or stochasticity influence the dynamics, and where computer simulation needs to be used to generate theory. In each of the eight chapters, they deal with a specific modeling approach or set of techniques designed to capture a particular biological factor. They illustrate the methodology used with examples from recent research literature on human and infectious disease modeling, showing how such techniques can be used in practice. Diseases considered include BSE, foot-and-mouth, HIV, measles, rubella, smallpox, and West Nile virus, among others. Particular attention is given throughout the book to the development of practical models, useful both as predictive tools and as a means to understand fundamental epidemiological processes. To emphasize this approach, the last chapter is dedicated to modeling and understanding the control of diseases through vaccination, quarantine, or culling. Comprehensive, practical introduction to infectious disease modeling Builds from simple to complex predictive models Models and methodology fully supported by examples drawn from research literature Practical models aid students' understanding of fundamental epidemiological processes For many of the models presented, the authors provide accompanying programs written in Java, C, Fortran, and MATLAB In-depth treatment of role of modeling in understanding disease control

The contributions by epidemic modeling experts describe how mathematical models and statistical forecasting are created to capture the most important aspects of an emerging epidemic. Readers will discover a broad range of approaches to address questions, such as Can we control Ebola via ring vaccination strategies? How quickly should we detect Ebola cases to ensure epidemic control? What is the likelihood that an Ebola epidemic in West Africa leads to secondary outbreaks in other parts of the world? When does it matter to incorporate the role of disease-induced mortality on epidemic models? What is the role of behavior changes on Ebola dynamics? How can we better understand the control of cholera or Ebola using optimal control theory? How should a population be structured in order to mimic the transmission dynamics of diseases such as chlamydia, Ebola, or cholera? How can we objectively determine the end of an epidemic? How can we use metapopulation models to understand the role of movement restrictions and migration patterns on the spread of infectious diseases? How can we capture the impact of household transmission using compartmental epidemic models? How could behavior-dependent vaccination affect the dynamical outcomes of epidemic models? The derivation and analysis of the mathematical models addressing these questions provides a wide-ranging overview of the new approaches being created to better forecast and mitigate emerging epidemics. This book will be of interest to researchers in the field of mathematical epidemiology, as well as public health workers.

"... a fun and readable book that engages the imagination and retains the interest of the clinically oriented reader while conveying an understanding of the direct implications of molecular characteristics of infectious agents to the practice of medicine.." –Emerging Infectious Diseases, January 2010 "... provides a valuable overview of the basic principles and issues pertaining to the pathogenesis and prevention of infectious diseases. The illustrations, the chapter summaries with relevant information, and the case studies are all particularly useful for the targeted readers. The book is well designed and manages to convey the general concepts of the various aspects of infectious diseases without overwhelming the reader with too much information... recommended for students, trainees, or physicians who desire a well-illustrated textbook that is easy to read and that addresses the basic aspects of infectious disease." –Clinical Infectious Diseases, 2010 The study of infectious diseases has undergone major changes since its infancy when it was largely a documentation of epidemics. It has now evolved into a dynamic

phenomenon involving the ecology of the infectious agent, pathogenesis in the host, reservoirs and vectors, as well as the complex mechanisms concerned in the spread of infection and the extent to which this spread occurs. Rapid globalization has led to unprecedented interest in infectious diseases worldwide and their effect on complex population dynamics including migration, famine, fire, war, and terrorism. It is now essential for public health officials to understand the basic science behind infectious disease and, likewise, students studying ID must have a broader understanding of the implications of infectious disease in a public health context as well as clinical presentation and prevention. The clear demand for an integrated approach has led to the publication of this text. Check out the student companion site at [www.wiley.com/go/shettyinfectiousdisease](http://www.wiley.com/go/shettyinfectiousdisease)

There are at least two populations involved in any infectious disease process: the population of parasites that cause the disease and the population of hosts that are infected. *Parasitic and Infectious Diseases: Epidemiology and Ecology* focuses on the interface between these two populations. The various chapters demonstrate how combined field, experimental, and theoretical studies aid in our understanding of the dynamics of infectious disease processes and in formulating control strategies. Moving from the basics of mathematical modeling and epidemiological principles to case studies of human, livestock, and wild animal infections, the editors have assembled a book of tremendous value to researchers in ecology, parasitology, medical and veterinary sciences, infectious disease, epidemiology, and other related fields of study. Key Features \* Introduction of mathematical modeling for the novice \* Case studies covering a spectrum of infections in humans, livestock, and wild animals \* Integration of field, laboratory, and theoretical approaches \* Development and illustration of key concepts in interactions between infectious agents and their host populations \* Written and edited by internationally recognized leaders in the field

There is now near undisputed scientific consensus that the rise in atmospheric concentration of greenhouse gases causes warming at the Earth's surface. Global warming will also have impacts on human health. We focus here on vector-borne infectious diseases because climatic variables are major determinants of the geographical distribution of the cold-blooded insect and tick species that can transmit viruses, bacteria and other microparasites to humans. The distribution of vectors is thus one important component of infection risk. We review the methods that have been developed in the past few years to determine and to model the distribution of species under actual and hypothetical environmental conditions and show how mathematical models have been used in this context. Remote sensing technology offers progressively better environmental and climatic data which can be employed in conjunction with Geographic Information Systems (GIS) and spatial statistical techniques to determine the distribution of vector species under different scenarios. Mathematical models can help to elucidate many aspects of infectious disease dynamics. The available studies lead to the expectation that climate change affects the transmission dynamics of vector-borne infectious diseases. However, the details and the degree of these effects are very uncertain. In order to predict more reliably the effects of extreme climate variability or climate change on infectious disease dynamics more data on the interaction between ecological, epidemiological, economical and social processes are needed.

The topic of infectious disease epidemics has recently attracted substantial attentions in research communities and it has been shown that the changes of human behaviors have significant impacts on the dynamics of disease transmission. However, the study and understanding of human reactions into spread of infectious disease are still in the very beginning phase and how human behaviors change during the spread of infectious disease has not been systematically investigated. Moreover, the study of human behaviors includes not only various enforced measures by public authorities such as school closure, quarantine, vaccination, etc, but also the spontaneous self-protective actions which are triggered by risk perception and fear of diseases. Hence, the goal of this research is to study the impacts of human behaviors to the epidemic from these two perspectives: spontaneous behavioral changes and public intervention strategies. For the sake of studying spontaneous changes of human behaviors, this research first time applied evolutionary spatial game into the study of human reactions to the spread of infectious disease. This method integrated contact structures and epidemics information into the individuals' decision processes, by adding two different types of information into the payoff functions: the local information and global information. The new method would not only advance the field of game theory, but also the field of epidemiology. In addition, this method was also applied to a classic compartmental dynamic system which is a widely used model for studying the disease transmission. With extensive numerical studies, the results first proved the consistency of two models for the sake of validating the effectiveness of the spatial evolutionary game. Then the impacts of changes of human behaviors to the dynamics of disease transmission and how information impacts human behaviors were discussed temporally and spatially. In addition to the spontaneous behavioral changes, the corresponding intervention strategies by policy-makers played the key role in process of mitigating the spread of infectious disease. For the purpose of minimizing the total lost, including the social costs and number of infected individuals, the intervention strategies should be optimized. Sensitivity analysis, stability analysis, bifurcation analysis, and optimal control methods are possible tools to understand the effects of different combination of intervention strategies or even find an appropriate policy to mitigate the disease transmission. One zoonotic disease, named Zoonotic Visceral Leishmaniasis (ZVL), was studied by adopting different methods and assumptions. Particularly, a special case, backward bifurcation, was discussed for the transmission of ZVL. Last but not least, the methodology and modeling framework used in this dissertation can be expanded to other disease situations and intervention applications, and have a broad impact to the research area related to mathematical modeling, epidemiology, decision-making processes, and industrial engineering. The further studies can combine the changes of human behaviors and intervention strategies by policy-makers so as to seek an optimal information dissemination to minimize the social costs and the number of infected individuals. If successful, this research should aid policy-makers by improving communication between them and the public, by directing educational efforts, and by predicting public response to infectious diseases and new risk management strategies (regulations, vaccination, quarantine, etc.).

As we known, infectious diseases can be transmitted from one region to another due to extensive travel and migration. Meanwhile, different regions have different demographic and epidemiological characteristics. To capture these features, multi-patch epidemic models have been developed to study disease transmission in heterogeneous environments. In Chapter 1, a susceptible-infectious-susceptible patch model with nonconstant transmission coefficients is formulated to investigate the effect of media coverage and human movement on the spread of infectious diseases among patches. In chapter 2, I propose a multi-patch model to study the effects of population dispersal on the spatial spread of malaria between patches. In Chapter 3, based on the classical Ross-Macdonald model, I propose a periodic malaria model to incorporate the effects of temporal and spatial heterogeneity in disease transmission. Chapter 4 is

