
Preface

In this new century mankind faces ever more challenging environmental and public health problems, such as pollution, invasion by exotic species, the emergence of new diseases or the emergence of diseases into new regions (West Nile virus, SARS, Anthrax, etc.), and the resurgence of existing diseases (influenza, malaria, TB, HIV/AIDS, etc.). Mathematical models have been successfully used to study many biological, epidemiological and medical problems, and nonlinear and complex dynamics have been observed in all of those contexts. Mathematical studies have helped us not only to better understand these problems but also to find solutions in some cases, such as the prediction and control of SARS outbreaks, understanding HIV infection, and the investigation of antibiotic-resistant infections in hospitals.

Structured population models distinguish individuals from one another according to characteristics such as age, size, location, status, and movement, to determine the birth, growth and death rates, interaction with each other and with environment, infectivity, etc. The goal of structured population models is to understand how these characteristics affect the dynamics of these models and thus the outcomes and consequences of the biological and epidemiological processes. There is a very large and growing body of literature on these topics. This book deals with the recent and important advances in the study of structured population models in biology and epidemiology. There are six chapters in this book, written by leading researchers in these areas.

In Chap. 1, Population Models Structured by Age, Size, and Spatial Position, Glenn Webb systematically introduces population models with age, size, and spatial structure. The theory of semigroups of linear and nonlinear operators in Banach spaces is used to analyze these models and many numerical simulations are included to illustrate the theoretical results, as an aid to readers. A brief and historical introduction on age structured models is given in the Introduction. Section 1.1 focuses on population models structured by two factors, size and spatial position. Basic assumptions and definitions, illustrative examples, and simulations are presented. Fundamental theorems are stated and proved. Results are then established for population models structured by

age and spatial position in Sect. 1.2. In Sect. 1.3 population models structured by all three factors, namely, age, size, and spatial position, are studied. As an example, a model of tumor growth with cell age corresponding to the cell cycle, cell size corresponding to cell growth and division, and cell position in space corresponding to cell motility and migration is discussed.

An important class of spatial models deals with metapopulations. A metapopulation is a group of populations of the same species that occupy separate patches and are connected by dispersal. Spatially implicit metapopulation models with discrete patch-size structure lead to infinite systems of ordinary differential equations, as do host-macroparasite models which distinguish hosts by their parasite loads, and prion proliferation. In Chap. 2, *Infinite ODE Systems Modeling Size-structured Metapopulations, Macroparasitic Diseases, and Prion Proliferation*, Maia Martcheva and Horst Thieme develop a general theory on the properties of the solution semiflows generated by infinite systems of ordinary differential equations. The chapter consists of 14 sections. In Sect. 2.2, homogeneous linear Kolmogorov systems are discussed. Section 2.3 addresses semilinear systems. Sections 2.4–2.11 focus exclusively on metapopulation models. Boundedness of solutions of general metapopulation models is studied in Sect. 2.4, while Sect. 2.5 focuses on how the absence of migration or colonization of empty patches can cause extinction. In Sects. 2.6–2.11, a more specific metapopulation model is studied. Topics addressed include the existence of compact attractors, stability of equilibria, metapopulation persistence, etc. Finally, results are applied to analyze specific metapopulation models, specific host-macroparasite models, and prion proliferation models in Sects. 2.12, 2.13, and 2.14, respectively.

In the classical diffusive epidemic models introduced in Chap. 1, the spatial domains are usually assumed to be homogenous. However, in reality that is not the case – one needs to consider heterogeneous environments. In Chap. 3, *Simple Models for the Transmission of Microparasites between Host Populations Living on Non-coincident Spatial Domains*, William E. Fitzgibbon and Michel Langlais focus on modeling the direct and indirect transmission of a microparasite between host populations living on non-coincident spatial domains. The goal is to provide a mathematical approach to model the environmentally driven transmission of microparasites between host populations living on distinct spatial domains. A key assumption is the possibility for the microparasite to persist in the environment once it is released by infective individuals. Besides criss-cross transmission, indirect transmission occurs through contacts between susceptible hosts and the contaminated part of the environment. A critical example is the indirect contamination of human populations by animals when the parasite is benign for animals but lethal to humans. This is actually the case for Hantaviruses for which rodents are the main reservoir population, and more generally for many emerging infectious diseases. Various deterministic models can be developed, ranging from unstructured populations – basic ODE systems – to spatially structured multi-patch and reaction–diffusion models to handle heterogeneous environments.

Age structures, as introduced in Chap. 1, are also important to consider both from a chronological point of view – juveniles vs. adults – and from an epidemiological point of view – variable virulence.

The emergence of diseases that are transmitted by vectors, such as the West Nile virus and Dengue fever, raises challenging issues not only epidemiologically but also mathematically. In Chap. 4, *Spatiotemporal Patterns of Disease Spread: Interaction of Physiological Structure, Spatial Movements, Disease Progression and Human Intervention*, Stephen A. Gourley, Rongsong Liu, and Jianhong Wu are concerned about the effects of demographic and disease ages and spatial movements of hosts on the spatiotemporal spread patterns of certain diseases, with special emphasis on West Nile virus. They start with a short review of some standard models for the transmission dynamics of vector-borne diseases in homogeneous environments and populations. In Sect. 4.2 they focus on structured vector-borne diseases with particular reference to West Nile virus. As the juvenile and adult birds (the hosts) have different spatial movement behaviors, the main model is of the McKendrick–von Foerster type for age-structured bird populations. Various sufficient conditions are given for the system to evolve to the disease-free state and for the stability of this equilibrium. Age-structured control measures are considered in Sect. 4.3, and appropriate mathematical models are derived and used to assess the effectiveness of culling as a tool to eradicate WNV. The results show that eradication of WNV is possible by culling the mosquitoes at either the immature or the mature phase, even though the size of the mosquito population is oscillating and stays above a certain level. The interaction of individual movement and physiological status is considered in Sect. 4.4 with an application to the spatial spread of WNV. Finally, patchy models for the spatial spread of WNV are formulated and analyzed in Sect. 4.5.

To describe the complex dynamics of ecological systems, mathematical models frequently have a large number of variables. In Chap. 5, *Aggregation of Variables and Applications to Population Dynamics*, attention is directed to aggregation of variables in population and community dynamics. Pierre Auger, Rafael Bravo de la Parra, Jean-Christophe Poggiale, Eva Sanchez, and T. Nguyen-Huu introduce aggregation methods for different types of models, such as ordinary differential equations, discrete equations, delay differential equations, and partial differential equations based on the method of separation of time scales. In Sect. 5.2 the aggregation of variables for ODE systems is developed, geometric singular perturbation theory and normally hyperbolic manifolds are introduced, along with slow and fast systems, aggregation and emergence, and illustrative examples are given. Section 5.3 addresses aggregation methods for discrete models. In Sect. 5.4 the method of aggregation is also applied to partial differential equations and delay equations. Section 5.5 presents several applications in population and community dynamics.

In 1983, R. Freter and collaborators developed a simple chemostat-based model of competition between two bacterial strains, one of which is capable of wall-growth, to illuminate the role of bacterial wall attachment on the

phenomenon of colonization resistance in the mammalian gut. In Chap. 6, The Biofilm Model of Freter: A Review, Mary Ballyk, Don Jones, and Hal Smith have re-formulated the model in the setting of a tubular flow reactor, extended the interpretation of the model as a biofilm model, and provided both mathematical analysis and numerical simulations of solution behavior. In Sects. 6.1 and 6.2, the original Freter model is introduced and then is generalized and reformulated as a chemostat-based model. In Sect. 6.3, the one-dimensional thin tube flow reactor model with biofilm is proposed and analyzed, and special cases such as an advection dominated flow reactor and mobile wall-adherent cells, are considered. The three-dimensional flow reactor models are studied in Sect. 6.4. Section 6.5 focuses on mixed culture models, the associated eigenvalue problems are considered, and simulations are carried out.

This book can be used for various purposes. It is suitable as a textbook for a mathematical biology course or a summer school at the advanced undergraduate and graduate level. It can also be used as a reference book by researchers looking for either interesting and specific problems to work on or useful techniques and discussions of some particular problems. Since the book contains the most recent developments in some fields of mathematical biology and epidemiology, we hope that researchers at all levels will find the book inspiring and useful for their research and study.

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