

Preface

This book is an introductory text to the methods and tools that are nowadays widely used and accepted in the mathematical epidemiology literature. It is intended to start from a beginner level and accelerate to research level. It targets upper undergraduate mathematics students, and mathematics, physics, and engineering graduate students. The book will also be suitable for mathematics researchers who wish to build a background and advance to research level in mathematical epidemiology. The book is expected to be useful to mathematical epidemiologists as a reference text.

Chapter 1 discusses some historical aspects of modeling infectious diseases. It also introduces a number of epidemiological concepts with their definitions. Finally, Chap. 1 includes general ideas about the modeling process, how we go from a biological question to a mathematical model, and how we answer biological questions based on conclusions from the model. Chapter 2 introduces the basic epidemic models without demography as well as a comparison to data. Simple single-equation epidemic models are analyzed. Chapter 3 deals with how and when demographic variables are included in epidemic models. It also includes complete analysis of the basic SIR model with demography. Analysis of planar systems is presented. Hopf bifurcation is introduced and applied to a model with saturating incidence. Chapter 4 brings in vector-borne diseases and treats their modeling in the context of ordinary differential equations (ODEs) and delay-differential equations. Chapter 5 is devoted to building more complex models with various components. Most of the widespread techniques for the computation of the reproduction number are introduced and illustrated on examples. Chapter 6 discusses statistical techniques for fitting models to data and for selecting the model that best represents the data. The first six chapters use standard and relatively elementary mathematical techniques and may be appropriate for a more general audience.

Chapters 7–11 treat more advanced epidemiological models and build appropriate mathematical techniques that are more involved. Chapter 7 is devoted to the mathematical analysis of complex epidemiological models. Global stability is considered via Lyapunov functions. The possibility of multiple equilibria via backward bifurcation is also introduced. Chapter 8 is devoted to multistrain interactions. The chapter begins by establishing the competitive exclusion principle. Furthermore,

it introduces mechanisms for coexistence. Analysis of multistrain models is illustrated. Chapter 9 is devoted to modeling control strategies in the context of single-strain and multistrain diseases. Herd immunity and proportion vaccinated are introduced. The chapter discusses the phenomenon of strain replacement. Optimal control techniques are presented and applied to specific examples. Chapter 10 introduces the most basic ecological models such as predation and competition and includes the spread of a disease in animal populations subject to predation or competition. Complex dynamical behavior such as chaos is shown in a three-dimensional system of ODEs. Chapter 11 focuses on zoonotic diseases in general and avian influenza in particular. Basic models of avian influenza are introduced and compared to data. Control strategies are evaluated. Nonautonomous modeling is treated.

Chapters 16–14 are devoted to partial differential equation (PDE) age-structured epidemic modeling. Chapter 16 introduces host–age structured models. After a brief introduction of age-structured population models, the chapter proceeds by discussing age-structured SIS (susceptible–infected–susceptible) and SIR (susceptible–infected–removed) models. Chapter 13 introduces a basic SI model with age since infection. Pease’s influenza model is also discussed, and oscillations are obtained. Chapter 14 is devoted to immuno-epidemiological modeling. It includes immunological modeling, linking within-host models to epidemiological models and computation of relevant reproduction numbers. Chapter 15 is devoted to spatial aspects of epidemiology. Multipatch models with Lagrangian and Eulerian movement are considered. Furthermore, simple diffusion models are introduced, and a rabies epidemic model with diffusion is discussed. Chapter 13 introduces the basic epidemic models in a discrete setting. It also includes tools for local analysis of discrete dynamical systems. More complex discrete models are built, and the next-generation approach for the computation of the reproduction number in discrete settings is discussed.

This book is intended as a comprehensive text on mathematical epidemiology. However, it does not include some important topics that are an integral part of the subject. Two important topics that are missing are stochastic epidemic modeling and network disease modeling. These were not included to keep the length of the book within limits and because of the limited expertise of the author in those specific topics. There are several books that focus on these topic separately and involve epidemic modeling.

Chapters from this book can be used as an upper undergraduate or graduate text, as well as for summer courses. Chapters 1–6 are appropriate for an undergraduate course on mathematical epidemiology or as a supplemental text to an undergraduate mathematical biology class. Chapters 2–11 and 16 are appropriate for an introductory graduate class on mathematical epidemiology. Chapters 16–15 are more advanced and are appropriate for a PDE-focused graduate mathematical biology class. Exercises are provided after each chapter to help the reader understand and retain the material as well as to develop necessary skills to advance to research.

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