

# Preface to the Second Edition

Our textbook *Mathematical Models in Population Biology and Epidemiology* has reached its first decade and in the process it has captured and maintained the interest of a sufficient number of members of the computational, mathematical, modeling, and theoretical biology communities that the writing of a revised, updated and extended edition has gained the support of Springer. The field was already immense a decade ago when we took on the writing of this book, and our choices of what to include in the book were somewhat arbitrary, namely those that satisfied our interests, philosophies, and egos. Today, the research in the topics closer to our interest has grown so much that the writing of a book that heavily intersects with the field of population biology is beyond the confines of a single volume. So following the adage “why fix something that is not broken (even if old),” we have decided to maintain the core of the first edition; correct some of the errors, typos, and confusing paragraphs (while unknowingly introducing new ones); include a new chapter on the spatiotemporal dynamics of populations and expand the sections that focus on disease dynamics and control. We hope that this new edition is not only fatter but also better.

The emergence and/or reemergence of infectious diseases such as SARS, tuberculosis, and influenza are used to justify our substantial expansions of the epidemiology chapters (9 and 10). Further, this volume gives additional emphasis to the study of models that capture the dynamics of single epidemic outbreaks, influenza models, and parameter estimation.

Furthermore, a new chapter (8) is devoted to the study of the dynamics of spatially structured populations. Specifically, we have introduced the basic diffusion, reaction–diffusion, and metapopulation modeling frameworks as a *primer* for readers interested in a central topic in mathematical biology. A substantial number of additional exercises have been added, and the number of projects focused on biology has been doubled in this edition.

As in all new efforts, we have here played the primary role of “collectors” of the insights; questions and thoughts of many individuals, particularly current and former students and alumni of MTBI (Mathematical and Theoretical Biology Institute, <http://mtbi.asu.edu/>). MTBIers have helped shape this book for the past 15 years,

in a variety of ways. For example, many problems and projects have been motivated or have been adapted from the 144 technical reports generated over those 15 years, all collected in an accessible web site (<http://mtbi.asu.edu/research/archive>). We would like to thank particularly the contributions of the following MTBIs, including graduate students and faculty, Juan Aparicio, Leon Arriola, H. T. Banks, Faina Berezovskaya, Naala Brewer, Erika Camacho, Reynaldo Castro, Gerardo Chowell, Ariel Cintron-Arias, Maytee Cruz-Aponte, Mustafa Erdem, Arlene Evangelista, Zhilan Feng, Jose Flores, Luis Gordillo, Christopher Kribs-Zaleta, Raquel Lopez, Dori Luli, Emmanuel Morales, Romarie Morales, Ben Morin, Anuj Mubayi, Miriam Nuno, Anarina Murillo, David Murillo, Dustin Padilla, Kehinde Salau, Fabio Sanchez, Baojun Song, Karyn Sutton, Karen Rios-Soto, Ilyssa Summers, Steve Tennenbaum, Griselle Torres-Garcia, Jose Vega, Xiaohong Wang, Steve Wirkus, and Abdul-Aziz Yakubu. In addition, several individuals and colleagues found typos or mistakes in the first edition. We want to thank Malay Banerjee, Eric Cytrynbaum, Kathleen Dearing, Jonathan Dushoff, David Gerberry, Luis Gordillo, Jeff Moehlis, Steve Krone, Simon Levin, Marcin Mersan, Joseph Mugisha, Mason Porter, Dan Rubin, Hal Smith, V. P. Stokes, and Pauline van den Driessche for their keen eyesight and the kindness used to inform us of these mishaps.

We thank Kamal Barley, who provided invaluable help in redrawing most of the figures and constructing the index. Furthermore, we want to acknowledge particularly Ben Morin, David Murillo, and Sunmi Lee for providing solutions to a large number of problems. Our colleague Sergei Suslov and his students Jose Vega and Raquel Lopez provided a substantial number of problems and projects that are now incorporated in Chapter 8. In addition, David Kramer found many improvements as a copyeditor, and Donna Chernyk, our editor at Springer, supplied a great deal of help.

Some of the work of many of the people who had a part in the production of this book has received support from the Department of Defence, MITACS (Mathematics of Information Technology and Complex Systems), the National Science Foundation, NSERC (Natural Sciences and Engineering Research Council), the Sloan Foundation, and the Offices of the Provost and President of Arizona State University.

Finally, we want to thank our families for their love and patience despite the fact that we shamelessly used weekends and family times in this endeavor.

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This book is intended to inspire students in the biological sciences to incorporate mathematics in their approach to science. We hope to show that mathematics has genuine uses in biology by describing some models in population biology and the mathematics that is useful in analyzing them, as well as some case studies representing actual, if somewhat idealized, situations. A secondary goal is to expose students of mathematics to the process of modeling in the natural and social sciences.

A realistic background in mathematics for studying this book is a year of calculus, some background in elementary differential equations, and a little matrix theory. The mathematical treatment is based less on techniques for obtaining explicit solutions in “closed form”, to which students in elementary mathematics courses may be accustomed, than on approximate and qualitative methods. The emphasis is on describing the mathematical results to be used and showing how to apply them, rather than on detailed proofs of all results. References to where proofs may be found are given. Our hope is that students in the biological sciences will cover enough mathematics in their first two years of university to make this book accessible in the third or fourth year. Some review notes on the mathematics needed may be found at <http://www.cdm.yorku.ca/rev2.pdf>.

For many problems, the use of a computer algebra system can give many insights into the behavior of a model, especially for generating graphical representations of solutions. Some of the exercises and projects in the book either require the use of a computer algebra system or are simplified considerably by one. At this writing, Maple, Matlab, and Mathematica are widely used systems; students should become proficient in using at least one of them. In addition, the more specialized dynamical systems program XPP or its Windows version WinPP is very useful for studying dynamical systems and is especially valuable for differential–difference equations and equations with time lags. This program, created by Bard Ermentrout, may be downloaded from

<http://ftp.math.pitt.edu/pub/bardware/winpp.zip>

The more elaborate version XPP may be run under Windows on an X-Windows server and may be downloaded from

<http://ftp.math.pitt.edu/pub/bardware/xpp4w32.zip>

Matlab is also suitable for differential–difference equations and equations with time lags.

There are some topics that in earlier times would have been appendices in this book. These include some mathematical ideas such as Taylor approximation and the elements of linear algebra, and also some programs for solving problems with Maple, and WinPP. These topics, which we consider as the components of a virtual appendix, and some detailed solutions to selected exercises will be found in the form of PDF files at a future web site.

Answers to selected exercises are still given in the book as an appendix. Genuine understanding of the material in the book requires working of exercises; this is not a spectator sport. Answers in the back of the book are to be used to *check* your work, not to lead you to the solution.

In addition to exercises, there are several more extended descriptions of models, which call for readers to fill in some gaps. These are designated as Projects, and they may be given as group assignments.

The book concentrates on population biology. One of the practical sides of population biology is resource management. Another aspect is the study of structured population models. Mathematical epidemiology is an example, with populations structured by disease status. The core of the book, which should be included in any beginning modeling course, is Chapters 1, 2, 4, and the first five sections of Chapter 5. These chapters cover elementary continuous and discrete models for single-species populations and interacting populations. They include examples and exercises that may be too simplistic for more experienced students, who may progress through this material a little more rapidly than beginners. Chapters 9 and 10, on mathematical epidemiology, are also on a relatively elementary level and may be studied by students with relatively little background. Chapter 3, on continuous models with delays, Chapter 6, on harvesting and its implications in resource management, Chapter 7, on population models with age structure, and Chapter 8, on population models with spatial structure, as well as the later sections of Chapters 5 and 9, are more demanding mathematically. This material should probably be reserved for students with more mathematical background and some experience in biology.

The bibliography includes not only the books and papers to which reference is made in the text but also related works which pursue further some of the topics in the book. The book is meant to be an introduction to the principles and practice of mathematical modeling in the biological sciences, one which will start students on a path; it is certainly not the last word on the subject.

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