



PREFACE

In the not so distant past, the sciences of biology, chemistry, and physics were seen as more or less separate disciplines. Within the last half-century, however, the lines between the sciences have become blurred, to the benefit of each. Somewhat more recently, the methods of mathematics and computer science have emerged as necessary tools to model biological phenomena, understand patterns, and crunch huge amounts of data such as those generated by the human genome project. Today, virtually any advance in the life sciences requires a sophisticated mathematical approach. Characterization of biological systems has reached an unparalleled level of detail, and modeling of biological systems is evolving into an important partner of experimental work. As a result, there is a rapidly increasing demand for people with training in the field of biomathematics.

Training at the interface of mathematics and biology has been initiated in a number of institutions, including Rutgers University, the University of California at Los Angeles, North Carolina State University, the University of Utah, and many others. In 2001, a National Research Council panel found that “undergraduate biology education needs a more rigorous curriculum including thought provoking lab exercises and independent research projects.” To improve quantitative skills, faculty members should include more concepts from mathematics and the physical sciences in biology classes. Ideally, the report says, “the entire curriculum would be revamped.”¹ As the demand for academic programs that facilitate interdisciplinary ways of thinking and problem solving grows, many of the challenges for creating strong undergraduate programs in mathematical biology have become apparent. The report *Math & Bio 2010: Linking Undergraduate Disciplines* summarizes the results of the project *Meeting the Challenges: Education Across the Biological, Mathematical, and Computer Sciences*² and emphasizes that interdisciplinary programs should begin as early as the first year of college education, if not in high school. In one of the articles, an editorial reprinted from the journal *Science* and used in the report, the author Louis Gross specifically underscores the importance of finding ways to “teach entry-level quantitative courses that entice life science students through meaningful applications of diverse mathematics to biology, not just calculus, with a few simple biological examples.”³

The book that you are about to read, our *An Invitation to Biomathematics*, was conceived and written with this exact goal in mind. This book is meant to provide a glimpse into the diverse world of mathematical biology and to invite you to experience, through a selection of topics and projects, the fascinating advancements made

possible by the union of biology, mathematics, and computer science. The laboratory manual component of the text provides venues for hands-on exploration of the ever-present cycle of model development, model validation, and model refinement that is inherent in contemporary biomedical research. The textbook aims to provide exposure to some classical concepts, as well as new and ongoing research, and is not meant to be encyclopedic. We have tried to keep this volume relatively small, as we see this text used as a first reading in biomathematics, or as a textbook for a one-semester introductory course in mathematical biology. It is our hope that after reading this *Invitation*, you will be inspired to embark on a more structured biomathematical journey. We suggest considering a classical textbook, such as Murray's *Mathematical Biology*, to gain a systematic introduction to the field in general. We also encourage you to delve deeper into some of the more specialized topics that we have introduced, or to take additional course in mathematical biology.

The textbook is divided into two parts. In Part I, we present some classical problems, such as population growth, predator-prey interactions, epidemic models, and population genetics. While these have been examined in many places, our main purpose is to introduce some core concepts and ideas in order to apply them to topics of modern research presented in Part II. Because we also felt that these topics are likely to be covered in any entry-level course in mathematical biology, we hope that this organization will appeal to college and university faculty teaching such courses. A possible scenario for a one-semester course will be to cover all topics from Part I with a choice of selected topics from Part II that is, essentially, modular in nature. The diagram in Figure 1 outlines the chapter connectivity. Table 1 presents brief chapter descriptions by biological and mathematical affiliation.

A committed reader who has had the equivalent of one semester-long course in each of the disciplines of calculus, general biology, and statistics should be able to follow Chapters 1 to 10. With these prerequisites, we believe that the book can be read, understood, and appreciated by a wide audience of readers. Although Chapters 11 and 12 also comply with those general prerequisites, a quality understanding of the fundamental concepts covered there may require a somewhat higher level of general academic maturity and motivation. Thus, although Chapters 11 and 12 can be considered optional in essence, we would like to encourage the readers to explore them to the extent and level of detail determined by their individual comfort level.

Our rule while writing this book was that the biology problem should lead the mathematics, and that we only present the mathematics on a need-to-know basis and in the amount and level of rigor necessary. As a consequence, very few mathematical theorems are proved or even discussed in the text. We limited ourselves to the minimal

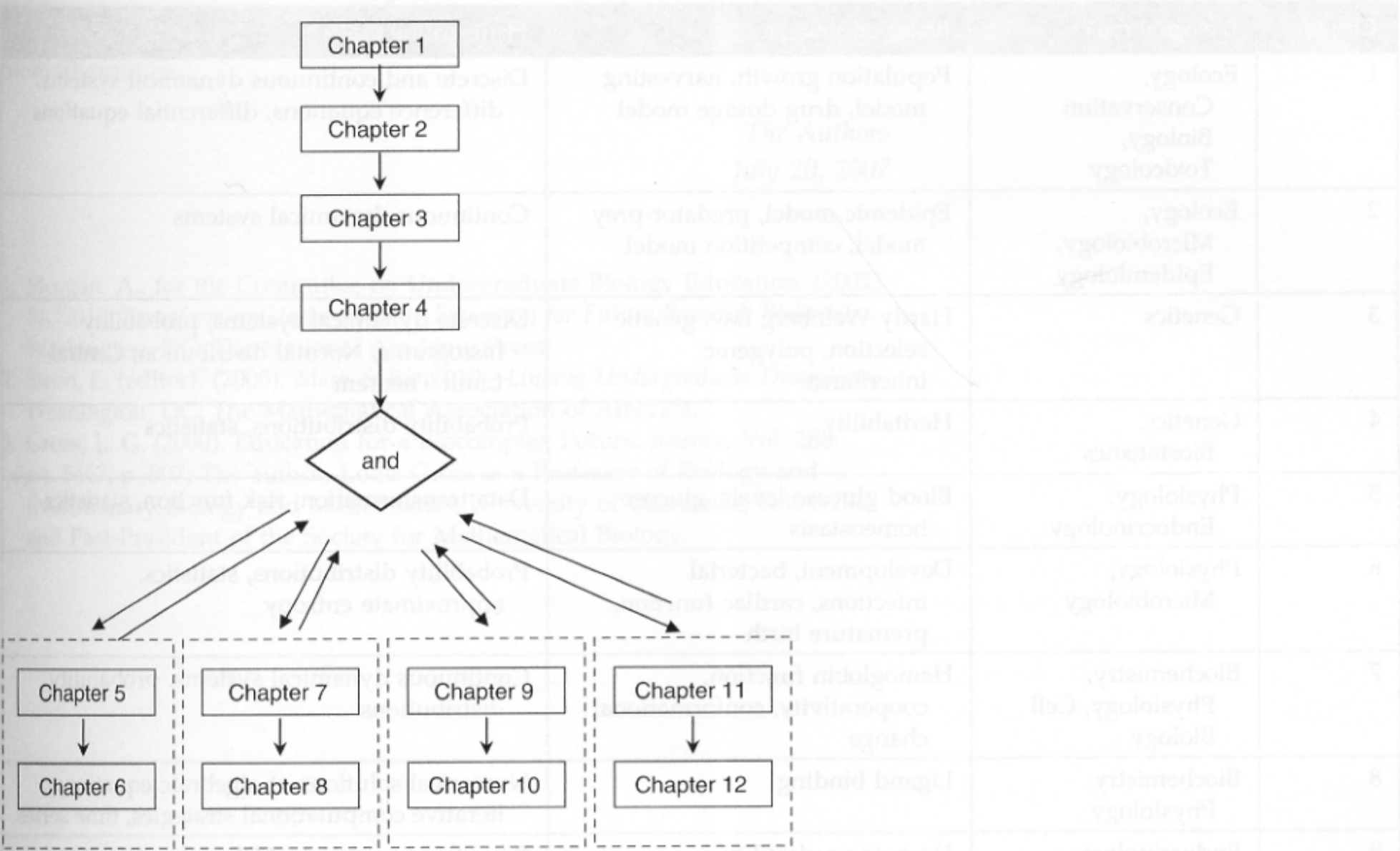


FIGURE 1.

mathematical terminology necessary for understanding, formulating, and solving the problem, relying on the reader's intuition for the rest. We felt that in the interest of showing how the tools of mathematics and biology can blend together and work as one when needed, we should resist the urge for possible generalizations (an urge that is almost second nature for those of us trained in the field of theoretical mathematics). The choice not to explore many of the possible exciting mathematical venues that stem from some of the topics and projects was deliberate, and we apologize to those readers who wish we had included them.

We would like to thank all of our students at Sweet Briar College and the University of Virginia, especially Jennifer McDonaugh, Jamie Jensen, and Suzanne Harvey, for providing valuable comments and opinion throughout the development and classroom testing of the textbook and laboratory manual manuscripts. We also thank our colleagues Drs. Marc Breton, Jeff Graham, Stan Grove, David Housman, Eric Marland, Pamela Ryan, Philip Ryan, Karen Ricciardi, and Bonnie Schulman for their feedback on selected chapters and/or laboratory projects, and Anna Kovatcheva for collecting the data used in Exercise 1 of Chapter 4. We appreciate the help of Dr. Stefan Robev and of Ryan King, who carefully proofread the entire first draft of the manuscript, and of Jane Carlson, who assisted with its early technical editing. We are also indebted to all

Chapter	Biological topics	Biological subtopics	Mathematical topics
1	Ecology, Conservation Biology, Toxicology	Population growth, harvesting model, drug dosage model	Discrete and continuous dynamical systems, difference equations, differential equations
2	Ecology, Microbiology, Epidemiology	Epidemic model, predator-prey model, competition model	Continuous dynamical systems
3	Genetics	Hardy-Weinberg law, genetic selection, polygenic inheritance	Discrete dynamical systems, probability histograms, Normal distribution, Central Limit Theorem
4	Genetics, Biostatistics	Heritability	Probability distributions, statistics
5	Physiology, Endocrinology	Blood glucose levels, glucose homeostasis	Data transformation, risk function, statistics
6	Physiology, Microbiology	Development, bacterial infections, cardiac function, premature birth	Probability distributions, statistics, approximate entropy
7	Biochemistry, Physiology, Cell Biology	Hemoglobin function, cooperativity, conformational change	Continuous dynamical systems, probability distributions
8	Biochemistry, Physiology	Ligand binding	Numerical solutions of algebraic equations, iterative computational strategies, time series
9	Endocrinology, Physiology, Cell Biology	Hormone pulsatility	Periodic components, FFT, pulse-detection algorithms
10	Endocrinology, Physiology, Cell Biology	Hormone networks	Continuous dynamical systems with delays
11	Physiology, Cell Biology, Molecular Biology	Circadian rhythms	Confounded time series, rhythm analysis
12	Physiology, Cell Biology, Molecular Biology	Gene chips, molecular biology of circadian rhythms	Data normalization, clustering strategies, time series, rhythm analysis

TABLE I.
Chapter topics by biological and mathematical affiliation

of our editors at Academic Press/Elsevier: Chuck Crumley, David Cella, Kelly Sonnack, Nancy Maragioglio, Luna Han, and Sally Cheney, for their encouragement and assistance throughout. Our deep gratitude goes to Tom Loftus who put many hours into editing the final draft of the manuscript for style and language consistency. Finally, we appreciate the support of the National Science Foundation under the Department of Undergraduate Education awards 0126740 and 0304930, and the support of the National Institutes of Health under NIDDK awards R25 DK064122, R01 DK51562, and R25 DK064122.

You are now invited to turn the page and begin your exploration of biomathematics.

The Authors

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1. Morgan, A., for the Committee on Undergraduate Biology Education. (2002). *BIO2010: Transforming Undergraduate Education for Future Research Biologists*. Washington, DC: The National Academy Press.
2. Steen, L. (editor). (2005). *Math & Bio 2010—Linking Undergraduate Disciplines*. Washington, DC: The Mathematical Association of America.
3. Gross, L. G. (2000). Education for a Biocomplex Future. *Science*, Vol. 288, no. 5467, p. 807. The author, Louis Gross is a Professor of Ecology and Evolutionary Biology and Mathematics, University of Tennessee, Knoxville, and Past-President of the Society for Mathematical Biology.

PROCESSES THAT CHANGE WITH TIME: INTRODUCTION TO DYNAMICAL SYSTEMS

Using Data to Formulate a Model

Darwin Viewed Continuous Models

A Continuous Population Growth Model

The Logistic Model

An Alternative Derivation of the Logistic Model

Long-Term Behavior and Equilibrium States

Analyzing Equilibrium States

The Malthus Model for Discrete Population Growth

A Population Growth Model with Delay

Modeling Psychological Mechanisms of Drug Elimination

Using Computer Software for Solving the Models

Some BERKELEY MADONNA Specimens

Applied Biology Laboratory Exercises for Chapter 1

Building a good mathematical model is a challenging task that requires a solid understanding of the nature of the system being modeled, as well as the mathematical tools being used to describe it. Because mathematical models are quite diverse, it is difficult to specify a process that would apply to all problems. However, there are fundamental principles that facilitate and guide the creative process. They are:

1. Initially, a model should be simple.
2. It is crucial to test the model under as many conditions as reasonable.
3. If the model seems to be successful in some ways but fails in others, try to modify the model rather than starting over.

In this chapter, we discuss how biological models of one variable change over time. The first model we study is growth of a population. Our initial attempt is based on numerical data; later, we build the model based on conjectures about "how populations should grow." Both models yield essentially the same result, and although these constructions are successful in the short term, both are flawed because the long-term behavior they predict is