

Preface

Mathematical biology is a fast growing field which is concerned with problems that arise in biology. The aim is to address biological questions using mathematics. The mathematical models that are used to address these questions depend on the specific biological context. They include dynamical systems, probability, statistics, and discrete mathematics. The approach in addressing a biological question is to develop a mathematical model that represents the biological background needed in order to address the question, to show that simulations of the model are in agreement with known biological facts, and, finally, to provide a solution to the original question. This approach to mathematical biology was carried out in two recent books: *Introduction to Mathematical Biology*, by C.-S. Chou and A. Friedman (Springer, 2016) and *Mathematical Modeling of Biological Processes* by A. Friedman and C.-Y. Kao (Springer, 2014). Both of these books were based on a one-semester course (the first one for undergraduate students and the second for master's students) taught over several years at The Ohio State University in Columbus, Ohio. Each of the books included MATLAB simulations and exercises. The present monograph considers biological processes that are described by systems of partial differential equations (PDEs). It focuses on modeling such processes, not on numerical methods and simulations. On the other hand it also includes results in mathematical analysis of the mathematical models, or of their simplified versions, as well as many open problems.

The monograph is addressed primarily to students and researchers in the mathematical sciences who do not necessarily have any background in biology, and who may have had little exposure to PDEs. We have included in an Appendix a “short course” in PDEs in order to familiarize the reader with the mathematical aspects of the models that appear in the book. The first chapter introduces the basic biology that will be used in the book. The second chapter introduces the basic blocks in building models, for example how to express the fact that a ligand activates an immune cell. The third chapter gives several simple examples of models on population dynamics. The fourth chapter develops two models of cancer. The choice of parameters in the cancer models, as in all other PDE models, is critically important if the models are to have a predictive value. In Chapter 5, we illustrate how to estimate the parameters of the first cancer models of Chapter 4 using both experimental data and some “reasonable” assumptions.

Chapter 6 describes mathematical results inspired by cancer models, including stability of spherical tumors and symmetry-breaking bifurcations, and it also suggests many open problems.

Chapter 7 addresses the question of the risk of atherosclerosis associated with cholesterol levels. The model develops a system of PDEs that describe the growth of a plaque in the artery. Chapter 8 describes mathematical results and open problems

for a simplified model of plaque growth. Chapters 9 and 10 follow the format of Chapters 7 and 8: Chapter 9 develops a model of wound healing, and Chapter 10 describes mathematical results and open problems associated with this model.

Almost all the PDE models introduced in this book are free boundary problems, that is, the domain where each PDE system holds is unknown in advance, and its boundary has to be determined together with the solution to the PDE system.

This book was written for the 2018 NSF-CBMS conference on “Mathematical Biology: Modeling and Analysis”, hosted by Howard University in Washington, DC, during May 21–25, 2018. It is our hope that this monograph will demonstrate to the reader the challenges, the excitement, and the opportunities for research at the interface of mathematics and biology.

It is finally my pleasure to express my thanks and appreciation to Dr. Xiulan Lai for typing the manuscript and drawing all the figures.

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