

Preface

Mathematical biomedicine is a fast developing interdisciplinary field of research that connects the natural and exact sciences in an attempt to respond to the challenges raised by biology and medicine. Biomedical research covers such diverse areas as the study of disease progression and treatment, drug development, and the analysis of epidemic trends and patterns, to name just a few. Mathematical methods in biomedicine therefore come from a correspondingly large number of fields of research that include mathematical physics, computational methods, control theory, combinatorics, statistics, and many more.

As in any research aimed to solve “real-world” problems, mathematical models in biomedicine must be grounded on experimental data. The information and model parameters usually come from *in vitro* or *in vivo* experiments, but are only rarely based on patient data. Unfortunately, quite often data are not sufficient to allow for an accurate and reliable parameter estimation. In the study of an infectious disease, the rate of infection typically varies between locations and from one time period to another. In other cases, the underlying medical processes are not fully understood and mathematical models become a tool to suggest biologically testable hypotheses.

There exist a large number of mathematical methods and procedures that can be brought in to meet the modeling and simulation challenges of understanding and predicting biological processes. This book is not meant to be a textbook or a monograph dedicated to the systematic study of any specific disease or a family of diseases. Instead, it is meant to illustrate the breadth and depth of research opportunities that exist in the general field of mathematical biomedicine. The book consists of five parts which can be read independently of each other, but are arranged to give the reader a broader picture of specific research topics and the mathematical tools that are being applied in its modeling and analysis.

There is a slight emphasis on issues related to cancer. One part not only deals with *cancer modeling* and addresses important topics like cancer stem cells, but it also focuses on specific cancers such as glioblastoma multiforme, an especially aggressive form of brain tumor. This naturally leads to the question of *treatment* and to a range of issues from modeling of gene therapies to pharmacokinetics of drugs to questions of how to optimize cancer treatment protocols. The latter topic

is addressed not only for traditional treatment approaches such as chemotherapy or radiotherapy, but also for more novel procedures that involve anti-angiogenic treatments which aim at blocking the migration of new blood vessels and capillaries to the tumor. More generally, the role of the *blood vessels* and their dynamics is presented in the context of cancer (tumor-angiogenesis) and both vascular diseases resulting in blood vessel abnormalities such as aneurysm.

Another important aspect in the treatment of any disease is the understanding of the role that the *immune system* plays in its prevention and cure. In this book, the important concepts of immuno-dominance and viral epitopes are considered. Improving our understanding of these aspects helps in the study of specific diseases. One chapter presents an up-to-date mathematical study of one of the most devastating diseases of recent times, namely HIV/AIDS. Infectious diseases can be analyzed from many angles that range from the study of the spread of the disease in the human body to the spread of the infection in the population. The latter is the subject of *epidemiology* and in the book seasonal effects of epidemiological models are described which are important for diseases such as malaria, cholera, or tuberculosis.

All these topics will be studied using a palette of mathematical tools ranging from discrete cellular automata to cell population-based models described by ordinary differential equations to nonlinear partial differential equations representing complex time- and space-dependent continuous processes. The authors employ both stochastic and deterministic methods to analyze biological phenomena in various temporal and spatial settings. Despite the wide range of topics covered, we readily acknowledge that the book does not in any way contain a comprehensive overview of mathematical methods and models used in modern biomedicine. Rather, the chapters highlight some topics that we believe are at the same time both in the mainstream and on the cutting edge of biomedical research. The book provides surveys as well as suggestions for possible future research directions by including open questions and new challenges. We hope that it will be of interest to both the mathematical and the biomedical communities and to both researchers working in the field and those who might consider entering it. Much of the material is presented in a way that allows young researchers and graduate students to use it as a starting point for their own work. We believe that the book will achieve its goal if, on the one hand, it raises the awareness of the vast array of topics awaiting researchers in the field of biomedicine and, on the other hand, it shows the power and richness of mathematical methods and tools that are being used to address the challenging problems in this field.

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