

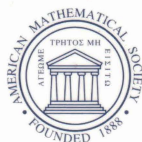
CONTEMPORARY MATHEMATICS

410

Mathematical Studies on Human Disease Dynamics Emerging Paradigms and Challenges

AMS-IMS-SIAM Joint Summer Research Conference on
Modeling the Dynamics of Human Diseases:
Emerging Paradigms and Challenges
July 17–21, 2005
Snowbird, Utah

Abba B. Gumel, Editor-in-Chief
Carlos Castillo-Chavez
Ronald E. Mickens
Dominic P. Clemence
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Preface

This volume contains the Proceedings of the AMS-IMS-SIAM Summer Research Conference on “Modeling the Dynamics of Human Diseases: Emerging Paradigms and Challenges” held at the magnificent Snowbird Summer and Ski Resort, Utah, July 17-21, 2005. The main aim of the conference was to bring together leading and upcoming researchers to discuss the latest advances and challenges associated with the modeling of the dynamics of emerging and re-emerging diseases, and to explore various control strategies. The conference featured sixteen invited one-hour plenary talks, eight talks each of 30 minutes duration, and a Poster session. Group discussions, where the participants were subdivided into subgroups with each subgroup brainstorming on some well-chosen topics (often stemming from the earlier presentations of that particular day), were also held. Members of each subgroup presented their conclusions to the general group.

This book is a collection of some of the most significant recent advances, trends, and challenges in mathematical modeling of human diseases. It contains 21 research papers, each of which is fully refereed by at least two reviewers. Contributions range from new modeling and mathematical (and computational) approaches to expository articles on emerging trends. Numerous diseases, such as cancer and tumor growth, foot-and-mouth, hantavirus, HIV, HPV, influenza, rotavirus, and vector-borne diseases, were considered. One of the major highlights of the conference was the discussion on the role of modeling in homeland security, vis-à-vis the deliberate release of infectious agents.

The Editors gratefully acknowledge the support of the sponsors, namely: the National Science Foundation (NSF), the American Mathematical Society (AMS), the Institute of Mathematical Statistics (IMS), and the Society of Industrial and Applied Mathematics (SIAM). We are grateful to Mr. Wayne Drady, AMS Conference Coordinator, for the excellent and tireless job he has done in ensuring that the conference went very smoothly, and for stocking the Hospitality Room at all times. Kudos also to Ms. Christine M. Thivierge (Editorial Assistant, AMS) and Sam White (Production Editor, AMS) for the efficient, professional, and diligent way they handled the publishing process. We are thankful to their colleagues at the Production and Technical Support departments for their help and patience in responding to the authors' questions. Finally, in addition to thanking the authors

for contributing their articles, we are very grateful to the many anonymous reviewers for their constructive criticisms and suggestions, which have enhanced the quality and clarity of the volume.

Abba Gumel (Editor-in-Chief)

Carlos Castillo-Chavez (Editor)

Ronald E. Mickens (Editor)

Dominic P. Clemence (Editor)

January 2006

Prologue

No problem facing humanity in the next century is more compelling than the changing epidemiological environment of infectious and other diseases. The World Cancer Report estimates that global cancer rates could increase by 50% in the next 15 to 20 years (<http://www.who.int/mediacentre/news/releases/2003/pr27/en/>). Emerging pathogens—some variants on familiar themes such as influenza, some reemergent enemies of the past such as tuberculosis, and some apparently novel forms such as SARS and HIV—plague humanity. Emergence of novel pathogens has always been part of our evolutionary history, but the rates of change and emergence have been greatly accelerated through our own activities: directly through the emergence of drug resistance because of our profligate use, for example of antibiotics and anti-malarials, and indirectly through our increased mobility and our impacts upon our environment.

Such challenges mandate the integration of a wide variety of disciplines, from cell biology, immunology and genomics, to population and community ecology, to climatology and the social sciences. These require that researchers relate phenomena on diverse scales of space and time, and translate the actions of individual agents into their macroscopic consequences, bridging scales of organizational complexity. Such integration mandates the application of mathematical and computational modeling, and the expansion of the frontiers of the mathematics of infectious diseases. Infectious disease modeling is one of the oldest and richest topics in mathematical biology, and has become accepted as integral to public health practice, in large part because researchers have maintained close contact with the empirical dimensions of the subject. But as the potential for high-speed computation has advanced, threats such as pandemic flu and bioterrorism have fueled the creation of ever-more-detailed models that track individual agents, and incorporate reams of information on their demographic and epidemiological characteristics, and their behavioral patterns. This is a welcome advance, but has run ahead of complementary analytical investigations to aid in understanding the behavior of these high-dimensional models, and in developing more robust reduced-dimensional versions.

Gumel et al. have taken an important step in that direction, bringing together a diverse collection of researchers in a book that provides a fair sampling of current mathematical research and challenges in human diseases. Most notable is that this book recognizes the central role of developing nations in the emergence of novel pathogens, and the need to involve researchers from these developing nations in addressing these problems. Over the last quarter century, there has been a remarkable expansion of research capacity in developing nations concerned with

mathematical modeling of disease, and this volume will provide a bridge to the future.

This present book illustrates both the diversity of the epidemiological challenges we face, and also the diversity of the mathematical approaches that will be needed to address them.

Simon Levin, Princeton University

January 2006

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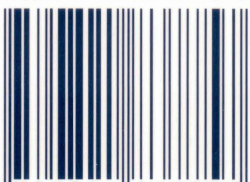
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This volume contains the proceedings of the AMS-IMS-SIAM Joint Summer Research Conference on Modeling the Dynamics of Human Diseases: Emerging Paradigms and Challenges, held in Snowbird, Utah, July 17–21, 2005.

The goal of the conference was to bring together leading and upcoming researchers to discuss the latest advances and challenges associated with the modeling of the dynamics of emerging and re-emerging diseases, and to explore various control strategies. The articles included in this book are devoted to some of the significant recent advances, trends, and challenges associated with the mathematical modeling and analysis of the dynamics and control of some diseases of public health importance. In addition to illustrating many of the diverse prevailing epidemiological challenges, together with the diversity of mathematical approaches needed to address them, this book provides insights on a number of topical modeling issues, such as the modeling and control of mosquito-borne diseases, respiratory diseases, animal diseases (such as foot-and-mouth disease), cancer and tumor growth modeling, influenza, HIV, HPV, rotavirus, etc. This book also touches upon other important topics, such as the use of modeling in homeland security and some review and new results on various modeling paradigms including network, stochastic and deterministic formulations together with the use of optimal control and related methods for evaluating control strategies.

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