Maia Martcheva An Introduction To Mathematical Epidemiology

Focussing on stochastic models for the spread of infectious diseases in a human population, this book is the outcome of a two-week ICPAM/CIMPA school on "Stochastic models of epidemics" which took place in Ziguinchor, Senegal, December 5–16, 2015. The text is divided into four parts, each based on one of the courses given at the school: homogeneous models (Tom Britton and Etienne Pardoux), two-level mixing models (David Sirl and Frank Ball), epidemics on graphs (Viet Chi Tran), and statistics for epidemic models (Catherine Larédo). The CIMPA school was aimed at PhD students and

Post Docs in the mathematical sciences. Parts (or all) of this book can be used as the basis for traditional or individual reading courses on the topic. For this reason, examples and exercises (some with solutions) are provided throughout. From a mathematical point of view, physiologically structured population models are an underdeveloped branch of the theory of infinite dimensional dynamical systems. We have called attention to four aspects: (i) A choice has to be made about the kind of equations one extracts from the predominantly verbal arguments about the basic assumptions, and subsequently uses as a starting point for a rigorous mathematical analysis. Though differential equations are easy to formulate (different mechanisms don't interact in infinites imal time intervals and so end up as separate terms in the equations) they may be hard to interpret

rigorously as infinitesimal generators. Integral equations constitute an attractive alternative. (ii) The ability of physiologically structured population models to increase our un derstanding of the relation between mechanisms at the i-level and phenomena at the p-level will depend strongly on the development of dynamical systems lab facilities which are applicable to this class of models. (iii) Physiologically structured population models are ideally suited for the for mulation of evolutionary questions. Apart from the special case of age (see Charlesworth 1980, Yodzis 1989, Caswell 1989, and the references given there) hardly any theory exists at the moment. This will, hopefully, change rapidly in the coming years. Again the development of appropriate software may turn out to be crucial.
This book introduces advanced

mathematical methods and techniques for analysis and simulation of models in mathematical epidemiology.
Chronological age and class-age play an important role in the description of infectious diseases and this text provides the tools for the analysis of this type of partial differential equation models. This book presents general theoretical tools as well as large number of specific examples to guide the reader to develop their own tools that they may then apply to study structured models in mathematical epidemiology. The book will be a valuable addition to the arsenal of all researchers interested in developing theory or studying specific models with age structure.
This book describes the uses of different mathematical modeling and soft computing techniques used in epidemiology for experiential research in projects such as how infectious diseases

progress to show the likely outcome of an epidemic, and to contribute to public health interventions. This book covers mathematical modeling and soft computing techniques used to study the spread of diseases, predict the future course of an outbreak, and evaluate epidemic control strategies. This book explores the applications covering numerical and analytical solutions, presents basic and advanced concepts for beginners and industry professionals, and incorporates the latest methodologies and challenges using mathematical modeling and soft computing techniques in epidemiology. Primary users of this book include researchers, academicians, postgraduate students, and specialists.
Mathematica Laboratories for Mathematical Statistics with CD-ROM
From Cells to Populations
with applications to Astronautics,

Robotics, Economics, and Engineering
Chaos in Ecology
Epidemics
EVEQ2000 Conference in Levico Terme (Trento, Italy), October 30–November 4, 2000

This volume summarizes the state-of-the-art in the fast growing research area of modeling the influence of information-driven human behavior on the spread and control of infectious diseases. In particular, it features the two main and inter-related "core" topics: behavioral changes in response to global threats, for example, pandemic influenza, and the pseudo-rational opposition to vaccines. In order to make realistic predictions, modelers need to go beyond classical mathematical epidemiology to take these dynamic effects into account. With contributions from experts in this field, the book fills a void in the literature. It goes beyond classical texts, yet preserves the rationale of many of them by sticking to the underlying biology without compromising on scientific rigor. Epidemiologists, theoretical biologists,

biophysicists, applied mathematicians, and PhD students will benefit from this book. However, it is also written for Public Health professionals interested in understanding models, and to advanced undergraduate students, since it only requires a working knowledge of mathematical epidemiology.
KEY BENEFIT: This reference introduces a variety of mathematical models for biological systems, and presents the mathematical theory and techniques useful in

analyzing those models. Material is organized according to the mathematical theory rather than the biological application. Contains applications of mathematical theory to biological examples in each chapter. Focuses on deterministic mathematical models with an emphasis on predicting the qualitative solution behavior over time. Discusses classical mathematical models from population , including the Leslie matrix model, the Nicholson-Bailey model, and the Lotka-Volterra

predator-prey model. Also discusses more recent models, such as a model for the Human Immunodeficiency Virus - HIV and a model for flour beetles. KEY MARKET: Readers seeking a solid background in the mathematics behind modeling in biology and exposure to a wide variety of mathematical models in biology.
This is the only book that teaches all aspects of modern mathematical modeling and that is specifically designed to introduce undergraduate

students to problem solving in the context of biology. Included is an integrated package of theoretical modeling and analysis tools, computational modeling techniques, and parameter estimation and model validation methods, with a focus on integrating analytical and computational tools in the modeling of biological processes. Divided into three parts, it covers basic analytical modeling techniques; introduces computational tools used in the modeling of biological problems; and includes various problems from epidemiology, ecology, and physiology. All chapters include realistic biological examples, including many exercises related to biological questions. In addition, 25 open-ended research projects are provided, suitable for students. An accompanying Web site contains solutions and a tutorial for the implementation of the computational modeling techniques. Calculations can be done in modern computing languages such

as Maple, Mathematica, and MATLAB?.
CD-ROM contains text, data, computations, and graphics.
Stability Analysis of Nonlinear Systems
Spaces of Measures and their Applications to Structured Population Models
Structured Population Models in Biology and Epidemiology
A Two-sex, Age-structured Population Model in Discrete-time
Dynamic Systems and Applications
Analysis, Theory, and

Applications
Chaos in Ecology is a convincing demonstration of chaos in a biological population. The book synthesizes an ecologically focused interdisciplinary blend of non-linear dynamics theory, statistics, and experimentation yielding results of uncommon clarity and rigor. Topics include fundamental issues that are of general and widespread importance to population biology and ecology. Detailed descriptions are included of the mathematical, statistical, and experimental steps they used to explore nonlinear dynamics in ecology. Beginning with a brief overview of chaos theory and its implications for ecology. The book continues by deriving and rigorously testing a mathematical model that is closely wedded to biological

mechanisms of their research organism. Therefrom were generated a variety of predictions that are fundamental to chaos theory and experiments were designed and analyzed to test those predictions. Discussion of patterns in chaos and how they can be investigated using real data follows and book ends with a discussion of the salient lessons learned from this research program Book jacket.

Based on lecture notes of two summer schools with a mixed audience from mathematical sciences, epidemiology and public health, this volume offers a comprehensive introduction to basic ideas and techniques in modeling infectious diseases, for the comparison of strategies to plan for an anticipated epidemic or pandemic, *and to deal with a disease outbreak in real time. It covers detailed case studies for diseases including pandemic influenza, West Nile virus, and childhood diseases. Models for other diseases including Severe Acute Respiratory Syndrome, fox rabies, and sexually transmitted infections are included as applications. Its chapters are coherent and complementary independent units. In order to accustom students to look at the current literature and to experience different perspectives, no attempt has been made to achieve united writing style or unified notation. Notes on some mathematical background (calculus, matrix algebra, differential equations, and probability) have been prepared and may be downloaded at the web site*

of the Centre for Disease Modeling (www.cdm.yorku.ca).
The book is a comprehensive, self-contained introduction to the mathematical modeling and analysis of disease transmission models. It includes (i) an introduction to the main concepts of compartmental models including models with heterogeneous mixing of individuals and models for vector-transmitted diseases, (ii) a detailed analysis of models for important specific diseases, including tuberculosis, HIV/AIDS, influenza, Ebola virus disease, malaria, dengue fever and the Zika virus, (iii) an introduction to more advanced mathematical topics, including age structure, spatial structure, and mobility, and (iv) some challenges and opportunities for the future. There are exercises of varying

degrees of difficulty, and projects leading to new research directions. For the benefit of public health professionals whose contact with mathematics may not be recent, there is an appendix covering the necessary mathematical background. There are indications which sections require a strong mathematical background so that the book can be useful for both mathematical modelers and public health professionals.

The book investigates stability theory in terms of two different measure, exhibiting the advantage of employing families of Lyapunov functions and treats the theory of a variety of inequalities, clearly bringing out the underlying theme. It also demonstrates manifestations of the general Lyapunov method,

showing how this technique can be adapted to various apparently diverse nonlinear problems. Furthermore it discusses the application of theoretical results to several different models chosen from real world phenomena, furnishing data that is particularly relevant for practitioners. Stability Analysis of Nonlinear Systems is an invaluable single-sourse reference for industrial and applied mathematicians, statisticians, engineers, researchers in the applied sciences, and graduate students studying differential equations.
Stochastic Epidemic Models with Inference
Mathematical and Computational Approaches to Immunology
Mathematica Laboratories for Mathematical Statistics
Mathematical Reviews

Mathematical Models in Epidemiology
Frontiers in Mathematical Biology
An Introduction to Mathematical EpidemiologySpringer
Structured population models are transport-type equations often applied to describe evolution of heterogeneous populations of biological cells, animals or humans, including phenomena such as crowd dynamics or pedestrian flows. This book introduces the mathematical underpinnings of these applications, providing a comprehensive analytical framework for structured population models in spaces of Radon measures. The unified

approach allows for the study of transport processes on structures that are not vector spaces (such as traffic flow on graphs) and enables the analysis of the numerical algorithms used in applications. Presenting a coherent account of over a decade of research in the area, the text includes appendices outlining the necessary background material and discusses current trends in the theory, enabling graduate students to jump quickly into research.

This volume tackles a variety of biological and medical questions using mathematical models to understand complex system dynamics. Working in collaborative teams of six, each with a senior research mentor, researchers developed new mathematical models to address questions in a range of application areas. Topics include retinal degeneration, biopolymer dynamics, the topological structure of DNA, ensemble analysis, multidrug-resistant organisms, tumor growth modeling, and geospatial modeling of malaria. The work is the result of newly formed collaborative groups begun during the Collaborative Workshop for Women in

Mathematical Biology hosted by the Institute of Pure and Applied Mathematics at UCLA in June 2019. Previous workshops in this series have occurred at IMA, NIMBioS, and MBI.
This book grew out of the discussions and presentations that began during the Workshop on Emerging and Reemerging Diseases (May 17-21, 1999) sponsored by the Institute for Mathematics and its Application (IMA) at the University of Minnesota with the support of NIH and NSF. The workshop started with a two-day tutorial session directed at ecologists, epidemiologists, immunologists,

mathematicians, and scientists interested in the study of disease dynamics. The core of this first volume, Volume 125, covers tutorial and research contributions on the use of dynamical systems (deterministic discrete, delay, PDEs, and ODEs models) and stochastic models in disease dynamics. The volume includes the study of cancer, HIV, pertussis, and tuberculosis. Beginning graduate students in applied mathematics, scientists in the natural, social, or health sciences or mathematicians who want to enter the fields of mathematical and theoretical epidemiology will find this book useful.

An Introduction to Mathematical Biology

Proceedings of the Conference on Mathematical Biology and Dynamical Systems, the University of Texas at Tyler, 7-9 October 2005

Hemorrhagic Fever with Renal Syndrome, Tick- and Mosquito-Borne Viruses

Evolution Equations: Applications to Physics, Industry, Life Sciences and Economics

Collaborations of Consequence

Introduction to the Foundations of Applied Mathematics

This book reviews how mathematical and computational approaches can be useful to help us understand how killer T-cell responses work to fight viral infections. It also demonstrates, in a writing style that exemplifies the point, that such mathematical and computational approaches are most valuable when coupled with experimental work through interdisciplinary collaborations. Designed to be useful to immunoligists and viroligists without extensive computational background, the book covers a broad variety of topics, including both basic immunological questions and the application of these insights to the understanding and treatment of pathogenic human diseases. Mathematical models are increasingly being used to examine questions in infectious disease control. Applications include predicting the impact of vaccination strategies against common infections and determining optimal control strategies against HIV and pandemic influenza. This book introduces individuals interested in infectious diseases to this exciting and expanding area. The mathematical level of the book is kept as simple as possible, which makes the book accessible to those who have not studied mathematics to university level. Understanding is further enhanced by models that can be accessed online, which will allow readers to explore the impact of different factors and control

strategies, and further adapt and develop the models themselves. The book is based on successful courses developed by the authors at the London School of Hygiene and Tropical Medicine. It will be of interest to epidemiologists, public health researchers, policy makers, veterinary scientists, medical statisticians and infectious disease researchers.
The common experience in solving control problems shows that optimal control

as a function of time proves to be piecewise analytic, having a finite number of jumps (called switches) on any finite-time interval. Meanwhile there exists an old example proposed by A.T. Fuller [1961) in which optimal control has an infinite number of switches on a finite-time interval. This phenomenon is called chattering. It has become increasingly clear that chattering is widespread. This book is devoted to its exploration. Chattering obstructs the direct use of Pontryagin's maximum principle because of the lack of a nonzero-length interval with a continuous control function. That is why the common experience appears misleading. It is the hidden symmetry of Fuller's problem that allows the explicit solution. Namely, there exists a one-parameter group which respects the optimal trajectories of the problem. When published in 1961, Fuller's example incited curiosity, but it was considered only "interesting" and soon was

forgotten. The second wave of attention to chattering was raised about 12 years later when several other examples with optimal chattering trajectories were 1 found. All these examples were two-dimensional with the one-parameter group of symmetries.
This publication represents the culmination of the National Academies Keck Futures Initiative (NAKFI), a program of the National Academy of Sciences, the National Academy of Engineering, and the National Academy

of Medicine supported by a 15-year, $40 million grant from the W. M. Keck Foundation to advance the future of science through interdisciplinary research. From 2003 to 2017, more than 2,000 researchers and other professionals across disciplines and sectors attended an annual "think-tank" style conference to contemplate real-world challenges. Seed grants awarded to conference participants enabled further pursuit of bold, new research and ideas generated at the

conference.
Molecular and Cellular Biology of Viruses
Mathematical Modeling and Soft Computing in Epidemiology
Mathematical Epidemiology
A Course in Mathematical Biology
Essential Mathematical Biology
Experimental Nonlinear Dynamics
This volume is a collection of papers on various areas of current interest in mathematical biology, such as epidemic disease modeling, including the effects of vaccination and strain replacement; immunology, such

as T-Cell dynamics and the mechanism of phagocytosis; knot theory; DNA computation; and Boolean networks.
This book is designed to be a practical study in infectious disease dynamics. The book offers an easy to follow implementation and analysis of mathematical epidemiology. The book focuses on recent case studies in order to explore various conceptual, mathematical, and statistical issues. The dynamics of infectious diseases shows a wide diversity of pattern. Some have locally persistent chains-of-transmission, others persist

spatially in 'consumer-resource metapopulations'. Some infections are prevalent among the young, some among the old and some are age-invariant. Temporally, some diseases have little variation in prevalence, some have predictable seasonal shifts and others exhibit violent epidemics that may be regular or irregular in their timing. Models and 'models-with-data' have proved invaluable for understanding and predicting this diversity, and thence help improve intervention and control. Using mathematical models to understand infectious disease dynamics has a very rich history in epidemiology. The field has seen broad expansions of theories as well as a surge in real-life application of mathematics to dynamics and control of infectious disease. The chapters of Epidemics: Models and Data using R have been organized in a reasonably logical way: Chapters 1-10 is a mix and match of models, data and statistics pertaining to local disease dynamics; Chapters 11-13 pertains to spatial and spatiotemporal dynamics; Chapter 14 highlights similarities between the dynamics of infectious disease and parasitoid-host dynamics; Finally, Chapters

15 and 16 overview additional statistical methodology useful in studies of infectious disease dynamics. This book can be used as a guide for working with data, models and 'models-and-data' to understand epidemics and infectious disease dynamics in space and time.
The goal of this book is to search for a balance between simple and analyzable models and unsolvable models which are capable of addressing important questions on population biology. Part I focusses on single species simple models including those which have been used to predict the growth of human and animal

population in the past. Single population models are, in some sense, the building blocks of more realistic models -- the subject of Part II. Their role is fundamental to the study of ecological and demographic processes including the role of population structure and spatial heterogeneity -- the subject of Part III. This book, which will include both examples and exercises, is of use to practitioners, graduate students, and scientists working in the field.

This text provides essential modeling skills and methodology for the study of infectious diseases through a one-semester modeling course or directed individual studies. The book includes mathematical descriptions of epidemiological concepts, and uses classic epidemic models to introduce different mathematical methods in model analysis. Matlab codes are also included for numerical implementations. It is primarily written for upper undergraduate and beginning graduate students in mathematical sciences who have an interest in mathematical modeling of infectious diseases. Although written in a rigorous mathematical manner, the style is not unfriendly to nonmathematicians.

Modeling the Interplay Between Human Behavior and the Spread of Infectious Diseases

An Introduction to Infectious Disease Modelling

Frontiers In Orthogonal Polynomials And Q-series

Killer Cell Dynamics

Mathematical Models in Population Biology and Epidemiology

Progress in Mathematical Ecology

Elements of Mathematical Ecology provides an introduction to classical and modern mathematical models, methods, and issues

in population ecology. The first part of the book is devoted to simple, unstructured population models that ignore much of the variability found in natural populations for the sake of tractability. Topics covered include density dependence, bifurcations, demographic stochasticity, time delays, population interactions (predation, competition, and mutualism), and the application of optimal control theory to the management of renewable resources. The second part of this book is devoted to structured population models, covering spatially-structured population models

(with a focus on reaction-diffusion models), age-structured models, and two-sex models. Suitable for upper level students and beginning researchers in ecology, mathematical biology and applied mathematics, the volume includes numerous clear line diagrams that clarify the mathematics, relevant problems thoughout the text that aid understanding, and supplementary mathematical and historical material that enrich the main text.
This work examines how the life history parameters effect the stable age distribution of the different classes and

compares these results with the standard single sex model. The conditions necessary for a population projected forward in time to reach a stable age distribution is analyzed. The conditions for existence are dependent on the nature of the mating function, i.e. the rate at which the two sexes find each other and mate. In addition, the assumptions under which these mating functions are constructed have important implications for the dynamics of the population and ultimate age distribution, stable or not. An analysis of when including both sexes becomes essential to the understanding of reproductive strategies, examination of whether a population fulfils the necessary assumptions about mating to make certain statements about population growth, growth rates and relative fitness, and outlining an accessible approach to modeling the joint life histories will be of practical value. Toward this end, a framework for discrete-time two-sex models with age structure is developed. In addition a marriage (mating) function based on an analogy with foraging theory and preferences based on the

predispositions of one age group for another is proposed. Some of the properties of these models and their solutions are also investigated.
Presents models of renewable and non-renewable resources and provides analytical methods to explore contemporary resource problems.
The book is a comprehensive, self-contained introduction to the mathematical modeling and analysis of infectious diseases. It includes model building, fitting to data, local and global analysis techniques. Various types of deterministic dynamical models are considered:

ordinary differential equation models, delay-differential equation models, difference equation models, age-structured PDE models and diffusion models. It includes various techniques for the computation of the basic reproduction number as well as approaches to the epidemiological interpretation of the reproduction number. MATLAB code is included to facilitate the data fitting and the simulation with age-structured models.

Natural Resource Economics

An Introduction to Mathematical Epidemiology

Age Structured Epidemic

Modeling

Elements of Mathematical Ecology

Theory of Chattering Control

Quantitative Modeling with Mathematical and Computational Methods

FOAM. This acronym has been used for over ?fty years at Rensselaer to designate an upper-division course entitled, Foundations of Applied Ma- ematics. This course was started by George Handelman in 1956, when he came to Rensselaer from the Carnegie Institute of Technology. His objective was to closely integrate mathematical and physical reasoning, and in the p- cess enable students to obtain a qualitative understanding of the *world we live in. FOAM was soon taken over by a young faculty member, Lee Segel. About this time a similar course, Introduction to Applied Mathematics, was introduced by Chia-Ch'iao Lin at the Massachusetts Institute of Technology. Together Lin and Segel, with help from Handelman, produced one of the landmark textbooks in applied mathematics, Mathematics Applied to - terministic Problems in the Natural Sciences. This was originally published in 1974, and republished in 1988 by the Society for Industrial and Applied Mathematics, in their Classics Series. This textbook comes from the author teaching FOAM over*

the last few years. In this sense, it is an updated version of the Lin and Segel textbook.
The international conference on which the book is based brought together many of the world's leading experts, with particular effort on the interaction between established scientists and emerging young promising researchers, as well as on the interaction of pure and applied mathematics. All material has been rigorously refereed. The contributions contain much material developed after the conference, continuing research and incorporating additional new results and improvements. In addition, some up-to-date surveys

are included.
Integrating computers into mathematical statistics courses allows students to simulate experiments and visualize their results, handle larger data sets, analyze data more quickly, and compare the results of classical methods of data analysis with those using alternative techniques. This text presents a concise introduction to the concepts of probability theory and mathematical statistics. The accompanying in-class and take-home computer laboratory activities reinforce the techniques introduced in the text and are accessible to students with little or no experience with

Mathematica. These laboratory materials present applications in a variety of real-world settings, with data from epidemiology, environmental sciences, medicine, social sciences, physical sciences, manufacturing, engineering, marketing, and sports. Included in the book are parametric, nonparametric, permutation, bootstrap and diagnostic methods. Permutation and bootstrap methods are discussed side by side with classical methods in the later chapters. Includes a CD-ROM with 238 laboratory problems written as Mathematica notebooks.

This self-contained introduction to the fast-growing field of

Mathematical Biology is written for students with a mathematical background. It sets the subject in a historical context and guides the reader towards questions of current research interest. A broad range of topics is covered including: Population dynamics, Infectious diseases, Population genetics and evolution, Dispersal, Molecular and cellular biology, Pattern formation, and Cancer modelling. Particular attention is paid to situations where the simple assumptions of homogenity made in early models break down and the process of mathematical modelling is seen in action.
Annual Report of the Biometrics Unit, Department of Plant

Breeding and Biometry
An Introduction to Mathematical Modeling of Infectious Diseases
NAKFI's 15 Years Igniting Innovation at the Intersections of Disciplines
Using Mathematics to Understand Biological Complexity
Current Developments in Mathematical Biology

This book is a printed edition of the Special Issue "Progress in Mathematical Ecology" that was published in Mathematics In this new century mankind faces ever more challenging environmental and publichealt hproblems,suchaspollution,in vasionbyexoticspecies,theem-gence of new diseases or the emergence of diseases into new regions (West Nile virus,S ARS,Anthrax,etc.),andtheresur genceofexistingdiseases(in?u enza, malaria, TB, HIV/AIDS, etc.). Mathematical models have been successfully used to study many biological, epidemiological and medical problems, and nonlinear and complex dynamics have been observed in all of those contexts. Mathematical studies have helped us not only to better understand these problems but also to ?nd solutions in some cases, such as the prediction and control of SARS outbreaks, understanding HIV infection, and the investi- tion of antibiotic-resistant infections in hospitals. Structuredpopulat ionmodelsdistinguishindividua lsfromoneanother- cording to characteristics such as age, size, location, status, and movement, to determine the birth, growth and death rates, interaction with each other and with environment, infectivity, etc. The goal of structured population models is to understand how these characteristics a?ect the dynamics of these models and

thus the outcomes and consequences of the biological and epidemiolo- cal processes. There is a very large and growing body of literature on these topics. This book deals with the recent and important advances in the study of structured population models in biology and epidemiology. There are six chapters in this book, written by leading researchers in these areas.
Describes most popular computational methods used to solve problems in electromagnetics Matlab code is included throughout, so that

the reader can implement the various techniques discussed Exercises included
Viruses interact with host cells in ways that uniquely reveal a great deal about general aspects of molecular and cellular structure and function. Molecular and Cellular Biology of Viruses leads students on an exploration of viruses by supporting engaging and interactive learning. All the major classes of viruses are covered, with separate chapters for their replication and expression strategies, and chapters for mechanisms such as attachment that are

independent of the virus genome type. Specific cases drawn from primary literature foster student engagement. End-of-chapter questions focus on analysis and interpretation with answers being given on the website (half for students, all for instructors). Examples come from the most-studied and medically important viruses such as HIV, influenza, and poliovirus. Plant viruses and bacteriophages are also included. There are chapters on the overall effect of viral infection on the host cell. Coverage of the immune system is focused on the interplay between host defenses and viruses, with a separate chapter on medical applications such as anti-viral drugs and vaccine development. The final chapter is on virus diversity and evolution, incorporating contemporary insights from metagenomic research. Key selling feature: Readable but rigorous coverage of the molecular and cellular biology of viruses Molecular mechanisms of all major groups, including plant viruses and bacteriophages, illustrated by example Host-

pathogen interactions at the cellular and molecular level emphasized throughout Medical implications and consequences included Quality illustrations available to instructors Extensive questions and answers for each chapter
Models and Data using R
Computational Electromagnetics
Emphasizing Simulation and Computer Intensive Methods
Mathematical Approaches for Emerging and Reemerging Infectious Diseases: An Introduction
This volume aims to highlight

trends and important directions of research in orthogonal polynomials, q-series, and related topics in number theory, combinatorics, approximation theory, mathematical physics, and computational and applied harmonic analysis. This collection is based on the invited lectures by well-known contributors from the International Conference on Orthogonal Polynomials and q-Series, that was held at the University of Central Florida in Orlando, on May 10 – 12, 2015. The conference was dedicated to Professor Mourad Ismail on his 70th birthday. The editors strived for a volume that would inspire young researchers and provide a wealth of information in an engaging format. Theoretical, combinatorial and computational/algorithmic aspects are considered, and each chapter contains many references on its topic, when appropriate. Contents: Mourad Ismail (Richard Askey) Binomial Andrews – Gordon – Bressoud Identities (Dennis Stanton) Symmetric Expansions of Very Well-Poised Basic Hypergeometric Series (George E Andrews) A Sturm – Liouville Theory for Hahn Difference Operator (M H Annaby, A E Hamza and S D Makharesh) Solvability of the

Hankel Determinant Problem for Real Sequences (Andrew Bakan and Christian Berg)Convolution and Product Theorems for the Special Affine Fourier Transform (Ayush Bhandari and Ahmed I Zayed)A Further Look at Time-and-Band Limiting for Matrix Orthogonal Polynomials (M Castro, F A Grünbaum, I Pacharoni and I Zurrián)The Orthogonality of Al–Salam–Carlitz Polynomials for Complex Parameters (Howard S Cohl, Roberto S Costas-Santos and Wenqing Xu)Crouching AGM, Hidden Modularity (Shaun Cooper, Jesús Guillera, Armin Straub and Wadim Zudilin)Asymptotics of Orthogonal Polynomials and the Painlevé Transcendents (Dan Dai)From the Gaussian Circle Problem to Multivariate Shannon Sampling (Willi Freeden and M Zuhair Nashed)Weighted Partition Identities and Divisor Sums (F G Garvan)On the Ismail–Letessier–Askey Monotonicity Conjecture for Zeros of Ultraspherical Polynomials (Walter Gautschi)A Discrete Top-Down Markov Problem in Approximation Theory (Walter Gautschi)Supersymmetry of the Quantum Rotor (Vincent X Genest, Luc Vinet, Guo-Fu Yu and Alexei Zhedanov)The

Method of Brackets in Experimental Mathematics (Ivan Gonzalez, Karen Kohl, Lin Jiu and Victor H Moll)Balanced Modular Parameterizations (Tim Huber, Danny Lara and Esteban Melendez)Some Smallest Parts Functions from Variations of Bailey's Lemma (Chris Jennings-Shaffer)Dual Addition Formulas Associated with Dual Product Formulas (Tom H Koornwinder)Holonomic Tools for Basic Hypergeometric Functions (Christoph Koutschan and Peter Paule)A Direct Evaluation of an Integral of Ismail and Valent (Alexey Kuznetsov)Algebraic Generating Functions for

Gegenbauer Polynomials (Robert S Maier)q-Analogues of Two Product Formulas of Hypergeometric Functions by Bailey (Michael J Schlosser)Summation Formulae for Noncommutative Hypergeometric Series (Michael J Schlosser)Asymptotics of Generalized Hypergeometric Functions (Y Lin and R Wong)Mock Theta-Functions of the Third Order of Ramanujan in Terms of Appell – Lerch Series (Changgui Zhang)On Certain Positive Semidefinite Matrices of Special Functions (Ruiming Zhang) Readership: Graduate students and researchers interested in orthogonal polynomials and