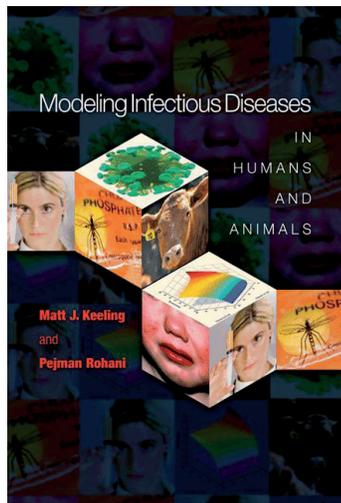


## Modeling Infectious Diseases in Humans and Animals



Matt J. Keeling and Pejman Rohani; Princeton University Press, Princeton; 384 pp.; 2008; US\$65 or £38.95; ISBN 978 0 691 11617 4 (hardback)

Since the publication in 1991 of Anderson and May's seminal work<sup>1</sup>, mathematical modelling of infectious diseases has become firmly established as one of the key tools available to epidemiologists to understand, predict and control the spread of infectious diseases in human, animal and plant populations. Accordingly, the field has undergone rapid growth, stimulated by high profile outbreaks such as avian influenza and foot-and-mouth disease. The present volume is a timely addition to the expanding literature on the subject, bringing together several of the most salient developments, by two authors with considerable experience, both practical and theoretical.

Throughout, the focus is on directly transmitted microparasite infections, though Chapter four contains some material on vector-transmitted infections. The book begins with two introductory chapters in which the basic mathematical theory of infectious diseases is presented, encompassing the homogeneously mixing SIR (susceptible–infected–removed) model and some of its variants. These chapters

establish an accessible writing style, maintained throughout the book, striking just the right balance between clarity and mathematical complexity, with more difficult points dealt with in boxed asides to avoid interrupting the flow. Chapter three addresses the difficult problem of heterogeneities due to variation in individual risk factors, age and temporal effects. Rather than getting bogged down in the intricate details of such models, the authors choose to give a flavour of the complexities involved by focusing on some simple cases. Here, as elsewhere, they use the excellent pedagogic device of flagging up the key points with highlighted one-sentence summaries at strategic points in the argument.

The next four chapters focus on important recent developments, which move well beyond the scope of existing books on the subject. Thus, Chapter four takes the wider perspective of evolution biology and discusses multi-pathogen and multi-host models. This is a key area of current research, essential to understanding phenomena such as strain variation in influenza, and the emergence of antibiotic resistance. The material presented in this chapter tends to be of a more conceptual nature than elsewhere in the volume, reflecting the many open problems. Chapter five discusses temporal forcing, which has proved critical to our understanding of many childhood infections such as measles. The mathematical complexities of non-linear dynamical systems are avoided without losing their flavour, with emphasis on such topics as harmonic resonance, bifurcation diagrams and attractors. Chapter six discusses approaches to stochasticity—primarily through the incorporation of process noise into differential equation models, though properly stochastic (individual-based) models are briefly touched upon. The chapter contains useful pointers to algorithmic implementations, as well as discussion of critical community size, extinction and importations. Chapter seven provides a very thorough and enlightening discussion of spatial models, grounded in experience of the 2001 outbreak of foot-and-mouth disease in the UK.

The chapter covers a great diversity of approaches, encompassing meta-populations, lattice models and cellular automata, networks and their pairwise approximations.

Finally, Chapter eight provides a unified treatment of control measures, including vaccination of human and wildlife populations, pulse vaccination, isolation and contact tracing. Here, as throughout, the key issues and concepts are brought to life with detailed case studies of human and animal infections.

A great strength of this book is its authoritative and accessible presentation of advanced topics. The authors skilfully demonstrate the contribution that sophisticated mathematical techniques can make to our understanding of infectious diseases, and to the practical public health problems of how best to control them. The authors' commendable commitment to accessibility is reinforced by numerous practical examples drawn from a wide range of human, animal and plant infections, and by online provision of computer code for many of the models presented in the book. There are many informative figures and few typographical errors. A minor irritant is the occasional reference mentioned in the text but missing from the bibliography. Overall, however, the production standard is extremely high.

Inevitably, a book on infectious diseases cannot realistically seek to cover the entire field. A statistically-minded reader cannot but notice the marginal place afforded in this book to applied probability and statistical inference. Stochastic models such as chain binomial models and branching processes get but a passing mention, while the stochastic SIR and SIS (susceptible–infectious–susceptible) models fare only marginally better, in spite of the important insights they offer. More recent developments, such as household models, go unmentioned. Statisticians might also be surprised to read that statistical inference for infectious disease models is “hampered by underdeveloped appropriate inferential methodologies” (p. 49). In fact, since the seminal work of Becker<sup>2</sup>, statistical methods in this field have undergone further

major development, including data augmentation techniques, serological and outbreak surveillance, improved methods for estimation from serological survey data and vaccine models, not to mention the wholesale revolution brought about by Markov chain Monte Carlo methods.

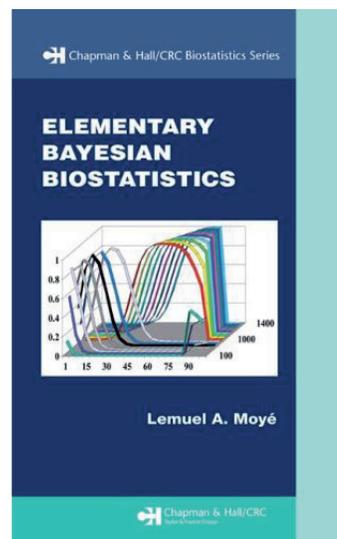
However, such sectional criticisms do not in any way detract from the broader and enthusiastic appreciation that the authors have provided an impressive, readable and topical account of the modern mathematical theory of infectious diseases and its numerous practical applications. This volume is a worthy successor to Anderson and May's treatment of the subject, and is essential reading for all epidemiologists, biologists and statisticians working on infectious diseases.

### References

1. Anderson, R. M. and May, R. M. (1991) *Infectious Diseases of Humans: Dynamics and Control*. Oxford: Oxford University Press.
2. Becker, N. (1989) *Analysis of Infectious Disease Data*. London: Chapman and Hall.

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## Elementary Bayesian Biostatistics



Lemuel A. Moyé; Chapman and Hall/CRC, Boca Raton, FL; xxi + 377 pp.; 2008, US\$79.95; ISBN 1 58488 724 9