Books

Modelling infectious diseases in humans and animals

An informative textbook, *Modeling infectious diseases in humans and animals* is written by a mathematician (Matt Keeling of the University of Warwick, Coventry, UK) and a physicist (Pejman Rohani of the University of Georgia, Athens, GA, USA). The authors assume in the reader a fairly sophisticated knowledge of mathematics and computational techniques, and the book is clearly aimed at advanced undergraduates or graduate students with a strong background in mathematics. A series of mathematical models, of increasing complexity, is clearly presented and the reader is taken through the appropriate mathematical analyses. A particularly nice feature of this book is that it includes web-based mathematical exercises.

The authors begin by describing simple epidemic models (focusing on the classic susceptible–infected–recovered model and its modifications) and then quickly progress to multi-pathogen/multi-host and temporally forced models, stochastic dynamics, and spatial models. Each chapter carefully explains the mathematical structure of a particular model (most of the models are based on a series of ordinary differential equations) and concludes with a few examples of the application of this type of model to a specific infectious disease of animals or human beings. Since the research of both authors is concerned with modelling childhood diseases, they have mainly selected examples from this area of modelling. Admittedly, this book is a textbook aimed at explaining some of the methodologies of modelling and does not intend to be a review of the literature of this field. However, I was disappointed that models of diseases of major medical importance such as HIV, tuberculosis, malaria, or hospital-acquired infections were not covered. Consequently, the reader is not made aware of the very large body of modelling literature that has focused on diseases that have great importance to public health.

The field of modelling infectious diseases is divided into two camps: those who believe that simple mathematical models are useful for understanding epidemiology and making predictions, and those who believe that complex models are necessary for making accurate predictions. Both simple and complex models have advantages and disadvantages. Simple models are constructed on the basis of a few assumptions (that are usually made transparent) and a few parameter values. Generally, these models are thoroughly analysed both mathematically and numerically. Uncertainty analyses have been used to make predictions from simple models (ie, the predicted outcomes have error bars). Multivariate sensitivity analyses have been used to investigate the effect of all of the assumptions and ranges in parameter estimates on the predictions. Simple models have therefore provided a great deal of insight into the dynamics and control of infectious diseases. However, if a model is over-simplified, important processes can be omitted and the model will have limited usefulness. Complex models are built on the basis of many assumptions (that may not be explained and therefore can not be evaluated) and a multitude of unknown parameter values (that are often specified as single point estimates). Surprisingly, so far, complex epidemiological models have not been adequately analysed to determine the sensitivity of their results to assumptions and parameter values. These complex models have generally been used to simulate single scenarios to make predictions; these predictions could be highly inaccurate because of the many unknowns in the model. Therefore, paradoxically, although complex models may appear to be more realistic than simple models, their predictions can sometimes be less accurate and give a misleading sense of certainty.

Keeling and Rohani conclude that the future of infectious disease modelling should be to develop very complex models and use them as predictive tools. I agree, in part, with their conclusion. However, I believe that it is always important to begin by constructing a simple model and then, if necessary, linking it with a complex model. The complex model should be built in a series of stages from the simple model and carefully explored at each stage by uncertainty and multivariate sensitivity analyses. This approach would enable the structure of the complex model to become more transparent, and the necessary degree of model complexity to be clearly assessed. To develop more useful models (whether they are simple or complex), modellers need to build close collaborations with infectious disease experts and biostatisticians. To construct more realistic models, modellers also need to use more sophisticated statistical techniques when fitting models to data, and for parameterisation, validation, and verification.

Keeling and Rohani have produced an excellent textbook that will introduce mathematicians to the field of infectious disease modelling. Hopefully, after reading this book mathematicians will be motivated to build collaborations with infectious disease experts and biostatisticians.

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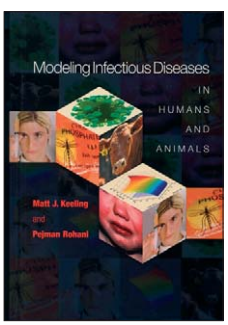

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For more on **sensitivity and uncertainty analysis of complex models of disease transmission** see *Int Stat Rev* 1994; **62:** 229–43 and http://www.semel.ucla.edu/biomedicalmodeling/index.asp