
Modelling the Spread of Infectious Diseases

Chair: Patrick Brown (Cancer Care Ontario)

LIN ZHANG, University of Guelph

Comparing Bayesian Statistical Models of Infectious Disease Outbreaks via Probability Scoring

Model comparison and assessment are key components in statistical modeling. Here we consider these components for infectious disease models. The approach taken will be to develop the tool of proper probability scoring rules to assess calibration and sharpness of probabilistic forecasts for spatio-temporal epidemic models. Scoring rules work by rewarding a numerical value to a model based on the predictive distribution and on the infection/non-infection event observed. We show how such methods can be used and compare the performance of different probability score-based methods.

LILIA LETICIA RAMIREZ RAMIREZ, Instituto Tecnológico Autónomo de México (ITAM)

Simulation of Infectious Disease Spread as a Tool to Evaluate Control Measures During an Epidemic Outbreak

SIMID (SIMulation of Infectious Diseases) is a program developed with the Region of Peel, Ontario, and Infonaut Inc. to picture general scenarios for outbreaks of directly transmissible diseases. Its main goal is to facilitate for health officers and decision makers the evaluation of diverse control measures, such as prophylactic vaccination, school closures and isolation. The program was implemented for the Region of Peel, using its social and demographic characteristics to model an individual contact network with emphasis on school contacts. In this presentation we talk about the program's theoretical bases, its algorithms, its main characteristics and its possible extensions.

NADIA BIFOLCHI, University of Guelph

Spatial Approximations of Network-based Individual Level Infectious Disease Models

Often, when modeling infectious disease spread, the complex network through which the disease propagates is approximated by simpler spatial information. Here, we simulate epidemic spread through various contact networks and fit spatial-based models in a Bayesian framework using Markov chain Monte Carlo methods. These spatial models are individual-level models which account for the spatio-temporal dynamics of infectious disease. The focus here is on choosing a spatial model which best predicts the true probabilities of infection, as well as determining under which conditions such spatial models fail.

LORNA DEETH, University of Guelph

Variations of the Deviance Information Criterion for Infectious Disease Models

The deviance information criterion (DIC) is a model comparison tool suited for complex models fitted within a Bayesian framework. Since its development, variations of the DIC have been proposed for application to missing data models. The DIC as a method of model selection is investigated when applied to latent conditional individual-level models (LC-ILMs), a class of models that can be used for infectious disease modeling, and which display mixture model-like characteristics due to their dependence on a latent grouping variable. The effectiveness of the traditionally defined DIC is compared to alternative definitions, to assess which is most applicable for LC-ILMs.

CHEN ZHANG, Memorial University of Newfoundland

Estimation and Forecasting of a Lag 2 Dynamic Model for Infectious Diseases

We discuss estimation and forecasting of an extension to lag 1 longitudinal dynamic model for correlated data used by Oyet & Sutradhar (2011) for modelling the spread of infectious disease. The lag 1 model only allow individuals with infectious at time point $t - 1$ to cause new infectious at time point t . Clearly, if at time point $t - 2$, there is an individual who is still infected by

the disease, it is possible for this individual to infect others at time point t . The present model discussed in this paper allows for such a possibility.

RAJAT MALIK, University of Guelph

Modeling the Spread of Influenza within Households in Hong Kong

Individual-level models (ILMs) can be used to model the spread of infectious diseases in discrete time. The key feature of these ILMs is that they can take into account covariate information on susceptible and infectious individuals as well as shared covariate information such as geography or contact measures. Here, such ILMs are fitted in a Bayesian framework using Markov Chain Monte Carlo techniques to data from a study on influenza within households in Hong Kong during 2009. The focus here is to estimate the effect of vaccination on infection risk and choose a model that best fits the disease spread.