Spatial Modelling for Infectious Disease

Chair: Karen Kopciuk (Alberta Health Services and University of Calgary)

DANIEL GILLIS, University of Guelph

Disease Source Classification Using Multivariate Spatial Poisson Mixture Models

Enteric disease data obtained from the Canadian Institute for Health Information provides motivation to extend mixture literature to label disease based on infection source. Mixtures are used to classify data as foodborne or waterborne. Two spatial models are presented and compared to the standard CAR spatial model described by Besag et al., 1991. The models account for spatially indexed disease by applying independent or dependent conditionally autoregressive spatial priors in the log linear term of each of the mixture components. All models are compared via simulation, with application to Alberta Gastrointestinal disease data (1992-1998).

YE LI, University of Toronto

Geostatistical Model for Spatially Aggregated Disease Incidence Data

Clinical data on the locations of syphilis cases in North Carolina are modelled with the aim of finding areas of abnormally high risk. Inference is complicated by uncertainty of case locations due to the aggregation in the population reporting census regions. A model is introduced consisting of a continuous random spatial surface with aggregated responses and fixed covariate effects. The process is modelled on a fine lattice and Bayesian inference is performed using Markov Chain Monte Carlo with data augmentation. Simulations studies are carried out to compare with the Besag-York-Mollié model and a model assuming the exact locations are known.

GRACE PUI SZE KWONG, University of Guelph

Computationally Efficient Forms of Spatial Infectious Disease Models

Individual-level models (ILMs) for infectious diseases, fitted in a Bayesian MCMC framework, are an intuitive and flexible class of models that can take into account population heterogeneity via various individual-level covariates. ILMs containing a geometric distance kernel to account for geographic heterogeneity provide a natural way to model the spatial spread of many diseases. However, in even only moderately large populations, the likelihood calculations required can be prohibitively time consuming. It is possible to speed up the computation via a technique which makes use linearized distance kernels. We examine some methods of carrying out this approximation and compare their performances.

JOURDAN GOLD, University of Guelph

Effects of Time-line Uncertainty in Infectious Disease Modelling

Because of the complexity of infectious disease systems, one often makes simplifying assumptions in their modeling process. These assumptions, while computationally convenient, could lead to a poorly fitted model. We can account for data uncertainty explicitly but this may cause computational problems. A simulation study was performed to ascertain the effects of ignoring timeline uncertainty. Results will be presented that quantify the trade-off between model inferential quality and computational-time, using a family of discrete-time heterogeneous infectious disease models known as individual-level models. Modeling approaches will vary from those under 'fixed data' assumptions to those under a 'full data augmentation approach'.

LORNA DEETH, University of Guelph

Mixtures of Individual-level Models for Infectious Disease Modelling

Individual-level models (ILMs) are a class of models that have been used to describe the spatiotemporal spread of infectious diseases. However, current ILMs do not account for (hidden) population heterogeneity, and instead assume a homogeneous population. A mixture ILM (MILM) is proposed that is an adjustment to a simple, spatial ILM, and allows for population heterogeneity with respect to certain model parameters. A simulation study was conducted in which both the simple ILM and MILM were fit to simulated epidemic data, and the respective posterior predictive abilities were assessed.

ROB DEARDON, University of Guelph

Posterior Predictive Approach to Goodness-of-Fit for Infectious Disease Models

In complex non-linear models, such as spatio-temporal infectious disease models, it is often unclear how best to ascertain goodness-of-fit. Often such models are fitted within a Bayesian statistical framework, since such a framework is ideally placed to account for the many areas of data uncertainty. Within a Bayesian context, a major tool in assessing goodness-of-fit is the posterior predictive distribution. Here, we examine different test statistics and ascertain how well they can detect model misspecification via a simulation study.