Bayesian non-parametric inference for stochastic epidemic models

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Despite the enormous attention given to the development of methods for efficient parameter estimation in stochastic epidemic models, there has been relatively little activity in the area of non-parametric inference. The infection rate function is usually assumed to take some parametric form with at most a few parameters (e.g. the homogeneous-mixing model), which can be too rigid to fit the data and assumes that an individual's infectiousness is fixed.

In this talk we are concerned with the development of novel non-parametric methods within a Bayesian framework. The proposed methodology involves modelling the infection process, e.g. using a step function, and trying to infer it having only partially-observed data, which is usually the case when modelling disease outbreak data. An efficient RJ-MCMC algorithm is employed which enables estimation of the force of infection as well as the unobserved times at which individuals become infected. The proposed framework offers far more flexible inference and additionally enables us to assume that an individual's infectiousness can vary over time.

We apply the proposed methodology to simulated and real outbreak data and compare with the standard parametric models. Finally, we discuss alternative choices for modelling the intensity of the infection processes such as P- and B-splines.

**Keywords:**
Stochastic epidemic model; Bayesian inference; non-parametric methods; reversible jump Markov Chain Monte Carlo.