Likelihood-based Inference for Stochastic Epidemic Models, with application to High-resolution Contact Tracking Data

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Abstract

Stochastic epidemic models such as the Susceptible-Infectious-Removed (SIR) model are widely used to model the spread of disease at the population level, but fitting these models present significant challenges when missing data or latent variables are present. In particular, the likelihood function of the partially observed data is typically considered intractable. We will discuss recent advances that enable likelihood computations without model simplifications in the presence of missing infection and recovery times, as well as latent variable methods that enable sampling methods. Motivated by a study of influenza transmission with social contact tracking data, we then present a data-augmented MCMC algorithm for fitting parameters of the SIR model when the underlying contact network evolves through time, and is dependent on individuals' disease statuses. We demonstrate how accounting for the dynamics of the epidemic and network models jointly is crucial for valid inference, and apply the method to analyze data from the eX-FLU study of influenza on a college campus.