

Spatial models of infectious disease transmission: data and computation

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Parameter estimation for individual-level mechanistic models of infectious disease transmission can be computationally intensive. The “gold standard” for parameterizing such models is to use a Monte Carlo method such as Markov chain Monte Carlo (MCMC) within a Bayesian framework. However, two problems are typically encountered using such an approach.

First, much of the data we would wish to observe are latent in infectious disease systems. For example, the times of infection and recovery are almost always censored in some way. Second, since the susceptible individual infectivity rates are usually cumbersome, nonlinear functions that vary between individuals, this results in a likelihood function which is also computationally cumbersome. Further, since in a method such as MCMC, the likelihood needs to be recalculated many, many times for different parameter values, the overall data analysis can take a very long time for even moderately large populations. The first problem is typically solved by treating uncertain/missing data such as infection and recovery times as nuisance parameters, incorporated into the Bayesian analysis via data augmentation. Unfortunately, substantially increasing the dimensionality of the parameter set as this does, also exacerbates the second problem.

Various methods in the literature have been suggested to deal with such problems. These include the use of: linearizing part of the likelihood to allow us to avoid the need to recalculate the entire likelihood each MCMC iteration; Gaussian Process emulation methods; so-called approximate Bayesian computation (ABC) techniques; data-sampling- and data-aggregation-based likelihood approximations; and supervised learning/classification-based methods of inference. Each, however, introduces some level of approximation to the true posterior we are really interested in.

Here, we review some of these methods, explaining some of the advantages and disadvan-

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tages inherent in each approach.