

**INFERENCE FOR EPIDEMIC MODELS USING APPROXIMATE BAYESIAN COMPUTATION**

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Computing the posterior distribution for spatio-temporal models of infectious disease epidemics can be computationally time consuming if the outbreak is large and/or takes place within a large population of individuals (e.g. the UK foot-and-mouth outbreak of 2001). If we are using a technique such as Metropolis-Hastings Markov chain Monte Carlo (MH-MCMC) to carry out inference for our model, then this can lead to serious practical problems, since we have to calculate the likelihood many times.

One approach that is being developed, which can help alleviate such problems, is that of approximate Bayesian computation. This technique avoids the need to calculate the posterior every iteration by basing acceptance or rejection of parameters, as part of the MCMC chain, on the result of simulation from the model. That is, for given parameters, data is simulated from the model, and then some metric of the difference between the observed data and the simulated data is used to determine acceptance or rejection. This leads to an MCMC chain that is a dependent sample of an approximation to the posterior distribution. This is useful if the simulation and metric calculation process can be carried out more quickly than the calculation of the posterior.

Issues that need to be considered include, which metrics are most suitable (e.g. is the metric sufficient?), how 'close' the simulated data needs to be to the original data for a proposed move to be accepted (i.e. tolerance), and how quickly can we simulate a spatio-temporal epidemic from the model?