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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.