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Modeling the Spread of Influenza within Households in Hong Kong

Individual-level models (ILMs) can be used to model the spread of infectious diseases in discrete time. The key feature of these ILMs is that they can take into account covariate information on susceptible and infectious individuals as well as shared covariate information such as geography or contact measures. Here, such ILMs are fitted in a Bayesian framework using Markov Chain Monte Carlo techniques to data from a study on influenza within households in Hong Kong during 2009. The focus here is to estimate the effect of vaccination on infection risk and choose a model that best fits the disease spread.