

Quantifying the mean epidemic dynamics from large scale stochastic simulations.

Kyle Hickmann

Department of Mathematics
Tulane University, New Orleans

Abstract

In our work a population of susceptible individuals is viewed as a complex network in which links represent probability of disease transmission from one individual to another. The epidemic will display different dynamic behavior dependent on the index case in the network. We have developed tools to study the dynamics of disease spread within a large population from an ensemble of these stochastic simulations. Previous work has shown that, for highly heterogeneous populations, the dynamics of an epidemic can be approximated by a deterministic model. However, there has not yet been a rigorous study of how stochastic simulations approach the deterministic limit or how the deterministic model may be inferred from stochastic simulation data. In this research we outline an algorithmic way to infer the mean behavior of an epidemic in a large population from a set of stochastic disease simulations. We show that our methods allow us to quantify the extent to which the deterministic model fits the stochastic data. These results simplify the identification of important features of an epidemic from an ensemble of simulations.