Quantifying Uncertainty in Model Predictions: Stages of the Network Modeling

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Abstract

The use of network models has been increasingly important to infer problems on stochastic processes such as epidemics. Epidemics behave differently based on the type of population structure, often represented by networks. Although complex, epidemics can be studied through three general stages: (1) a stochastic stage, in which the underlying distribution of times to infect specific percentages of the population varies, (2) a deterministic stage, where a system of ordinary equations can be use to calculate model parameters, and lastly (3) a final stochastic stage, where very few individuals remain infected in the population. Using the Susceptible-Infected (SI) epidemic model, we focus on the first stage of the epidemic as we aim to describe the distributions of time required for specific percentages of the population to become newly infected. At a specific time, these distributions converge to a stationary distribution specific to different networks (here: complete, dimensional, and Erdos-Renyi distributions). Upon convergence, the epidemic enters its second stage, the deterministic stage. Non-parametric statistics were used to determine at which point the distributions were not statistically different. Our preliminary results showed that the time to infect the percentages of the newly infected converged faster (~20%) under the complete network and the distribution of times all followed a Gamma distribution. Furthermore, the time to infect the percentages of the newly infected converged faster (~20%) under the complete network and the distribution of times all followed a Log-Normal distribution. Furthermore, the distribution of times converged at 45, 35, and 25%, respectively, for Erdos-Renyi networks with p = 0.1, 0.5, and 0.9 respectively. Understanding the epidemic through these stages can help tailor it so as to provide as accurate an estimation of the progression of a disease as possible.