

Population dispersion and equilibrium infection frequency in a spatial epidemic

Maria Duryea^a, Thomas Caraco^a, Geoffrey Gardner^a, William Maniatty^b,
Boleslaw K. Szymanski^b

^a*Department of Biological Sciences, University of Albany, Albany, NY 12222, USA*

^b*Department of Computer Science, Rensselaer Polytechnic Institute, Troy, NY 12180, USA*

Abstract

Spatially detailed epidemic models commonly invoke probabilistic cellular automata to predict population-level consequences of localized interactions between infectious and susceptible individuals. Most such models equate local and global host density; the resulting spatial uniformity implies that each individual interacts with the same number of neighbors. However, many natural populations exhibit a heterogeneous spatial dispersion, so that the number of contacts capable of transmitting an infection will vary among interaction neighborhoods. We analyze the impact of this variation with a probabilistic cellular automaton that simulates a spatial epidemic with recovery. We find that increasing spatial heterogeneity in host density decreases the frequency of infection at endemic equilibrium, and consequently increases the divergence between mean-field predictions and observed levels of infection.

Keywords: Cellular automaton; Mean-field approximation; Simulation study; Spatial epidemic