

Verifying Spatially-Explicit Simulation of Virulence Evolution Via Analytical Models

Boleslaw K. Szymanski (Computer Science, RPI)

William A. Maniatty (Computer Science, SUNY Albany), and

Thomas Caraco (Biological Sciences, SUNY Albany)

When pathogen strains differing in virulence compete for hosts, spatial structuring of disease transmission can govern both evolved levels of virulence and patterns in strain coexistence. We develop a spatially detailed model of superinfection, a form of contest competition between pathogen strains; the probability of superinfection depends explicitly on the difference in levels of virulence. We apply methods of adaptive dynamics to address the interplay of spatial dynamics and evolution.

We developed a simulation of the detailed model that indicates that spatial structure constrains disease virulence. The mean-field approximation predicts evolution to criticality; any small increase in virulence capable of dynamical persistence is favored. However, pair approximation of the detailed model agrees with the simulation spatial structure constraining disease virulence. Increased spatial clustering reduces the maximal virulence capable of single-strain persistence and, more importantly, reduces the convergent-stable virulence level under strain competition. The spatially detailed model predicts that increasing the probability of superinfection, for given difference in virulence, increases the likelihood of between-strain coexistence. When strains differing in virulence can coexist ecologically, our results may suggest policies for managing diseases with localized transmission. Comparing equilibrium densities from the pair approximation, we find that introducing a more virulent strain into a host population infected by a less virulent strain can sometimes reduce total host mortality and increase global host density.

The presentation is based on a paper “Spatially structured superinfection and the evolution of disease virulence” by Thomas Caraco, Stephan Glavanakov, Shengua Li, William Maniatty, and Boleslaw K. Szymanski that will appear in *Theoretical Population Biology*, 2006.