

Emerging Infectious Diseases and Agent-based Models: Moving Epidemiology from Analyzing Pattern to Simulating Process

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Abstract

This paper presents a conceptual framework describing the utility of spatially-explicit Agent-Based Models (ABMs) in simulating emerging infectious diseases and designing proactive policy measures to minimize contagion.

Background and Relevance

The sudden appearance of diseases like SARS (Enserink & Vogel, 2003), the devastating impacts that diseases like Ebola have had on both human and wildlife communities (Leroy et al., 2004), the fear that diseases like Avian Bird Flu have caused (Sengupta et al., 2007), and the immense social and economic costs created by viruses like HIV (Piot et al., 2004) underscore our need to understand and simulate the processes that underlie infectious diseases and predict their emergence. Epidemiological models to date have utilized a combination of mathematical and statistical modeling techniques, but have generally not incorporated explicitly spatial, temporal, and disaggregated dimensions in one system. For example, Susceptible-Infected-Recovering (SIR) models incorporate time but not space, whereas spatial statistics and cluster analysis incorporate space but not time. Further, spatial statistics and cluster analysis are useful tools to explore spatial patterns once a disease emerges, but are not adequate to forewarn policy-makers about impending outbreaks so appropriate measures can be taken. This is a lost opportunity because infectious disease outbreaks are by their very nature both (1) spatially structured and (2) result from individual interactions in a spatially heterogeneous landscape.

Methods

A means around the lack of spatial structuring and simulation of individual interactions are ABMs incorporated within geospatial software. An ABM simulates the interactions between biological individuals and their landscape through the use of computer code to represent each individual as an agent in a 'virtual' environment stored within a GIS. Further, the computer code representing an individual must possess the following four properties: (a) autonomous behavior, (b) ability to sense its environment and other agents, (c) ability to act upon its environment alone or in collaboration with other agents, and (d) possession of rational behavior (Woolridge & Jennings, 1995). Additionally, researchers have pointed out that intelligent agents should not only be able to respond to, but also learn from, their environment. Humanistic characteristics such as beliefs, desires, intentions, and emotions and trust also could form a part of agent behavior (Shoham, 1993). Computational models of boundedly rational decision-

making behaviour are available to develop computer code that fulfills the criteria of autonomy, awareness, reactivity, and rationality.

ABMs (a growing area of interest in GIScience (Sengupta & Sieber, 2007)) are ideal environments within which the complexity of disease transmission resulting from interactions between individuals and of individuals with their landscape can be simulated over time and space. The emergence of a disease is simulated by focusing on the on individual and their interactions with one another over a simulated landscape which may give rise to epidemics. Because each individual is represented independently, agents can exhibit heterogeneities in traits that are of interest in the context of disease dynamics (disease type, probability of transmission, or mortality). Further, the agents move within a specified landscape whose characteristics can be modified (e.g., varying in the extent of ecotone which has transmission probability for a specific pathogen elevated to a specific level). This allows agent-based models to represent complex systems where the solutions are non-deterministic and often have a stochastic component represented by probabilities (e.g., a particular type of interaction in a specific landscape, such as disease transmission or mortality, has a certain probability of occurrence at each time step). General patterns resulting from the interactions thus begin to emerge when the simulation has been run iteratively multiple times. These “emergent properties” include features such as disease spread, all of which occur at the population level rather than the individual level. Thus, simulating individual interactions lead to emergent properties (i.e., the potential for an epidemic) that cannot be predicted in advance of running the simulations.

Conclusions

Understanding how spatial patterns of disease incidence or risk are generated (i.e., simulating the processes rather than analyzing the patterns) provides a useful epidemiological tool for monitoring emerging infectious diseases. Rather than reacting to changes in disease dynamics that result from anthropogenic modifications to landscapes leading to increased contact between infected individuals, researchers can predict what will happen if a particular change were to occur and potentially design means to mitigate the effects. As new diseases emerge, we can react to them and understand the reasons for their emergence after the fact, or we can take a proactive approach and try to understand the principles that govern the emergence of novel diseases in general. In concluding, this paper argues that the latter approach is preferable and has the greatest potential to benefit human health.

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