

Workshop on Agent-Based Modeling of Complex Spatial Systems
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Agent-Based GeoComputation is not about building models. It is, ultimately, about the art and science of addressing complex spatial problems with computers; for sound inference on matters of importance. An appropriate model is necessary, but not sufficient. Consider the complementary laboratory tools and practices sufficient for inference with agent-based computational laboratory research for effective responses to complex geographic emergencies.

Our methodological advances in computational laboratory tools and practices have been driven by a potential pandemic influenza emergency due to an unusually deadly (H5N1) influenza pandemic spreading worldwide among migrating, wild, and domestic birds. H5N1 influenza currently kills more than half of its human victims. If it adapts to spread easily among humans, it could lead to a global influenza pandemic far more severe than the flu pandemic of 1918-1919.

Our research uses complementary computational laboratory tools to evaluate relative geographical risks via patterns of inter-city hierarchical diffusion of pandemic influenza, and to optimize geographic deployment of limited resources to inhibit the inter-city spread of pandemic influenza. The crucial substantive challenge harnesses advantages of geographic structure to clarify relative risks and to amplify the protective leverage of available resources, in order to target advanced preparation, minimize mortality, and gain time for vaccine production and administration. The crucial methodological challenge is to conduct sufficient sensitivity and risk analyses of the model and of recommended interventions to provide as much information as possible for decision-makers, in the event that model results must be used to recommend deployments of interventions during a pandemic emergency.

The epistemological insights and methodological extensions driven by responding to this potential emergency provide helpful guidelines for effective calibrations, experimental designs, optimizations, and risk analyses of spatial agent-based computational laboratory research.

Complementary Mathematical Modeling of Complex Dynamic Systems

Although respective limitations and advantages of mathematical versus agent-based models of complex dynamic systems are most commonly considered with respect to their roles as methodological substitutes (see for example Rahmandad and Sterman (2004)), there exist significantly complementary roles for which understanding their differences is also vital.

First, hybrid models using Dynamic Agent Compression (Wendel and Dibble (2007)) can harness efficiency and scaling gains by using mathematical equations rather than representative agents. For which temporal nuances of sacrificed discretization may become important to understand even for generalizations that appear to be lossless in other ways.

Second, standard mathematical models of complex dynamic systems such as SEIR models of epidemic diffusion in aspatial populations (Anderson and May 1991) may be cast as official standards against which behavior of agent models should be benchmarked. To do so, however, requires explicit consideration of the agent-based effects due to discretization as well as of those due to spatial structure in agent models (Durrett and Levin (1994), Keeling and Grenfell (2000), and Rahmandad and Sterman (2004)).

Complementary Genetic Algorithm Inference, Optimization, and Risk Analysis

Miller (1998) proposed to use a supervisory genetic algorithm to perform what he called “active nonlinear tests” (ANTs) by using the genetic algorithm to challenge each simulation model by seeking outcomes that provide exceptions or counter-examples to its usual results. This section briefly discusses a generalization of Miller’s ANTs to the broader problem of providing effective search and optimization across both treatment domains and outcome ranges for a model.

Systematic analysis of model behavior typically involves millions of simulation runs, each controlled by sweeping across discrete lists of values for sensitive model parameters, for each treatment variable of interest, and for seeds to control one or more random number series for stochastic simulations.

Of far greater importance scientifically, the standard focus on exploring model behavior via combinatorial sweeping across regularly spaced parameter values is a blind search for significant outcomes. As illustrated in Figure 1, regularly spaced parameter values may be entirely unrelated to the truly important parameter values where model outcome reach significant extrema.

Ideally, we would like to be able to search for interesting behavior in the outcome space rather than sweeping blindly in parameter space. As illustrated in Figure 2, a supervisory genetic algorithm allows us to do so with far greater efficiency than brute force combinatorial sweeping of parameter spaces. The genetic algorithm can be set up to search across combinations of key parameters for extreme values of single or multiple combinations of outcome variables, based on results from one or more stochastic replications of the scenario that is associated with each combination of key parameters. In addition, the greater economy in searching for key scenarios releases computational resources that may in turn be used to simulate sufficient stochastic replications for each to be able to distinguish statistically significant differences among scenario outcomes.

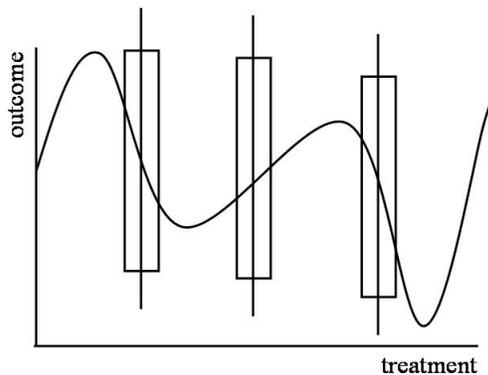


Figure 1: Running only a few stochastic replicates of each treatment level can result in variances so large that the signal becomes lost in the noise. Similarly, selecting treatment levels blindly via random or regular spacing may completely miss important local and global extrema.

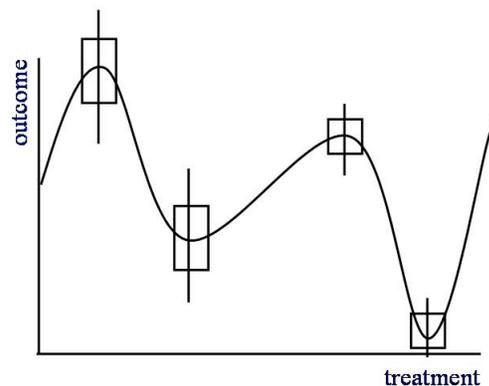


Figure 2: In contrast, an ideal experimental design runs enough stochastic replicates for reliable inference. Similarly, data-driven experimental designs may provide guidance for identification of key values for treatment variables and for basins of attraction leading to common outcomes.

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