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# Modelling to contain pandemics

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Agent-based computational models can capture irrational behaviour, complex social networks and global scale — all essential in confronting H1N1, says **Joshua M. Epstein**.

As the world braces for an autumn wave of swine flu (H1N1), the relatively new technique of agent-based computational modelling is playing a central part in mapping the disease's possible spread, and designing policies for its mitigation.

Classical epidemic modelling, which began in the 1920s, was built on differential equations. These models assume that the population is perfectly mixed, with people moving from the susceptible pool, to the infected one, to the recovered (or dead) one. Within these pools, everyone is identical, and no one adapts their behaviour. A triumph of parsimony, this approach revealed the threshold nature of epidemics and explained `herd immunity', where the immunity of a subpopulation can stifle outbreaks, protecting the entire herd.

But such models are ill-suited to capturing complex social networks and the direct contacts between individuals, who adapt their behaviours — perhaps irrationally — based on disease prevalence.

Agent-based models (ABMs) embrace this complexity. ABMs are artificial societies: every single person (or `agent') is represented as a distinct software individual. The computer model tracks each agent, `her' contacts and her health status as she moves about virtual space — travelling to and from work, for instance. The models can be run thousands of times to build a robust statistical portrait comparable to epidemic data. ABMs can record exact chains of transmission from one individual to another. Perhaps most importantly, agents can be made to behave something like real people: prone to error, bias, fear and other foibles.

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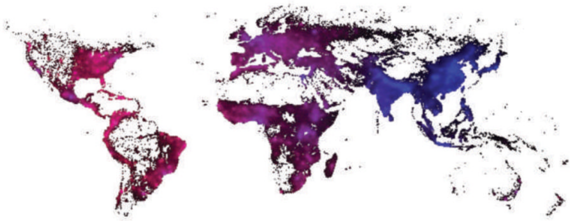
Such behaviours can have a huge effect on disease progression. What if significant numbers of Americans refuse H1N1 vaccine out of fear? Surveys and historical experience indicate that this is entirely possible, as is substantial absenteeism among health-care workers. Fear itself can be contagious. In 1994, hundreds of thousands of people fled the Indian city of Surat to escape pneumonic plague, although by World Health Organization criteria no cases were confirmed. The principal challenge for agent modelling is to represent such behavioural factors appropriately; the capacity to do so is improving through survey research, cognitive science, and quantitative historical study.

Robert Axtell and I published a full agent-based epidemic model[1] in 1996. Agents with diverse digital immune systems roamed a landscape, spreading disease. The model tracked dynamic epidemic networks, simple mechanisms of immune learning, and behavioural changes resulting from disease progression, all of which fed back to affect epidemic dynamics. However, the model was small (a few thousand agents) and behaviourally primitive.



Simulation of a pandemic beginning in Tokyo.

Now, the cutting edge in performance is the Global-Scale Agent Model (GSAM)[2], developed by Jon Parker at the Brookings Institution's Center on Social and Economic Dynamics in Washington DC, which I direct. This includes 6.5 billion distinct agents, with movement and day-to-day local interactions modelled as available data allow. The epidemic plays out on a planetary map, colour-coded for the disease state of people in different regions — black for susceptible, red for infected, and blue for dead or recovered. The map pictured shows the state of affairs 4.5 months into a simulated pandemic beginning in Tokyo, based on a plausible H1N1 variant.

For the United States, the GSAM contains 300 million cyber-people and every hospital and staffed bed in the country. The National Center for the Study of Preparedness and Catastrophic Event Response at Johns Hopkins University in Baltimore is using the model to optimize emergency surge capacity in a pandemic, supported by the Department of Homeland Security.

Models, however, are not crystal balls and the simulation shown here is not a prediction. It is a `base case' which by design is highly unrealistic, ignoring pharmaceuticals, quarantines, school closures and behavioural adaptations. It is nonetheless essential because, base case in hand, we can rerun the model to investigate the questions that health agencies face. What is the best way to allocate limited supplies of vaccine or antiviral drugs? How effective are school or work closures?

Agent-based models helped to shape avian flu (H5N1) policy, through the efforts of the National Institutes of Health's Models of Infectious Disease Agent Study (MIDAS) — a research network to which the Brookings Institution belongs. The GSAM was recently presented to officials from the Centers for Disease Control and Prevention in Atlanta, Georgia, and other agencies, and will be integral to MIDAS consulting on H1N1 and other emerging infectious diseases. In the wake of the 11 September terrorist attacks and anthrax attacks in 2001, ABMs played a similar part in designing containment strategies for smallpox.

These policy exercises highlight another important feature of agent models. Because they are rule-based, user-friendly and highly visual, they are natural tools for participatory modelling by teams — clinicians, public-health experts and modellers. The GSAM executes an entire US run in around ten minutes, fast enough for epidemic `war games', giving decision-makers quick feedback on how interventions may play out. This speed may even permit the real-time streaming of surveillance data for disease tracking, akin to hurricane tracking. As H1N1 progresses, and new health challenges emerge, such agent-based modelling efforts will become increasingly important.

## References

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