TeraGrid-based epidemiological modeling helped policymakers evaluate strategies for responding to the H1N1 flu epidemic.

Asking “What If?” About H1N1

Spread of H1N1 in the Washington, DC area—From the epidemiological modeling by Shawn Brown and colleagues, this graphic shows infected individuals per square mile, coded by color (increasing from blue to red), at the peak of the epidemic. Courtesy: Shawn Brown, PSC
he 2009 H1N1 flu epidemic raised many questions for public-health officials they hadn’t faced as seriously before:

• Should schools be closed? If yes, when and for how long?
• With a limited amount of vaccine, what groups—children, elderly, caregivers—should be vaccinated first?
• What about antivirals? Given limited supplies, what communities should get these relatively new medications and in what quantity?

During 2009, two National Institutes of Health MIDAS (Models of Infectious Disease Agent Study) research groups—one in Pittsburgh, one in Texas—relied on TeraGrid resources and applied two different, but complementary approaches to model the H1N1 outbreak. Their results, produced in real time during the epidemic, informed health care decision-makers locally, nationally and internationally. The MIDAS program helps health officials prepare for outbreaks by using computational tools to mimic how infectious disease spreads through populations.

Lauren Ancel Meyers, a MIDAS scientist at The University of Texas at Austin, used TACC’s Lonestar system to model H1N1 transmission within and among U.S. cities. Her model optimized choices for how to distribute the U.S. stockpile of antiviral medication, roughly 50 million doses. She presented her results and consulted with officials at BARDA (the U.S. Biomedical Advanced Research and Development Authority), with the U.S. Centers for Disease Control and Prevention in Atlanta, GA and the British Columbia Centre for Disease Control.

Her modeling showed that relatively simple strategies, such as regular releases of the stockpile to cities in proportion to their populations, worked as well as more complex approaches. Her findings are especially pertinent for the future, since they indicate that antivirals can save lives and reduce transmission prior to the availability of a vaccine.

“The U.S. antiviral stockpile,” says Meyers, “can play a critical role in early mitigation of future flu pandemics.”

PSC scientist Shawn Brown is co-principal investigator for the University of Pittsburgh Graduate School of Public Health’s MIDAS Center of Excellence led by Donald Burke. Brown and his collaborators used PSC’s Pople system to model H1N1 on a regional basis, both in Allegheny County, Pennsylvania (which includes Pittsburgh) and the Washington, DC metropolitan area.

“Our models are a virtual laboratory to ask questions you can’t ask with real populations,” says Brown. “We build a population, pretend to infect them with the flu, and then look at mitigation strategies, such as vaccinations or school closure, and see what effect they have.”

Using an agent-based model, a very detailed approach, Brown and colleagues found, for instance, that to close schools less than two weeks may slightly increase infection rates, and that schools may need to be closed eight weeks or longer to have a significant impact. Their modeling also supported recommendations by the U.S. Advisory Committee on Immunization Practices that priority be given to vaccinations for people at risk for severe complications. They found that prioritizing at-risk individuals, rather than only high transmitters (i.e., children), may result in slightly more cases of flu, but reduces serious disease and death, and overall economic cost.

Brown and his colleagues consulted with the Allegheny County Health Department and health officials for the state of Pennsylvania as well as BARDA, the U.S. Department of Homeland Security, and the President’s Council of Advisors on Science and Technology.

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