

Validation for flu prediction

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Network scientist Alessandro Vespignani's predictions about the spread of the H1N1 in 2009 were highly accurate, according to new validation studies. Credit: Brooks Canaday

(Medical Xpress)—In 2009, the H1N1 virus slipped into the blood-streams of more than 40 million people around the world. In just four months, it killed more than 14,000 individuals as it traveled from Mexico to India on its most favored vehicle: humans. As travelers moved about the planet via airplanes and cars, the pathogen followed, creating an epidemic the likes of which had not been seen since the 1970s.

At the time, Alessandro Vespignani was at the University of Indiana, where he began tracking the disease with as much attention as the Centers for Disease Control. Vespignani—now the Sternberg Family Distinguished University Professor of physics, computer science, and health sciences at Northeastern University—and his research team built a computational model called [GLEAM](#), or Global Epidemic and Mobility Model, which they used to predict the outbreaks as they surfaced around the globe.

In the last three years, the team has been tirelessly working to validate its predictions. To that end, its recently published article in the journal *BMC Medicine* offers definitive proof of a strong agreement between the predictions and the real-life surveillance data collected in 2009.

"Although we knew the prediction of the model were in pretty good agreement in several places of the world," said Vespignani, "here we produce a very extensive validation on more than 45 countries."

To model disease spreading, GLEAM integrates three data "layers." The first uses a population database, which was developed by a team at Columbia University and provides a high-resolution population density map of the entire planet. The second uses local commuting flows and airline transportation databases to estimate [human mobility](#) within and between countries, respectively. Finally, an epidemic layer accounts for the behavior of the disease itself, including information such as incubation and transmission times.

Operating from within the proverbial eye of the storm in 2009, the team used the model to forecast the week of the epidemic's peak in 48 countries in the Northern Hemisphere. In 42 of these countries, the forecasts were directly on target; in the other five, the team's predictions were off by only one to two weeks.

Normally, flu season peaks months after H1N1 did, making even the two-week variation a considerably good result. "This is the first large-scale validation of a computational model that pulled out predictions in real time," said Vespignani. "It shows that computational models have acquired the maturity to provide useful information and at the same time points out the way on how to improve and develop better models and tools."

More information:

www.biomedcentral.com/1741-7015/10/165/abstract

Provided by Northeastern University

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