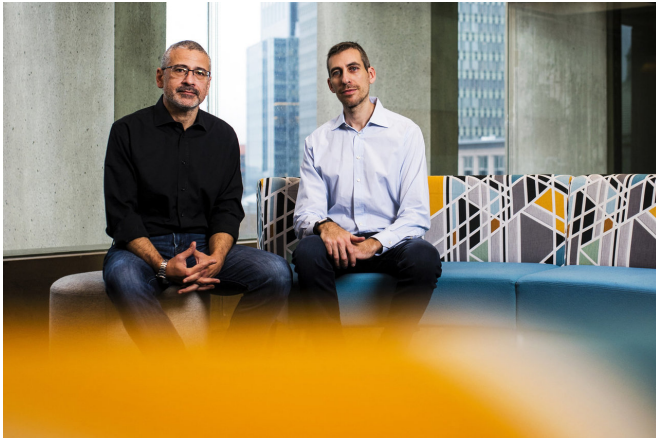


Tracking an epidemic requires computer models—but what if those models are wrong?

20 November 2018, by Laura Castañón



Credit: Northeastern University

Whether they're tracking the future spread of an epidemic, or determining where best to distribute a vaccine during an outbreak, today's disease researchers depend on reliable computer models.

Now, [researchers](#) at Northeastern are taking another look at one of the basic assumptions of these models: that in the early stages of an epidemic, the average [number](#) of new cases caused by each infected person is relatively constant.

"This number is never constant," said Alessandro Vespignani, the Sternberg Family Distinguished University Professor of Physics, Computer Science, and Health Sciences. "The evidence from the data is shattering the classic perspective."

Simple models typically show the start of an epidemic as an exponential curve based on this number, which is known as the basic reproductive number. Patient zero gets the flu. She spreads it to

two people. Each of them spreads it to two additional people, and so on. The curve only begins to level off when so many people are sick that it becomes difficult to find healthy people to cough on.

But real [epidemics](#) don't behave in such easy-to-graph ways. At Northeastern's Laboratory for the Modeling of Biological and Socio-technical Systems, Vespignani and his colleagues have been analyzing networks to build more realistic models.

Their early models started with the idea that people spend most of their time within their own social networks, which would affect the spread of a disease. Patient zero is more likely to infect her friends and family than a stranger who lives across town. But their recent paper published in *Proceedings of the National Academy of Sciences* goes a step further: It shows that not all networks are created equal.

The team analyzed the differences between types of social networks, such as workplaces, households, and communities, and layered them into a larger model. Vespignani expected that each layer would have a unique basic reproductive number.

"Actually, it was completely different," said Vespignani, who is the director of Northeastern's Network Science Institute. "The reproductive number that we used in the past doesn't work in realistic situations."

Marco Ajelli, an associate research scientist at Northeastern and a senior author on the recent paper, was the first to realize that the dynamics were more complicated than they had thought. Even within those individual layers, the basic reproductive number was constantly changing. A

middle-schooler from a big family is going to infect many more people in his household than a retiree who lives alone, Ajelli said. And epidemics tend to tear through high-traffic places like schools and offices at the start, then slow down as they reach more isolated areas.

"During different times of the epidemic, you have different combinations of different kinds of contacts," Ajelli said. "You have to combine all that information together."

The team used the data from a 2009 outbreak of swine flu in Italy and the Netherlands to see if the model would accurately line up with the fluctuations of a real [epidemic](#). The researchers collected information on Italian and Dutch social dynamics as well as the disease itself.

"It's really long, and sometimes even tedious, work," Vespignani said, "studying the household structure in that place, getting the workplace statistics, and then merging that into this huge synthetic reconstruction of the world. But it's very important."

They found that their model was able to follow the growth and spread of the disease much more accurately than models using a constant basic reproductive number. But currently, it's a model that is specific to Italy, the Netherlands, and places with similar contact networks. To use this [model](#) in other areas, Vespignani and his team will need detailed data on societies all over the world.

In the meantime, Vespignani and Ajelli have proposed that disease modelers rely on a different method to predict the spread of epidemics. Instead of using a single basic reproductive number, researchers can use the data from real outbreaks as they occur to determine the reproductive number for each day.

"You can use that number to produce better simulations, better forecasts, and have more grip on the actual spread of the disease in the population, without making guesses about what's happening," Vespignani said.

More information: Quan-Hui Liu et al.,

"Measurability of the epidemic reproduction number in data-driven contact networks," *PNAS* (2018). www.pnas.org/cgi/doi/10.1073/pnas.1811115115

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