How can we get ahead of a virus? Math

Authorities are using mathematical modelling to predict a variety of outcomes as flu spreads through the population

BY RANDY SHORE, VANCOUVER SUN   NOVEMBER 7, 2009

One of the key tools used by medical authorities to get ahead of a virus as it races through a population is mathematical modelling, which uses computers and a whole host of data to mimic the behaviour of the virus in human populations.

As you take your simple model and add layers of complexity to it, you gain the power to predict a variety of outcomes based on variables such as when the vaccination program starts, how many people are vaccinated before the virus begins to spread widely or who you decide to vaccinate first -- super-spreaders such as school children or low-spreaders such as nursing home clients.

Modelling used today is based on the pioneering work of British epidemiologists W.O. Kermack and A.G. McKendrick, who coined the ideas of the reproductive number, the number of new cases that result from each infection; and the generation time, how long it takes new cases to occur.

The resulting model predicts an attack rate -- how quickly a virus will spread through a given population until those spreading the virus start running into more people with immunity than people who have none. At that point, the pandemic starts to wane and we transition to herd immunity, in which even those without immunity are protected because it is so difficult for the virus to spread.

The H1N1 flu has a reproductive number between 1.3 and 1.8. That means each infection will generate about one-and-a-half new cases, said University of Toronto epidemiologist David Fisman, a researcher for the MITACS [Mathematics of Information Technology and Complex Systems] network based in Vancouver.

He noted the bubonic plague that killed 20 per cent of the people in Europe had a reproductive number of 1.2.

He was quick to point out that death is almost certain with the plague and very rare for the swine flu, which is considered mild even for an influenza.

Armed with these numbers, scientists led by the B.C. Centre for Disease Control's director of mathematical modelling Babak Pourbohloul used a computer program populated by 2.4 million nodes, one representing each person in the Lower Mainland. Models can represent populations ranging from a small village to the entire world.

Researchers assign the nodes different characteristics based on what is known about the population, such as how many people are a particular age, how many work in hospitals and in offices and how many are in kindergarten and likely to wipe their noses with their hands.

"We try to connect all those nodes in the way that people connect to each other on a regular day," said Pourbohloul.

Researchers then infect a few nodes and run the program that simulates the spread of the virus thousands or even millions of times to see which scenarios occur most often and use that to predict how the virus will behave in the real world.

That predictive model helps health authorities decide what they should do to either head it off -- which they do fairly successfully with the seasonal flu -- or manage the wildfire-like spread of a pandemic virus to minimize the number of deaths that occur.

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