



Lessons From Past Outbreaks Can Inform Public Health Policy Now

Scientific approaches to infectious disease transmission models can help us make better decisions regarding the COVID-19 pandemic.

For the millions, if not **billion-plus**, people now confined, trying to juggle work, kids and assorted COVID-19 worries, questions abound: When is the situation going to get back to normal? Has the number of cases peaked yet? If my parents need to go to hospital, will there be respirators for them?

Looking for answers, even the least scientifically minded among us has by now read scores of articles on the mathematical models and risk models meant to guide authorities about the next control measures to take. In the United Kingdom, the media hotly debated the virtues of the **Imperial College model**, which informed the government’s earlier strategy of creating a “herd immunity”. In the United States, the Institute for Health Metrics and Evaluation (IHME) model, used by the White House to chart the pandemic, regularly makes **headlines**.

Earlier this month, INSEAD invited **Stephen Chick**, INSEAD Professor of Technology and Operations Management, the Novartis chair of Healthcare Management and the academic director of the INSEAD Healthcare Management Initiative, to share some insights gleaned from two decades working on such models. More than 1800 online participants tuned in to the third webinar of the INSEAD series, **Navigating the Turbulence of COVID-19**.

The basic risk model most of us are familiar with is

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linear, such as a decision tree with arrows. Let’s say that you are trying to assess John’s risk of cancer. John has various risk factors. But if his neighbour, Fatima, also has cancer, it changes very little to John’s risk of getting it. By and large, each case is independent. However, in the case of a virus like COVID-19, if Fatima is infected, she can and does influence John’s risk of infection. Community behaviour influences outcomes. And the sequence of events through time matters as well. What we need are nonlinear, dynamic models fully reflecting the interdependence of the pieces of the puzzle.

Striking the right balance

Such dynamic models include the rate of contacts, potentially infectious contacts, the probability of transmission per infectious contact, and the duration of time over which somebody who is infected will have those potentially infectious contacts, said Chick. Complexities such as information about the social structures where transmission can occur (e.g. schools or public transport), multiple routes of transmission, different characteristics of individuals such as age or medical history add to the model.

An important lesson is that we can alter the direction of the epidemic if we act on these parameters. Social distancing and frequent hand washing can reduce the rate of infectious contacts, as we all know by

now.

One challenge is to reach “a balance between how rich is the model, how expressive it is, while keeping it simple enough so that you can run it quickly to get some good insights,” said Chick. Every model makes assumptions, so none will be perfect, but they all help us make better decisions if we are careful with our choice of model.

Another challenge is weighing the different elements of the model appropriately. Chick gave the following analogy: If the model is about estimating your risk of being hit by a truck that’s coming at you as you’re standing in the street, wind resistance around the truck is clearly not as important as your ability to jump out of the way. Resources can and should be prioritised on the parameters known to have the biggest impact.

Dealing with uncertainty

Of course, a new type of infectious disease like COVID-19 will create uncertainty about some of the input parameters at least. For example, we may not know exactly the contact rate or the infectivity. Obviously, it would be unethical to infect people just to gauge the probability of infection. What we can do is see whether the prediction from our chosen model matches what is seen in reality. From there, we can iterate and refine.

That’s something Chick did with some **models** he built for the British government regarding Creutzfeldt–Jakob disease (CJD) with a team at University of Sheffield and their health technology assessment group. The government had been considering how to prevent the CJD prion from transmitting via surgical instruments. That was a **£500 million question** over five years, as this would have been the cost of replacing surgical instruments (after a single use) in order to prevent infection. It was impossible to collect data about whether people would get CJD from exposing them to the causative prion because that’s unethical. In eliciting uncertainty about the important parameters, the researchers generated a variety of disease trajectories. By observing the actual disease trajectory and refining knowledge about the parameters driving that infection, it became possible to improve decision making.

What to do when the first vaccines are developed

Chick pointed out that we can learn from past influenza pandemic models, while comparing them to the current crisis. Referring to **research** done in the early 2000s by Hill and Longini, Chick said that it answered a very interesting question: “Given a limited amount of vaccine, if we had to vaccinate folks for an influenza pandemic, should we vaccinate

the elderly first or should we vaccinate some other population subgroup first?”

Considering that the elderly have a much higher probability of dying from influenza, a reasonable initial reaction might be to focus on vaccinating them. But once researchers started to model the infectious disease transmission and its dynamics, they found that it was critical to vaccinate a younger population.

That’s because disease transmission can be very rapid amongst youths, who can then transmit it to grandma and grandpa. So, in that particular case, “you may save more lives in the elderly by vaccinating kids,” Chick explained.

Beyond the prioritisation of vaccination in a given country, there is a need to consider how to allocate vaccines across borders. In the context of an influenza outbreak, **research** by Chick, Mamani and Simchi-Levi proposed a contractual mechanism to coordinate vaccination to reduce the overall financial burden of infection globally and the total number infected.

Takeaways for policymakers

A key takeaway for public health decision makers is that models, especially the dynamic ones we need, don’t grow overnight. They take years to develop and refine. Governments should fund properly the teams that such work requires.

The good news is that efforts from one outbreak can be carried to the next. The H1N1 flu model is useful now as we tackle the COVID-19 crisis, said Chick. But each outbreak will have its own unique characteristics and it can take time to collect reliable data to update models. However, even before these data come in, having a model to build on can save lives.

A second takeaway is that the choice of the model does matter. Models contain implicit assumptions regarding capacity and aggregate behaviour, so picking the wrong model can lead to poor decision making. With Brennan and Davies, Chick proposed a **new taxonomy of model structures**, which helped governments in the **UK** and **France** choose the right model to predict health benefits and costs of interventions more accurately. Selecting the optimal model among all those available becomes even more critical when resources are constrained.

A third takeaway is that we shouldn’t be surprised if the nonlinear dynamics of disease transmission results in **counterintuitive measures**. For example, in 1993, a Cryptosporidiosis outbreak infected a quarter of the population living in Milwaukee, Wisconsin, leading to 1000 hospitalisations and **69**

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deaths, the majority in patients with AIDS. Initially, it seemed that providing special filters for immunocompromised individuals was a better and cheaper solution than an imperfect, ozone-based, supplemental municipal treatment of water. In the absence of human-to-human transmission, that made sense. But once new **nonlinear dynamic risk models** (developed by Chick, Soorapanth, Koopman and Brown) factored in the possibility of direct or indirect human transmission, the supplemental municipal treatment could prove more cost effective – a US\$100 million question. In **further work**, Chick, Soorapanth and Koopman used endemic data to provide an alternative to waiting for, identifying and measuring an outbreak.



In the presence of much uncertainty about disease and transmission parameters, models can help quantify this uncertainty and thus guide where data collection efforts should be focused. Furthermore, every government should work on data exchangeability. Science will advance the fastest if we can all benefit from the experience of other countries.

This is not the last outbreak we will experience, said Chick. And as the then-president of the European Research Council, **said** this month: “[A]t a time like this, the very best scientists in the world should be provided with resources and opportunities to fight the pandemic, with new drugs, new vaccines, new diagnostic tools, new behavioural dynamic approaches based on science, to replace the oft-improvised intuitions of political leaders.”

INSEAD’s webinar series “Navigating the Turbulence of COVID-19” feature expert inputs on key issues surrounding pandemic control and current countermeasures around the world. Join them [here](#).

Stephen Chick is a Professor of Technology and Operations Management and the Academic Director of the **Healthcare Management Initiative** at INSEAD. He directs the **Middle East Health Leadership Programme**, part of INSEAD’s Executive Education programme.

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