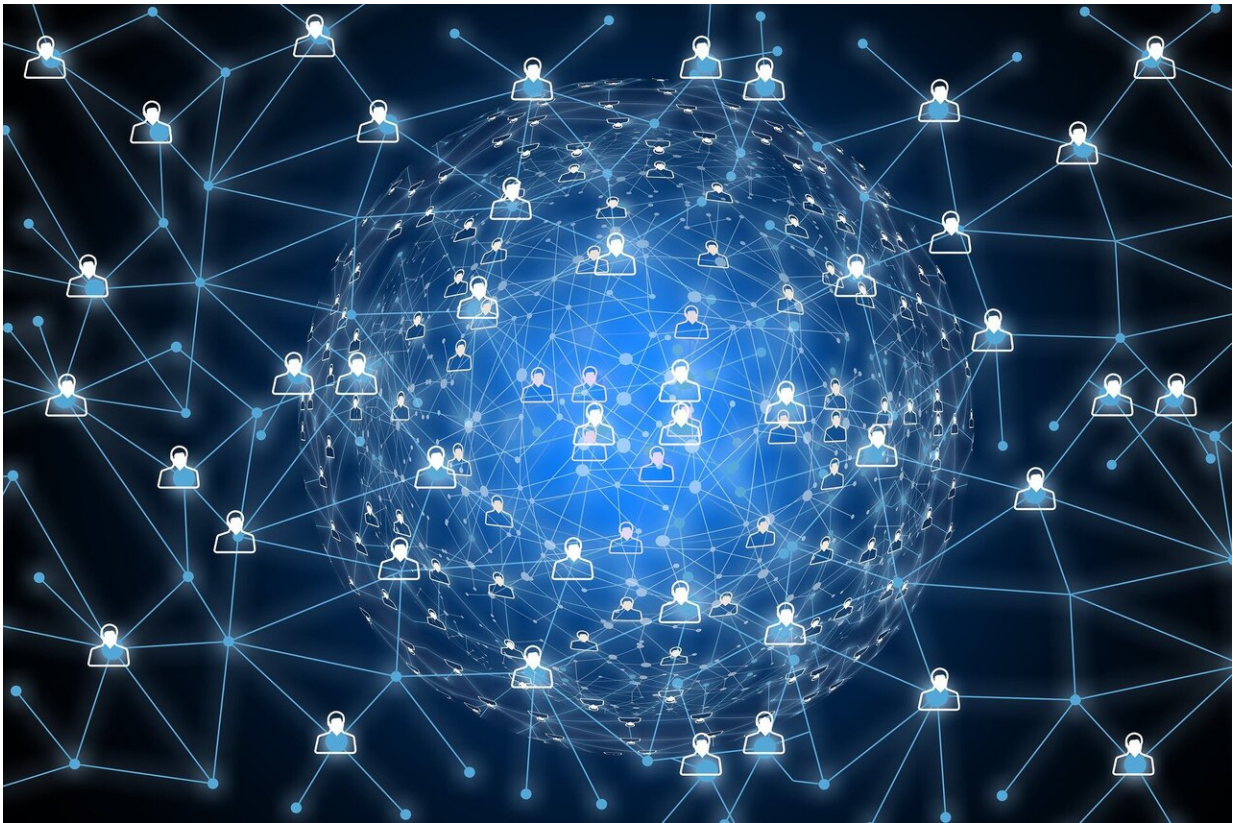# Mathematical model will monitor spread of COVID-19

May 21 2020, by Lindsey Valich

Credit: CC0 Public Domain

University of Rochester researchers are using their expertise in mathematical modeling to help answer one of the biggest questions surrounding the pandemic and quarantine: When is this going to end?

Gourab Ghoshal, an associate professor of physics, mathematics, and computer science, and Andrew White, an assistant professor of chemical engineering, recently received a National Science Foundation grant to create a [mathematical model](#) that will monitor the spread of COVID-19. Both White and Ghoshal are computational researchers and are able to conduct their research remotely during the campus shutdown. Combining their expertise in modeling both epidemiology and molecular simulation, the researchers hope to create a unique tool that will help policymakers make informed decisions about reopening the country.

"We need to turn on the lights to get more information to eradicate this disease," Ghoshal says. "This is very difficult because we have to scale up testing, do contact tracing, convince people to make behavioral changes. It would be helpful to have an estimate for how transmissible the disease is in real time."

Measuring infection rates: R_0 versus R effective

As anyone who has seen the 2011 movie Contagion knows, the estimate of a virus's infection rate is represented by the mathematical term "R_0," pronounced "R naught." If R_0 equals five, for example, every person who is infected with a virus will infect an average of five people. If R_0. is greater than one, the virus is spreading and the outbreak will continue, but if R_0 is less than one, the disease is declining and will eventually die out.

While R_0 is used to describe the intensity of a disease outbreak, it is really only relevant at the beginning of a pandemic. As the pandemic progresses, other factors, such as social distancing or quarantines, affect the infection rate.

"At every point in time, you want to monitor the effective transmissibility of the disease, independent of how many people actually

have it: what is the likelihood that somebody goes out and who do they infect?" Ghoshal says.

In order to take into account fluctuating situations and behaviors over the course of a pandemic, Ghoshal and White's model will produce what is known as R effective, which is R_0 as a function of time: the number of people who can be infected by an individual at any given time. At the beginning of a pandemic, for example, R effective may be five, but once a quarantine is in place and progresses, R effective could be less than one.

"That is good because it means you're in a situation where the pandemic might die down, but then the moment you start easing lockdowns, there's a good chance that can take off again," Ghoshal says. "Our model might be able to give you what R effective is in real time."

Local officials will be able to use Ghoshal and White's model to monitor infection rates on a day-to-day basis, and will better be able to determine whether opening businesses causes infection rates to spike.

"The mayor of a specific town would know the R effective today and tomorrow and can say, "Ok, I'll open up all the coffee shops' and can see what the R effective is, and can open up more businesses if the R effective stays down or close things if the R effective goes up," Ghoshal says.

The challenge of speed and accuracy

Researchers are able to calculate R_0 and R effective by inputting data into mathematical models. There are several data variables that are used to most accurately calculate R effective: (S)usceptible; (E)xposed; (A)symptomatic but infectious; symptomatic and (I)nfectious; (R)ecovered; and (D)eceased.

The problem with many of the current models that use this SEAIRD framework is that they are a trade-off between accuracy and simplicity: as models become increasingly sophisticated, they become more data intensive so they can't be deployed quickly. Simple models, on the other hand, require fewer data inputs and can be deployed more quickly, but they are often not as accurate.

Ghoshal and White hope to develop a model that is somewhere in between.

"Our model will be easily deployable and will make reasonably accurate predictions really fast, in a scalable fashion," Ghoshal says.

To do this, the researchers are taking the epidemiology models Ghoshal works on and feeding them into a framework called maximum entropy biasing that White has successfully used to simulate molecular dynamics.

The researchers input into the model the two variables they find to be most reliable—the mortality rates and hospitalization rates, which are numbers easily obtained from open source data at the state and county level. A maximum entropy biasing framework allows the model to account for any other variables that are unknown—individuals who don't show any symptoms, but are still able to infect others, for instance—so researchers don't have to input every factor.

"Maximum entropy basically means that we aren't going to find all the parameters, so we're going to put on this bias term that accounts for things we don't know," White says. "This is a new direction that people haven't explored."

Inputting just these two variables and using maximum entropy biasing will produce the R effective for a region at any point in time. The nature of the model means it could also be deployed for future disease

outbreaks as well.

"Another pandemic is bound to happen unless we change our ways," Ghoshal says. "In the initial phase, when there's very little data available, we hope this particular tool can start to turn the lights on, if not in the entire apartment, at least in one room, before more people die."

Provided by University of Rochester

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