Physicists develop powerful tool to predict the spread of COVID-19

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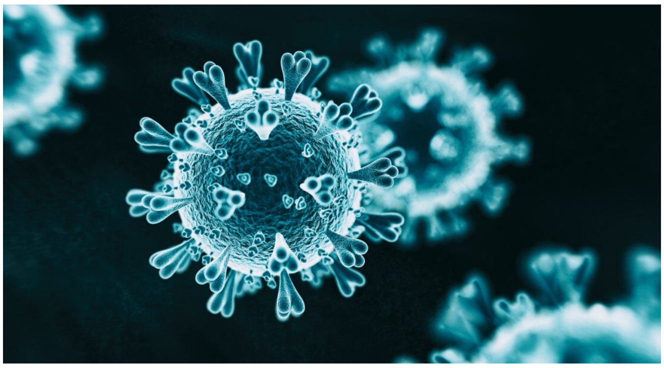

Credit: Niels Bohr Institute

How extensive should a shutdown be when a new COVID outbreak occurs? Should testing capacity be expanded? And at what pace should tracing occur? Physicists from the University of Copenhagen's Niels Bohr Institute have developed a new model that can more effectively predict the progression of COVID outbreaks in Denmark, while pointing out how to best manage increasing caseloads. The model enhances the ability to deal with the current pandemic and heightens Denmark's preparedness for future epidemics.

When the Danish authorities implement COVID-19 shutdowns and precautions, their actions are based on mathematical models that simulate how the virus will progress. Now, Mathias Heltberg, Christian Michelsen, Emil Martiny, Mogens H. Jensen and Troels Petersen of the Niels Bohr Institute have innovated an "agent-based model" that, as a new feature, includes specific characteristics of Denmark's population, such as the geographic distribution of Danes and their network interactions.

"We have developed a model that pushes the boundaries of how we can model and predict the progression of disease across the country. It is a tool that, among others, the Statens Serum Institute can use to better predict and estimate the progress of this disease across Denmark over time. It will allow us to be better equipped to manage COVID in the future," says Mathias Heltberg.

Among other things, the model can provide knowledge about how extensive the impact of local shutdowns will be, so as to disturb and affect the fewest number of people possible as a result of precautionary measures. It can also provide answers as to whether testing capacity should be bolstered locally or add clarity about the best approach when infections increase in a specific area—whether, for example, it is better to expand testing capacity and contact tracing as opposed to instituting shutdowns.

Can predict how quickly infections will spread

The new model distinguishes itself by being based on the activity of individuals. Mathias Heltberg and his colleagues have had access to the geographic location of the populace by studying Danish home sales over the past 13 years. With the help of Statistics Denmark, the researchers have also looked at family structures: how many people live together, where people work, how far they commute, the number of contacts people have every day, etc. Being statistical samples, no citizen monitoring is involved.

"We'll never be able to predict whether an office party in some town will end up becoming a super-spreader event, where 30 people become infected by a single party-goer. Isolated events cannot be predicted, as they are by their very nature, entirely random. What we can predict is the extent to which people in different areas interact with each other and how quickly infection will spread between areas. This is what is key to predicting how quickly the disease will progress geographically across Denmark, and whether, for example, we can prevent larger outbreaks by shutting down regionally instead of nationwide," explains Mathias Heltberg.

Stands to improve preparedness in the future

The model provides Danish authorities with a managerial tool that can be used to prevent some people from becoming infected in the future. The hope among researchers is that it will become a tool that can save lives. Not just in relation to COVID, but for any future epidemic. The model can also be applied to predict other diseases with other types of DNA, that infect differently, because the basic mathematical framework is the same.

Action must be taken immediately—but it won't be as bad as we fear

The model allows researchers to incorporate the effects of people living in densely populated cities, as well as those living in the countryside.

"When people live near to one another, the risk of contagion is naturally greater than in less dense living conditions. Of course, there are individual differences, but at a statistical level, it becomes obvious," says Associate Professor Troels Petersen, who is normally a particle physics researcher.

Of these, two conclusions come to light—both of a positive nature:

"First of all, we tend to overestimate the level needed to achieve herd immunity and thereby both how many need to be infected before the pandemic can no longer spread, as well as where the pandemic will infect. This is because certain people have far more contagious contacts and will statistically contract COVID sooner. However, once they have had it, those with many contacts are removed from the equation (due to their immunity), so there is a preponderance of those with fewer contacts left, who will infect fewer, etc. In this way, the curve one sees at first will not be representative of the disease's characteristics," says Christian Michelsen, a Ph.D. student at the Niels Bohr Institute.

Additionally, the research points out the importance of implementing the necessary interventions as soon as possible during the course of the pandemic.

"At the beginning, the virus is driven by those with many contacts, making it important to limit their potential for infecting others. So, to be certain that the health care sector doesn't become overwhelmed, while avoiding restricting too many people for too long, one must implement the tightest restrictions possible at the very beginning," explains Mathias Heltberg.

Heltberg points out that it makes little sense to debate the correctness of interventions or compare the strategies of various countries. Because we remain in an early phase, where the disease's progress can be slowed via a shutdown.

"There are still things that we don't know about this disease, including how long a previously infected person will retain their immunity. But when a vaccine arrives, the number of people we need to vaccinate in order to stop the spread of the virus will probably be lower than what was predicted earlier in the curve. And it won't take quite as many vaccines until we approach something resembling immunity among the population," adds Mathias Heltberg.

Provided by Niels Bohr Institute