

[COVID Information Commons \(CIC\) Research Lightning Talk](#)

[Transcript of a Presentation by Leila Hedayatifar \(New England Complex Systems Institute\)
October 10, 2023](#)



[Title: Effects of preventive protocols in COVID spread, an agent-based framework](#)

[Leila Hedayatifar CIC Database Profile](#)

[NSF Award #: 2032536](#)

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[Transcript](#)

Slide 1

Ok, hello everyone, it's my pleasure that I'm here in this webinar. Yes, the previous webinar was more than one year ago and it was on the results we got for the first project that we did for an NSF-granted project. This is a new direction that we are going through. Here, I'm going to present the study and investigation that we did to check the effects of preventative protocols in COVID using an agent-based framework.

Slide 2

First, I want to talk about why we study epidemic models. Epidemic models help us understand how infectious disease spreads through a society. These models provide us with insights about different factors that are crucial for developing effective public health interventions. They also allow us to make predictions about the potential impact of a pandemic and help assess the effectiveness of interventions like vaccination, social distancing, travel restrictions, and other preventions. Also, policy makers rely on epidemic models to formulate evidence-based policies and guidelines. One of the most important things is that sharing simplified epidemic models with the public can enhance understanding of disease transmission dynamics. For the public, something very simple, understandable.

Slide 3

Based on these thoughts that we had in our mind, we developed a model in Net Logo. Net Logo is a multi-agent modeling environment and programming language designed for simulating complex systems and modeling agent based frameworks. It allows you to have a figure for the whole model that you are developing and set the parameters. You can consider different situations for them, like the slider or the switch on and off icons.

Slide 4

It also allows you to have plots and figures that show you how the model is evolving over time, including how different compartments of the model are changing over time. I'm going to talk about these figures later.

Slide 5

Now, I'm going to go through different parts of the model that we developed - an agent based model. It specifies the dynamics by which a population of agents engage in interactions and undergo evolution throughout time. So we have a network of agents that are connected to each other and we consider different parameters and attributes for these agents or individuals in our network. First is the connections. These connections represent a network. We have a set of numbers, nodes, or agents and then we have the average node degree which represents the connections for each node. We connected the different nodes to each other based on that average number. Then, we relocate the nodes and put the nodes that they are connected to close to each other. This simulates the local connections for each person. Then, over that, we create long-distance connections that simulate if people travel to another location or if they move to a different location and make connections with people who are not usually close to them. Then, we consider the demographic parameters like age and gender. For age and gender, we have the option that if you want to consider those effects in the model, if you want to consider the age distribution, or want it to be a random distribution, or you want to use the U.S. age population distribution, that is pulled from the census. We are able to check the age range or the male to female percentage of the population. This allows us to simulate different environments, which was one of the interesting things that we wanted to study. The other is the health risk levels. We considered four different health risks: people who are older than 65 years old, pregnant women, and people with some health conditions or serious health conditions. It's possible for the model to define how many cases we want to have in our simulation and we see what happens in the model.

Slide 6

Then, we apply the SIR model. It's a fundamental epidemiological model that is based on some differential equations used to understand and analyze the spread of infectious disease. It has three different compartments: individuals who are susceptible to the disease but have not yet been infected, individuals who are currently infected with the disease and are capable of spreading the disease to other people, and individuals who were infected with the disease and recovered and are now immune to further infection for a period of time. We have the parameters for them. First,

the initial infected cases that guaranteed the start of the spread of the disease. Then, we have the chance of getting COVID, which is the probability of transmission of COVID. This can be changed based on different variants of COVID. We have the infection period of time and immunity period of time. The parameters we have for the symptomatic cases and asymptomatic cases, including the active duration that they can transmit the disease. We also have the distribution we have for the symptomatic cases. The other parameter that was important for us was Long COVID. We wanted to be able to study it or not. It's just considered based on a threshold, after that threshold if they still have symptoms, they're going to be considered Long COVID. And a small portion of the cases were super immune - it's very small, but as it was reported in the model and in the data, we considered it in the model.

Slide 7

Preventative protocols are the precautionary ways that people help to prevent spread of a disease. The ones that we had for COVID included wearing masks, social distancing, or quarantining sick people, and also the vaccination. For these preventative models, we considered two different sets of parameters: the precaution percentages, which relates to how people behave, and the vaccination percentages. For vaccination, we considered if we wanted to have vaccinations in the model or not. Should it be the percentage of people vaccinated, the vaccination's efficiency, also the decay in the vaccination's efficiency, and also the vaccination priority (this allowed us to start vaccinating people who are in a high-risk level).

Slide 8

The compartment model, in our modeling, these type of models allow us to have agents in a specific status and we can track the number of agents in each compartment over time. If we click on the setup, we're going to have a set of the nodes with the defined average connections, long-distance connections, and other attributes that I explained in the previous slides. Then, at each time point, the model checks the statuses of the agents and updates that status based on the previous status of their neighbors. Then, by running the model, we can see how different compartments of the model are changing in the system, in the model, over time. Also, there are some other measurements that we can do. For instance, we were interested in the number of re-infected agents in the model. How many times, how many nodes, or what percentage of nodes are re-infected again? We also wanted to know the productivity. The productivity is calculated based on the asymptomatic cases - they are not productive during the time that they are symptomatic. We are calculating the percentage of people who have symptoms.

Slide 9

All of these things that I have explained so far and the model in Net Logo allows us to go through the model, play with the parameters, and see how different parameters or preventive policies can change the behavior of the system. How the situation changes and different compartments of the systems change. But if you want to see the average behavior of the system, we need to do multiple realizations. For this, we need to make an ensemble of multiple realizations with the same set of parameters. Based on that, we can analyze the average behavior of the system and explore various potential outcomes of the model. Here, I'm going to show you

a setup of parameters used when we run the model. We're going to see different situations happen because we have different randomness. We have some randomness in the model and that randomness over time can change the behavior of the system.

Slide 10

We made some realizations. For any set of the parameters - here I'm going to show you just some of the results that we found based on our model. For each of these figures and for each point we run the model 100 times. We did the average calculation for each of those runs. I have four figures here and I'll try to explain these four figures in a short amount of time. The x-axis represents the probability of transmission, which is the chance of getting COVID. On the x-axis, we have the average number of infections per node. That shows how many times they got infected. The color bar represents the average duration of the pandemic and how many times we run the code. The stop time of the code is the time that we no longer have any infected cases or immune cases in the model. This graph represents the average node degree - at the beginning of the pandemic, if you remember, policy makers tried to convince people to reduce their connections, to minimize their connections with other people. Here, we show that by going from high degrees of connection to low degrees of connection, you can see that even in high degrees of connection with low probabilities of transmission, the disease is going to spread very fast in the system. The average number of infections is around one, which means that most of the cases see infection very fast, in a very short amount of time. But as the connections are reduced, we see that there is a shift to higher probabilities that the disease will not spread - it takes time for the disease and we have many reinfections, cases where people get re-infected. In very low degrees, even for very high probability of transmissions, the run time for the model is higher even with the few cases where there are re-infections. So it takes more time when we reduce the connection. It takes more time for the disease to be spread in society and then recirculate.

Slide 11

For the long-distance connections, again, we see that when we go from 0% long-distance connections to 20% long-distance connections, the behavior changes. You can see that, again, we have a change in the probability of transmissions. When we have a lot of long-distance connections, traveling even for short amounts of time, the disease is going to spread fast. But when we eliminate long-distance connections, the disease takes more time to spread and there are fewer re-infection cases.

Slide 12

Here, I'm showing the average duration in the y-axis. For precautions, we went from 0% to 100%. You see that when the precaution is zero, even with low probability of transmission, we have a peak in the duration of the pandemic. It takes a long time to circulate in society and there is a high rate of infection. However, as we go to higher precaution levels, like the one we see here where precaution is at 100%, not all the cases get infected and the spread of the disease halts quickly.

Slide 13

This figure represent the the results for the vaccination percentage. You can see that even with a small vaccination percentage, we see a big change in the number of cases and in the duration of the pandemic. For higher probabilities, also, the time is changing, which is very important because at the beginning - remember that these vaccinations started after three months - so we were interested to see how it was going to impact other situations. I didn't show it here, but you can see that even small changes can make a lot of differences.

Slide 14

So, in conclusion, I can say that our model depicts the spread of a virus within a population, considering a number of initial infected cases and whether it can propagate throughout the entire population or be contained before infecting some individuals. And based on those figures, I can say that reducing both local and long-distance connections, on average, acts as a deterrent to the rapid spread of the disease. Implementation of precautionary and vaccination policies not only decelerates the spread of the disease but also lowers the likelihood of reinfection. These are some of the results for this work, which is still in progress. We're going to have many more results in the future.

Slides 15-16

I want to acknowledge my colleagues in this work. Thank you for listening.