

How Local Interactions Impact the Dynamics of an Epidemic”

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(based on the article by Lydia Wren and Alex Best)

I. Introduction

The Susceptible-Infected-Recovered (SIR) model is a simple way to predict disease spread. After the coronavirus pandemic of 2020, Lydia Wren and Alex Best of the University of Sheffield noticed the absence of spatial and social structure (“locality”) within the SIR model. In their article, “How Local Interactions Impact the Dynamics of an Epidemic,” Wren and Best achieve a simplistic solution. This paper will cover the details of Wren and Best’s article and extend their findings.

Wren and Best incorporate a locality variable into their own SIR model, which determines whether infected individuals transmit the disease through “local” (neighbor-to-neighbor) interactions, “global” (random) interactions, or any manner in between. The more common or close an interaction, the more “local” the interaction. They also introduce “density,” which is a term for how probable an individual is susceptible, infected, or recovered. The idea here is that more dense populations have a higher probability of being infected.

To incorporate social and spatial structure in the SIR model, Wren and Best use approximate mathematical models and stochastic simulations of epidemics. These simulations produce graphs, which the authors use to propose practical ways to minimize epidemic spread.

II. Models

In the SIR model, N represents a constant population size (let’s say 1) with no births or deaths. Its components, S , I , and R , represent the fraction of the population that is susceptible, infected, or recovered respectively. Transmission rate and recovery rate are incorporated, and immunity is permanent.

Wren and Best add a locality parameter to this model which takes into account spatial structure. This parameter, L , when equal to 0, represents purely global interactions. As L

increases, interactions become more and more local until $L=1$, which is when interactions are purely local. They take the SIR equations for calculating the number of susceptible or infected individuals, and adapt them to calculate the probability of an individual being susceptible or infected. This probability is dependent upon the locality of an interaction between one who is infected with one who is susceptible. Each individual is represented by a single cell in a square lattice which represents the entire population.

Each cell has a density, which is the probability of an individual being susceptible, infected, or recovered. Each adjacent pair of cells also has a density. Wren and Best formulate equations for calculating these pair densities, which is the probability that a random pair of neighboring sites are a mixture of SS, SI, SR, II, IR, and RR, where S = susceptible, I = Infected, and R = recovered.

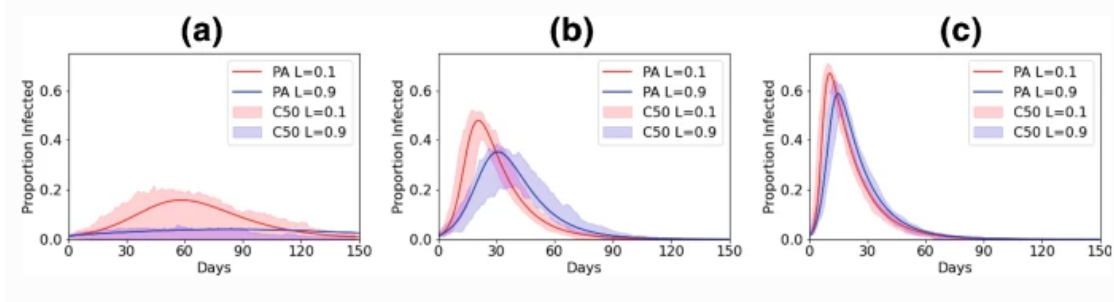
Next, they introduce the reproductive ratio, which is the measure of the average number of secondary infections caused by an infected individual. This could also be defined as how easily the disease is transmissioned, as a higher reproductive ratio means that more individuals are likely to get infected. On the other hand, a lower reproductive ratio means that it is harder for the disease to be transmissioned. The initial growth rate of the epidemic will be slower with the greater degree of local interactions.

Stochastic simulations incorporate the lattice described above. Then through the use of coding and the Gillespie algorithm, they are able to include the susceptible, infected, and recovered in the simulation. For each simulation, the program selects a completely random cell in the lattice to be infected. As time goes on, infected individuals infect those around them and recover after a specified number of days. The day of the epidemic's peak, the peak itself, and the total percent of the population that is infected are all tracked and graphed.

III. Results

Wren and Best's explanation of how local and global interactions as well as how the reproductive ratios affect the epidemic curves are best explained by the figure 1 graphs. There are three graphs, where (a) is when the reproductive ratio is at 2, (b) is when reproductive ratio is 5, and finally when (c) reproductive ratio is at 0. These different reproductive ratios then have two variables such as global interaction as well as local interaction. It is very clear that the global interaction within all three graphs has an increased infection rate whereas the local interaction has significantly less infections. This result illustrates to us that if we take into account local interactions from the beginning of an epidemic we are able to lessen the infection rate significantly. Of course we have to understand that there are different degrees of local and global interactions as at each step when local interaction lessens and goes towards a global interaction the infection rate increases, where when the reproductive rate reaches .5 the local interaction becomes a global interaction, resulting in the curves in red we see in figure 1.

Fig. 1



We then go deeper into the results as the three variables that we create, percentages of the population infected by day 300, the percentage of the population infected at the peak and the day of the peak. These variables help describe any potential targets in setting a public health policy as one policy that we conclude would help regulate an infection would be to control movement.

Within the three variables Wren and Best noticed that they all have overlapping IQR's at least up

to $L=0.4$ where it is still considered a local interaction, but as the L reaches higher values the infected rate moves away from local interaction at a rapid rate. Through their findings they also found that when the reproductive rate increases, the number of overlapping IQRs increase, meaning that the curve is increasing in more infected individuals on both local and global interactions. They are able to find the average pair approximation through the results within the IQRs, which allows for us to understand minimum and maximum of infection in both local and global interactions.

Using local interactions as a control mechanism, we were able to come up with a way to reduce infection rate through enforcing movement restrictions. If we restrict movement, we are able to create a more localized interaction which greatly impacts the infection rate. To create a scenario of how movement can be represented, Wren and Best created two equations which describe the susceptible individuals and the infectious individuals. The first equation is the global interaction between the two, and the second equation is the local interaction between the susceptible and the infectious individuals. It is easily seen that the global interactions have a huge spike in infection which then levels out, whereas local interactions will have a continuous infectious rate which will be easier to manipulate and manage in real world applications.

IV. Discussion

The novelty of Wren and Best's model is to "explore how epidemics over short timescales can be restricted by different degrees of local interactions, not just at the extremes of purely global or purely local infections." As our graphs indicated, moving from predominantly global interactions to predominantly local significantly reduces the infected percentage of a population.

However, as we transition from global to local interactions, the infected percentage does not decrease linearly, but is almost flat until L is about 0.5, and then we see a drastic decrease. This would suggest that epidemics transmitted by as many local interactions as global ($L = 0.5$), will affect a population about as much as if all interactions were global ($L = 0$). This is because when $L > 0.5$, a substantial number of global interactions will seed enough local outbreaks to cover a wide spread of the population. But when $L < 0.5$, there are not enough global transmissions, and much of the population will never interact with an infected person. While limiting global travel should decrease disease spread, the observation above seems to indicate that travel restrictions will only have a significant effect if imposed in the epidemic's earliest stages. That is, before there are too many global interactions ($L > 0.5$) for it to matter.

While our model shows us that restricting global interactions early leads to less infections, we must remember that we assumed a constant population and permanent immunity, and we are using a simple SIR model. In reality, we must account for births and deaths. People may not stay immune forever, or the disease may mutate and cause a "2nd wave". In the case of Covid-19, an SEIR model may be more helpful, where E stands for the percentage of the population that is exposed but unsure whether or not they are infected. Additionally, we cannot expect limiting global interactions alone will protect us from an epidemic if we are ignoring other practical measures such as hand-washing, face-covering, and social distancing. Regardless, our model provides a valuable nuance on the SIR model by showing how spatial and social structure impact the dynamics of an epidemic.

V. Extension

To extend the results of our paper, we adapted the code used for the stochastic simulations. Originally, the code modeled a population of 625, represented by a $N \times N$ matrix

where $N=25$. The recovery rate was set to $1/14$, meaning an infected individual recovers after 14 days. Also the number of initial infected was 5, or 0.008% of the 625 people.

In our first extra set of simulations, we ran tests for a recovery rate of $1/7$ with R_0 's of 2, 5, and 10. The results followed the same trends as the graphs with a recovery rate of $1/14$. However, the “day of peak” and “peak infected” for each L value was slightly decreased. This was expected, because if infected individuals recover in half the time, then the peak number of infected people will not accumulate as quickly, and the day of peak will also be delayed.

In our second set of extra simulations, we ran tests for different values of IO , which was our variable for the initial number of infected individuals. We tried with an IO of 1, first at R_0 values of 2, 5, and 10. We noticed that the data was much more spread out than when IO equaled 5. The boxes of the box-and-whisker plot were bigger, meaning the inner quartiles covered a wider range of data points. This is because less initial infected individuals allows for more and more variability, since there are less data points for the results to converge.

Additionally, the “peak infected,” “day of peak,” and “total infected” were close to 0 for all values of L except 0. When $L=0$, the “peak infected” and “day of peak” was about the same as it was for $IO=5$. The reason for this sudden jump at $L=0$, is because with only 1 initial infected, you need purely global interactions to cover a significant area of the matrix.

Finally, we tried an IO of 25, and we saw trends very similar to when IO was 5, except the “total infected” was almost at 100% for any L value. The purpose of running these extra simulations is to show that the authors’ methods can be manipulated for epidemics of varying conditions. Also, we were able to gain extra insights into theoretical epidemic spread.

Bibliography

Wren, L., Best, A. How Local Interactions Impact the Dynamics of an Epidemic. *Bull Math Biol* 83, 124 (2021). <https://doi.org/10.1007/s11538-021-00961-w>

Source Code

GitHub - abestshef/latticeSIR: Python code for stochastic simulations of an SIR epidemic on a lattice. <https://github.com/abestshef/latticeSIR>