

Modeling Epidemics using Networks

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1 Introduction

The COVID-19 pandemic has shown us the importance of having knowledge about epidemics and their progression. Modelling epidemics can help in forming and enforcing policies at the correct times. They can help us be well prepared for upcoming times of crises, and even help in preventing them altogether. They also allow us to test our policies on simulations, which can help in understanding when to relax lock downs, reopen economies and how to revert back to normalcy without causing a resurgence of the epidemic.

Traditional mathematical modeling of epidemics is based majorly on ordinary differential equations (ODEs). However these models neglect the difference in susceptibility of individuals in the population, relationships between individuals in the populations or the different behaviour patterns and structures of interactions of individuals in the populations.

These nuances are important in describing the spread of epidemics even at large scale levels, and neglecting these is a major drawback of traditional models. The structural relationships between individual agents can be taken into account by network modeling of epidemics. This paper first discusses the most common model for epidemics, the SIR model, and contrasts it with network models for epidemics.

2 Objective

This main objective of this paper is to introduce network modeling of epidemics. Prior to discussing network modeling, we discuss the traditional non-network models, in particular the SIR model in detail, to serve as a contrast to the network models. This is followed by a brief description about networks, and then network based SIR models are discussed. We also discuss using a cellular automata based simulation for network based models.

3 Non Network Models

3.1 Compartmental Models

Compartmental models are a very general modelling technique. They are often applied to the mathematical modelling of infectious diseases. The models

are most often run with ordinary differential equations (which are deterministic), but can also be used with a stochastic (random) framework, which is more realistic but much more complicated to analyze.

Many models exist to track the behaviour of an epidemic as it spreads through a community. The majority of these are Compartmental models, in which people are classified according to their disease condition. Kermack and McKendrick's SIR model is a particularly well-known example of such a paradigm (1927). 2 Individuals are either susceptible (S), infected (I), or removed (R) in this model (R). Persons begin in S and progress to I and eventually R, which comprises individuals who have either recovered (or are otherwise immune) or died, depending on their interactions with already contagious individuals and the characteristics of the disease (such as how contagious it is). The SIS ("susceptible-infected-susceptible") model, in which recovered individuals can be reinfected and thus re-enter the pool of the susceptible, and the SEIR ("susceptible-exposed-infected-removed") model, which incorporates a new health status for individuals who have been exposed to the virus and have been removed from the pool of the susceptible, are two other categorical models. Once the parameters are set, the flow of newly infected people in these models is determined by the number of people who are already sick as well as the number of people who are vulnerable at any particular time.

3.1.1 The Standard SIR Model

Many models are derivatives of the SIR model, which is one of the simplest compartmental models. The model is divided into three sections: -

S: The number of people who are vulnerable. When a susceptible person comes into "infectious contact" with an infectious person, the susceptible person catches the disease and moves to the infectious compartment.

I: The total number of infected people. These are people who have been infected with the virus and are capable of infecting others.

R: stands for the amount of people who have been removed (and are now immune) or who have died. These are people who have been infected with the virus and have either recovered and entered the removed compartment or died. The number of deaths is believed to be insignificant in comparison to the entire population. This compartment is also known as the "recovered" or "resistant" compartment.

The number of persons in each compartment at any one time is rep-

resented by these variables (S , I , and R). We make the precise numbers a function of t (time) to illustrate that the number of susceptible, infectious, and removed individuals may vary over time (even if the total population size remains constant): $S(t)$, $I(t)$, and $R(t)$. These functions can be worked out for a given disease in a specific community in order to predict and control possible outbreaks.

The SIR system without so-called vital dynamics (birth and death, sometimes called demography) described above can be expressed by the following system of ordinary differential equations:

$$\frac{dS}{dt} = -\frac{\beta IS}{N}$$

$$\frac{dI}{dt} = \frac{\beta IS}{N} - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$

This system is non-linear, however it is possible to derive its analytic solution in implicit form. Firstly note that from:

$$\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0$$

Therefore, it follows that:

$$S(t) + R(t) + I(t) = \text{constant} = N$$

where N represents the constant population. Note that the above relationship implies that one need only study the equation for two of the three variables. Secondly, we note that the dynamics of the infectious class depends on the following ratio:

$$R_o = \frac{\beta}{\gamma}$$

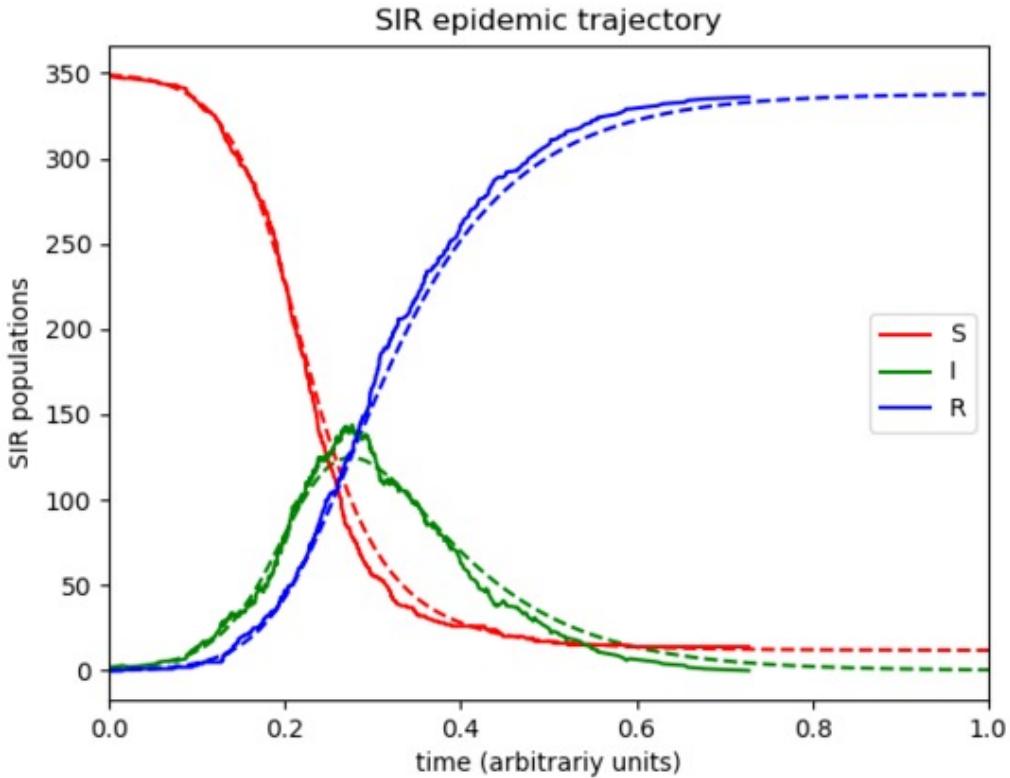


Figure 1: A single realization of the SIR epidemic as produced with an implementation of the Gillespie algorithm and the numerical solution of the ordinary differential equation system (dashed).

The so-called "basic reproduction number" is a number that is used to determine how many (also called basic reproduction ratio). This ratio is calculated as the estimated number of new infections (also known as secondary infections) from a single infection in a population of all susceptible individuals.

The flow from susceptible to infected is proportionate to the total number of both susceptible and infected in the classic SIR model. This technique aims to represent the idea that the likelihood of infection for a given virus's transmissibility is determined by how frequently infected individuals interact with those who are still susceptible.

A disease to which no one has immunity (as is likely the situation with COVID-19) begins with a small number of infected and a vast pool of susceptible persons, according to the SIR model. As the infection spreads across the population and the number of sick people grows, the rate of new infections rises quickly while the rate of elimination remains constant, causing the number of infected people to grow even faster.³ Without any interventions or behavioural adjustments, the number of new infections every day rises to a peak and then falls. The drop is due to the fact that there are fewer and fewer vulnerable persons in the community, limiting the number of people who can be infected. The spread of the disease will slow down and eventually peter out as the number of vulnerable individuals falls and a bigger share of the population becomes immune through recovery. Herd immunity is the result of a large number of immune individuals providing protection to the community.

3.2 Variations on the basic SIR model

3.2.1 The SIS model

Some infections, for example, those from the common cold and influenza, do not confer any long-lasting immunity. Such infections do not give immunity upon recovery from infection, and individuals become susceptible again.

4 Network Models

4.1 What does network model mean

A network model is a database model that is designed to represent objects and their relationships in a flexible way. The network model's schema, which is regarded as a graph with arcs for relationship kinds and nodes for object types, is a unique characteristic. The network model's schema, unlike other database models, is not limited to a lattice or hierarchy; instead, a graph replaces the hierarchical tree, allowing for more basic relationships with the nodes.

4.2 History of network model

Charles Bachman was the original inventor of the network model. In 1969, the Conference on Data Systems Languages (CODASYL) Consortium developed the network model into a standard specification. A second publication was introduced in 1971, which later turned into the basis for virtually all implementations. It was widely supplanted by the Relational Model later on because of its higher-level, more declarative interface.

4.3 Advantages of the Network Model

The network model's key advantage is its capacity to address the hierarchical model's lack of flexibility, of which it is intended to be a direct progression. In the network model, each child (referred to as a "member") might have several parents (referred to as "owners"), resulting in more complicated, many-to-many interactions. The following are some of the advantages of the network model:

- Simple Concept: This approach, like the hierarchical model, is simple to understand and implement.
- Ability to Manage a Variety of Relationships: The network model can handle one-to-one (1:1) relationships as well as many-to-many (N: N) relationships.
- Data is easily accessible: When compared to the hierarchical paradigm, data access is easier.
- Data Integrity: Because of the parent-child relationship, there is always a connection between the parent and kid segments in a network model.
- Independence of data: In a network, data independence is preferable.

4.4 Drawbacks of Network Model

- System Complexity: Because each record must be kept via pointers, the database structure becomes more complex.
- Because a large number of pointers is required, insertion, updates, and deletion become more difficult.

- Lack of Structural Independence: Any change in structure necessitates a change in application, resulting in structural dependency.
- Incomplete Flexibility: While the network model is more flexible than the hierarchical model, it still cannot satisfy all relationships by designating another owner.

4.5 A Network SIR Model of Epidemics

The use of a network, consisting of nodes and links, to portray patterns of interaction is a fundamental component in using the network technique to mimic an epidemic. The nodes represent individuals or families, while the linkages describe the contacts that could transfer disease. The presence of a link could indicate that two persons work in the same plant or attend the same school, and that a disease could be transmitted between them in that environment. Importantly, when there is no link between two people, such as when they live on opposite ends of the country, the disease does not instantaneously transmit from one to the other. Figures 2 and 3 show two different types of networks that will be discussed later. The nodes are the numbered blue circles, and the lines linking them are the edges.

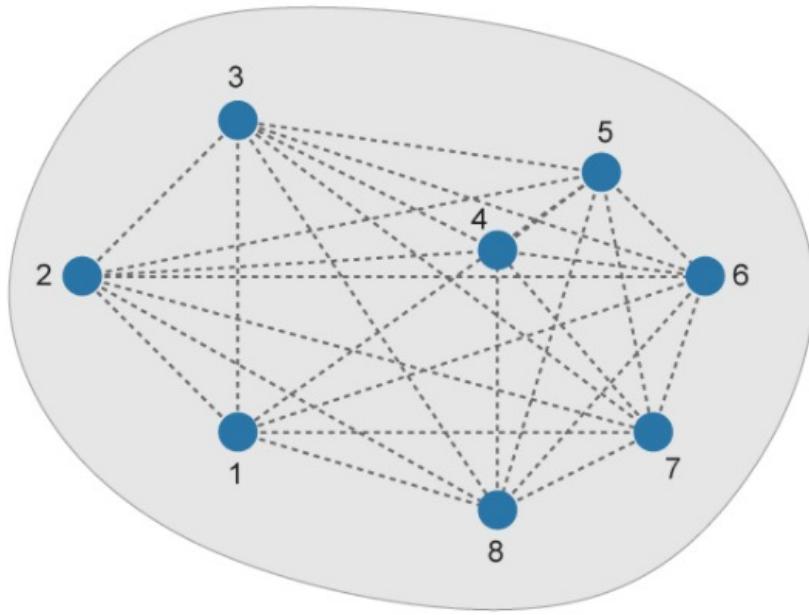


Figure 2: The Complete Network in the SIR Model

A fundamental component of using the network approach to mimic an epidemic is the portrayal of patterns of interaction using a network, which consists of nodes and links. The nodes represent individuals or families, whereas the linkages describe potential disease spreaders. The presence of a link could indicate that two persons work at the same plant or attend the same school and that disease could spread between them in such an environment. Importantly, when there is no connection, such as when two people live on opposite sides of the country, the sickness does not instantly move from one to the other. Figures 2 and 3 show two different types of networks that will be discussed further. The nodes are the numbered blue circles, and the links are the lines that connect them.

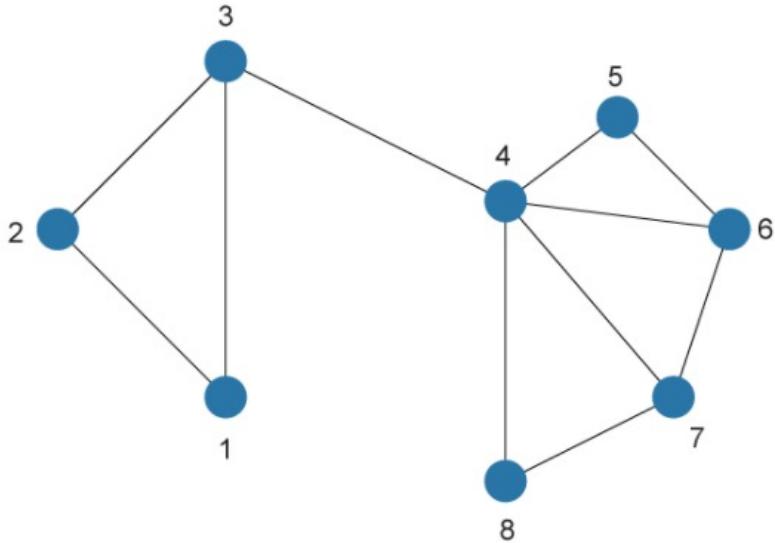


Figure 3: An incomplete Network with Link Heterogeneity

The baseline SIR model is a specific instance within the context of a network model, with two properties: To begin with, every pair of persons in the population has the potential to be linked (such a network is said to be complete). Second, each and every person has the same number of links as everyone else (such a network is homogeneous in its structure). Figure 2 depicts these assumptions in a simple eight-node network. A dashed line connects each pair of nodes, showing that under the SIR situation, the disease can possibly spread between any two individuals in the population. This is an extreme scenario, because the conditions of completeness and homogeneity are rarely met in most situations. Figure 3 depicts a new network that uses the same eight nodes but adds heterogeneity to the connection patterns—not all nodes are directly connected by a link and the link patterns are not all the same. This is an extreme scenario, because the conditions of completeness and homogeneity are rarely met in most situations. Figure 3 depicts a different network with the same eight nodes but with connection patterns that are more heterogeneous—not all nodes are directly connected by a link, and the number of linkages that each node has varies. We'll argue that disregarding such variation obscures some key characteristics of disease transmission that a more flexible network model can reveal.

The increased granularity of the network model comes at a price. The data required to fully map out a given interaction network, for example, could be prohibitively expensive to get. Furthermore, network models are more difficult to work with than simpler models, and they are frequently solved using simulations. However, we suggest that the valuable insights such models can provide into disease spread may make the expenses worthwhile.

5 Cellular Automata

5.1 Cellular Automata

A cellular automaton is a grid of "coloured" cells that evolves over a number of discrete time steps according to a set of rules dependent on the states of neighbouring cells. The rules are then iteratively implemented for as many time steps as are desired.

5.2 Network Cellular Automata

Nodes in a network of connections are referred to as cells. In contrast to traditional cellular automata, cells are abstracted to a higher level and do not necessarily represent a volume partition of space. In fact, a network may typically be mapped to any number of dimensions. The cells in Figure 4-30 are drawn on a 2D-periodic grid, however it should be emphasised that this grid specification is not part of the network's description; it is simply a method of drawing the network in a logical manner.

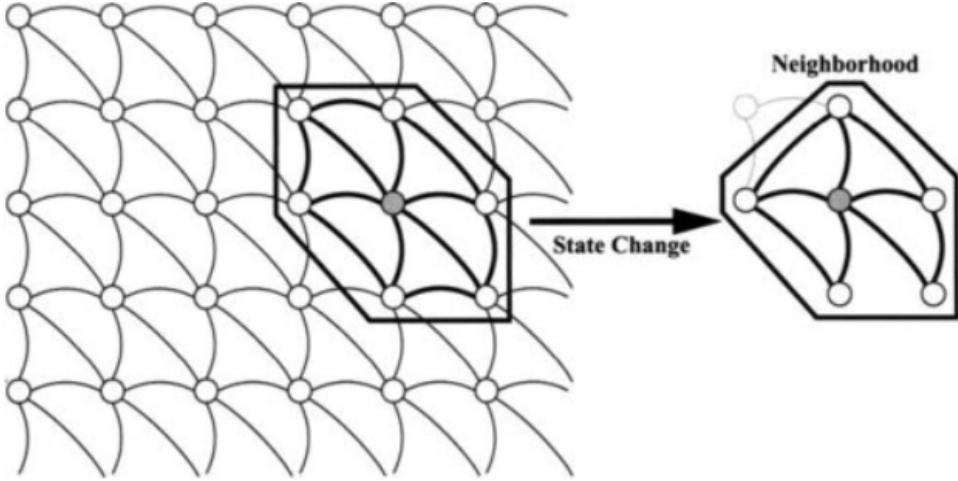


Figure 4: Network cellular automata

6 Cellular Automata SIR Simulation

In this section, we attempt to simulate the spread of an infectious disease using the concepts of cellular automata and SIR modelling with graphs that we have discussed previously.

6.1 Our Model

In our CA model, we assume each cell houses one individual, that can have 3 states, Susceptible, Infected or Removed/Recovered.

Python was used to visualize the CA model depiction of the spatial disease propagation. The disease spreads through the cellular world based on probabilities of infection and recedes based on probability of recovery and number of susceptible individuals. At each time step, there is a probability of a S cell becoming infected according to $P_i(\nu) = 1 - e^{-K\nu}$, where ν is the number of neighbor cells infected and K is a measure of how infectious the disease is.

Similarly, each I-cell can become recovered based on probability P_c or parameter b from the previous ODE model for SIR.

6.1.1 Base parameters

We have set the size of our automation world to be 50x50. Our choice for values of the constants mentioned above are:

Case 1:

$$k = 0.3$$

$$P_c = 0.3$$

Case 2:

$$k = 0.7$$

$$P_c = 0.3$$

As mentioned before k is a measure of how infectious the disease is, and P_c is the probability of recovery for an infected person.

6.1.2 Topology of cellular world

We have implemented a CA model that has a topology of a toroid. This was done to give all cells equal number of neighbour cells. The vertical edges of the cellular automaton have neighbours on the opposite vertical edge, and similarly for the horizontal edges.

We consider a Moore neighbourhood for our model, such that every cell has 8 neighbour cells.

6.1.3 Infection origins

We have considered two different cases for the focal points of the epidemic.

The first case deals with a central focal point, where the disease originates from the center of the cellular automaton.

The second case deals with a 'patchy' configuration of infection origin.

6.2 Simulation Results

We successfully simulated the spread of an epidemic using cellular automata. Our model consists of a population of size 2500 (50x50 grid) and 150 timesteps. 'S' stands for susceptible (blue), 'R' for recovered (black), and 'I' for infected (red).

The result of the two cases are given below. For each case we display photos from the simulation at given timesteps, and we also present the final SIR counts vs. time graphs for the simulations. The key for all the graphs stands that S is Blue, I is yellow and R is green.

We also analyse and compare the two cases:

6.3 Case 1 : $k = 0.3$, $P_c = 0.3$

Following are the graphs from the simulation for Case 1, when the initial configuration is an infected center:

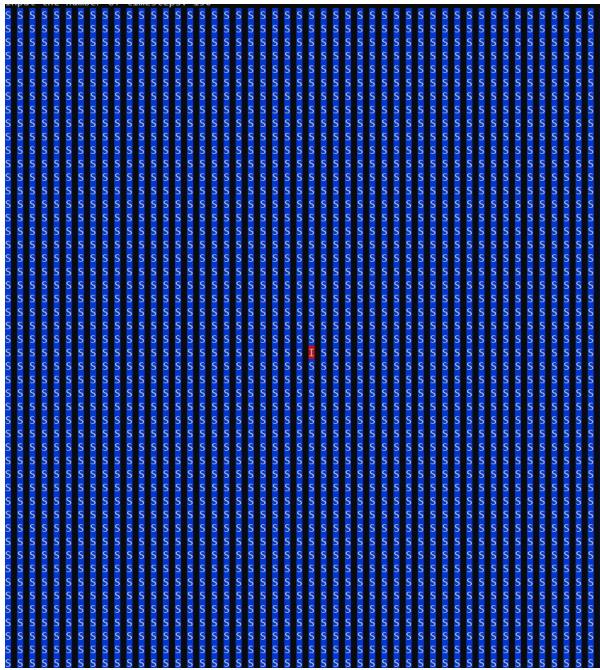


Figure 5: Timestep 0

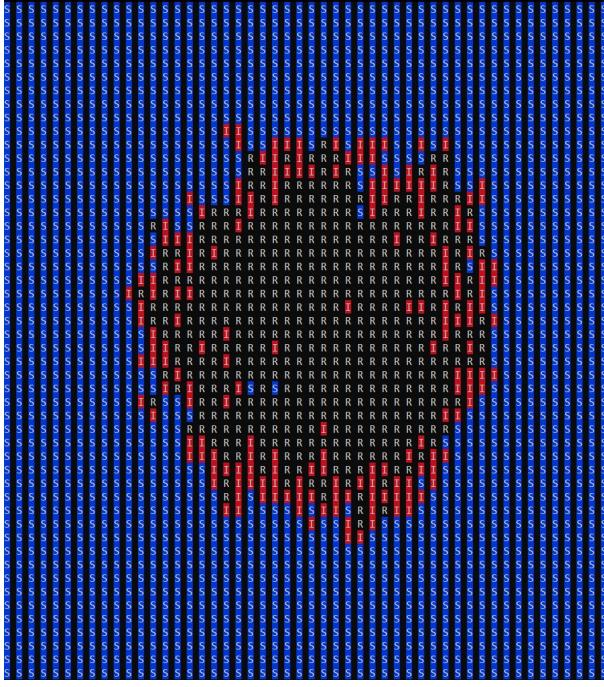


Figure 6: Timestep 20



Figure 7: Timestep 60

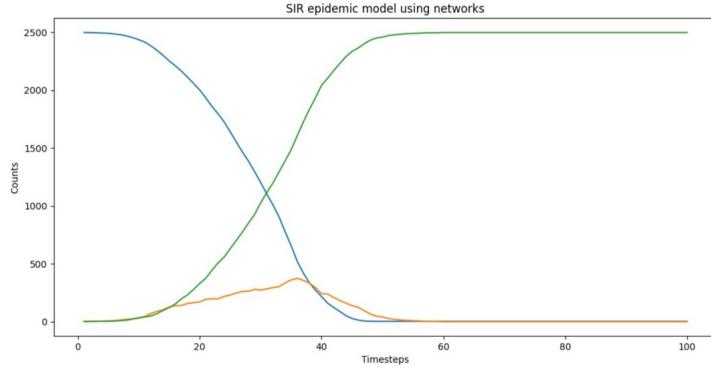


Figure 8: SIR counts vs. Time

Following are the graphs from the simulation for Case 1, when the initial configuration is a patchy infected population:

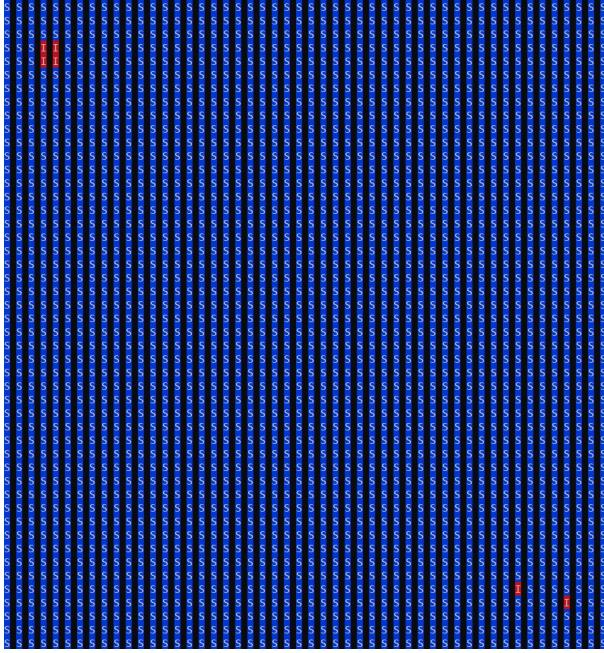


Figure 9: Timestep 0

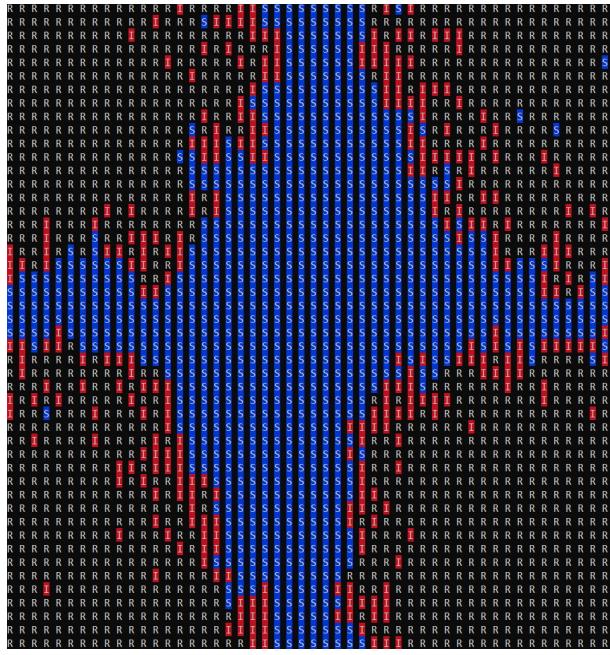


Figure 10: Timestep 25



Figure 11: Timestep 53

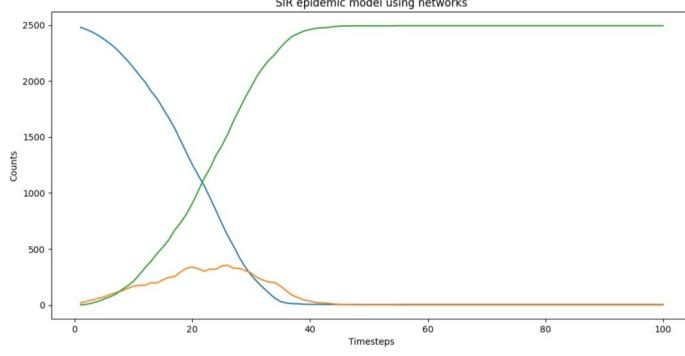


Figure 12: SIR counts vs. Time

6.4 Case 2: $k = 0.7$, $P_c = 0.3$

Following are the graphs from the simulation for Case 2, when the initial configuration is an infected center:

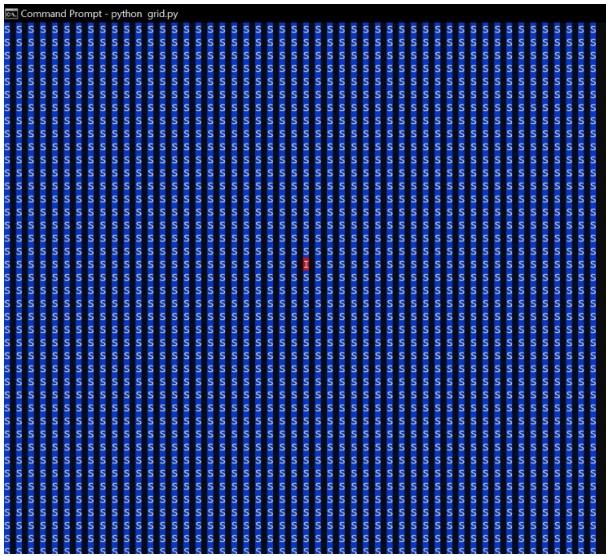


Figure 13: Timestep 0

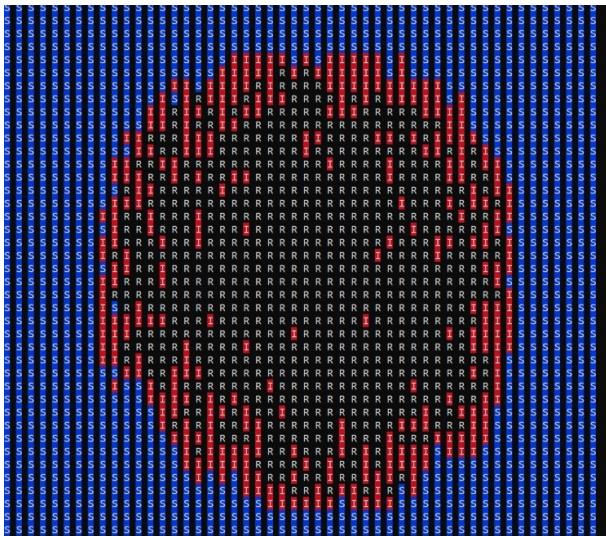


Figure 14: Timestep 16

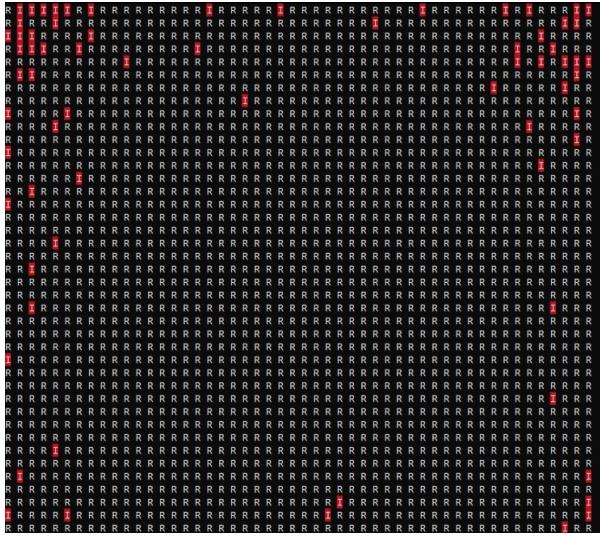


Figure 15: Timestep 31

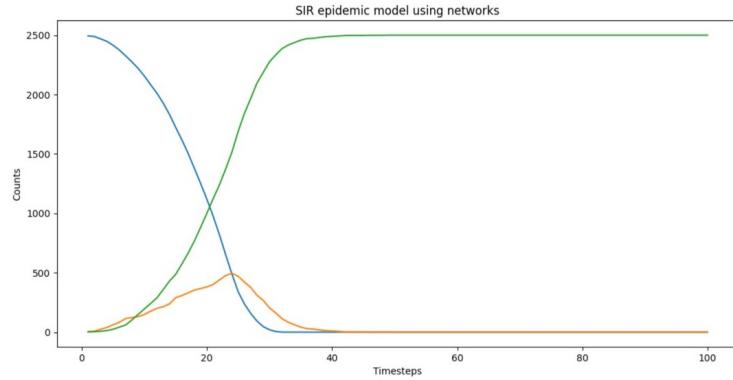


Figure 16: SIR counts vs. Time

Following are the graphs from the simulation for Case 2, when the initial configuration is a patchy infected population:

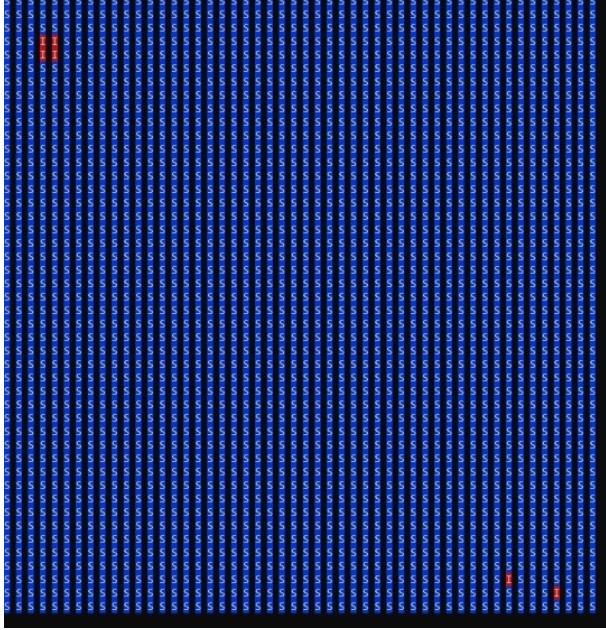


Figure 17: Timestep 0

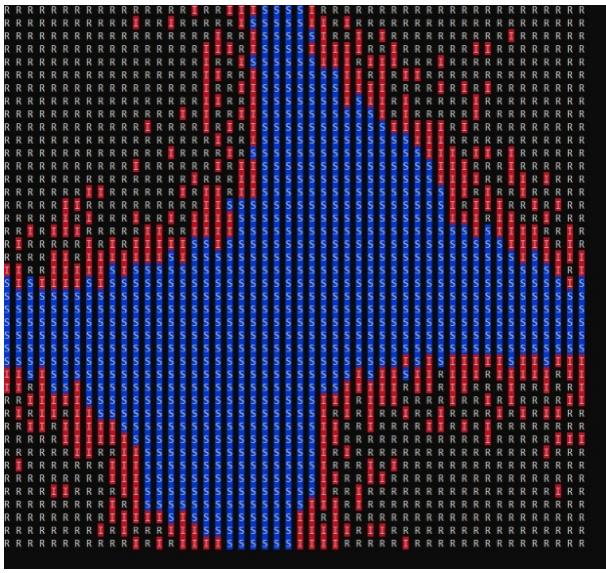


Figure 18: Timestep 16



Figure 19: Timestep 25

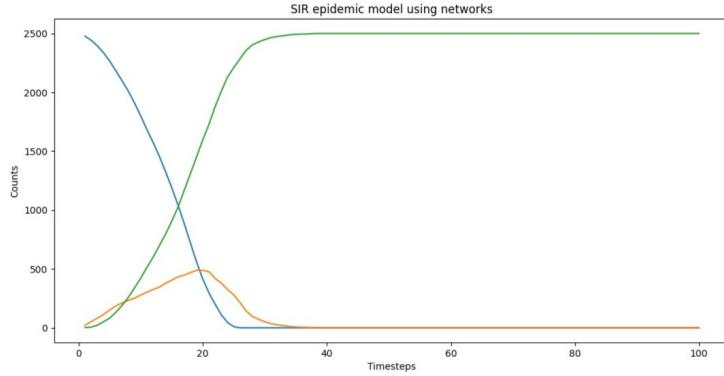


Figure 20: SIR counts vs. Time

6.5 Analysis of Simulation

When the initial configuration is infection in the center of the population , we see the following results: Initially, one cell was infected by the disease. Gradually, the disease started spreading to the cell's 8 adjacent neighbors. The spread is not equal in all directions. Infected people are recovered/removed after some time. Recovered/Removed people do not get infected again. After

a few timesteps, almost half of the population was infected and the majority of infected people were recovered/removed. We ran simulations on different numbers of rows and timesteps. The majority of our simulations show a similar pattern. We begin with an infected cell that spreads the infection to its neighbors. These cells are recovered leaving a dark spot in the middle and eventually, all the infected cells are recovered. A key observation is that some of the cells were not infected ever. This is because all the neighboring cells were already recovered/removed or not infected at all. After saturation of the population, that is when no more of the susceptible individuals can be infected, we see that individuals gradually recover/get removed, and in the end we have a pattern with individuals that were never affected, and all others that have recovered/been removed.

When the initial configuration is patchy, the infection is not in the middle but at one of the corners in patches. The infection from one corner is spread to other corners since the shape of the population is toroidal meaning the cells at the corners are connected to the cells at opposite corners and can spread the infection to these cells. After a few timesteps the simulation has black patches at all 4 corners of the population from the recovery of infected corner cells. Similarly, as before, after saturation of the population, all individuals that were once affected gradually recover and eventually, the pattern reaches a standstill/equilibrium .

The difference between cases 1 and 2 is that 2 has a higher value of K. Thus, the disease is more infectious and hence spreads faster. We therefore see that the stages of progression in Cases 1 and 2 remain same, but they come at earlier timesteps in Case 2, for both the center and patchy case.

The spread of a disease in a population was studied using various models in this report. Building on the foundation of the compartmental model, specifically studying the SIR model we developed a baseline understating of the spread and pattern of spread. Further, we looked into the working of networks and a network-based SIR model and the differences and advantages it has over a basic compartmental model. We used a cellular automata model as a basic version of the network and simulated the spread of disease.

6.6 Simulation code

Below is the novel code for our simulation:

```
1  
2 import math
```

```

3 import sys
4 import random
5 import time
6 import matplotlib.pyplot as plt
7 from colorama import init
8 from termcolor import colored
9
10 init()
11
12
13 def copyarr(a,temp):
14
15     for i in range(len(a)):
16
17         for j in range(len(a[0])):
18
19             temp[i][j] = a[i][j]
20
21
22 def printarr(a):
23
24     for i in range(len(a)):
25
26         for j in range(len(a[0])):
27
28             if a[i][j]==0:
29                 print(colored('S', 'white', 'on_blue') ,end = " ")
30             elif a[i][j]==1:
31                 print( colored('I', 'white', 'on_red') ,end = " ")
32             elif a[i][j]==2:
33                 print( colored('R', 'white', 'on_grey') ,end = " ")
34
35     print()
36
37
38 def countinfns(a,r,c):
39
40     n = len(a)
41     m = len(a[0])
42     cnt = 0
43
44     if a[r-1][c-1]==1:
45         cnt+=1
46
47     if a[r-1][c]==1:

```

```

48     cnt+=1
49
50     if a[r-1][(c+1)%n]==1:
51         cnt+=1
52
53     if a[r][c-1]==1:
54         cnt+=1
55
56     if a[r][(c+1)%n]==1:
57         cnt+=1
58
59     if a[(r+1)%n][c-1]==1:
60         cnt+=1
61
62     if a[(r+1)%n][c]==1:
63         cnt+=1
64
65     if a[(r+1)%n][(c+1)%n]==1:
66         cnt+=1
67
68     return cnt
69
70 def counts(a):
71     sus=0
72     inf = 0
73     rec=0
74
75     for i in range(len(a)):
76         for j in range(len(a[0])):
77
78             if a[i][j]==0:
79                 sus+=1
80             elif a[i][j]==1:
81                 inf+=1
82             elif a[i][j]==2:
83                 rec+=1
84
85     return (sus,inf,rec)
86
87 def timestep(a,olda):
88     k = 0.7
89
90     for r in range(len(olda)):
91
92         for c in range(len(olda[0])):

```

```

93
94
95     if olda[r][c]==2:
96         continue
97
98     elif olda[r][c]==0:
99
100        #person is susceptible
101
102        v = countinfns(olda,r,c)
103
104        p = 1 - math.exp(-k*v)
105
106        a[r][c] = random.choices([0,1],weights = (1-p,p),k=1)
107        [0]
108
109        #print(v,a[r][c],r,c)
110
111    elif olda[r][c]==1:
112
113        #person is infected
114        pc = 0.3
115        a[r][c] = random.choices([2,1],weights = (pc,1-pc),k
116        =1)[0]
117
118        #print(a[r][c])
119
120
121
122 #initial map
123 a = []
124 temp = []
125 n = int(input("Input the number of rows"))
126 for i in range(n):
127     b = []
128     c = []
129     for j in range(n):
130         c.append(0)
131         b.append(0)
132     temp.append(c)
133     a.append(b)
134
135 #infecting the center
136 a[len(a)//2][len(a[0])//2] = 1

```

```

136 a[3][3] = 1
137 a[3][4] = 1
138 a[4][3] = 1
139 a[4][4] = 1
140
141 a[43][42] = 1
142 a[44][46] = 1
143
144 #timesteps
145 t = int(input("Input the number of timesteps "))
146
147
148 printarr(a)
149 #printarr(temp)
150
151 total = t
152 scnts = []
153 icnts = []
154 rcnts = []
155 time = []
156
157 while t>0:
158
159     print("Timestep" + str(total-t))
160
161     copyarr(a,temp)
162     timestep(a, temp)
163     t-=1
164
165     z = counts(a)
166     scnts.append(z[0])
167     icnts.append(z[1])
168     rcnts.append(z[2])
169     time.append(total-t)
170
171     printarr(a)
172
173 plt.title("SIR epidemic model using networks")
174 plt.xlabel("Timesteps")
175 plt.ylabel("Counts")
176 plt.plot(time, scnts, label = "susceptible")
177 plt.plot(time, icnts, label = "infected")
178 plt.plot(time, rcnts, label = "removed/recovered")
179
180 plt.show()

```

7 Conclusion

The spread of a disease in a population was studied using various models in this report. Building on the foundation of the compartmental model, specifically studying the SIR model we developed a baseline understanding of the spread and pattern of spread. Further, we looked into the working of networks and a network-based SIR model and the differences and advantages it has over a basic compartmental model. We used a cellular automata model as a basic version of the network and simulated the spread of disease.

8 References

Following is the list of references used in our report:

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