Modeling of Virus Spread using Cellular Automata

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Abstract

This paper describes and tests a simple program to simulate the spread of viral diseases in a homogenous population. To achieve this model, we develop an excitable media system using a technique named cellular automata.

A sample population is chosen, and three small pockets are considered the epicenters of the virus spread. The proposed system simulation was created using the Python programming language. The ruleset used in the simulation is the same as used by the Hodgepodge Machine. Different scenarios were simulated and compared with each other by plotting charts for each. The results showed that virus spread could be significantly reduced by introducing the usage of masks and quarantining the infected people. In addition, some essential factors like the probability of a person wearing a mask or quarantining a person were introduced to study their effect on virus spread in more detail.

I. Introduction

Viruses are submicroscopic contaminating agents consisting of genetic codes, either DNA or RNA, coated by a protein layer. These agents can replicate themselves in the presence of living cells. These viruses are one of the leading causes of infectious diseases, which kill many people worldwide.

Humanity has faced many epidemics and pandemics in history. Black Death in Europe during the mid-1300s wiped out almost one-third of Europe's population. Around 1920, Spanish flu became a pandemic and caused the death of 20-50 million people. Between 1957-1958, the world saw the loss of 1 million lives due to the Asian flu [1]. The recent spread of COVID-19, classified as a pandemic, has been the leading cause of 5 million deaths and counting. Till now, 260 million people have been infected with this virus [2].

The spread of virus-caused illnesses in society has been hastened by an ever-increasing population and the capacity to travel to distant places in less time. Globalizing diversities and increasing populations are causing individual interactions to intensify. Due to this, people are becoming increasingly concerned about public health hazards, necessitating proactive measures to avert epidemics and pandemics. This apprehension has made epidemiologists' role of monitoring, preventing, observing, and controlling different diseases very significant and acknowledged. Many techniques are available and still used by scientists to study any disease by making statistical models, but they prove to be scarce and incomplete when focusing on vast spatial domains. Thus, it is essential to develop new techniques that leverage today's computational power to solve the problems faced while studying diseases.

To counter the spread of viral diseases, simulating the spread plays a crucial role in containing the disease. Simulations can be used to study the spread of the virus and help the local authorities plan accordingly. For example, imposing social restrictions, promoting clean and hygienic behavior, etc. Visuals provided by the simulations can help epidemiologists forecast, answer questions, study the spread pattern, and generate quality data. This can ultimately save many lives.

II. Background

A. Cellular Automata

Cellular Automata (CA) is a discrete computational model which is decentralized and can perform complex computation with the help of local information only [3]. There is a set of multiple automatons, which is arranged in a 2D grid fashion. Each of the automatons has a finite number of state values, which are updated synchronously or asynchronously at every timestamp using a state transition function. Due to its ability to define complex and non-linear dynamics in a more straightforward and concise way, this technique finds its way in various fields of application like simulating reaction processes, traffic jams, and so forth [4].

B. Hodgepodge Machine

Hodgepodge Machine [5] is a type of cellular automata primarily designed for heterogeneous catalytic reactions. Each automaton refers to the catalyst particles and can have more than two states. The degree of infection is correlated with the saturation of the catalyst's surface. Activities are synchronized through local interaction. This machine can simulate local infections as the healthy cell become infected by the neighbors, which then goes through different stages of infection until they become ill. After this, they automatically recover and fall back to their original state.

C. Related Work

Various researchers have worked on different techniques and ideas for the past couple of decades to simulate the behavior of virus spread among the population. One of the ideas [6] presented by Pfeifer *et al.* suggests using the S-I-R epidemic model, where S represents the number of susceptible, I represents the number of infected, and R represents the number of recovered people. This model can be formulated as

$$\frac{dS}{dt} = -\frac{\beta IS}{N}, \qquad S(0) = S0 \geq 0, \tag{1}$$

$$\frac{dI}{dt} = \frac{\beta IS}{N} - \gamma I, \qquad I(0) = I0 \geq 0, \tag{2}$$

$$\frac{dR}{dt} = \gamma I, \qquad R(0) = R0 \geq 0 \tag{3}$$

Here, β represents the contact rate, and $1/\gamma$ represents the average infectious period. This model was also supported by integrating it with cellular automata to include the factor of geological and demographic realities. Other factors included as an extension of the S-I-R model are natural birth, natural death, immigration, emigration, and passive immunity [7] [8]. The lifecycle of the disease was classified into five different phases: latent period, infectious period, recovered/removed, incubation period, and symptomatic period. The operation of the state transition function was to handle the mentioned factors and calculate deaths by diseases, immigrations, vectored infections, contact infections, spontaneous infections, apply the movement operation through Cellular Automata and repeat the process for the next cycle.

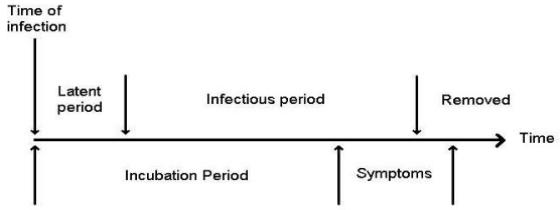


Figure 1: Life cycle of an infectious disease (Ching Fu S et al., 2003)

An article by Max Brenner [9] makes use of the Kermack-McKendrick model, which is the S-I-R model, for calculating the infected population over time. The simulation developed in this article is specifically for COVID19 assumes that there is no quarantining procedure for the infected people. Although, it takes some critical factors like social distancing and mask-wearing into consideration. The simulation also takes care of essential parameters concerning COVID19 as directed by trustworthy sources like CDC. The results signified the importance of social distancing and masks as the attack rate was higher when people were not following the protocols.

Senthil Athithan *et al.* [10] introduced their work based on dynamic cellular automata for the epidemic spread model. The idea considered three scenarios

- No movement allowed, and a non-patchy population
- No movement allowed but a patchy population
- Movement allowed, and a patchy population

Here, movement refers to the traveling of individuals across the simulation space. Patchy population refers to the non-homogenous spread of population across the simulation space. The first two scenarios use Moore's neighborhood for the simulation, while the third scenario uses extended neighborhood to consider the movement factor. Four other criteria further controlled the third scenario, i.e., which, when, and how many cells will move and the distance they will cover after one time.

Another similar approach to model the disease spread has been to develop a simulator named EPI-SIM [11]. This simulator makes the use of cellular automata, where each cell has its probability of risk of exposure and probability of contracting the virus. It is a four-state simulator with states named susceptible, latent, infected, and recovered/removed. A cell moves from susceptible to a latent state if it is surrounded by an infected cell in its neighborhood (Moore neighborhood). Moving further, latent cells become infected if they stay in that state for a particular period. The infected cells will either shift to die or recover in the next timestamp. At last, the recovered cells may become utterly immune to the virus or fall back to a susceptible state (finite immunity). The work done by Sangeeta Venkatachalam *et al.* [11] also experimented on other factors like contact rate, infectivity rate, the vaccination rate, and population difference.

III. METHODOLOGY

In this work, the proposed method for simulating the spread of the virus among the population uses the hodgepodge machine algorithm. Each cell in the 2D grid is considered an individual, each holding a state value and other information that can be set up during the simulation. On top of that, the method is extended to consider other essential factors like immunity, quarantine, and masks. This study has been done by programming the simulator in Python 3.8 and using libraries like Numpy, Pygame, Matplotlib, and Itertools for operations like calculation of the following states, plotting the states, and simulating the spread.

A. States of an Individual

An individual is defined as a class with multiple variables. The class also consists of a function to set corresponding values to the variables according to the situation in the simulation.

Variables defining the individual's condition are:

- *status:* This string value holds the condition label of the individual. It is divided into four types- healthy, infected, ill, recovered, and quarantine.
- *state_value:* This integer value denotes the level of seriousness of the condition of an individual. The value 0 represents healthy. Values greater than or equal to 1 but less than 5 are considered infected. Individuals with value 5 are ill. Recovered and quarantined individuals are allotted the value of 6 and 7, respectively.
- *immunity:* This integer value represents the immunity level of the individual after he/she has recovered from the disease. The value 0 means that there is no immunity after recovery. The value i, where i>0, defines the duration of the immunity, which is equal to the value itself.
- *mask:* This string value depicts whether the person is wearing a mask or not. It can hold only two values- "Yes" or "No," representing that a person wears a mask or does not wear a mask.

B. Neighborhood chosen

The two types of neighborhoods that can be implemented for virus spread simulation purposes are 4-cell Von Neumann and the 8-cell Moore neighborhood. Von Neumann neighborhood considers four cells around the central cell, i.e., left, right, up, and down. In contrast, Moore neighborhood considers eight cells around the central cell, i.e., left, right, up, down, top-left, top-right, bottom-left, and bottom-right. According to assumptions made while modeling, virus spread is all about the contact of cells with each other. In our proposed method, we will be simulating the scenarios using Moore's neighborhood as it is realistic.

We will then compare the scenarios and evaluate the results for each.

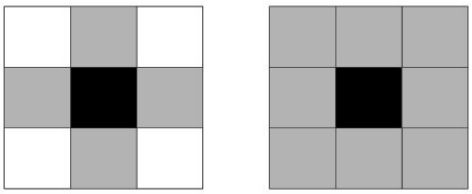


Figure 2: Von Neumann neighborhood (left) and Moore neighborhood (right) (Szymon Skoneczny, 2017)

C. Algorithm used

Our proposed simulation model uses the base algorithm of a hodgepodge machine. Designed initially to describe the Belousov-Zhabotinski reaction, this algorithm can also be used to imitate the prototype for virus spread across the population, updated synchronously. The algorithm can also be extended to add on various features, discussed later in the report. Although, the basic set of rules remains the same as follows:

Algorithm 1: Algorithm for virus spread in the population without any immunity or mask factor

for *cell* in 2d Grid:
  if (*cell* in 3 defined patches of population) **then**
    cell ← 0 or 1 (85% probability of 0's occurrence)
  else
    cell ← 0
  end if
end for
while True **do**
  for *cell* in 2D Grid:
    select 8 neighborhood cells
    count the infected and ill cells
    if (*cell.status* == "Healthy") **then**
      cell.status ← "Infected"
      cell.value ← min(ill, $floor\left(\frac{A}{k1}+\frac{B}{k2}\right)$),
      where:
      A – infected neighbors count
      B – ill neighbors count
      k1,k2 – some constants
    else if (*cell.state* == "Infected") **then**
      cell.state ← "Ill"
      cell.value← min(ill, $floor\left(\frac{S}{A}\right)+g$),
      where:
      S – sum of states of neighbors
      A – infected neighbors count
      g – spreading of infection
    else if (*cell.state* == "Ill") **then**
      cell.state ← "Recovered"
      cell.value ← *6*
    else if (*cell.state* == "Recovered") **then**
      cell.state ← *"Infected"*
      cell.value ← 1
    end if
  end for
end while

The algorithm described above helps to simulate the scenario in which a person does not gain immunity after his/her recovery and is again susceptible to the viral disease. This seems unrealistic while modeling the spread since there must be some immunity for a finite or infinite period. Therefore, this algorithm is improved by adding crucial aspects like insusceptibility, masks, and isolation to bring more realism to the simulation. The scenarios that are simulated are:

- A person with finite immunity
- A person with finite immunity and quarantining
- A person with finite immunity, wearing masks and quarantining
- A person with infinite immunity

D. Initializing the Simulator

The basic structure of the simulating environment remains the same for every scenario. The spatial region is of the size - 100×100 cells, making the population under simulation to be 10,000 cells or people in our case. The region is wrapped around, which means that cells on the extreme opposite ends can affect each other. Every cell or individual in this 2D grid can hold multiple state values, representing different phases, represented by different colors throughout the simulation. The blue color represents a healthy person. The color yellow, transitioning from a lighter shade towards a dark shade, represents the increasing illness level in an individual. Red represents an ill person, while green represents a recovered person. The individuals in grey represent people under quarantine.

When the simulation begins, three small patches are chosen, representing the starting points of the virus spread. The individuals present in these patches are arbitrarily allotted the state value of 0 and 1 with the probability that the individual has an 85% chance of being healthy or holding the value 0. Every individual in these patches has a 15% chance of being minorly infected with a state value of 1. The rest of the individuals in the grid are allotted the value 0 (healthy).

A count function is also programmed to count the number of healthy, recovered, and infected + ill at each step during the simulation and store the values in lists.

The proposed simulator focuses on modeling the spread of the virus according to the different circumstances that further depend on multiple factors. All the states are updated synchronously at every time step during the spread modeling of the disease.

E. Simulation - a person with no immunity

This simulation directly follows the approach explained in *algorithm 1*. The cells can only have seven states: 0 for healthy, 1 to 4 for infected, 5 for ill, and 6 for recovered. An infinite while loop runs for calculating the states at every step, which can be ended using the Esc key on the keyboard. After simulation, the S-I-R graph for healthy, infected + ill, and recovered individuals are plotted for further evaluation.

F. Simulation - a person with finite immunity

Modeling this scenario requires a slight change in the basic algorithm of the hodgepodge machine that is being followed in this report. During the ill stage of the individual, the immunity value for the individual is updated

to 30, 60, 90, or infinite days. Each immunity value is set to the individual with the probability of 0.45, 0.30, 0.15, and 0.10, respectively. During the recovery stage, the value is set to the 1st stage of infection only when the immunity period of a particular cell ends, which is calculated by subtracting the immunity value by one until it becomes zero. After simulating and visualizing the spread, the S-I-R graph is plotted for each cell state to be studied later and compared with other simulation scenarios.

G. Simulation – a person with finite immunity and quarantining when infected/ill

In addition to the algorithm described in the previous simulation, an additional state number 7 is added with the status set as "Quarantine." There are four infectious stages through which an individual can suffer. The proposed method considers the option of quarantine only when the individual is in the 4th stage of infection, i.e., he/she might have developed symptoms of infection that lead to his/her identification. At this stage, a quarantining probability is set for that individual depicting whether he/she would be quarantined or not. For simulation purposes, we have set this probability to 0.7, meaning that there are 70% chances that an individual at the 4th stage of infection will be quarantined. Also, the quarantine period for the simulation is set to 21 days or three weeks.

Under quarantine, the individual can not be ill. After the quarantine period gets over, the individual's status changes to "Recovered." Depending on the probability set, immunity gets built up for 30, 60, 90, or infinite days. Our simulation considers the probability for the immunities to be 0.45, 0.30, 0.15, and 0.10, respectively. When the immune period ends or becomes susceptible, the individual gets infected with the 1st stage. This simulation runs forever until the modeling saturates or the user ends it. Count charts are then plotted for further investigation of the model.

H. Simulation - a person with a finite immunity, wears masks and quarantine when infected/ill

A new factor of masks is added to this simulation. Each individual can have the value of the mask set to "No" or "Yes," depicting non-mask wearers and mask wearers. An assumption made for this simulation is that mask wearers are 100% safe from the infection spread.

During the initialization of the population, the simulation assumes that an individual has a 40% chance of wearing a mask if he was not wearing it earlier. This value is set as we consider that there is not much awareness amongst the population initially. When the person gets recovered, the likelihood of wearing a mask by an individual is set to 80%, representing more awareness related to the virus spread. The rest of the algorithm remains the same as the previous simulations.

I. Simulation - a person with infinite immunity

This scenario uses the same algorithm as used by the simulation for people with finite immunity. The only minor change is that we would be setting up the immunity value to be infinite. In this way, any individual who gets recovered from the illness can not get infected again by the viral disease spread. The S-I-R graph is plotted for this simulation to be compared with other scenarios for further studies and observations.

J. Research Questions

After running different simulations, we performed some evaluation on the results to answer these two research questions:

- What is the pattern of the spread in each simulation?
- How do different scenarios affect the spread of the virus?
- Which scenario is the best for containment of the disease?
- What are the suitable parameters to minimize the spread in the best scenario simulation?

The first research question is answered by visualizing the simulation until the spread stops or the user ends it. For different scenarios, there can be different visualizations or pattern formations.

The second research question is responded to by studying the charts plotted for each simulated scenario. The charts describe four variables: Healthy, Infected+Ill, Recovered, and Quarantined. These charts are compared with each other to study the spread in each.

The third research question is answered by comparing the results of each simulation under factors like maximum infections and spread time. This evaluation would help us choose the best scenario that can limit the spread more efficiently.

At last, to answer the fourth point, the parameters like quarantining, mask-wearing, immunity probabilities, and quarantining period are altered to determine the most suitable parameter for the best scenario simulation.

IV. RESULTS AND DISCUSSION

The plots used to study the spread of the virus are inspired by the S-I-R model. These models are one of the simplest compartmental models often used for the mathematical modeling of diseases. The goal of these models is to predict and answer the questions such as how a disease spreads, how many infections, or what is the duration of the spread. These models are helpful for epidemiologists to figure out essential measures that need to be taken to prevent disease spread.

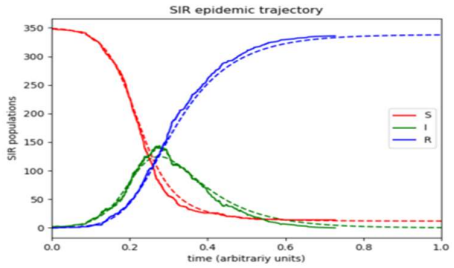
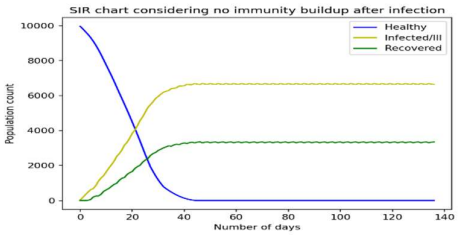


Figure 3: A sample SIR epidemic trajectory plot

They are based on differential equations, which provide three decisive parameters of the simulation study, i.e., "Susceptible," "Infected," and "Recovered/Removed." We have also added a fourth parameter for our study, named "Quarantine."

A. *Simulation outcomes for the person with no immunity*



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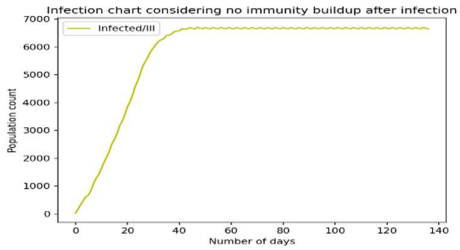


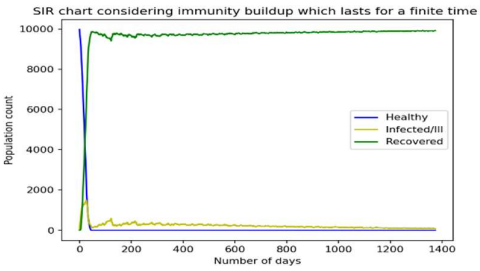
(b)

Figure 4: (a) SIR chart when there is no immunity buildup after infection, (b) Infections for the scenario.

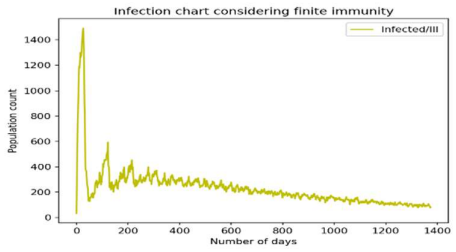
The results depict that the infection spreads quickly, and the number of infected and ill people reaches its maximum value of around 7000 people in 35 to 40 days. After reaching the peak, the increase in the count of infected individuals saturate. This is because there is no immunity buildup after the recovery stage. Therefore, this goes on loop forever, and there will not be any observable downward trend in the infection count.

In addition, it can be observed that the recovery growth also becomes stagnant after 35 to 40 days, with a maximum value of around 3000 recoveries. Visualizing the simulation shows a concentric spread of the disease for infinite time.

B. *Simulation outcomes for the person with finite immunity*



(a)

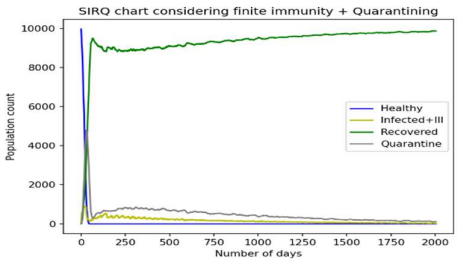


(b)

Figure 5: (a) SIR chart when there is finite immunity buildup after infection, (b) Infections for the scenario.

This simulation shows the importance of immunity that builds up after the person is infected. The first peak reaches more quickly (in around 25 days) than the previous simulation with no immunity consideration, but the peak value is far less than the non-immunity simulation. Also, some small peaks afterward represent the subsequent waves of infection, but their peak values are far below the first wave's value. On further simulating, until the infection graph saturates, we observed that it would take approximately 3000 days or eight years to dampen the infection count thoroughly. Also, it was noticed that the saturation was linear with a negative slope. The maximum peak infection count achieved was around 1500 people, far less than the previous simulation. The peak values of smaller waves follow this first wave by the peak values of 600, 450, 380, and so on, till the graph becomes smoother. The simulation showed a concentric spread of the virus, with a pause between consecutive waves for some time, followed by randomness in the spread.

C. *Simulation outcomes for the person with finite immunity and quarantining when infected/ill*



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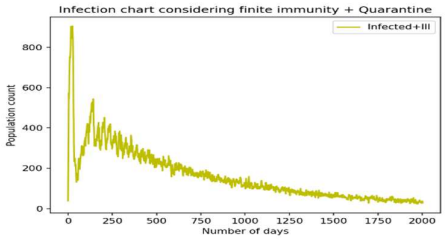


(b)

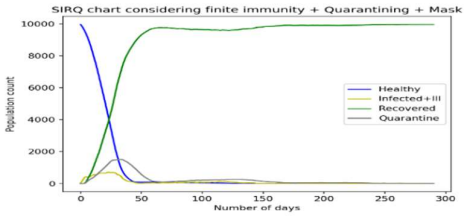
Figure 6: (a) SIRQ chart when there is finite immunity buildup, and the person can be quarantined, (b) Infections for the scenario.

The simulation results for the people with finite immunity and quarantining when infected/ill depicts a significant drop in the peak infections compared to the previous models. The spread timeline remains precisely the same as that of the model with finite immunity without quarantine, but the peak values differ. For this simulation, the peak value of the first wave was around 900 infectious and ill people compared to 1500 people in the previous model.

If we further compare this model with the previous model, we observe that the subsequent waves' peak values for this simulation were higher than the first peak value of infection. Also, the recovery plot for this model follows the growth pattern similar to a logarithmic function. The infection chart follows an exponential decay as compared to the linear decay in the previous simulation. The visualization started

with one concentric wave spreading across the entire population, followed by random infections.

D. Simulation outcomes for the person with a finite immunity, wearing masks and quarantining when infected/ill



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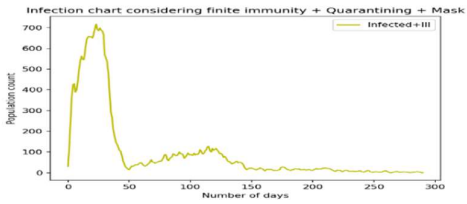
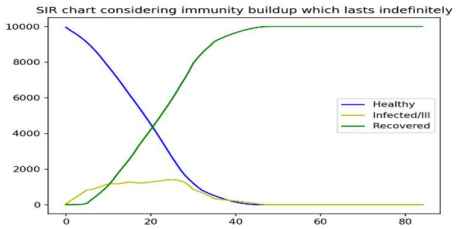


(b)

Figure 7: (a) SIRQ chart when there is finite immunity buildup after infection, the person wears a mask and can be quarantined (b) Infections for the scenario.

This simulation shows very promising results. There are only two visible waves of the infection, the first one being the highest wave. The maximum peak value is around 730. This means that around 730 people got infected in the first wave of the disease, which significantly improved compared to previous simulations. The first wave starts and ends within two months. The arrival of the second wave is significantly slower and represents the flattening of the curve with the peak value of 130 individuals. After around 150 days or five months, the spread slows down with an average of 10 cases a day. When the timeline hits around 300 days or 9.5 months, the spread stops with zero new infections in the population.

E. Simulation outcomes for the person with an infinite immunity



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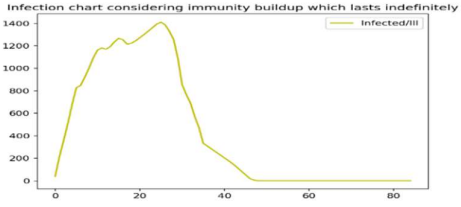

(b)

Figure 8: (a) SIR chart when there is infinite immunity buildup after infection, (b) Infections for the scenario.

When we simulated the situation where a person gets an infinite immunity buildup after getting the infection, we observed that although the infection timeline decreases significantly, the infection count is massive. Only one wave is generated with a maximum peak value of around 1400 individuals. After 45 days or 1.5 months, the infection count drops to zero. The simulation exhibited concentric waves for only one time before everybody got recovered.

F. Comparison between different scenarios

To figure out which scenario is best for containing the spread of the disease, we ran the simulation five times for each of the scenarios and calculated an average of the values describing the maximum count of infections, duration of the spread, and multiple disease waves.
The results that we observed from the simulation trials are recorded and tabulated as follows:

Table 1: COMPARISON TABLE FOR DIFFERENT SCENARIOS

Scenarios	***Maximum infections***	***Duration of the disease***	***Any subsequent waves***
No immunity	6700	∞	0
Finite immunity	1530	8-9 years	5+
Finite immunity + Quarantine	910	9-10 years	5+
Finite Immunity + Mask + Quarantine	730	8-9 months	1
Infinite Immunity	1500	1.5 months	1

Out of these, two scenarios are very likely to occur. One possible scenario is a population that develops post-infection finite immunity, followed by quarantining. It is observed that if an individual develops finite immunity after infection and there are 70% chances that he/she would be quarantined during the 4th stage of infection, the maximum number of infected people that a population would have is around 910 people. However, the primary concern with this scenario is the long-lasting effects in the form of multiple waves of infection. The simulation shows that it may last for more than nine years with subsequent waves after random intervals.

This leads us to the best possible scenario, i.e., a person developing finite immunity quarantines on infection and wears masks for protection. The simulation provides us with excellent results of 730 maximum infections with a total disease duration of 8 to 9 months.

These figures clearly project the importance of wearing masks, significantly reducing the infection spread timing. Also, it is essential to observe that only a single subsequent infectious wave is generated, which is significantly less in intensity than the first wave.

To study this scenario in more detail, we observe the simulation in detail by varying the parameters like quarantining, mask-wearing, and quarantining period and

observing the effects on maximum infection count. The study is tabulated in Table 2 as shown:

Table 2: COMPARISON TABLE BY VARYING THE PARAMETERS

Quarantine Probability	Mask Probability	Quarantine period	Max infection
0.2	0.2	7	800
		14	776
		21	770
	0.4	7	802
		14	782
		21	780
	0.7	7	660
		14	653
		21	641
0.4	0.2	7	784
		14	769
		21	747
	0.4	7	767
		14	751
		21	746
	0.7	7	641
		14	623
		21	625
0.7	0.2	7	742
		14	736
		21	738
	0.4	7	731
		14	725
		21	722
	0.7	7	594
		14	595
		21	585

Comparing the results by varying parameters suggests that the best scenario to contain the disease is to increase the quarantine probability, mask probability, and the quarantine period. This would ensure that the maximum infections get reduced and the virus spread is controlled effectively. The best results from our simulation on the test cases give us the maximum infections of 585 when the probability of a 4^{th} stage infected person being isolated is 0.7. Also, the mask probability of 0.7 suggests that a healthy person is very much aware of the virus and has a 70% chance of wearing a mask. Increasing the quarantine period to 21 days significantly helped in reducing the infections.

V. LIMITATIONS AND FUTURE WORK

Although this study simulated the virus spread in great detail, it has some limitations. As we know, there are various types of viruses, each having different characteristics and behavior in different environments. However, this project takes a generalized approach to modeling the virus spread in the population. In reality, there are various factors like population density, migration of people from one place to another, etc. However, the model developed in this project considers the population spread to be homogenous and non-moving. Also, we have not considered the death factor, and it is assumed that every person would eventually recover from the illness.

Some extensions to this study are proposed to improve this model further to make the simulation more real and apt according to the conditions. Future work can be done to set each individual's probability of getting infected based on his/her previous infection history. Factors like population density, movement of people, and more could be added. Under this model, only infected/ill are being quarantined. A feature can be added for a healthy person to get quarantined if he/she comes in contact with any infected. Work on including the parameters according to different viruses can be done to simulate the spread of particular diseases

VI. CONCLUSION

This study aimed to propose a method to simulate the spread of the virus in a homogenous population. Some experiments were conducted by simulating various scenarios of virus spread. Data were collected for various scenarios, and it was found that the best realistic scenario to contain the disease spread is when there is a finite immunity in the population after the infection. This is reinforced by people wearing masks and isolating themselves on getting infected or ill. On further drilling down into this model by varying various parameters, we found that the best virus spread suppression occurs when the quarantining probability, mask-wearing probability, and quarantining period are high. These results can help the epidemiologists and government authorities study the virus spread pattern and place restrictions like quarantining and mask-wearing to minimize damage and loss of life

VII. REFERENCES

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