

## Mini Project 2: Pandemic Flu Spread

---

Amirtha Ganesh Pugazhendhi (GTID : 903515950)  
Sukanya R Iyer (GTID : 903622016)

April 28, 2021

## CONTENTS

<b>1 ABSTRACT</b>	<b>3</b>
<b>2 BACKGROUND &amp; DESCRIPTION OF THE PROBLEM</b>	<b>3</b>
2.1 Phase 1 . . . . .	3
2.2 Phase 2 . . . . .	4
<b>3 METHODOLOGY</b>	<b>7</b>
3.1 Assumptions . . . . .	7
3.2 Simulation using Python . . . . .	7
<b>4 MAIN FINDINGS</b>	<b>10</b>
4.1 Scenario 1: Impact of vaccination . . . . .	10
4.2 Scenario 2: Impact of social distancing . . . . .	10
4.3 Scenario 3: Impact of quarantine . . . . .	11
4.4 Scenario 4: Impact of supply chain issues in the availability of vaccine . . . . .	11
4.5 Scenario 5: Impact of increase in number of neighbours . . . . .	12
4.6 Scenario 6: Impact of mutant virus . . . . .	13
<b>5 APPLICATIONS &amp; LIMITATIONS</b>	<b>14</b>
<b>6 CONCLUSION</b>	<b>15</b>
<b>7 REFERENCES</b>	<b>16</b>

# 1 ABSTRACT

This mini project in phase 1 studied the pandemic flu spread in a classroom of 21 elementary school kids. We tried to implement an SIR(Susceptible, Infected and Recovered) model to compute the infected number on students on daily basis. In our model we had assumed on Day 1, we have 20 of the kids as healthy and susceptible to flu. Tommy (the 21<sup>st</sup> kid) walks in with the flu and starts interacting with his potential victims. We then simulated this condition both in Python and Arena and our finding was that on average the infection lasts in the class for 15 days.

In phase 2, we are considering a larger population. Here some infectious people enter the population of susceptibles and some of the susceptibles become infected. We have further considered an incubation period until a person becomes infectious. We considered factors such as recovery, death, social distancing, effect of vaccination and calculated the number of people who eventually get infected and observed till when the epidemic lasts.

## 2 BACKGROUND & DESCRIPTION OF THE PROBLEM

### 2.1 Phase 1

For phase 1, the motivation for our simulation model was the SIR model. An SIR model is an epidemiological model that computes the theoretical number of people infected with a contagious illness in a closed population over time. The name of this class of models derives from the fact that they involve coupled equations relating the number of susceptible people  $S(t)$ , number of people infected  $I(t)$ , and number of people who have recovered  $R(t)$ . The model is denoted as SIR model abbreviating the same. [1] As implied by the variable function of  $t$ , the model is dynamic in that the numbers in each compartment may fluctuate over time. The SIR model is one of the simplest compartmental models, and many models are derivatives of this basic form. The model consists of three compartments:-

- $S$  is the number of susceptible candidates, who can be potentially infected.
- $I$  is the number of candidates infected, and with a capability to transmit it to the susceptible candidates.
- $R$  is the number of recovered individuals.

Recovered individuals' susceptibility to disease is specific to a given model, but they can't be reinfected in most cases. They may have a natural immunity, or they may have recovered from the disease and are immune from getting it again, or they may have the disease but are incapable of transmitting it (e.g. because they may have been placed in isolation). The mathematical model doesn't distinguish among those possibilities. The model we will consider assumes a time scale short enough that births and deaths can be neglected.

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. Schematic representation, differential equations, and plot for the basic SIR (susceptible, infectious, and recovered) model are given in figures 2.1 and 2.2. Model parameters are  $b$ , the transmission rate ( $b = 0.0005$ ), and  $c$ , the recovery rate ( $c = 0.05$ ). There is initially one infection in a population of 1,000 individuals.

$$\frac{\partial S}{\partial t} = -\beta SI \quad (2.1)$$

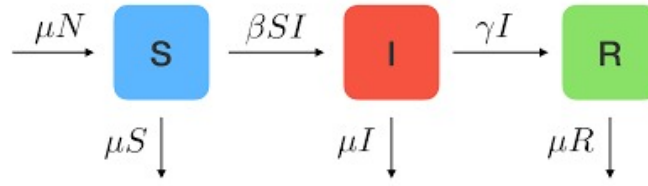


Figure 2.1: SIR model

$$\frac{\partial I}{\partial t} = \beta SI - \gamma I \quad (2.2)$$

$$\frac{\partial R}{\partial t} = \gamma I \quad (2.3)$$

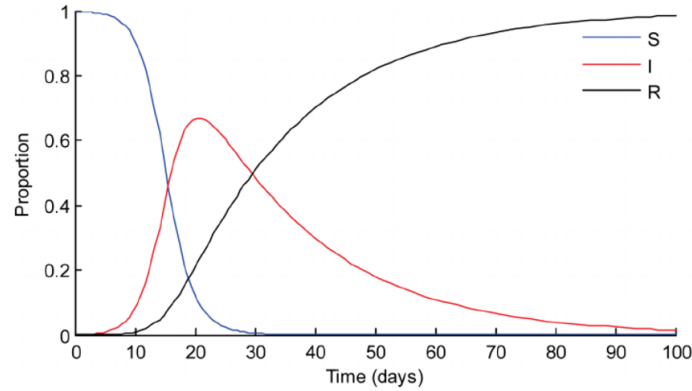


Figure 2.2: SIR epidemic trajectory

The problem given to us in phase 1 considered an elementary school setting with 21 students and one of the students, Tommy was infected on Day 1. All other 20 students were susceptible to the infection on day 1. Our model computed the number of students infected by the spread of the virus each day and finally arrived on the conclusion of the number of days the infection will last in the school.

## 2.2 Phase 2

Various extensions of the SIR model exist. For phase 2, we have used susceptible - exposed - infectious - quarantined - removed (SEIQR) compartmental model to model the pandemic dynamics with the removed compartment consisting of both the recovered patients and the deceased people. This model basically extends from the SIR model by adding incubation period and quarantine. Along with these, we also include mitigation methods (social distancing, masking) and long term resistance via vaccinations. Fig 2.3 gives an explanation of the different states considered in the model.[\[3\]](#)

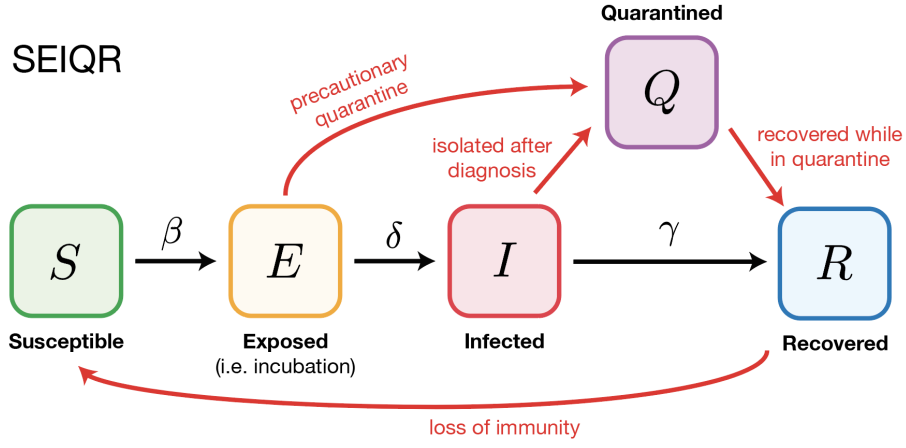


Figure 2.3: SEIQR epidemic trajectory

Simple dynamical equations are used to describe the evolution of epidemics. The basic reproduction number and the concept of herd-immunity are easily understood within the framework of, for example, the SIR model where the population is compartmentalised in susceptible, infected and removed classes. The dynamical equations [3] used in this model is shown below:

$$\frac{\partial S}{\partial t} = -\beta \frac{SI}{N} \quad (2.4)$$

$$\frac{\partial E}{\partial t} = \beta \frac{SI}{N} - \alpha E - \delta_1 E \quad (2.5)$$

$$\frac{\partial I}{\partial t} = \alpha E - \gamma I - \delta_2 I \quad (2.6)$$

$$\frac{\partial Q}{\partial t} = +\delta_2 I - \mu Q \quad (2.7)$$

$$\frac{\partial R}{\partial t} = \gamma I + \mu Q \quad (2.8)$$

In this model, the time variable, infection rate, removal rates from the infectious and the quarantine compartments are represented by  $t$ ,  $\beta$ ,  $\gamma$  and  $\mu$  respectively and  $\frac{1}{\alpha}$  represents the average latent period. The removal rates from the exposed and infectious compartments due to quarantine are represented by  $\delta_1$  and  $\delta_2$  respectively. It was also assumed that  $S + E + I + Q + R = N$ , where the total population  $N$  is constant. [4] A schema of the model in Fig 2.4 and the trajectory is shown in Fig 2.5.

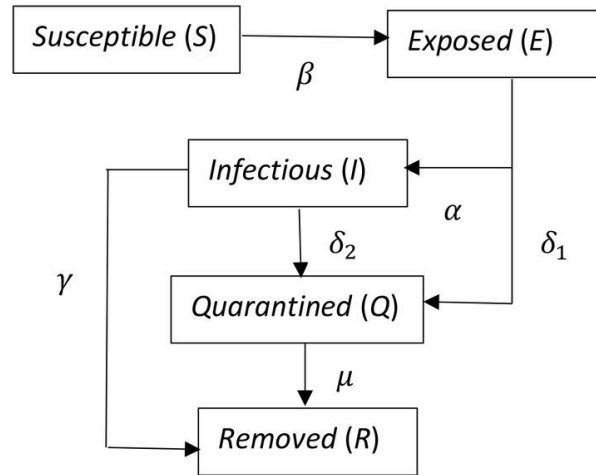


Figure 2.4: SEIQR block diagram

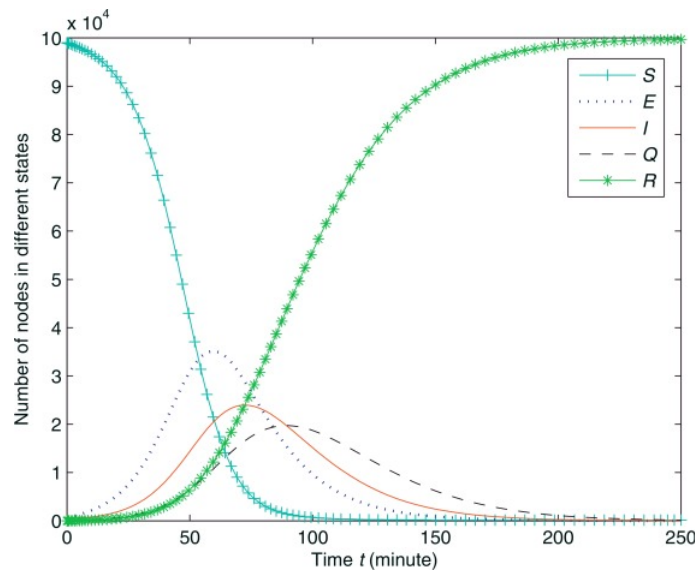


Figure 2.5: SEIQR epidemic trajectory

## 3 METHODOLOGY

### 3.1 Assumptions

- Once a person is infected and recovered the person is considered to be not susceptible to the flu and cannot be infected again. For a situation when person deceased because of infection they are removed from the population.
- In our model we are not considering precautionary quarantine state, i.e., the person does not have an option of going from exposed state to quarantine state so  $\delta_1 = 0$ .
- Chance of transmitting the infection by an infected person is defined by a random variable with Bernoulli distribution.
- In our model we have considered an incubation period as 4 days. Incubation period is defined as the time it takes for the infection to become active.
- We assume that providing vaccination (1 or 2 dose) to the population does not eliminate the infection completely but decreases the chance of getting infected significantly.
- For our model we restricted the infection spreading from one person to maximum 4 neighbours. For example in phase 1, the neighbourhood was say 21 students. Here in phase 2, one person's potential to infected is limited to 4 other people(based on the observations from COVID-19). We have also explored a case where there is increase in neighbours (refer scenario 5).
- We assume the infection period is for 14 days.
- We incorporated the concept of herd immunity i.e., after 90 % of the population get infected the population achieves herd immunity and the remaining 10 % do not get infected.
- The model is assuming that the people are readily accepting the vaccination.

### 3.2 Simulation using Python

We have used the below simulation model to showcase this problem. We have shown our analysis and results for the python model. Fundamentally, our program functions around the concept: any given person who is infected by our simulation's flu/disease has the potential to spread it to their neighbours(meaning the person they come in contact with) for the next 14 days. We have kept this neighbour count as a constant, as if it is kept varying there would be an exponential increase in the binomial probability of the spread. After getting infected they are considered to be recovered or deceased and no longer susceptible to the flu. The probability of an infected person to infect any other person he/she comes in contact with is 0.05 for the base model. In our python program we have used the following steps to simulate the flu spread:

- Our global parameters consists of the population count (1000), incubation period (4 days), infected period (14 days), neighbour count (3), probability of getting infected (0.05), probability of getting infected after vaccination dose 1 (0.00001), period of quarantine (10) and probability of recovery (0.97).
- We defined our simulation length that we want to simulate and created a data frame to collect the data of total number of infected, susceptible, recovered, deceased, quarantined.
- Using the functions defined for each state, for example: exposure to infection, getting infected, effect of social distancing, effect of quarantine we can simulate any scenario and observe the results. The results consists of number of people who got exposed, infected, quarantined, vaccinated, deceased and recovered.
- We have used lists to collect data of no. infected, susceptible, exposed, deceased, quarantined and recovered, probability of the infection is defined as 0.05 initially.

- The data frame is then used to collect the information and the populated data is used to observe the results of the simulation.

We have used the following functions in the model:

- Using the **social distancing** function we control the probability of infection. Here in our base model we reduce the infection probability from 0.05 to 0.01. Meaning that if social distancing is introduced the probability of people getting infected will be less. Also this function enables to reduce the infection probability for people who got vaccinated with first dose. We assumed this probability to be 0.000001.
- Using the **vaccine d1** function we are initially trying to get 1 % of population vaccinated with dose 1. We assume here that the infection is mitigated to some extent by the vaccination of dose 1.
- Using the **vaccine d2** function we are initially trying to get 0.5 % of population vaccinated with dose 2. We assume here that the infection is mitigated to some extent by the vaccination of dose 2.
- Using the **get exposed** function we are trying to expose the susceptible vaccinated population and susceptible non-vaccinated population. Here we introduce the incubation period, infected period, the probability of infecting the neighbours. For example we model that if a person is infected then after the incubation period(4 days) the infection becomes active and stays until the infection period gets over(14 days).
- The **update days exp**, **update days inf**, **update days qt** functions are used to create a list to update the number of days spent in each state.
- Using the **get quarantined** function we are calculating the number of quarantined people who were diagnosed with infection.
- Using the **results from infected**, **results from vaccine**, **results from quarantined** functions we are getting the total number of infected, vaccinated with 2 dose and quarantined people on daily basis.

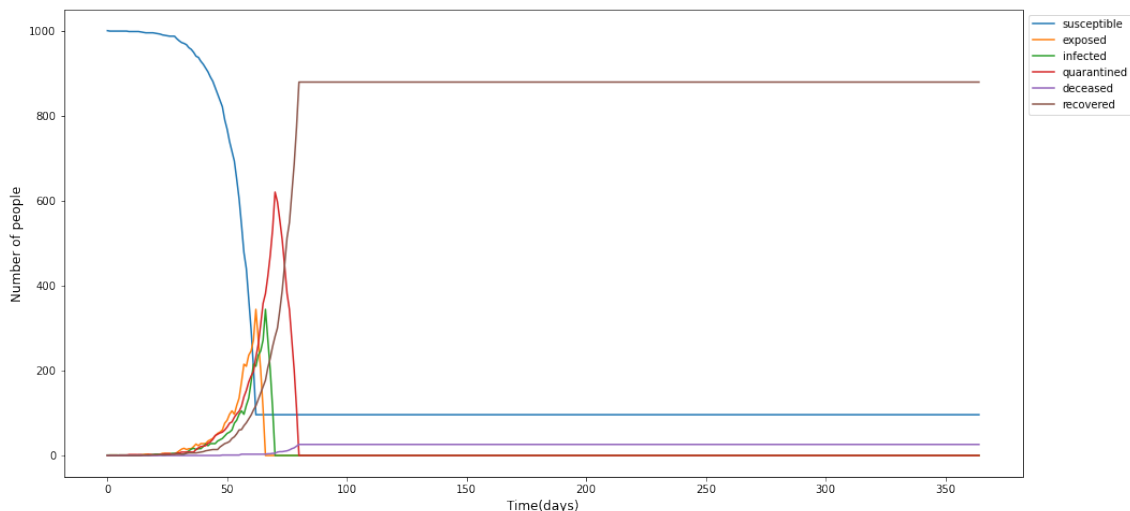


Figure 3.1: Pandemic Flu Spread Simulation using Python



From Fig. 3.1 we see that initially, the concentration of infectious people, grows approximately exponentially. The concentration of susceptible people, decreases at a constant rate as the disease invades the population (here the thousand people). It becomes flat towards the end due to the concept of herd immunity. In conjunction with the infectious folks recovering, this eventually causes the (net) growth rate of infected students to diminish and, eventually causes it to decay. And as the no. infected and susceptible comes down, the recovery rate increases. No. of exposed and people who quarantined also increase initially, reach a peak and then decreases.

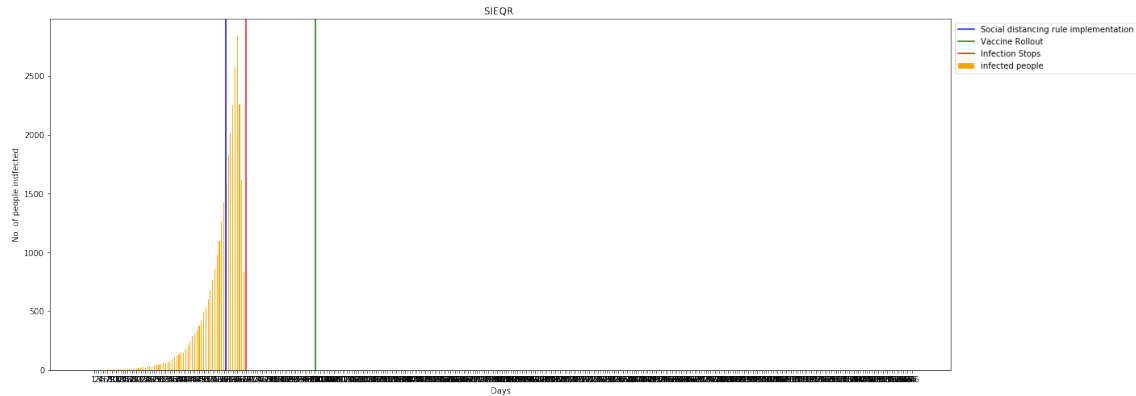


Figure 3.2: Pandemic Flu Spread Simulation using Python

## 4 MAIN FINDINGS

We have tried to showcase our learning's by defining scenarios. We executed our model for each one of them and summarized our results.

### 4.1 Scenario 1: Impact of vaccination

This scenario studies the impact of the spread of infection when both first and second dose of vaccination is made available to the population. We have considered following changes as compared to the base model:

Population: 1000 people

Vaccine roll out: 100 days

Social distancing start: 1000 days

Here we increase the social distancing to 1000 days so that we could focus our study on impact of vaccination.

**Observation:** We see the results as shown in Figure 4.1. We observe that as soon as the vaccination is rolled out there is a decrease in the infection. We also show when the infection stops.

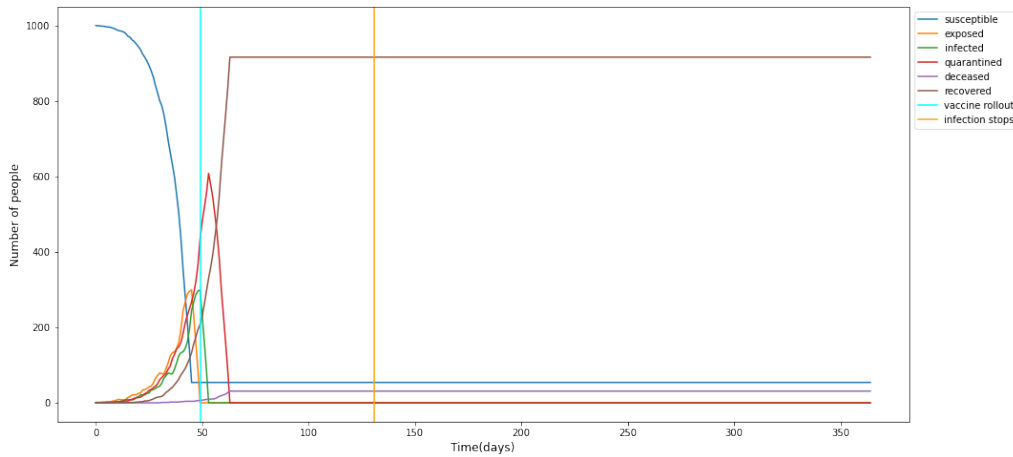


Figure 4.1: Pandemic Flu Spread Simulation - Impact of vaccination

### 4.2 Scenario 2: Impact of social distancing

In this scenario we study the impact of social distancing on the spread of the infection. We have considered following changes as compared to the base model:

Population: 1000 people

Vaccine roll out: 1000 days

Social distancing start: 30 days

We increased the vaccine roll out to large number so that we could study the behaviour with focus on social distancing factor.

**Observation:** We see the results as shown in Figure 4.2. We observe that once the social distancing is implemented the exposed and infected no. of people decreases and the results are quite realistic. We have also represented when the infection stops in the graph.

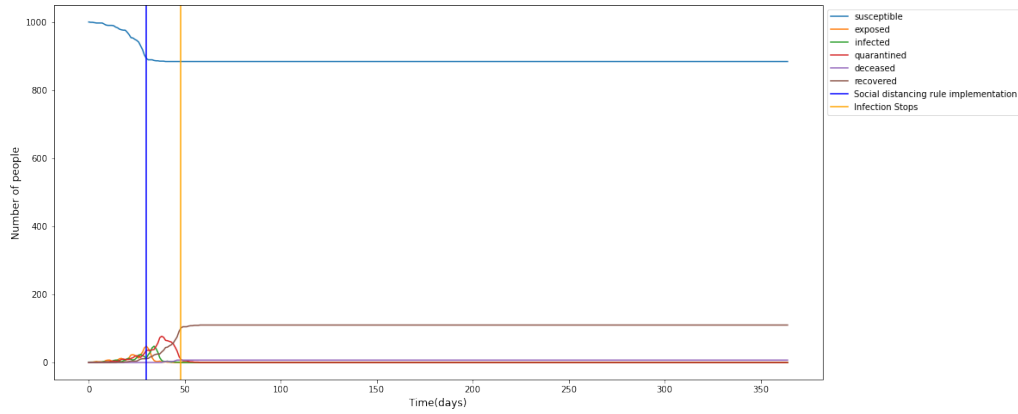


Figure 4.2: Pandemic Flu Spread Simulation - Impact of social distancing

### 4.3 Scenario 3: Impact of quarantine

In this scenario we study the impact of quarantine on the spread of the infection. This scenario is same as what we considered for base model, only we changed the population to 1000 to study the impact.

**Observation:** We see the results as shown in Figure 4.3. The no. of susceptible people comes down and becomes flat due to the herd immunity concept. The no. exposed and infected reach a peak and then decrease once quarantine period comes into effect. The quarantine period is basically the addition of the infection period and the no. of days exposed.

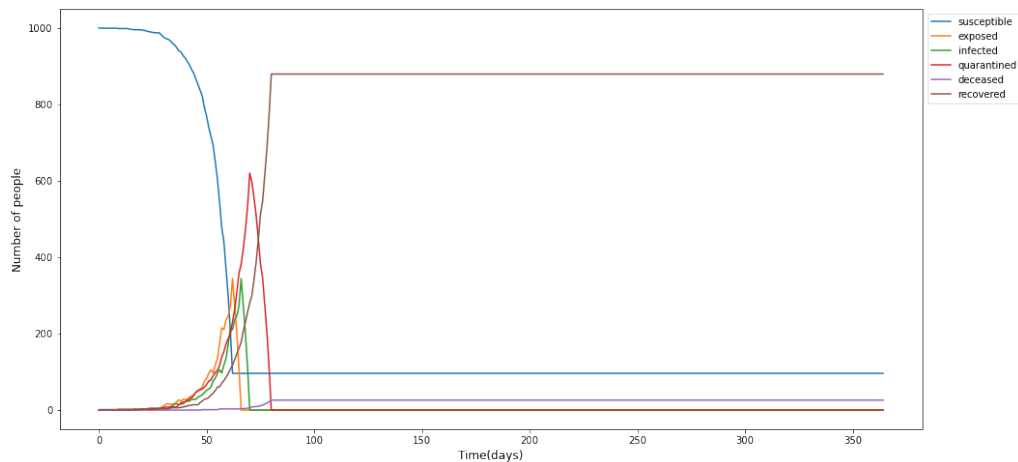


Figure 4.3: Pandemic Flu Spread Simulation - Impact of Quarantine

### 4.4 Scenario 4: Impact of supply chain issues in the availability of vaccine

In this scenario we study how the supply chain issues in the availability of vaccine affects the spread of the infection. We have considered following changes as compared to the base model:

Population: 1000 people

Vaccine roll out dose 1: 100 days

Vaccine roll out dose 2: 160 days

Social distancing start: 1000 days

Infection probability: 0.1

We increased the social distancing to large number so that we could study the behaviour with focus on vaccine roll out factor.

**Observation:** We see the results as shown in Figure 4.4. Here we see that there is a delay in roll out of vaccine dose 2 by 2 months or 60 days. We see how the infection, no. of susceptible people comes down after this period.

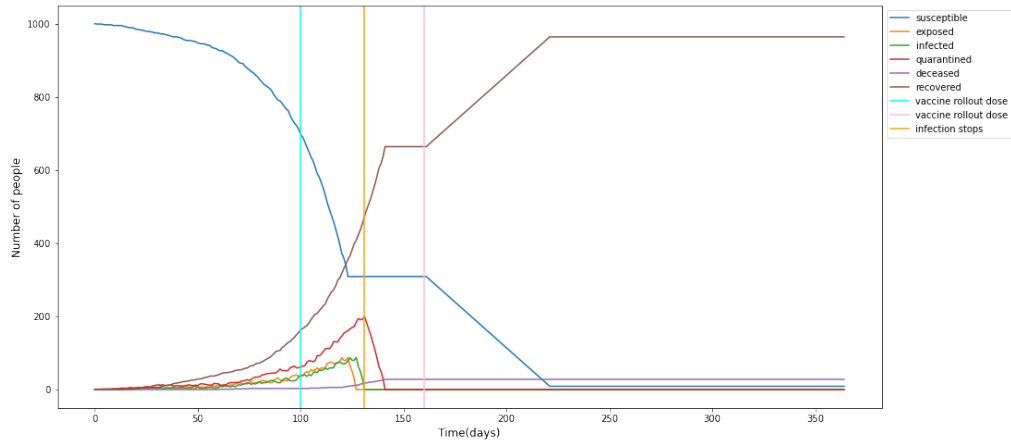


Figure 4.4: Pandemic Flu Spread Simulation - Impact of supply chain issues

#### 4.5 Scenario 5: Impact of increase in number of neighbours

In this scenario we study the impact of increasing the number of neighbours on the spread of the infection. We have considered following changes as compared to the base model:

Population: 1000 people

Vaccine roll out: 100 days

Social distancing start: 60 days

No. of neighbour: 5

**Observation:** We see the results as shown in Figure 4.5. We kept the day vaccine roll out and social distancing starts same as base model. We found that the increase in neighbour from 3 to 5 significantly increases the rate of infection.

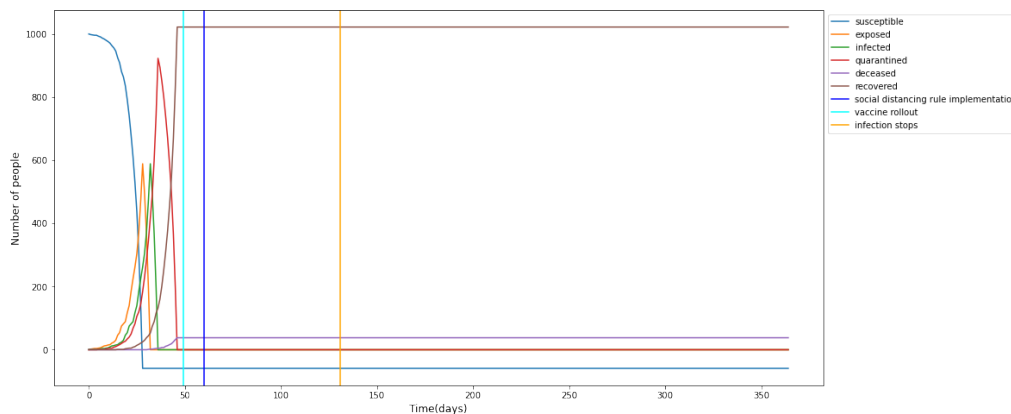


Figure 4.5: Pandemic Flu Spread Simulation - Impact of increase in number of neighbours

#### 4.6 Scenario 6: Impact of mutant virus

Population: 1000 people

Vaccine roll out: 100 days

Social distancing start: 1000 days

Infection probability: 0.15

**Observation:** We see the results as shown in Figure 4.6. We increased the social distancing to large number so that we could study the behaviour with focus on impact of mutant virus on the infection spread. We introduced a mutant virus on day 40 and observed how the infection rate, no. of exposed people rises as and then falls down after reaching a peak.

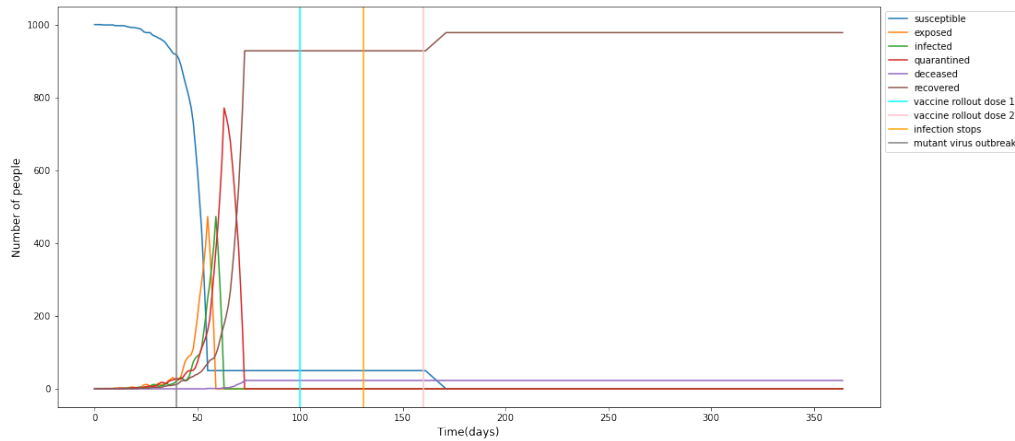


Figure 4.6: Pandemic Flu Spread Simulation - Impact of mutant virus

## 5 APPLICATIONS & LIMITATIONS

- The pandemic flu spread simulation analysis may prove useful in wide variety of fields. Studying this for a large population definitely gives a huge perspective which can be further developed and used as a standard tool used in epidemiology to study the spread of infectious disease. Because both infection rates and mitigation efforts such as vaccination, social distancing have a large impact on economic behavior, economists are now working with these models to better understand the interrelationships between public health measures and economic activity.
- Studying scenarios such as delay in availability of vaccine due to supply chain issues can be further utilised by the manufacturers to have better forecast of amount of vaccination needed and hence prevent any delays in future pandemic situations. It gives a good idea on the reaction of the population when there is vaccination available and how keen they are on the mitigation efforts.
- From health concerns to situations related with marketing, informatics or even sociology, several fields are using this epidemiological model as a first approach to better understand a situation. Several papers have studied, under epidemiological models, the adoption or abandonment of online social networks. Viral Marketing is another case where we can check through these kind of models how we can potentially reach a large and fast audience, through a cheap communication campaigns.
- Studying scenarios on social distancing can be used as an outreach and method to propagate the awareness among people on the benefits of such a behavior and how it can help mitigate the effects of the pandemic.
- Like any model, the model is not without **shortcomings**. One key limitation of the pandemic flu spread model is the assumption it makes regarding the frequency at which infected individuals meet with those who are susceptible, thereby generating opportunities for disease transmission. As in reality this situation can be very different and there maybe a case of super spreader events. Weddings, funerals and even large family parties (like birthdays or holiday dinners) are a few examples of regular events that turn into super spreaders, though there are plenty of other examples, too.
- Understanding the endemic equilibrium and defining the stability might not be accurate. This equilibrium arises as a balance between transmission of infection and replenishment of the susceptible pool, either through loss of immunity or demographic turnover. Establishing a criteria for the stability of the infection-free steady state and existence of an endemic steady state might be simple for basic models but might prove a difficult task for the complex ones. [5]
- The model also assumes uniform mixing across the entire population. This means that infections evolve as if any susceptible individual interacts with and could be infected by any infected individual across the population with equal probability which is not the case in reality.

## 6 CONCLUSION

We tried simulating the pandemic flu spread for a larger population using python. We played around simulating several scenarios and understanding the condition of flu spread in such situations. We observed different outcomes with each scenario run but the pattern observed are realistic. We even tested by trying different probabilities and observed how by increasing the probability of spreading the infection increases the number of people infected. We observed the impact of mitigation methods like social distancing, 1 dose and 2 dose of vaccination and saw how they vary the spread of infection.

We further recommend that adopting a network perspective can offer useful insights when modeling the spread of infectious diseases such as COVID-19. Relaxing the assumption of uniform random mixing and explicitly modeling interaction patterns via a network can provide a number of important insights about the spread of a disease that are not present in the baseline model. We think that in our model we have made assumptions about the pattern of interactions among individuals that most likely will not hold true in the real world.

In future the network perspective in the sense that heterogeneity in the number of contacts individuals have and the clustering of contacts, can change the behavior of the model in important ways, affecting the speed of the disease spread, long-run health outcomes, and the effects of the disease on economic activity. We can also explore the similar model on an international scale. New data sources such as social media, electronic health records can identify possible asymptomatic patients, infer human behavioral aspects, and facilitate tracking transmission chains. The challenges in the current SEIQR modeling paradigm must be considered carefully and model's effectiveness must be evaluated considering complicated clinical, behavioral, and other social aspects as well.

## 7 REFERENCES

### REFERENCES

- [1] Luz, P. M., Struchiner, C. J., Galvani, A. P. (2010). Modeling Transmission Dynamics and Control of Vector-Borne Neglected Tropical Diseases. *PLoS Neglected Tropical Diseases*, 4(10), e761. <https://doi.org/10.1371/journal.pntd.0000761>
- [2] Li, F., Meng, X., Wang, X. (2018). Analysis and Numerical Simulations of a Stochastic SEIQR Epidemic System with Quarantine-Adjusted Incidence and Imperfect Vaccination. *Computational and Mathematical Methods in Medicine*, 2018, 1–14. <https://doi.org/10.1155/2018/7873902>
- [3] Mathematical Modelling Versus Machine Learning for COVID-19, by Col Jung, The Startup Dec, 2020
- [4] Géhin, A., Goorah, S., Moheeput, K., Ramchurn, S. (2020). COVID-19 outbreak in Mauritius: Logistic growth and SEIR modelling with quarantine and an effective reproduction number. Cold Spring Harbor Laboratory. <https://doi.org/10.1101/2020.09.22.20199364>
- [5] Roberts, M., Andreasen, V., Lloyd, A., Pellis, L. (2015). Nine challenges for deterministic epidemic models. *Epidemics*, 10, 49–53. <https://doi.org/10.1016/j.epidem.2014.09.006>
- [6] Chen, S., Robinson, P., Janies, D., Dulin, M. (2020). Four Challenges Associated With Current Mathematical Modeling Paradigm of Infectious Diseases and Call for a Shift. *Open Forum Infectious Diseases*, 7(8). <https://doi.org/10.1093/ofid/ofaa333>
- [7] Mishra, B. K., Jha, N. (2010). SEIQRS model for the transmission of malicious objects in computer network. *Applied Mathematical Modelling*, 34(3), 710–715. <https://doi.org/10.1016/j.apm.2009.06.011>