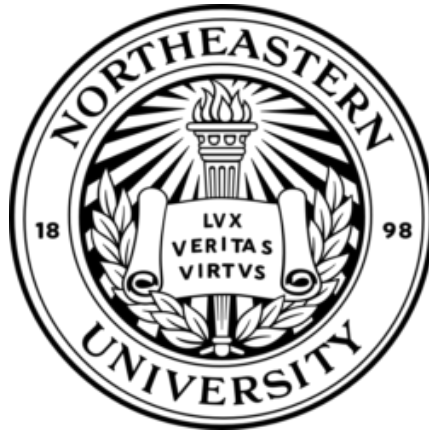


# Covid-19 Simulation

Project Report



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PROGRAM STRUCTURES AND ALGORITHMS ([INFO 6205](#))

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## Table of Contents

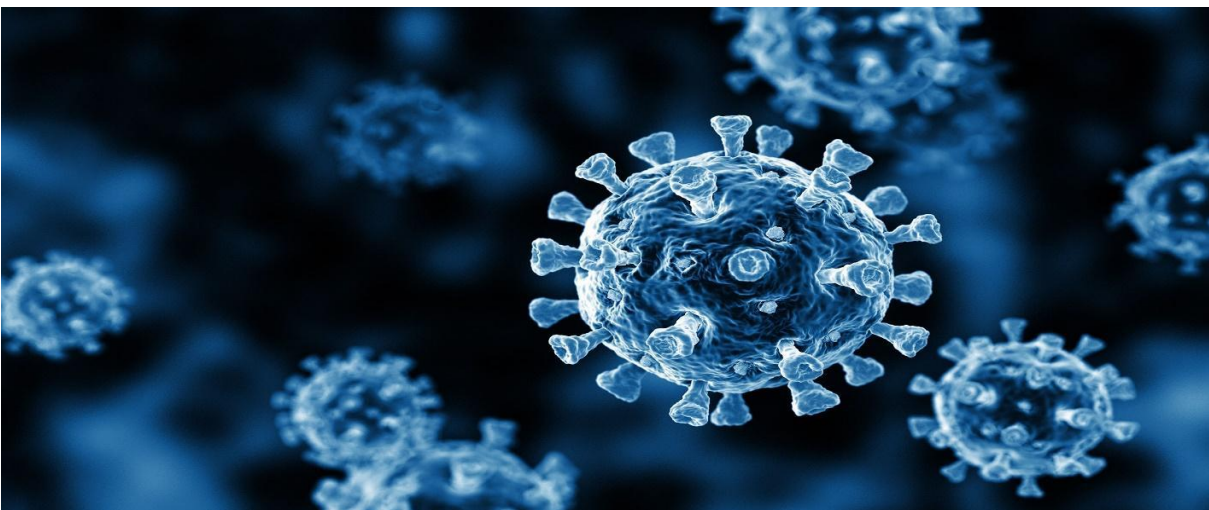
<b>INTRODUCTION</b>	<b>3</b>
<b>AIM OF THE PROJECT</b>	<b>4</b>
<b>PROJECT DETAILS</b>	<b>6</b>
Technologies used	6
Simulation Details	6
<b>IMPLEMENTATION</b>	<b>7</b>
Data Structures	7
Contact Tracing	7
<b>Scenarios</b>	<b>10</b>
Without Mask #1	10
Mask Mandatory #2	11
Comparison of Two Viruses #3	12
Vaccine Availability and Efficacy #4	14
Isolation Barrier and Quarantine #5	15
<b>Worst Case</b>	<b>15</b>
<b>Unit Test</b>	<b>16</b>
<b>Config File</b>	<b>17</b>
<b>CONCLUSION</b>	<b>18</b>
<b>FUTURE STUDY</b>	<b>19</b>
<b>REFERENCES.....</b>	<b>20</b>

# INTRODUCTION

A virus is a small collection of genetic code, either DNA or RNA, surrounded by a protein coat. A virus cannot replicate alone. Viruses must infect cells and use components of the host cell to make copies of themselves. Often, they kill the host cell in the process and cause damage to the host organism. Because viruses don't have the same components as bacteria, they cannot be killed by antibiotics; only antiviral medications or vaccines can eliminate or reduce the severity of viral diseases E.g., Covid-19.

The recent scare caused by the SARS-CoV-2 coronavirus pandemic has prompted a flurry of research into prevention and treatment strategies. Although certain infections are symptomatic, meaning they cause symptoms throughout the infection, others are asymptomatic, meaning they don't cause symptoms yet can still spread. The use of masks, social distancing, and limiting human movement are all thought to be significant factors in flattening the exponential curve of increasingly rising cases.

Today a year and a half since the first incident of the coronavirus and the various research done in the study of the Sars-Cov-2 virus over the same period, there is still a dire need for models that simulate the spread of the Covid-19 pandemic as accurate and as efficient as possible so that Public Health Departments can use to factor into their decision making to best control the disease.



## AIM OF THE PROJECT

The project aims to simulate various factors that affect the mass spreading of a viral disease. It also focuses on analyzing and determining the possible steps that can be taken in order to curtail the spread of the disease in the event of another major outbreak. Following are the factors that are taken into consideration for simulating the spread of the Covid-19 virus.

- Total population
- Infected population
- Rate of Infection
- Social Distancing
- Wearing Mask
- Following Quarantine / Isolation
- Contact Tracing
- Availability & Efficacy of Vaccine

### Important to points to take into consideration:

- i) **Population Density:** It is a measure of the total population in a given region that is either vulnerable to infection, has already been infected, or is resistant to the virus as a result of natural or vaccination-induced recovery.
- ii) **R Factor:** R-naught also known as the reproduction factor indicates the contagiousness of a disease. R-naught tells you the average number of people who will contract a disease from a single infected person. A R-naught value of **6.8** for a disease means that an infected person will transmit the disease to an average of 6 to 7 people who hadn't been infected nor vaccinated.

$$R_o = \beta * T$$

$\beta$  – Infection producing contacts per unit time;  $T$  – Infection period

- iii) **K-factor:** Different pathogens have different ways in which they transmit the infection hence the K-factor came into existence which is called the “Dispersion parameter”. It is the way of knowing whether a virus spreads in a steady manner or in big bursts, whereby one person infects many at once.

$$K = \text{Distribution} * \text{Infection}$$

Distribution → *measures the average number of people a host will contact while still infectious.*

Infection → *measures how likely an average person also becomes infected after contact with an infected individual.*

- iv) **The usage and effectiveness of masks:** Wearing masks is considered to have a good defensive effect and hence the rate of transmission is set to . Not wearing masks drastically increases the probability of a person getting infected so the rate of transmission is set to .
- v) **Availability of Vaccines:** Most of the vaccines available have an efficiency rate of around 85% to 95% so the rate of efficiency for this simulation is set as 90%. So the probability of a person becoming infected with covid who has not been infected and has been vaccinated is very less

## PROJECT DETAILS

### Technologies used

The simulation is developed using Python 3 with **TKinter** to create GUI. Graphics are rendered using **Matplotlib** library which provides sophisticated control over geometry, coordinate transformation, color management and text layout. **NetworkX** library is used to represent the graph data structure that is used in this project to establish the relationship between person and infection. Unit testing is implemented using **unittest** framework for Test Driven Development and **GitHub** is used as Version control software.

### Simulation Details

To model this simulation, various real-world variables that play a critical role in the spread of the covid-19 virus are taken into account. Furthermore, a variety of other factors contribute to the disease's spread, so this isn't a true-to-life simulation of the pandemic. However, using this model, a lot of key inferences could be made that may help us in suppressing the spread of the disease.

#### Details about the simulation:

- Simulation is initialized with a total population and some infected individuals carry the virus whose both values can be configured and are represented as colored balls in the figure.
- Some Important color code to be aware of during simulation:
  - **Green**: Healthy
  - **Red**: Infected/Unhealthy
  - **Grey**: Recovered
- Balls move randomly within the boundary of space and a healthy ball can be infected on colliding with an infected ball, which depends on a combination of factors such as rate of transmission and probability of getting infected.
- Infected balls can be asked to quarantine as soon they are found carrying the virus which puts them in a separate space away from healthy balls thereby greatly reducing the spread of the secondary infections.

## IMPLEMENTATION

Social interactions between susceptible and infected people are important during disease transmission, but not so much between uninfected people. The goal of this simulation is to create a communication network as people become infected. At each simulation stage, only infected people and their near contacts are generated. The key advantage of this model is the computational efficiency achieved when simulating a large-scale disease outbreak.

### Data Structures

In this simulation model below are the data structures used:

- The graph data structure is implemented using a adjacency lists to establish contact tracing and for arriving at the R and K factors of the virus.
- A node in a graph represents a person, and an edge between two nodes represents a relationship between two persons such that one person has contracted the disease from the other person.

### Contact Tracing

Contact tracing is the method of finding people who may have had contact with an infected person ("contacts") and then gathering additional information about them. Public health Department attempts to eliminate infections in the population by tracing the contacts of infected people, monitoring them for infection, isolating or treating the infected, and tracing their contacts. In this model we have achieved contact tracing of individuals and their role in spreading of the disease through the implementation of the Graph data structure. Wherein any connection between two individuals (two nodes) indicates that disease transmission has taken place from one person to another.

### Code Snippet for implementing Contact Tracing

```
for per in persons:
    if per.index == p.index or per.infected or per.recovered:
        pass
    else:
        d = p.get_dist(per.posx, per.posy, per.name)
        if d < r_transmission:
            if np.random.random() < p_transmission / 100:
                per.infect(frame)
                sizes[per.index] = 80
                print(p.name + "=>" + per.name)
                g.addEdge(p.name, per.name)
                print(g.graph)
```

### Code Snippet for Generating A Graph based on Contact Tracing

```
def vis(self):
    print("VIS")
    g = nx.DiGraph()
    g.add_nodes_from(self.graph.keys())

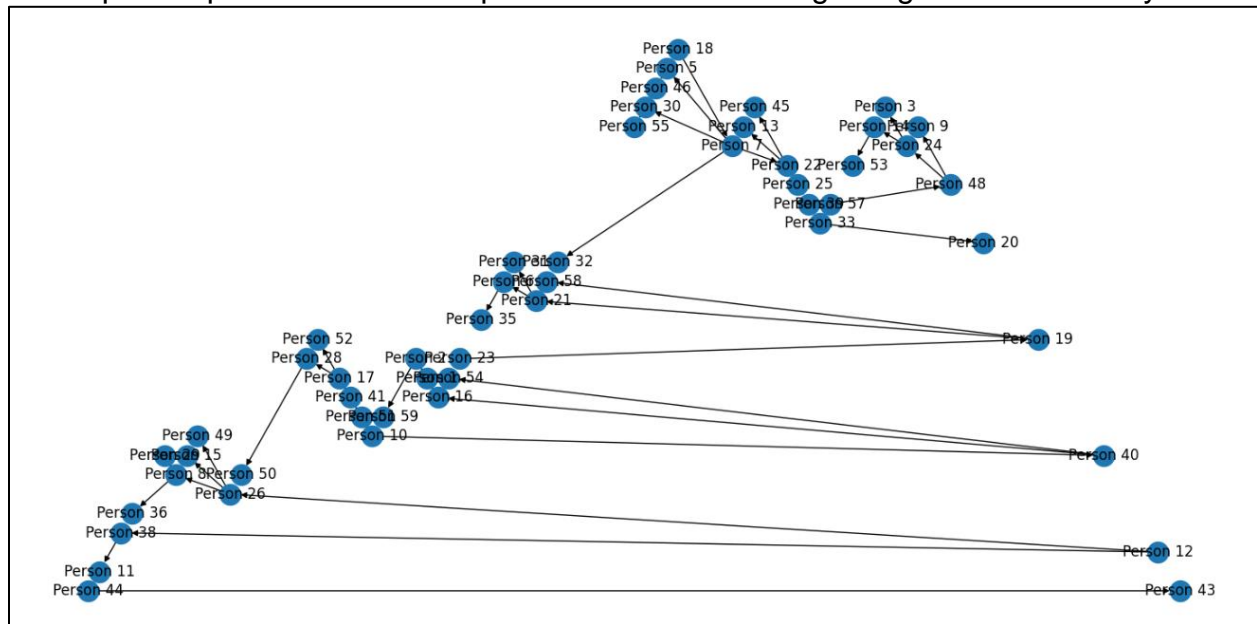
    for k, v in self.graph.items():
        g.add_edges_from([(k, t) for t in v])
    plt.clf()
    nx.draw_planar(g, with_labels=True, arrows=True)
    plt.savefig("RFactor.png")
    plt.clf()

    g1 = nx1.DiGraph()
    print("Self ", self.key)
    g1.add_node(self.key)
    for k, values in self.graph.items():
        for value in values:
            if k == self.key:
                print(f'{k} - {value}')
                g1.add_edge(k, value)

    plt1.clf()
    nx1.draw(g1, with_labels=True)
    plt1.savefig("KFactor.png")
```



A Sample Graph Generated to implement Contact Tracing using NetworkX library.



## Console Output Image of Contact Tracing:

```
C:\Users\naren\AppData\Local\Programs\Python\Python39\python.exe "C:/Spring 21/PSA/Aishwarya/INF06205-PSA-FinalProject/main.py"
After G0: Without Mask Mandate
20
Person 16==>Person 9
defaultdict(<class 'list'>, {'Person 16': ['Person 9']})
Person 9==>Person 5
defaultdict(<class 'list'>, {'Person 16': ['Person 9'], 'Person 9': ['Person 5']})
Person 9==>Person 19
defaultdict(<class 'list'>, {'Person 16': ['Person 9'], 'Person 9': ['Person 5', 'Person 19']})
Person 2==>Person 8
defaultdict(<class 'list'>, {'Person 16': ['Person 9'], 'Person 9': ['Person 5', 'Person 19'], 'Person 2': ['Person 8']})
Person 9==>Person 10
```

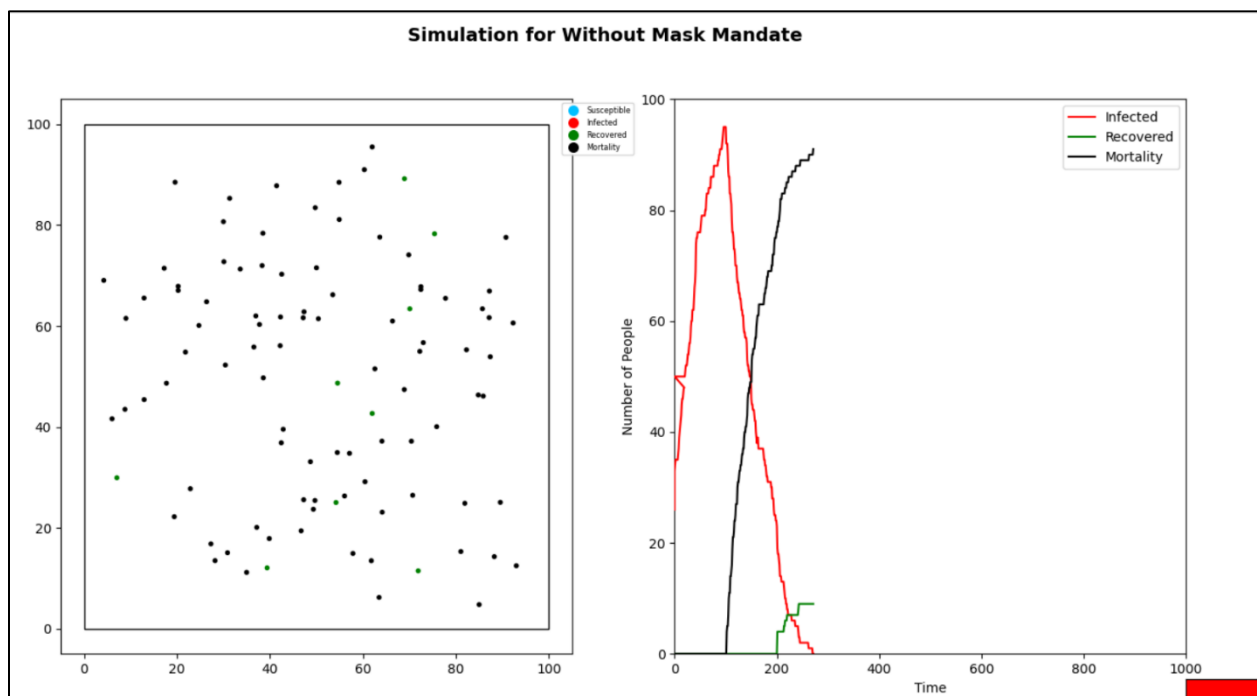
The following points about the findings can be deduced from the above output:

- Person 9 can be considered a patient now as he came in contact with an infected individual Person 16.
- Similarly Person 9 has infected Person 5 and Person 19.
- This contact tracing would be helpful in evaluating the measures such as quarantine's effect on disease transmission

## SCENARIOS COVERED

### i) Without Mask Mandate:

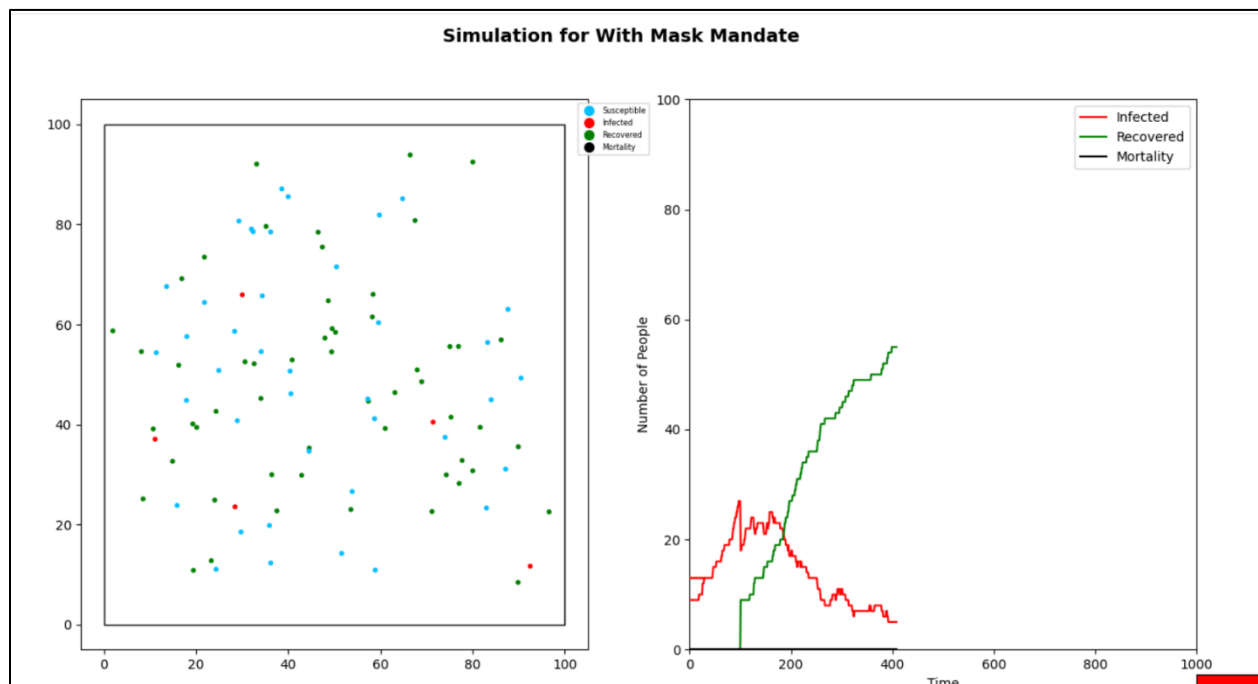
The situation involves no restrictions being enforced by the government or the public health department is simulated wherein people are neither asked to wear masks nor quarantine to flatten the curve. In this scenario, the transmission of the disease is the highest, as people move around places with absolutely no restrictions, and the effect of the mask factor is also not considered as there are no mandates to enforce people to wear them.



**Explanation:** The spread of the disease in this scenario is exponential as there are no restrictions enforced on the movement of people and mask mandate is also not applied. There is a very high chance of large outbreaks as a single infected individual can infect several other healthy individuals as not everyone wears a mask or has been exposed to the virus and is immune.

## ii) Mask Mandate:

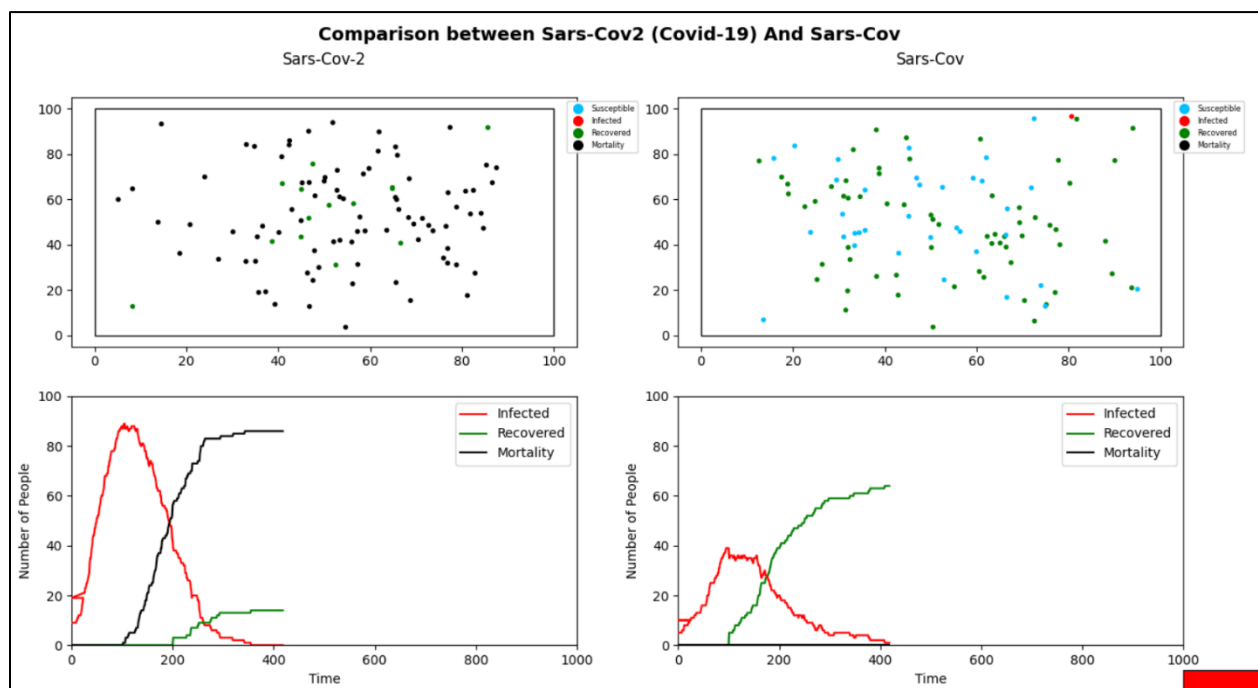
The situation of mask mandate being enforced in a particular region is being simulated wherein people are not asked to quarantine but are recommended to wear a mask when they step out to public places which lessens the contraction of the virus by a healthy individual.



**Explanation:** If a mask mandate is in place, but infected people are not quarantined, this graph illustrates the number of healthy people vs. infected people. In this scenario, without any appropriate vaccine, healthy people will contract the virus after a few days, and the number of infections will rise by a considerable amount, although not drastically as the mask is considered to have a good defensive effect.

### iii) Comparison of Two Viruses:

In this simulation, we are comparing two viruses (**Sars-Cov**) and Covid-19 (**Sars-Cov-2**) and how the order of growth (disease spread) is for these two different virus variants. Since it is the study of two viruses that were active at different periods we have made the playing ground even by not considering factors such as mask mandate or quarantine required.



**Explanation:** From the graph, the rate of growth for people getting infected by the covid-19 (sars-cov-2) is quite faster than that of the Sars-Cov as the rate of transmission is higher for covid-19 than Sars-Cov virus variant. Apart from that, the recovery time or incubation period is also higher for the covid-19 variant hence the people infected with the covid-19 virus consume a longer duration of time to recover.

## R-factor and K-factor of Two Viruses:

The **R-factor** which is the average number of person infected by a single individual for the Sars-Cov-2 (covid-19) is around ... in our simulation which is higher than the R-factor of the Sars-Cov virus variant which indicates that the covid-19 virus is highly transmissible than the Sars-Cov. We had achieved this by setting the rate of transmission rate and probability of infection higher than that of the Sars-Cov.

The **K-factor** which is the way of knowing whether a virus spreads in a steady manner or in big bursts, whereby one person infects many at once. It is entirely different from the R-factor because with R-factor we take the average which doesn't give us more information whereas with K-factor introduces the role of variability where a small number of people or a person might be responsible for a large outbreak of the infection which we overlook when considering the R-factor. So the concept of Super spreaders (a single patient or a small group of patients) comes into consideration.

- We have calculated the K-factor of the Covid-19 as well as that of the Sars-Cov virus by the identifying the super spreader of the virus transmission.
- Then we perform contact tracing to trace the people infected by this super spreader.

## Console Outputs:

```
Super Spreader SARS 2 Person 60
Super Spreader SARS 2 Person 60
K Factor for SARS 2 0.1373
R Factor for SARS 2 1.8431
Super Spreader SARS 1 Person 30
Super Spreader SARS 1 Person 30
K Factor for SARS 1 0.1154
R Factor for SARS 1 1.6154
```

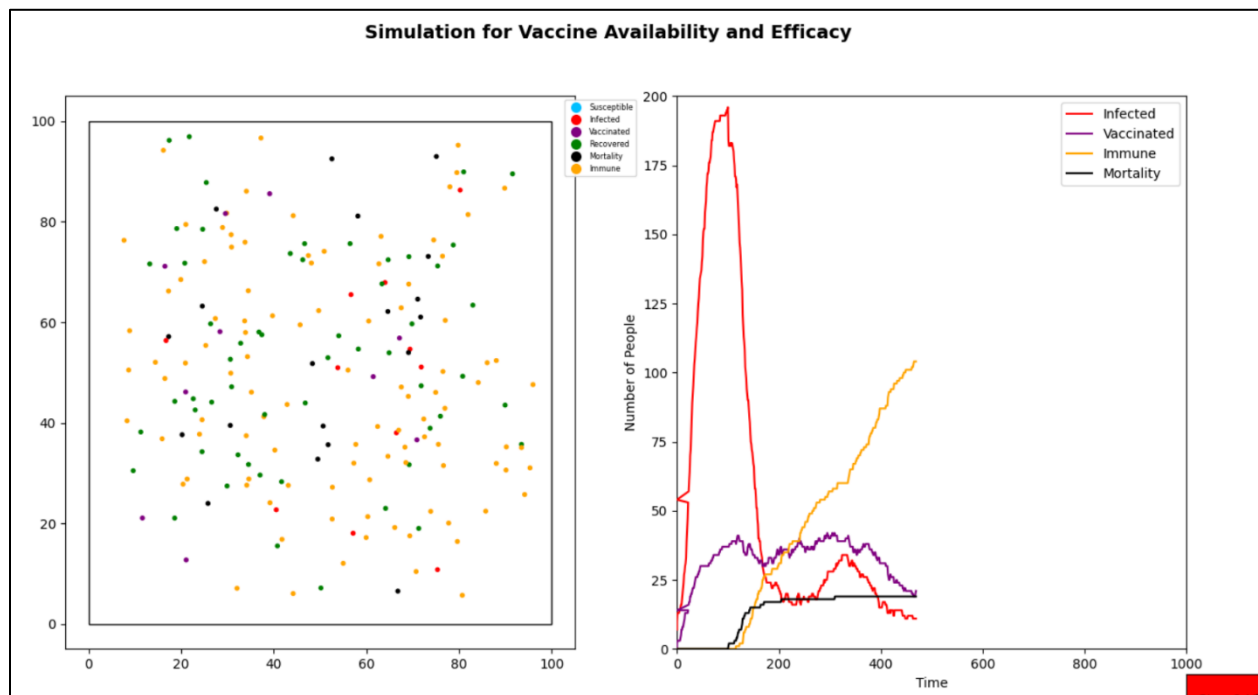
## Reasons to Consider K-factor:

- In the late stages of an outbreak, when the virus is almost eradicated, super-spreading events are important.
- Small K values indicate that a single infected individual will cause a large number of new cases in a short period of time. If this occurs, the epidemic could easily resurface.

## iv) Vaccine Availability and Efficacy:

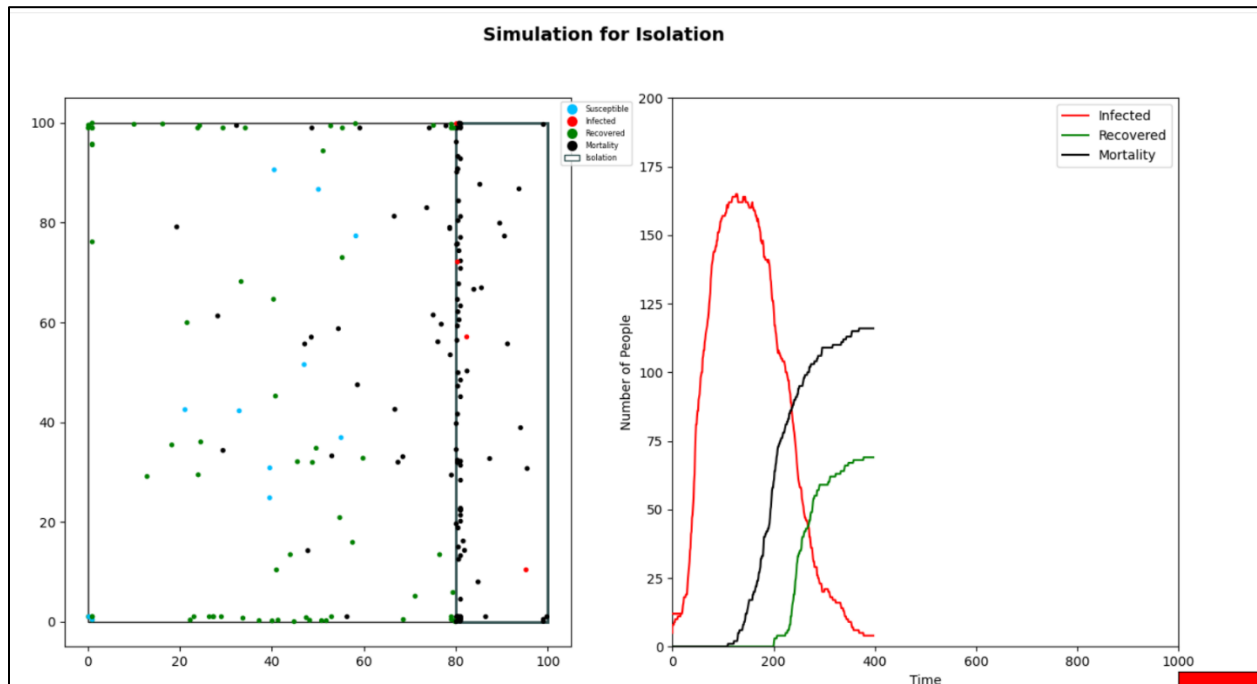
- We are simulating Vaccine availability and Efficacy by using below three factors:
  - Vaccine Availability per day percentage
  - Vaccine Efficacy percentage
  - Overall percentage of Vaccine taking place
- In the population of 200 people, daily only 20 percent people are getting vaccinated based on the availability. Only 30 percent of the vaccine is available for the total population. The efficacy of the vaccine is set to 50 percent i.e. 50% of the people will get immune and the remaining may get infected or die.

## Outputs:



### v) Isolation or Quarantine Effect on Infection:

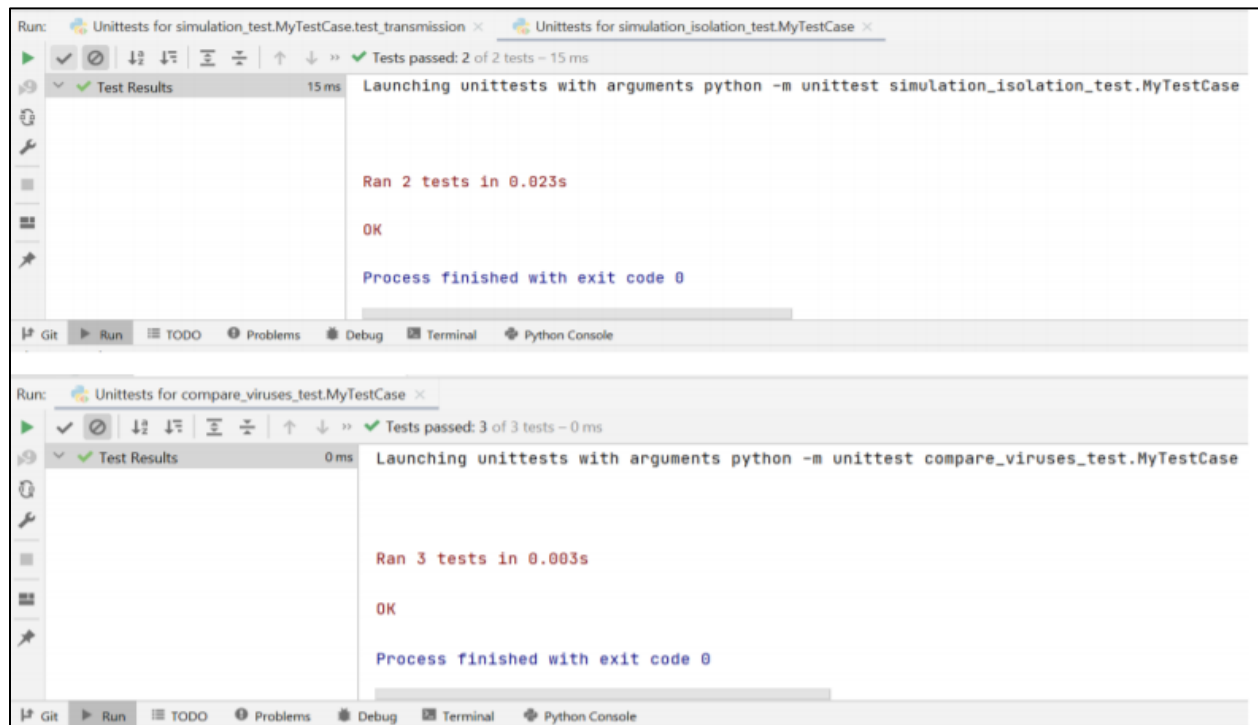
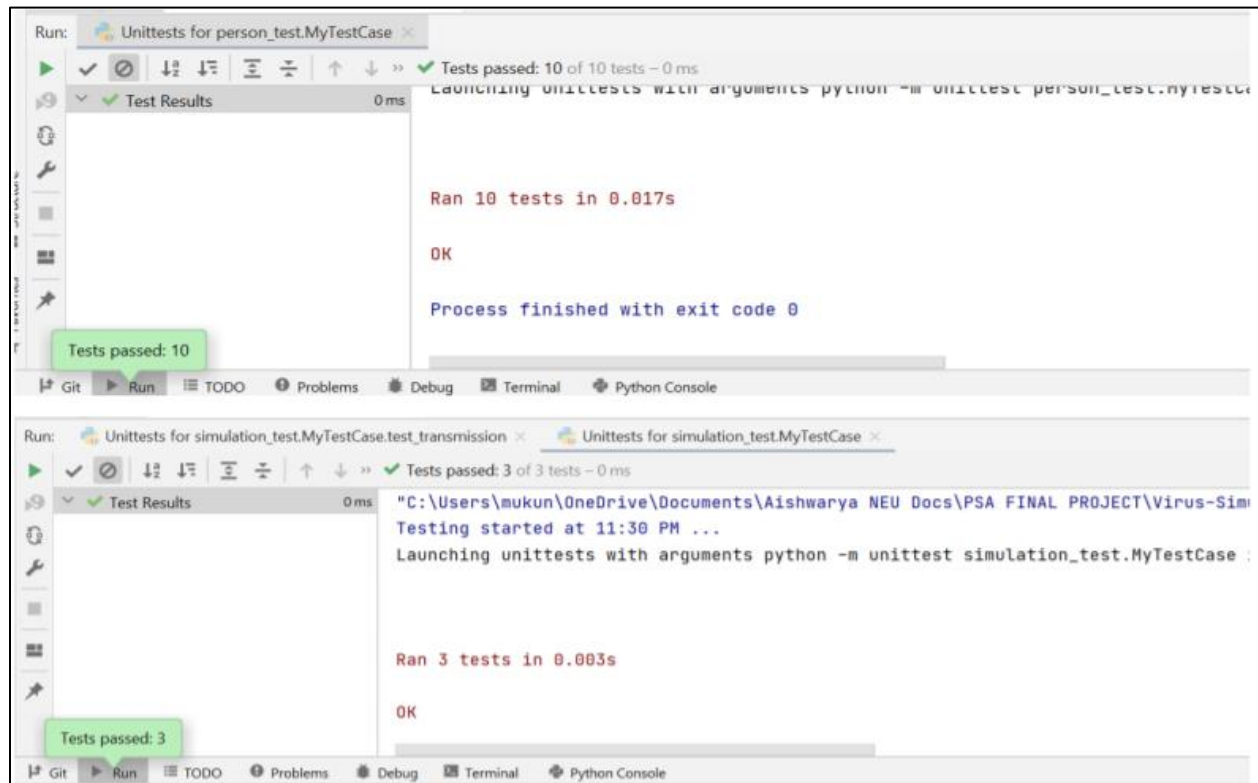
In this scenario we are trying to simulate the effect isolation has on the spread of the disease. So a patient on infection is advised to isolate or quarantine himself to lessen the spread of the infection.



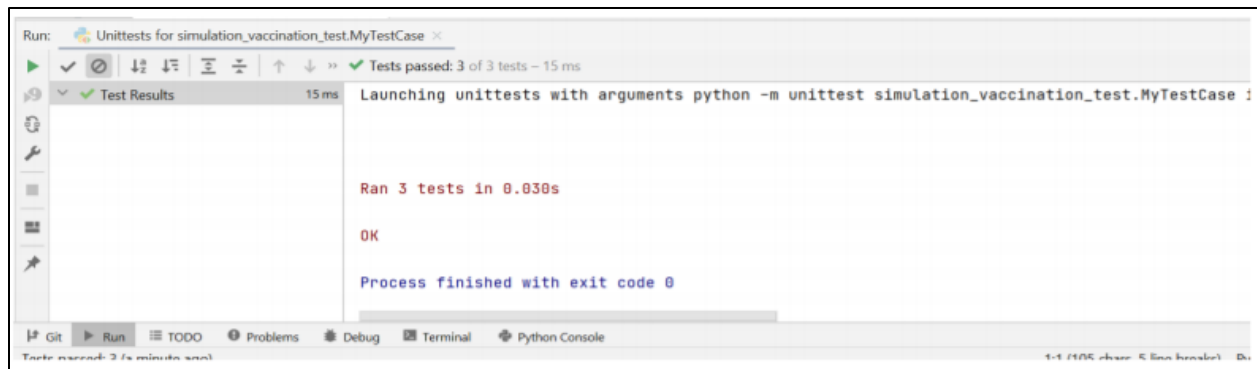
### Worst Case:

We are using Graph data structures. The worst-case scenario here is One person infecting all the other people in the region but it's practically impossible. The worst-case here is  $O(V+E)$

## Unit Test Cases:







## Config File:

Various parameters that are required for the variety of scenario simulations are defined via a configuration file called **config.ini** which can be easily edited.

```
#####
# Configuration file #
#####

[Covid 19 Parameters]

Population = 20
Infected_Percent = 20
Rate_Transmission = 2
Probability_Transmission = 80
Probability_Quarantine = 1
Recovery_Time = 100

[Mask_Mandate]

Population = 50
Infected_Percent = 4
Rate_Transmission = 2
Probability_Transmission = 1
Probability_Quarantine = 1
Recovery_Time = 100

[Comparison_Scenario]

Population = 100
Infected_Percent = 10
Rate_Transmission = 2
```

## Project Walkthrough Video:

[https://drive.google.com/file/d/1u2BVTGHJKAth\\_azGltNazthZ7\\_oqBVHQ/view?usp=sharing](https://drive.google.com/file/d/1u2BVTGHJKAth_azGltNazthZ7_oqBVHQ/view?usp=sharing)

## Conclusion

The relationship between the population and the number of contagious people in the population is depicted in this simulation model. We found that the plots indicate a simple 'tipping point': if we don't use the Mask mandate and Self-Isolation, the virus spread accelerates after a certain number of infections. The number of infections at their height is largely determined by how many people conform to the restrictions. Finally we can conclude from this simulation, that measures such as Mask mandate, Self-Isolation and Vaccine availability have a positive effect on the containment of the infection.

## **Future Study**

This model can be fine-tuned in the near future by integrating the heterogeneous population. The K-factor can also be researched upon and better included within our model to better predict the simulation.

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