

Virus Spread Simulation

Project Report



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COURSE

Program Structures and Algorithms (INFO6205)

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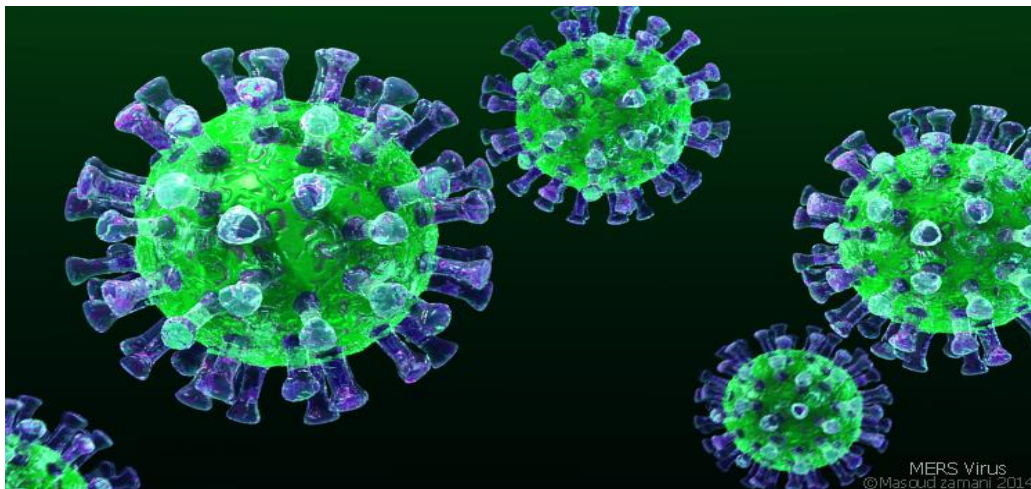
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INTRODUCTION

Virus is a submicroscopic agent that replicates inside a living cell of an organism and infect all types of life forms, from animals and plants to microorganisms, including bacteria. When infected by a virus, the host cell is forced to rapidly produce identical copies of the virus. While some infections are symptomatic i.e., they show usual symptoms during the infection, on the other hand there are asymptomatic i.e., they don't show any symptoms but capable of transmissions.

Recently, the widespread panic created by the coronavirus pandemic from SARS-CoV-2 has led to various research regarding prevention & treatment strategies. Social distancing is considered one of the important factors to flatten the exponential curve of rapidly increasing cases. The spread can be slowed down by avoiding public spaces and generally limiting the movement.

As there are occurrences of new and re-emerging SARS-CoV-2 disease outbreaks, there is a need for tools to simulate dynamics as accurate as possible and as efficient as possible so that public health officials can implement optimal intervention methods at the initial stages of outbreaks. Simulation models offer such tools for estimating the characteristics of a specific disease outbreak.



AIM OF THE PROJECT

The objective is to simulate spread of virus in a certain environment with the following factors:

- Total population / population density
- Infected population
- Infection rate
- Social Distancing
- Wearing Mask
- Following Quarantine
- Contact Tracing

Above mentioned factors can be modified to simulate & analyze different types of environment based on the different value of factors.

Many existing models allow us to gain insight into disease transmission process and to study threshold quantities such as basic reproduction number R_0 , and the more prominent K -factor which captures the dispersion of the infection, do not model a contact-network structure of the human network to study disease transmission.

Population Density: It is a measure of total population size (of susceptible and infected individuals, or others) needed to sustain an outbreak once it has appeared? In current model density is an input parameter by an epidemiologist who will analyze the model outcome and further use in strategies to control the spread.

R Factor: R_0 is the rate of transmission and is the average number of people infected by one infectious individual in a population with everyone susceptible. Higher values indicate greater infectivity.

$$R_0 = \beta \bar{i}$$

R_0 = basic reproduction number,

β = infection producing contacts per unit time, &

\bar{i} = mean infectious period

Some typical Ro values:

- Flu: 1.2
- Measles: > 10.0
- COVID-19: 2.0 – 4.0 (research still going on)

K-factor: It explains the dispersion of the infection and can be calculated as product of the rates of distribution and infection related to virus

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

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 a viral host

Virus having a k-factor of 1 is in a "steady" state of neither growth nor decline, while a k-factor greater than 1 indicates exponential growth and a k-factor less than 1 indicates exponential decline.

Some typical K values:

- Flu: 1.28
- Measles: <= 3.3
- COVID-19: 0.1-0.3 (research still going on)

Current model uses simulation technique that consider all the above factors.

PROJECT DETAILS

Technologies used

The simulation is developed using Java 8 with AWT & Swing APIs to create GUI. Graphics are rendered using Graphics2D library which provides sophisticated control over geometry, coordinate transformation, color management and text layout.

Unit testing is implemented using JUnit framework for Test Driven Development. GitHub is used as VCS & its Actions workflow for continuous integration of project.

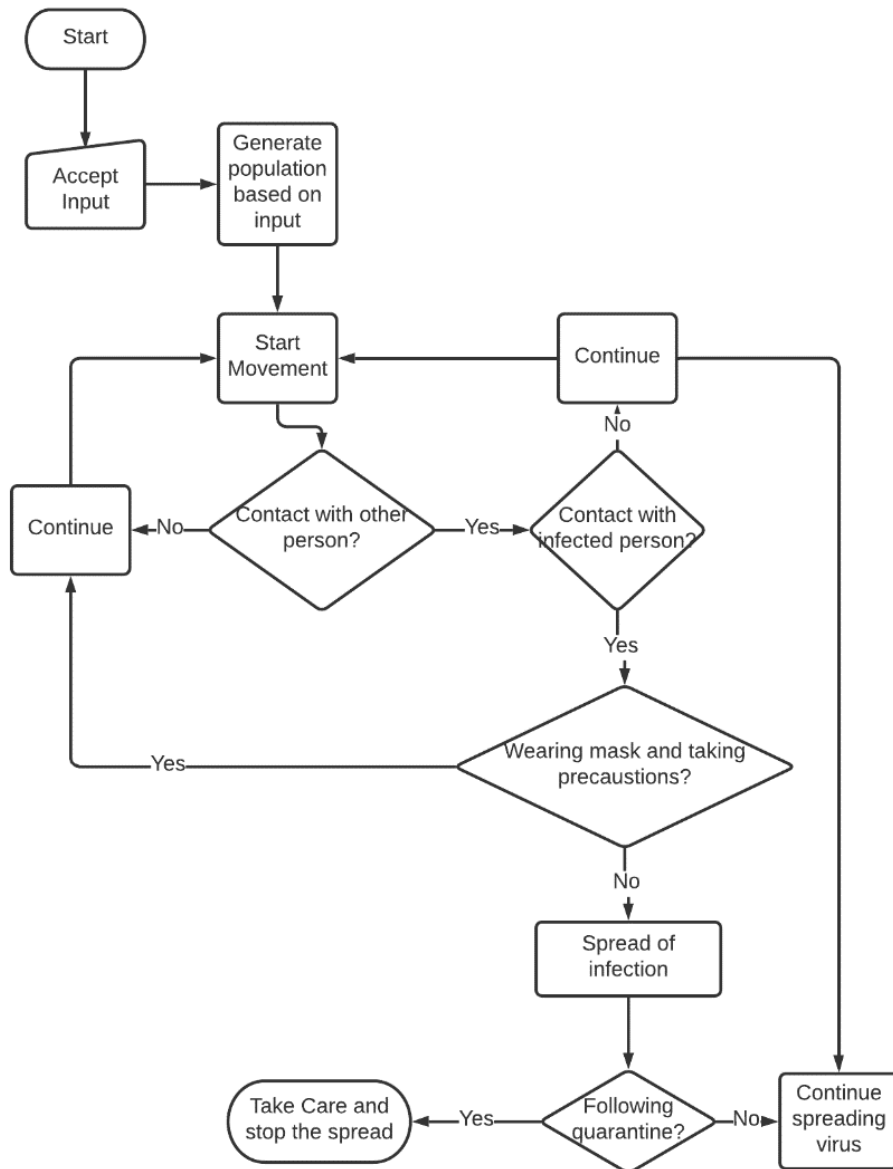
Simulation Details

It is not a 100% real world simulation as there are numerous more factors in the real world apart from ones discussed in the project. However, it could show how social distancing plays a key role in suppressing the spread of viruses like coronavirus.

Several details about the simulation are discussed below:

- Simulation is initialized with total population and some unhealthy population, represented by the balls.
- States of people are color coded in balls as follows:
 - **Green**: Healthy
 - **Red**: Infected/Unhealthy
 - **Orange**: Recovered
- Balls move randomly within the boundary of space and healthy ball can be infected by colliding with infected ball, which depends on rate of infection.
- Infected balls will be recovered after certain time period and can't be infected again.
- Any ball can be marked for social distancing or quarantine, which means it can't move during the simulation, but other balls can collide with it. Number of social distancing balls can be set from the panel.

Flow Diagram



IMPLEMENTATION

During disease transmission, the social contacts between susceptible and infected persons are significant, whereas contacts between uninfected persons are not significant. The overview of this simulation is building a contact network as people become infected at each simulation step by generating only infected persons and their close contacts. The main advantage of this simulation is computational efficiency when simulating disease outbreak with high prevalence in a large population.

Data Structures

In this simulation model below are the data structures used:

- List data structure is used to represent the population
- A graph data structure is used in contact tracing
- A node in a graph represents a person, and an edge between two nodes represents a relationship between two persons that would allow for disease transmission
- In this graph, edges can represent interaction between two nodes such that there are undirected graphs
- Prevalence at any point of time is a property of Person class and associated with a flag which identifies the infected person.

Contact Tracing

We assumed that the disease could transfer between any connected close individuals. Therefore, we are concerned with generating simple undirected graphs, i.e., no loops or multiple edges are allowed since we assume each susceptible person will be prone to infected from any of its infected contacts.


```

public void printContactTracing(LinkedHashMap<Person, List<Person>> contact_graph){
    for(Map.Entry<Person,List<Person>> entry : contact_graph.entrySet()){
        Person source = entry.getKey();
        List<Person> contactList = entry.getValue();

        System.out.print("Person " + source.getId() + " was infected and contracted to --> ");
        for(Person p: contactList){
            System.out.print(" " + p.getId());
        }
        System.out.println();
    }
}

```

We have simulated the virus progression with sample size e of 100 (total population) and considered till 300. This sample is representative of total united states population. Though we have not considered the heterogeneity of the population in this model but can be introduced in future studies.

Following mitigation factors were considered during the simulation:

1. Quarantine
2. Mask Mandate
3. Social Distancing

OUTPUT

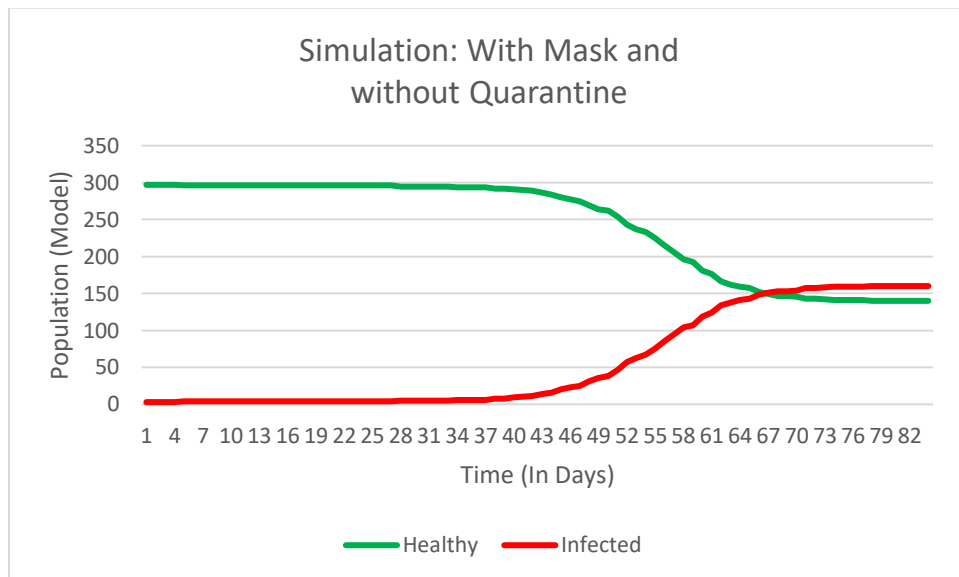
Model is implemented using multiple data structures in Java, and the time complexity is taken into consideration when getting and setting data.

Below mitigation factors are applied during simulation to understand the virus propagation:

Mitigation #1

Mask mandate is applied without quarantine in effect with 50% population following social distancing

Total Population	People wearing Mask	People following Social distancing	People in Quarantine
300	142	50%	0

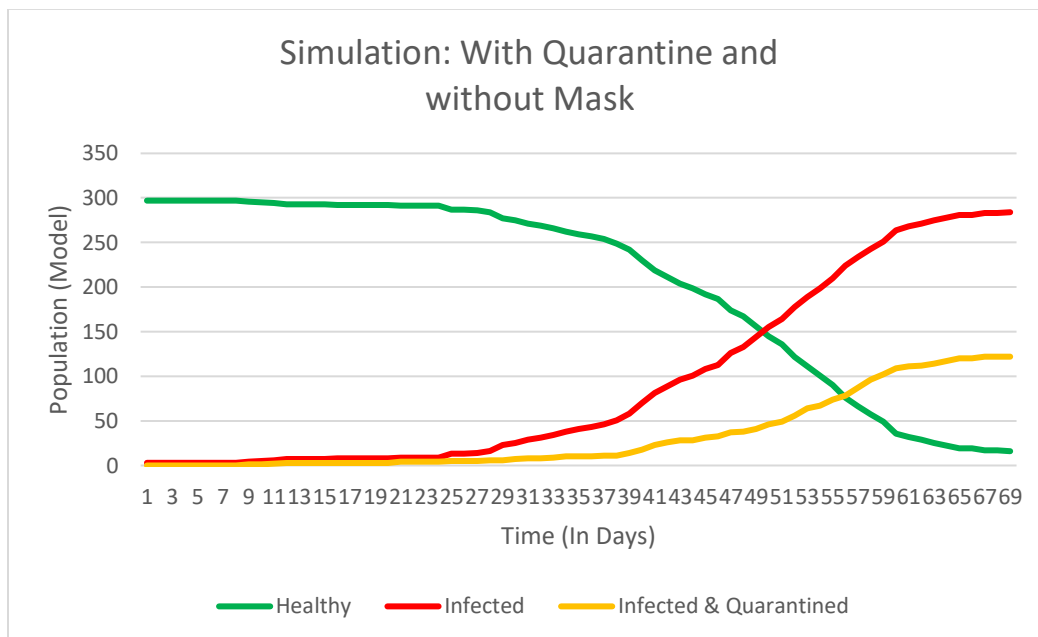


Explanation: This graph explains the number of healthy people vs Infected if there is a mask mandate in place, but infected people are not quarantined. In this case without an effective vaccine in place after few days the healthy people will contract virus and we can see that the infected will raise.

Mitigation #2

Quarantine mandate is applied with no mask mandate & 50% population following social distancing

Total Population	People wearing Mask	People following Social distancing	People in Quarantine
300	0	50%	135

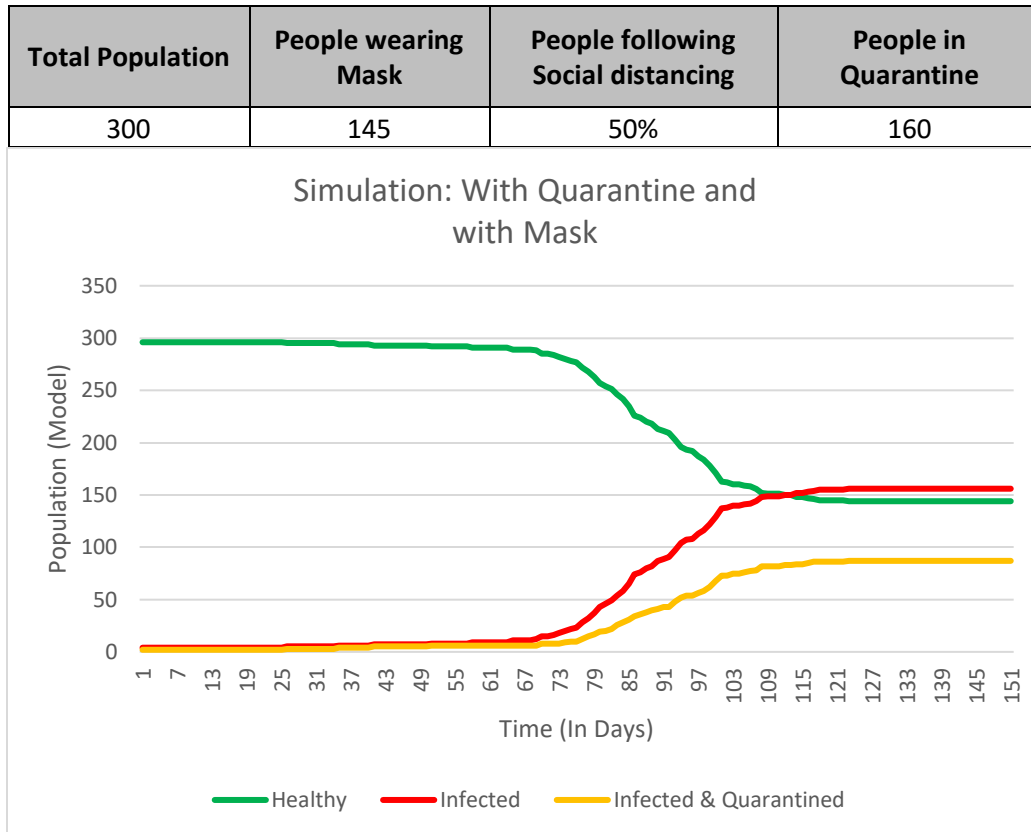


Result Explained:

This graph explains the number of healthy people vs Infected if there is quarantine in place, but no mask mandate. In this case without an effective vaccine in place after few days the healthy people will contract virus and we can see that the infected will raise, and the healthy people will decrease rapidly due to no mask mandate. Quarantine will be in line with infected people.

Mitigation #3

Quarantine mandate is applied along with mask mandate with 50% population following social distancing



Explanation: This graph explains the number of healthy people vs Infected if there is quarantine in place, along with mask mandate. In this case without an effective vaccine in place after few days the healthy people will contract virus and we can see that the infected will raise, and the healthy people will decrease slowly due to mask mandate. Quarantine will be in line with infected people. Even though there is rise in infected people after certain time there will not be rise in infections and the curve flattens for infected people and healthy people.

We can observe that with mask mandate and quarantine mandate along with 50% social distancing at one point in time infections will not increase and stabilize till effective vaccine will be release in market

Contact Tracing

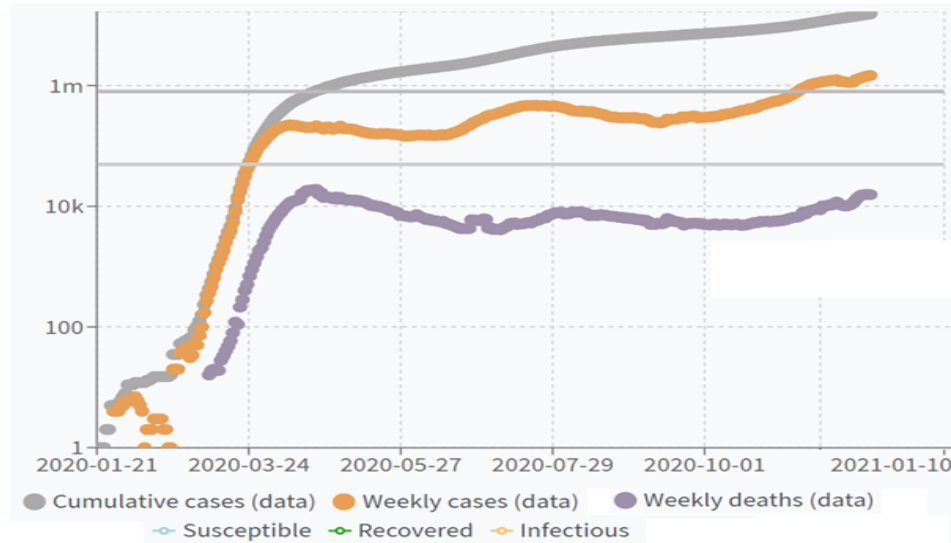
```
Person P-8617 was infected and contracted to --> P-7841
Person P-2843 was infected and contracted to --> P-7841
Person P-8837 was infected and contracted to --> P-8705 P-8837 P-4751 P-2308 P-0314
Person P-2373 was infected and contracted to --> P-8705
Person P-4751 was infected and contracted to --> P-8837
Person P-2308 was infected and contracted to --> P-8837
Person P-0314 was infected and contracted to --> P-8837 P-0314 P-5217
Person P-7306 was infected and contracted to --> P-8705
Person P-5217 was infected and contracted to --> P-0314 P-5217
Person P-2618 was infected and contracted to --> P-8705
```

Explanation: From the above figure we can conclude the following points about the results:

- Person P-8617 can be considered as patient 0
- Person P-8837 can be considered as Super Spreader as this person is transmitting the virus to 4 people which is highest in this simulation.
- This contact tracing will be useful in determining the impact of quarantine in spreading disease.

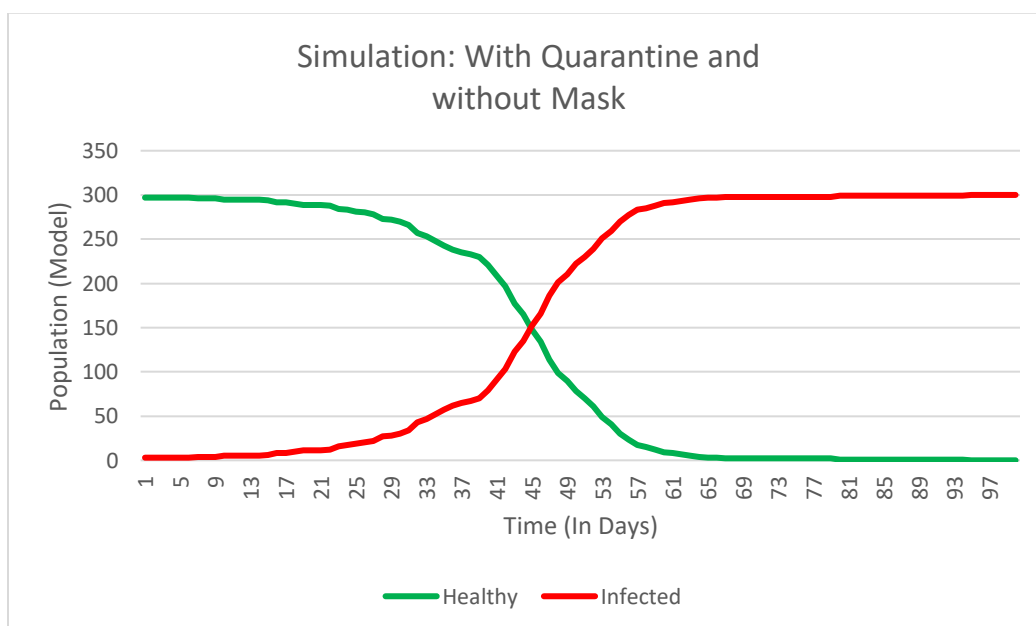
EVIDENCE

Below graph represents the united states population current case load due to virus:



Simulation with no mitigation applied (no mask and quarantine):

Total Population	People wearing Mask	People following Social distancing	People in Quarantine
300	0	50%	0



Result Explained: We have simulated the virus propagation without applying the mitigation factors. In case of 50% population following social distancing and not following mask mandate along with no one getting quarantined we observed that the infection will rapidly increase and reach highest level. In this scenario we see that the whole population will get infected.

In Ideal scenario after 50% population is infected, we will achieve herd immunity as the R-naught is expected to be 2.0 (research on going) in case of COVID-19. We have factored R-naught while considering the person in quarantine.

Screenshots

1. Simulation output if mask mandate is applied without quarantine

```
Total population: 300
Total wearing mask : 142
Total following quarantine: 0
Total population following social distancing163
```

Total	Healthy	Infected	Infected & Quarantined
300	297	3	0
300	297	3	0
300	297	3	0
300	297	3	0
300	296	4	0
300	296	4	0
300	296	4	0
300	296	4	0
300	296	4	0
300	296	4	0
300	296	4	0
300	296	4	0
300	296	4	0
300	296	4	0
300	296	4	0

2. Simulation output if quarantine mandate is applied with no mask mandate

```
Starting the simulation
Total population: 300
Total wearing mask : 0
Total following quarantine: 135
Total population following social distancing155
```

Total	Healthy	Infected	Infected & Quarantined
300	297	3	0
300	297	3	0
300	297	3	0
300	297	3	0
300	297	3	0
300	297	3	0
300	297	3	0
300	297	3	0
300	296	4	1
300	295	5	1
300	294	6	2
300	293	7	3
300	293	7	3
300	293	7	3
300	293	7	3
300	292	8	3
300	292	8	3

3. Simulation with Mask and Social Distancing factors

```
"C:\Program Files\AdoptOpenJDK\jdk-11.0.8.10-hotspot\bin\java.exe" "-javaagent:C:\Program Files\JetBrain
Start was pressed
Starting the simulation
Total population: 300
Total wearing mask : 145
Total following quarantine: 160
Total population following social distancing160
```

Total	Healthy	Infected	Infected & Quarantined
300	296	4	2
300	296	4	2
300	296	4	2
300	296	4	2
300	296	4	2

4. Simulation with no mitigation factors applied i.e. No Mask and No Quarantine

```
Total population: 300
Total wearing mask : 0
Total following quarantine: 0
Total population following social distancing154
```

Total	Healthy	Infected	Infected & Quarantined
300	297	3	0
300	297	3	0
300	297	3	0
300	297	3	0
300	297	3	0
300	297	3	0
300	297	3	0
300	296	4	0
300	296	4	0
300	296	4	0
300	295	5	0
300	295	5	0
300	295	5	0
300	295	5	0
300	295	5	0
300	294	6	0
300	292	8	0
300	292	8	0
300	290	10	0
300	289	11	0

CONCLUSION

Simulation model illustrates the interaction between the population, and the percentage of infectious people present in the population. We noticed that the plots show a clear 'tipping point': after 'n' number of infections, the virus spread starts accelerating if we will not apply Mask mandate and Self-Isolation. The peak number of infections strongly depends on how many people obey the self-isolation rules and mask mandate. However, reports have been going around that even without symptoms you can still be contagious, and remain contagious for quite some time after recovering, which makes such a self-isolation scenario and Mask mandate even more important and the simulation model confirms this in the case of SARS-CoV-2.

FUTURE STUDY

In near future this model can be fine-tuned by including the heterogenous population along with factors like hospital beds and emergency services. This will give even better picture of the virus propagation and load on the country.

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