

## Mini Project 1: Pandemic Flu Spread

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Amirtha Ganesh Pugazhendhi (GTID : 903515950)  
Apoorva N Srinivas (GTID : 903616049)  
Sukanya R Iyer (GTID : 903622016)

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# 1 ABSTRACT

This project studies the pandemic flu spread in a classroom of 21 elementary school kids. We have tried to implement an SIR(Susceptible, Infected and Recovered) model to compute the infected number on students on daily basis. In our model we have 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 have then simulated this condition both in Python and Arena and our major finding is that on average the infection lasts in the class for 15 days.

## 2 BACKGROUND AND DESCRIPTION OF THE PROBLEM

The motivation for our simulation model is 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. 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.

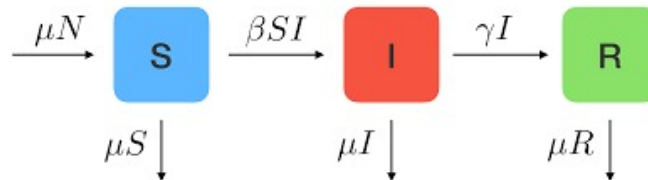


Figure 2.1: SIR model

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

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

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

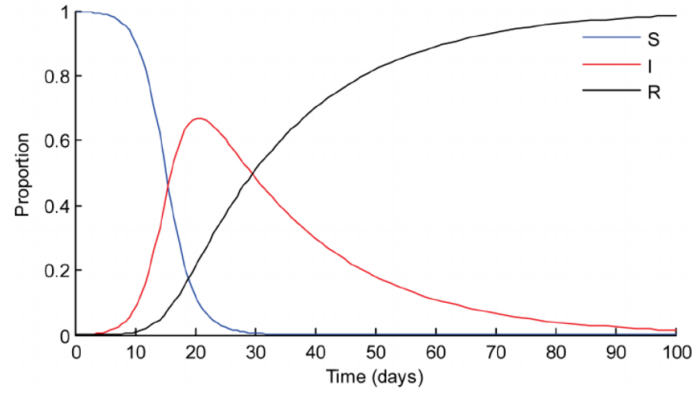


Figure 2.2: SIR epidemic trajectory

The problem given to us considers an elementary school setting with 21 students and one of the students, Tommy is infected on Day 1. All other 20 students are susceptible to the infection on day 1. Our model computes the number of students infected by the spread of the virus each day and finally arrives on the conclusion of the number of days the infection will last in the school. Each kid if infected will be infectious for 3 days i.e., there are 3 days that a student can transmit the infection to another student. Any infectious kid can infect the susceptible kids by a probability of  $p = 0.02$  and it is given that all kids and days are independent (so we have i.i.d. Bern(p) trials).

## 2.1 ASSUMPTIONS

- In our simulation model we have considered only the infection rate and we have not considered recovery
- Once a student is infected and recovered(after 3 days) the student is considered to be not susceptible to the flu and cannot be infected again.
- Chance of transmitting the infection by a student in the infectious state is defined by a random variable with Bernoulli distribution.

### 3 METHODOLOGY

We have used two simulation models to showcase this problem. We have shown our analysis and results for both the models.

#### 3.1 SIMULATION USING PYTHON

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 whoever they meet(21 students) for the next 3 days. After that they are considered to be recovered and susceptible to the flu. The probability of an infected student to infect any other student he/she comes in contact with is 0.02.

In our python program we have used the following steps to simulate the flu spread:

- We have introduced 5 functions primarily: to infect a student, to reduce the no of days of infection possible for infected person when a day is over, reduce the no of infected student, function to recover infected kids after 3 days of infection, function to track the count of number susceptible, infected and recovered.
- We defined our simulation length, no of trials that we want to simulate and created a data frame to collect the data of total number of infected, susceptible, recovered students.
- We have used lists to collect data of no infected, susceptible and recovered, probability of the infection is defined as 0.02.
- We have used two loops, the first loop calculates the no of infected students with their potential infection periods and the second loop uses Bernoulli random variable with  $p = 0.02$  to get the count of infected, susceptible and recovered students.
- The data frame is then used to collect the information and the populated data is used to observe the results of the simulation.

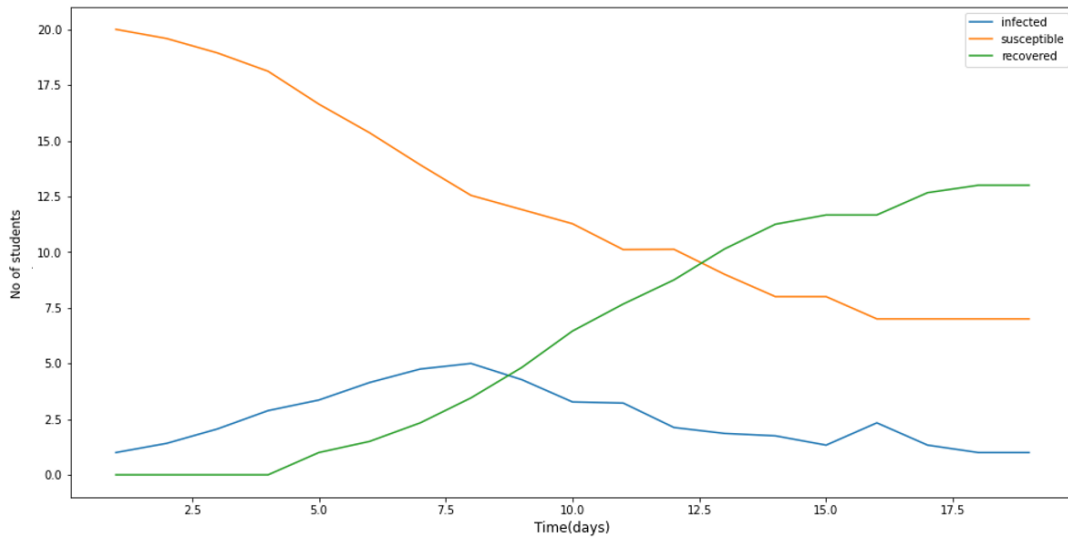


Figure 3.1: Pandemic Flu Spread Simulation using Python

From Fig. 3.1 we see that initially, the concentration of infectious candidates, grows approximately exponentially. The concentration of susceptible students, decreases at a constant rate as the disease invades the population(here the 21 students of elementary school). As a result, the frequency with which any given infectious individual comes into contact with a susceptible

individual decreases. 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 of students increases.

### 3.2 SIMULATION USING ARENA

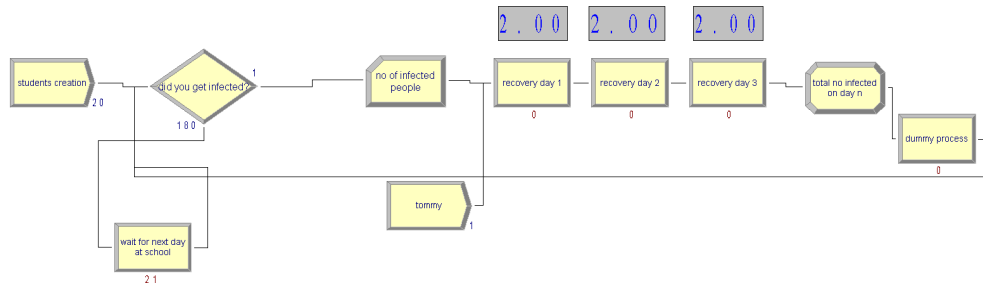


Figure 3.2: Pandemic Flu Spread Simulation using Arena

- In our arena model as depicted in figure 3.2 we have considered batch of 20 students as the input who stay in the system for 1 whole day.
- Tommy, the infected student enters the system as a separate entity.
- Decision model for Arena is different from Python as it accounts for all the people in different stages of recovery who infect the non infected students.
- Recovery Day 1, 2 and 3 are modeled as 1 day processes at the end of which the infected entity exits.
- People infected moved to recovery day 2 while these non infected go back in to the loop after delay of 1 day.
- The counter indicators tell the distribution of people among different stages of recovery for day 1,2,3.
- Record module used to record the students getting infected for first time and this count/entity is not accounted again in future.
- Assign module models a variable which is the sum of people in any stage of recovery at given point of time.

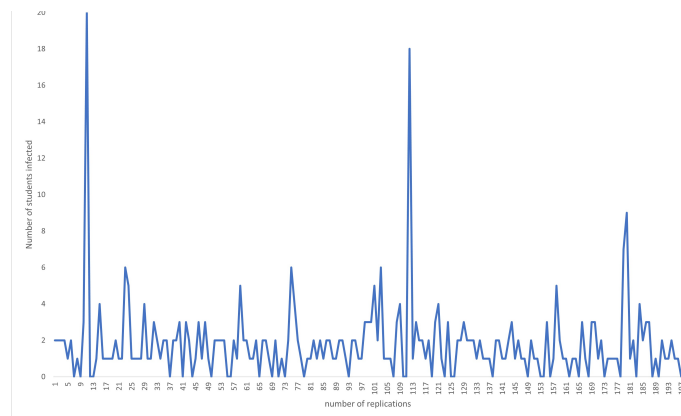


Figure 3.3: Replication vs number infected

- Fig 3.3 depicts the graph for replications vs number infected. Our arena simulation output report is depicted in Fig 3.4.

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Category Overview

March 7, 2021

Values Across All Replications

Simulation

Replications: 100 Time Units: Days

Queue

Time

Waiting Time	Average	Half Width	Minimum Average	Maximum Average	Minimum Value	Maximum Value
recovery day 1.Queue	0.2946	0.11	0.00	4.4211	0.00	9.0000
recovery day 2.Queue	0.00	0.00	0.00	0.00	0.00	0.00
recovery day 3.Queue	0.00	0.00	0.00	0.00	0.00	0.00

Other

Number Waiting	Average	Half Width	Minimum Average	Maximum Average	Minimum Value	Maximum Value
recovery day 1.Queue	0.03780000	0.03	0.00	1.6800	0.00	10.0000
recovery day 2.Queue	0.00	0.00	0.00	0.00	0.00	0.00
recovery day 3.Queue	0.00	0.00	0.00	0.00	0.00	0.00

Resource

Usage

Instantaneous Utilization	Average	Half Width	Minimum Average	Maximum Average	Minimum Value	Maximum Value
Resource 2	0.05660000	0.01	0.02000000	0.3800	0.00	1.0000

Number Busy	Average	Half Width	Minimum Average	Maximum Average	Minimum Value	Maximum Value
Resource 2	0.05660000	0.01	0.02000000	0.3800	0.00	1.0000

Number Scheduled	Average	Half Width	Minimum Average	Maximum Average	Minimum Value	Maximum Value
Resource 2	1.0000	0.00	1.0000	1.0000	1.0000	1.0000

Scheduled Utilization	Average	Half Width	Minimum Average	Maximum Average		
Resource 2	0.05660000	0.01	0.02000000	0.3800		

Total Number Seized	Average	Half Width	Minimum Average	Maximum Average		
Resource 2	2.8300	0.45	1.0000	19.0000		

User Specified

Counter

Count	Average	Half Width	Minimum Average	Maximum Average		
Counter 1	1.8300	0.45	0.00	18.0000		

Model Filename: C:\Users\Sukanya\Documents\School\Spring 2021\6644\simulation project\tria

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Figure 3.4: Arena simulation output

## 4 MAIN FINDINGS

(a). What is the distribution of the number of kids that Tommy infects on Day 1?

In our model we have considered that the probability that Tommy infects any individual susceptible kid on any of the three days is  $p = 0.02$ ; and we have considered that all kids and days are independent so that we have i.i.d. Bern(p) trials. We know that Bernoulli distribution is a special case of the binomial distribution where a single trial is conducted (so  $n$  would be 1 for such a binomial distribution). Thus our model validates this logic and from our results we found that the number of kids Tommy infects follows a binomial distribution. The formula for binomial distribution with the parameters we considered is given by,

$$P_x = \binom{n}{x} p^x q^{n-x}$$

where,

- $P$  = binomial probability of any susceptible student getting infected
- $x$  = number of times for a specific outcome (here getting infection) within  $n$  trials
- $\binom{n}{x}$  = number of combinations
- $p$  = probability of success in a single trial (here  $p = 0.02$ )
- $q$  = probability of failure in a single trial (here  $q = 0.98$ )
- $n$  = number of trials

(b). What is the expected number of kids that Tommy infects on Day 1?

For our simulation, on day 1 only Tommy is infected and we started our simulation from the next day. We calculated how many students he infected on second day for answering this question. We did 1000 trials considering 200 days with our simulation and found that on an average the number of infected students on the second day of simulation is: 1.401 student. This includes tommy as well thus  $1 - 1.396 = 0.396 = 0.4$  student get infected by tommy on day1. (approximately). This value can be validated by taking the mean of binomial distribution ( $np$ ) =  $200 * 0.02 = 0.4$  Refer fig 4.1.

(c). What is the expected number of kids that are infected by Day 2 (you can count Tommy if you want)?

On average on day 2 which is day 3 for our model, the number of infected students are: 1.882 students. Refer fig 4.1

```
mean_infected = df.groupby('days')['infected'].mean()
mean_infected
```

days	
1.0	1.000000
2.0	1.396000
3.0	1.882000

Figure 4.1: Expected number of kids that are infected on Day 1 and Day 2

(d). Simulate the number of kids that are infected on Days 1,2, . . . Do this many times. What are the (estimated) expected numbers of kids that are infected by Day  $i$ ,  $i = 1, 2, \dots$ ? Produce a histogram detailing how long the “epidemic” will last.

From our analysis we find that the epidemic lasts for 15 days. Refer to the fig 4.2.

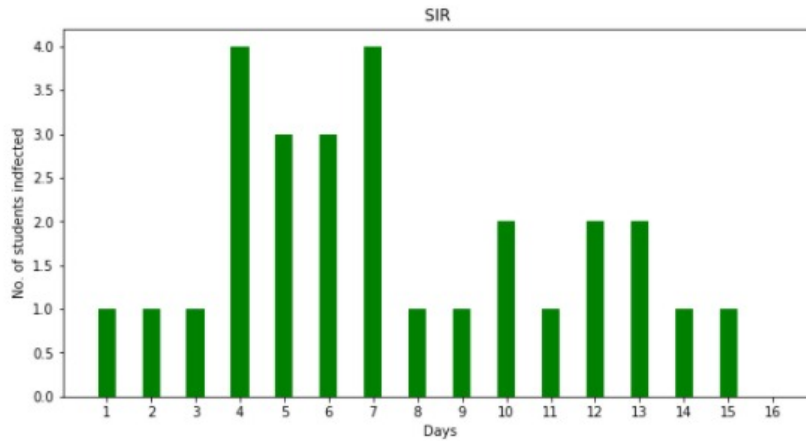


Figure 4.2: Expected number of days the epidemic lasts

Further analysis of the model leads to below **applications** and **limitations** :

- 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.
- The pandemic flu spread simulation analysis may prove useful in wide variety of fields. It 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 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.
- 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.
- 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.



## 5 CONCLUSION

We tried simulating the pandemic flu spread for a small data set consisting of 21 elementary students using python and arena. We played around simulating the condition of flu spread in both the software. We observed different outcomes with each simulation run but the distribution remained the same. We even tested by trying different probabilities and observed how by increasing the probability of spreading the infection the number of people infected increases. 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.