

Simulating Pandemic Flu Spread

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Abstract

How does the spread of a pandemic flu evolve in a classroom? Our project focuses on the applications-oriented problem (No. 3), which considers the flu spread set off by one kid in a classroom of 21 kids. In this project, we simulated how a pandemic could develop within a class under different conditions. In particular, we modeled how the number of kids who are susceptible to the infection, infected, and recovered could change over time.

We built our simulation model in Python and adapted it to the implementation in multiple scenarios. We first built a deterministic model to simulate the situation described in the problem. We then added randomness to the model by experimenting with different distributions of the infection probability to reflect the reality of a pandemic flu spread. Finally, we performed the sensitivity analysis to test our deterministic model under different parameter settings.

We found that the speed and intensity of the pandemic flu increase the most at the early stage of the pandemic outbreak. The pandemic will last longer, and the infection peak will come later as the recovery days for individuals increase. Through the stochastic simulation and the sensitivity analysis, we conclude that early detection and intervention of pandemic are critical to containing the spread. Protection measures such as isolation and social distancing will contribute the most at the early stage of identifying the virus.

Introduction

In this simulation project, we consider the spread of a pandemic flu in a classroom of 21 elementary school kids. At the beginning of the simulation, 20 of the kids are healthy and susceptible to the flu, and one kid (Tommy) is infected with the flu virus. The infected kid has the chance of contacting everyone in the classroom and spreading the flu to anyone he meets, at a probability p of 0.02 per day. For our initial deterministic model, we assume that, as in the problem description, any infected person will be infectious for 3 consecutive days. On any of the three days, any individual susceptible kid has a chance of 0.02 of getting infected by the infectious person. After 3 days of infection, the infected kid will fully recover and is immune to the flu.

The main questions that we would like to answer for this project include:

- How can we model the development of the infection chain initiated by Tommy over time?
- What is the distribution of student infections each day?
- How do we estimate the expected number of kids infected each day?
- What is the maximum number of kids that can stay infected on any given day?
- How long will the flu spread last among the students?

- When does the number of infections reach the peak?
- How long does the peak last?
- What precautionary measures can we recommend containing the spread of the pandemic?

To answer these questions, we divide our simulation approach into three parts:

1. Building a deterministic simulation model with the parameters given in the problem description, such as probability of being infected, time for recovery, and capable infection scope of every infected kid, and analyzing simulation output.
2. Creating a stochastic model to treat the key parameters given in the problem as unknown, introduce random variables as estimators for those parameters, and simulate the results for different distributions of the random variables in multiple replications.
3. Performing scenario and sensitivity analysis to determine the impact of e.g. class size, infection rate, required recovery time to develop immunity. Based on this, we can recommend relevant protection and precaution measures, e.g. isolation policy, optimal class size, intervention activity, etc. to contain the pandemic.

The remainder of this report is organized as following.

Methodology

- We first describe the methodology that we used to build the base deterministic model, including the theory behind the model, the input and output variables used in the model, and the main assumptions we made for the simulation.
- Then we run the deterministic model built in the Python environment and document the simulation results.

Main findings

- After running the deterministic simulation, we present the main findings and use them to answer the question a), b), and c) outlined in the problem description of this project.
- Then we move forward with the stochastic simulation and answer the question d) in the problem description. We also present our findings from three different stochastic cases.
- We continue with the sensitivity analysis and report our insights and recommendations.

Conclusion

We conclude our report with a project summary and discussion on the further improvement for our model.

Methodology

Deterministic Simulation

To solve the problem at hand, we will be using the well-established SIR model [1] to simulate the flu spread in a class of 21 students. As per the methodology defined for this model in [2], we will be dividing our fixed population into three categories. The sizes of these three categories vary as a function of time. These three variables along with supporting variables can be defined as following:

$S(t)$ = Number of individuals at time t , which are susceptible to get infected

$I(t)$ = Total number of individuals at time t , that are infected.

$R(t)$ = Total number of individuals who have recovered from the disease.

N = Population size. Equivalent to 21 students as per our problem statement.

In terms of the variables defined above, a particular non infected student is initially part of the $S(t)$ category and then moves to $I(t)$ category after getting infected from Tommy or another student. After completing the recovery period of three days, the student moves in the $R(t)$ category and remains in that category until the end of the pandemic. This statement highlights the first assumption in our methodology which states that a student who is infected once, gains immunity from the disease after the recovery period and therefore cannot get reinfected. A flow chart describing the aforementioned chain of events is shown in Figure 1:



Figure 1: Flow of population across category

Our main objective is to mathematically define the changes in the above-mentioned category with respect to small time interval denoted as Δt . After defining these changes for a small-time interval, we can let Δt go to zero and ultimately acquire derivatives of above-mentioned categories with respect to time. To formulate our problem, we can create a uniform time mesh given by $t_n = n * \Delta t$. The approximate value of S at t_n is given by S^n . S^n is a numerical approximation of the exact value of S at time t_n which is denoted by $S(t_n)$. Likewise, we can define I^n and R^n as numerical approximation of $I(t_n)$ and $R(t_n)$ respectively at time t_n .

We can start our solution formulation by first defining the change in $S(t)$ category in time interval ΔT . Theoretically speaking there can be in total n possible interactions between the students in S and I categories in a given time interval T . Given that out of these n possible interactions, m number of possible pairings actually occur, we can define the probability of student interacting in time interval T as $\frac{m}{n}$. This probability can be further defined for a unit time interval as following $\mu = \frac{m}{n*T}$.

Given that the total number of possible interactions are SI ; the expected number of meetings per time interval between students in S and I categories can be defined as μSI and total number of these meetings for a time interval Δt can be defined as $\mu SI \Delta t$. Out of $\mu SI \Delta t$ possible interactions, only a fraction of these

meetings will lead to the person getting infected. Given that out of y possible interactions, x number of people get infected, then the probability of getting infected is given by $p = \frac{x}{y}$. Hence, the expected number of students belonging to S category that can get infected in Δt time interval can be defined as $p\mu SI\Delta t$. By defining $\beta = p\mu$, we can simply our formula as $\beta SI\Delta t$. Using aforementioned derivation, we can define the change in S category as following:

$$S^{n+1} - S^n = -\beta S^n I^n \Delta t$$

At this stage, it is intuitive to observe that the loss in S category is equivalent to the gain in I category. This gain can be defined as following:

$$I^{n+1} - I^n = \beta S^n I^n \Delta t$$

However, in addition to this gain, there will be a loss in this category as well since some students who will get infected, will eventually move to R category after completing their recovery period. Given that a students out of b total number of infected students recover in a time period T , then the probability that one individual recovers in a unit time interval can be defined as $\gamma = \frac{a}{bT}$. Then for a small interval Δt , the number of infected people that can recover can be defined as $\gamma I \Delta t$. This quantity denotes the loss in the I category. Therefore, the equation for the change in I category can be updated as following:

$$I^{n+1} - I^n = \beta S^n I^n \Delta t - \gamma I^n \Delta t$$

The loss in I category is equivalent to gain in R category. Given that there is no loss in the R category the change for this category can be simply defined as following:

$$R^{n+1} - R^n = \gamma I^n \Delta t$$

The derivation process can be summarized as per following mathematical equations:

$$\Delta t = \text{Small time interval}$$

$$S^n = \text{Approximate value of } S \text{ at time } t_n$$

$$I^n = \text{Approximate value of } I \text{ at time } t_n$$

$$R^n = \text{Approximate value of } R \text{ at time } t_n$$

$$SI = \text{Total possible interactions of students in } S \text{ and } I \text{ categories}$$

$$n = \text{Theoretically possible pairings of students during time interval } T$$

$$m = \text{Actual possible pairings of students during time interval } T$$

$$\mu = \frac{m}{nT} = \text{Probability that people meet during time interval } T, \text{ per unit time}$$

$$\mu SI = \text{Expected number of meetings per unit time interval of } SI \text{ possible pairs of students}$$

$$\mu SI \Delta t = \text{Expected number of meetings during time interval } \Delta t \text{ of } SI \text{ possible pairs}$$

$$p = \frac{x}{y} = \text{Probability of getting infected, given } x \text{ people get infected in } y \text{ such meetings}$$

$$\beta = p\mu$$

$$p\mu SI\Delta t = \beta SI\Delta t = \text{Change in } S \text{ category for } \Delta t \text{ time interval}$$

$$\gamma = \frac{a}{bT} = \text{Probability that one individual recovers in a unit time interval}$$

$$S^{n+1} - S^n = -\beta S^n I^n \Delta t = \text{Change in } S \text{ category}$$

$$I^{n+1} - I^n = \beta S^n I^n \Delta t - \gamma I^n \Delta t = \text{Change in } I \text{ category}$$

$$R^{n+1} - R^n = \gamma I^n \Delta t = \text{Change in } R \text{ category}$$

To apply this methodology to our case study, we would need the input values of parameters β and γ and initial conditions for the three categories $S(0) = S_0$, $R(0) = R_0$ and $I(0) = I_0$. As per our problem statement initial conditions for our categories can be defined as following:

$$S_0 = 20 \text{ students}$$

$$I_0 = 1 \text{ student, Tommy}$$

$$R_0 = 0 \text{ students}$$

The main challenge is to determine the correct value of β and γ parameters. As per the definitions of β and γ defined above, the values for these parameters are usually defined as per observed data. However, as per our problem statement, observed data is not available, therefore we must define these parameters in an alternative manner. As per [3] and [4] β is defined as the infection rate and is the product of the transmission risk with the average number of contacts per day. Therefore, we can define β as following:

$$\beta = \text{Infection Rate} (= 0.02) * \text{Average_Contacts_Per_Day}$$

After defining β as per above equation we would have to make certain changes in our difference equations. In the updated equations the product $\beta S^n I^n \Delta t$ has to be divided by N which is equivalent to total number of students in class.

As per [5] and [6], the recovery rate parameter γ can be defined as the inverse of the time period that it takes a particular individual to recover from an infection. Therefore, for our case study γ should be $\gamma = \frac{1}{3}$. However, as per our problem statement, if we use the SIR model directly then the model will update the R category from day 1. As per our problem, an infected student recovers after 3 days and therefore, the R category should be updated on the third day. To take into account this effect, we have modified our difference equations such that, the addition in R category starts after the end of fourth day and any further addition in this category is equivalent to the new additions in the I category four days earlier. The first addition in R category on third day is 1, which is equivalent to Tommy getting recovered on day 3.

Taking these factors into account, our updated difference equations for the deterministic case look as following:

$$S^{n+1} - S^n = -\frac{\beta S^n I^n \Delta t}{N} = \text{Change in } S \text{ category}$$

$$I^{n+1} - I^n = \frac{\beta S^n I^n \Delta t}{N} = \text{Change in } I \text{ category where } n < 3$$

$$I^3 = 1$$

$$I^{n+1} - I^n = \frac{\beta S^n I^n \Delta t}{N} - I^{n-4} = \text{Change in } I \text{ category where } n \geq 4$$

$$R^{n+1} - R^n = I^{n-4} = \text{Change in } R \text{ category where } n \geq 4$$

Before applying the SIR model to our case study, it is important to list the main assumptions of this model. The underlying assumptions of this model are as following:

1. A student who is infected once, will recover after 3 days, and will gain immunity from the disease, thereby eliminating the possible of reinfection.
2. There is no latency period after a particular individual gets infected. This means, that once an individual gets infected, they are immediately likely to infect others from the next day.
3. The risk of contagion of infection is equal for all members of population

Stochastic Simulation

To analyze the impact of stochastic variables, we only change one variable into distribution each time. In the following discussion, the parameters we were experimenting on were mainly average number of contacts per student, recovery rate. We added randomness by assigning those parameters with uniform, exponential, and normal distributions. We simulated 60 days per round for a total of 100 rounds to get the average results.

Sensitivity Analysis

For the sensitivity analysis, we use the deterministic model as our base model. We compare the difference in the simulation output by changing the key parameters of the model. The input parameters that we want to vary are, for example, the infection probability p , the class size, and the time required for recovery after the infection. We will determine the impact of these input parameters on the model output and make recommendations for pandemic control accordingly.

Main Findings

Deterministic Simulation

For our first simulation, we used the following inputs:

$$S_0 = 20$$

$$I_0 = 1$$

$$R_0 = 0$$

$$\text{Average Contacts Per Day} = 20$$

$$D = \text{Duration of Simulation} = 30 \text{ Days}$$

$$dt = \text{Small Time Interval} = 1 \text{ Day}$$

$$\beta = \text{Infection Rate} (= 0.02) * \text{Average_Contacts_Per_Day}$$

The result of our first simulation is shown in Figure 2:

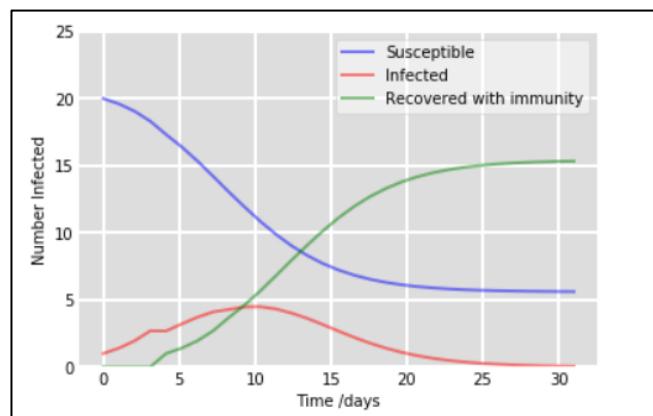


Figure 2: Deterministic Simulation Output

As per these results, the first and foremost inference that we can make is that the distribution for a particular student to get infected on any day is Bernoulli with probability of success defined as 0.02. Secondly, given that Tommy will be making multiple contacts on the first day and only a certain number of these contacts will lead to infection transmission to other students, we can state that the distribution of the number of kids that Tommy infects on Day 1 is Binomial with probability of success of 0.02 and number of trials equivalent to the number of contacts he makes on the first day.

From our simulation results we can determine that the estimated number of students who will get infected after day 1 is 0.4. This is the similar to the result we would get, if we multiply the probability of success to the number of contacts Tommy makes on day 1, assuming that Tommy makes contact with every other student on day 1. This value is equivalent to $0.02 * 20 = 0.4$.

By the end of day 2, estimated number of students that will get infected is 1.948, including Tommy. As per Figure 2, it appears that after 28 days, the pandemic ends since by then more than 20 students have recovered with immunity and the number of infected and susceptible students have declined to zero.

Stochastic Simulation

We mostly simulated deterministic cases in the previous section, which means that the probability of contacting and infecting other students was fixed for every day, every student. In this section, we will attempt to simulate our case using a stochastic method. We can investigate how the stochastic simulation model differs from the deterministic one by assigning probability to the contact rate, infection rate, and so on. We reasoned that this stochastic model would better reflect reality. We decided to utilize the SIR model to build stochastic simulation.

Deterministic base case:

Our basic model is to set average number of contacts as 15. As we can see from Figure 3 below, the infected number of students reach its maximum on the 18th day, the number of recovered students converged about at the 60th day.

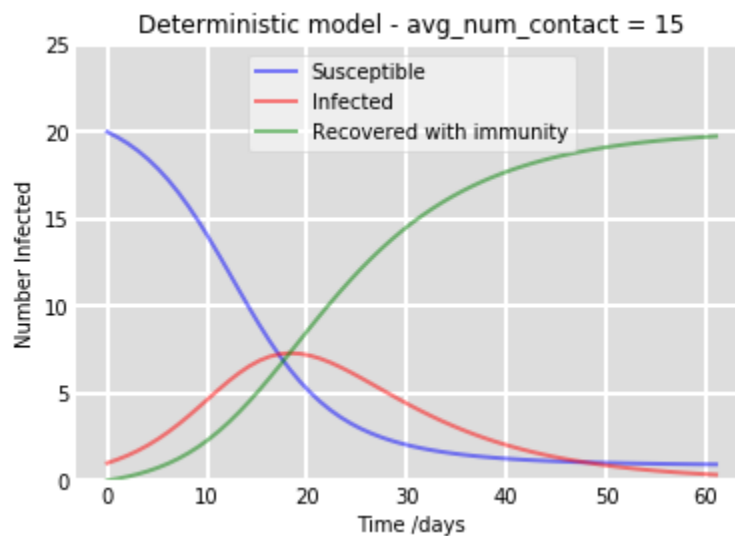


Figure 3: Deterministic Simulation Using SIR

Stochastic case:

Contact variation among days

Students in school may have a variety of activities and classes on any given day. As a result, we'd like to incorporate day-to-day variation into the average number of contacts per day. We assigned uniform, exponential, and normal distributions to our simulation model's daily contact number of students. The mean of our uniform, exponential, and normal distributions was set as 15.

For uniform distribution, we set the range for uniform distribution as 10 to 20. We found that the peak value of infected students and the equilibrium day of the simulation models were similar to our initial deterministic one, with slight differences in numbers because of randomness. After we run the simulation

100 times, we calculated the average infection peak day was 17.96, and almost converged at the 60th day. This result was very similar to deterministic case.

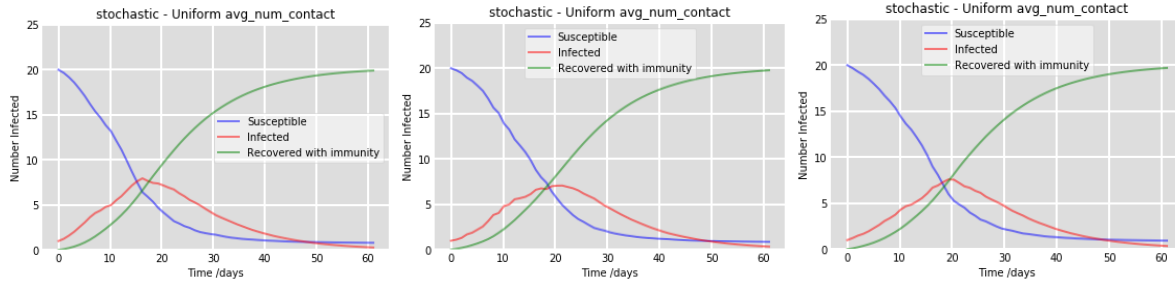


Figure 4: Stochastic Daily Contact Simulation Using Uniform Distribution

In terms of exponential distribution, we found that there were a lot of zigzag shapes in the curve and the peak day could vary a lot. We run the simulation 100 times, we calculated the average infection peak day was 18.9, and the convergence was getting later compared to the deterministic case.

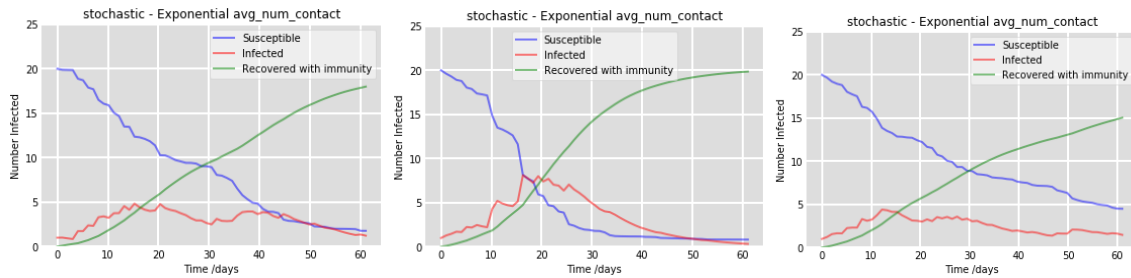


Figure 5: Stochastic Daily Contact Simulation Using Exponential Distribution

The normal distribution model was similar to the uniform distribution. The average infection peak day was 18.05, and the convergent day was 19.09. When we assigned it as normal distribution, we find that when we have higher variance, it would be similar to the uniform distribution. While if it has lower variance, the outcome is similar to the deterministic case.

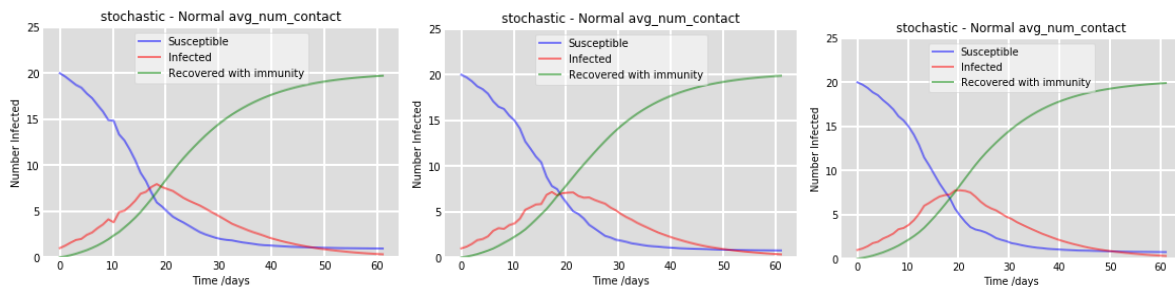


Figure 6: Stochastic Daily Contact Simulation Using Normal Distribution

We discovered that when the distribution is skewed to the right, the peak day is later than in the deterministic case.

Fitness variation among individuals

In this section, we'd like to look at the differences in fitness among students. Students with poor physical health may require more days to recover from the flu, and vice versa. We primarily used a uniform distribution, and we discovered that the situation in this model can vary greatly, as the stochastic recovery rate introduced relatively more variances into the model.

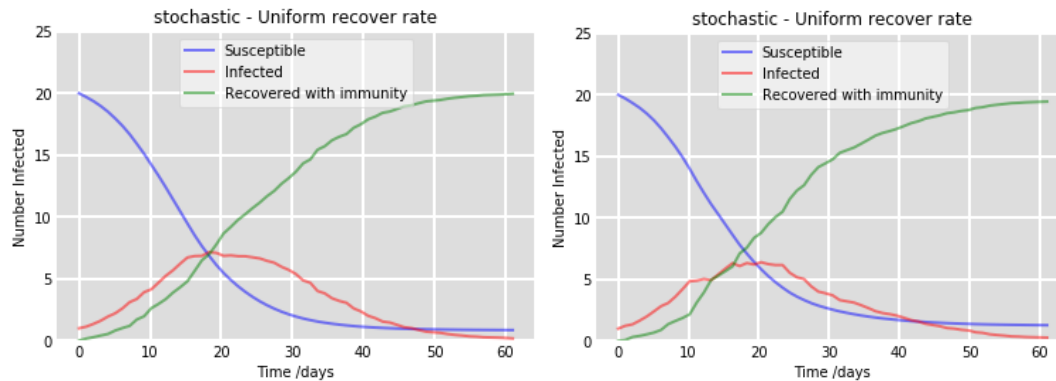


Figure 7: Stochastic Daily Fitness Situation Simulation Using Uniform Distribution

School policy interaction

The preceding sections were all predicated on the assumption that no school-level interception limits student contact. In practice, however, if there are more infected students, the school will most likely take measures to isolate them socially. To simulate this scenario, we will employ the second stochastic simulation model and include a negative relationship between the number of infected students and their contact. As shown in the graph below, this policy is beneficial in lowering the peak and halting the spread of flu early.

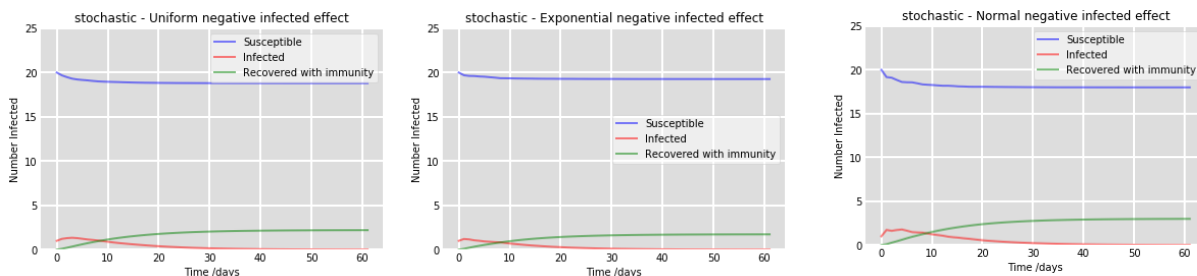


Figure 8: Stochastic School Policy Simulation Using Uniform, Exponential and Normal Distribution

Sensitivity Analysis

In the section of deterministic simulation, we modeled the pandemic flu spread under deterministic conditions. The key parameters were given and fixed for the simulation. For example, the probability that an infected kid can infect any individual susceptible kid during the infection period was given as $p = 0.02$. The infection period of an infectious kid was set for 3 days. In addition, the class size remained unchanged for 21 students, including Tommy. We also assumed that an infectious kid will have the chance to contact every other kid in the class during his or her infection period.

What if we want to know how the pandemic flu spread will look like with different values of the parameters? How fast will the pandemic spread if the flu is more contagious, meaning a higher probability of getting infected? How long will the pandemic last if the infection period is not 3 days but 5 days, or even longer? Will a smaller class size alleviate the flu spread? How will the maximum number of infections change in those scenarios? When will the infection peak occur? What appropriate actions can we take to reduce the spread of the pandemic flu? We are interested in the answers to these what-if questions. To answer them, we perform the sensitivity analysis on the deterministic simulation model described at the beginning of this chapter.

We will compare the simulation results by changing the following parameters:

1. The probability p that any infected individual can infect another person on any particular day during his or her infection period
2. The infection period inf_t in days of an infectious kid
3. The class size n
4. The average ratio r of the class that an infected kid will be able to contact on each day during his or her infection period

We will observe the following output of the simulation as we change the parameter values:

1. The day on which the pandemic stops in the class d_i
2. The maximum number of kids who stay infected on any day during the pandemic spread max_inf
3. The day on which the infection peaks max_inf_d
4. The number of days that the infection peak lasts for max_inf_len

Variation of infection probability p

We first perform the sensitivity analysis for the probability p . Below are the simulation results for $p = 0.02$, 0.04, 0.06, and 0.08

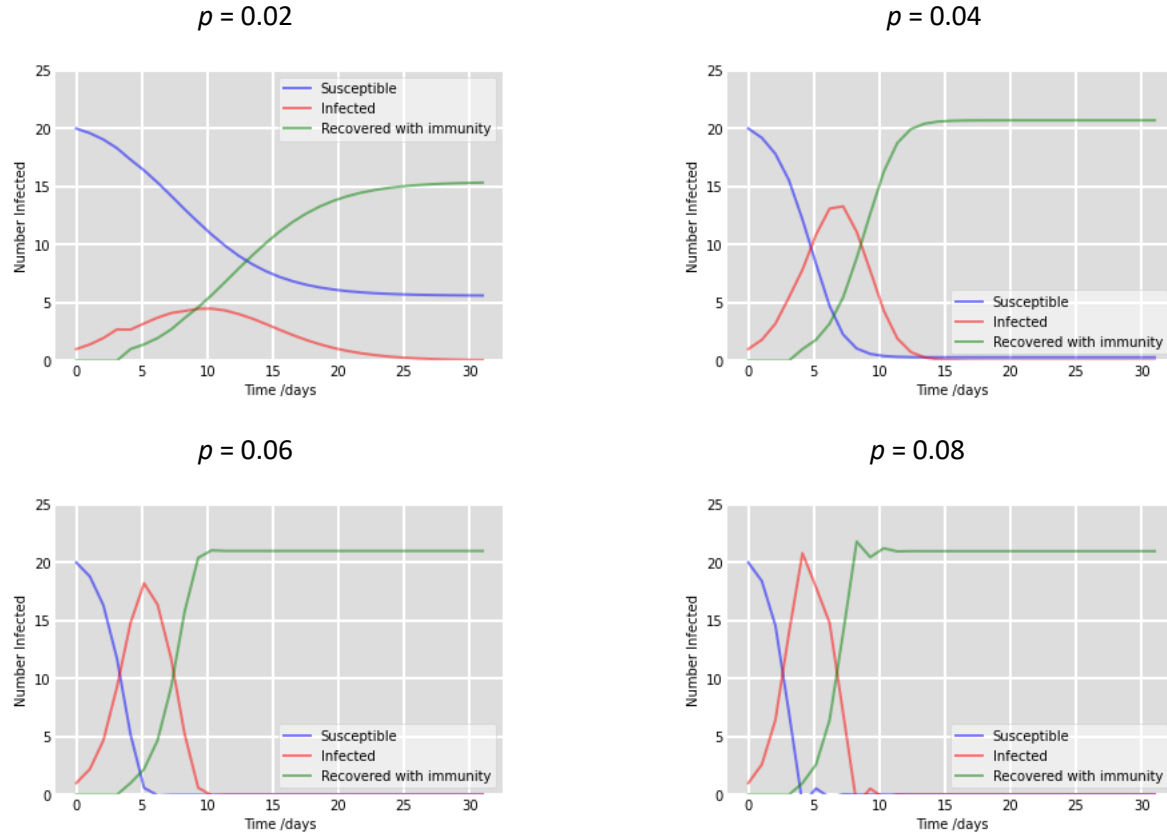


Figure 9: Simulation result with different infection probability p

Table 1: Sensitivity Analysis for Probability p

p	d_i	max_inf	max_inf_d	max_inf_len
0.02	28	4.49	10	1
0.04	15	13.30	7	1
0.06	10	18.21	5	1
0.08	8	20.80	4	1

We noticed that the increase of maximum number of infected kids tends to be slower as the infection probability rises. The maximum number of infections has tripled when the probability doubles from 0.02 to 0.04. Accordingly, the days on which the pandemic stops and peaks come earlier with the increasing probability, also with biggest jump from $p = 0.02$ to 0.04.

This suggests that the critical point of large flu outspread might be the early stage of virus mutation, where the infection probability increases. It is, therefore, important to contain the pandemic spread in the beginning of identifying the virus.

Variation of infection period in days with probability $p = 0.02$

Next, we look at the simulation results by changing the infection period in days. We begin with the infection probability $p = 0.02$

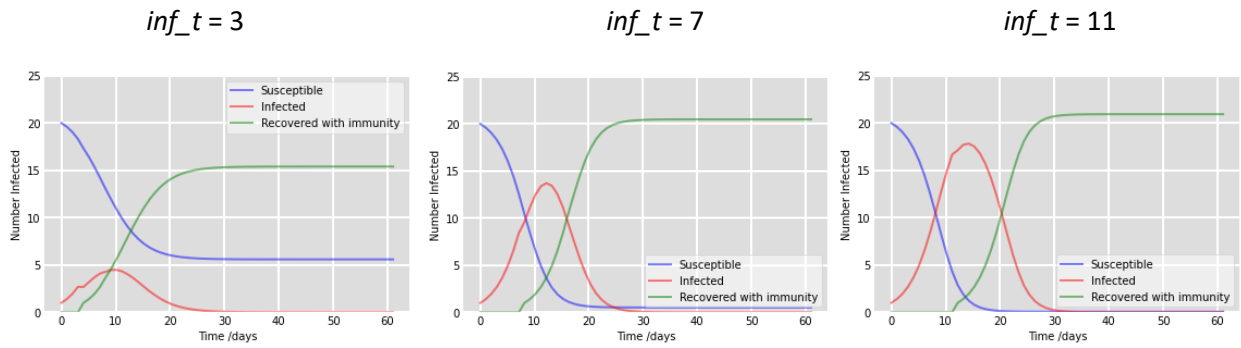


Figure 10: Simulation result with different recovery time in days under the infection probability $p = 0.02$

Table 2: Sensitivity Analysis for Infection Period inf_t with $p = 0.02$

Inf_t	d_i	max_inf	max_inf_d	max_inf_len
3	28	4.49	10	1
7	29	13.71	12	1
11	32	17.83	14	1
15	35	20.32	15	1

As the infection period prolongs, the pandemic lasts longer, and the infection peak comes later. The change of maximum number of infections shows a similar pattern to the that with the increasing infection probability. This implies that the pandemic disease with longer recovery time will extend the time for virus circulation, making it harder to stop and increasing the risk of further infection in a larger scope. The largest jump of infection strength occurs between the infection length of 3 to 7 days.

Variation of infection period in days with probability $p = 0.2$

Let's look at what happens for the different infection lengths on a pandemic with the infection probability $p = 0.2$.

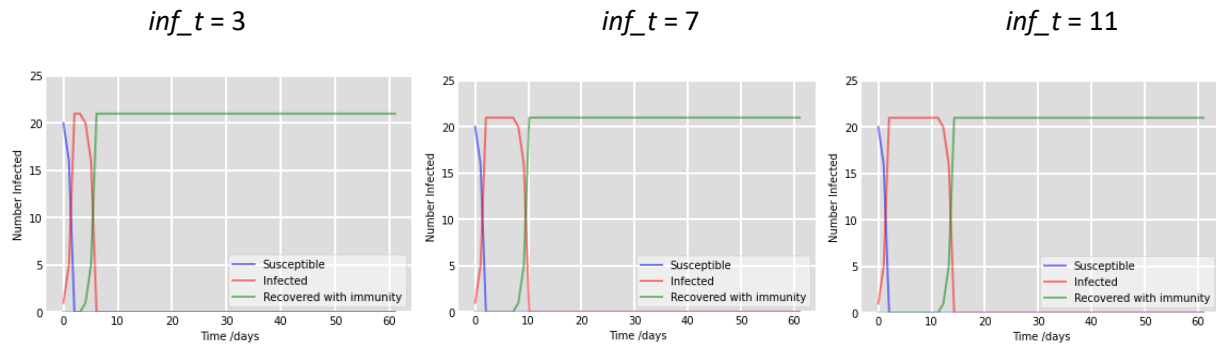


Figure 11: Simulation result with different recovery time in days under the infection probability $p = 0.2$

Table 3: Sensitivity Analysis for Infection Period inf_t with $p = 0.2$

Inf_t	d_i	max_inf	max_inf_d	max_inf_len
3	6	21	2	2
7	10	21	2	6
11	14	21	2	10
15	18	21	2	14

With the infection probability $p = 0.2$, it takes only two days for infection to reach the peak level, regardless of the recovery period for infected people. The entire class will be infected under all infection periods. Besides, the longer the recovery period is, the longer the infection peak will last. This reminds us that highly infectious virus, such as corona virus, with the infection probability of over 0.2 is able to infect a very large portion of the population in extremely short time. It is, therefore, important to identify this kind of highly contagious virus very early and implement special counter-measures to mitigate the severe impact of the pandemic.

Variation of class size

Finally, we look at the how the class size will affect the spread of the pandemic flu.

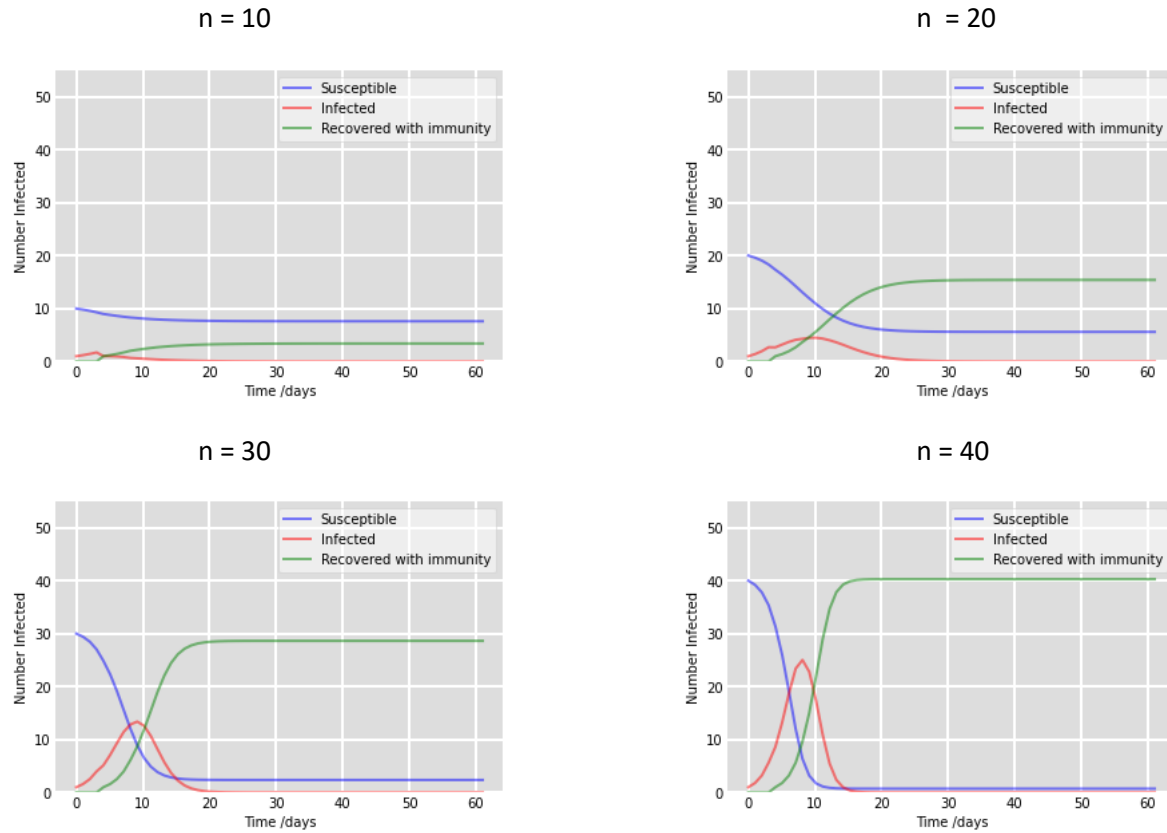


Figure 12: Simulation result with different class sizes

Table 4: Sensitivity Analysis for Class Size

n	d_i	max_inf	max_inf_d	max_inf_len
10	20	1.71	3	1
20	28	4.49	10	1
30	21	13.38	9	1
40	17	25.02	8	1

We can see that the ratio of the maximum number of infections to the class size increases significantly as the class size increases. This suggests that the pandemic spread is less effective in a smaller size of population. It implies that separation and isolation of infected individuals would help reduce the speed of virus infection. Therefore, it is important to implement appropriate distancing measures to contain the pandemic spread. Interestingly, the duration and the peak infection number drop with the class size larger than 20. This may be attributed to the decreasing circulation speed of the virus in a larger population if the recovery time is short, and the infection probability is low.

Conclusion and Discussion

In this project, we used simulation methods to investigate the various possibilities of flu spread in a class with one infected student.

We first investigated a deterministic method for estimating the number of infected students each day. Then we experimented with converting determined values into variables and comparing the results of uniform, exponential, and normal distributions. In addition, we used sensitivity analysis on our models to determine the importance of each parameter in our model.

In the deterministic scenario, we described our model in terms of difference equations and set the initial parameters β as a constant value which was derived from infection rate and average number of contacts per day. Moreover, we updated our R category as such that the first entry in this category would be 1 followed by the number of students who were infected four days earlier. From deterministic simulation, we were able to determine that after 28 days, the pandemic ends since by then more than 20 students have recovered with immunity and the number of infected and susceptible students have declined to zero.

For stochastic simulation, we find that adding randomness into our model can bring different outcomes each round, while if we keep the distribution symmetric and have higher variances, the peak point of infection and equilibrium point of the system would be similar to the deterministic case. Besides, we also found that if the school taking strict social distancing policies, the flu could be stopped in early stage.

In the sensitivity analysis, we used the deterministic model as the baseline and tested different combinations of the parameters for the simulation. We found that the spread of pandemic flu is closely related to the infection probability of an individual, the recovery time from the disease, and the class size. To successfully contain the pandemic, it is crucial to identify the virus early and take precautionary measures such as isolating infected people and keeping social distancing before the flu evolves.

We conclude our report with a project summary and discussion on the further improvement for our model. Our models were all predicated on the assumption that the classroom is a closed system, that the flu is not contagious, and so on. In reality, however, the situations are far more complicated. So, in the following steps, we'll try to simulate in a more open system and experiment with a larger number of parameters.

Besides, when we were considering the daily variation of students' contact rate, we used random numbers to simulate the variation. We could improve our simulation by collecting real world data of student's everyday activities and make our simulation model more accurate.

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