

# Math 142 Project Report

## 1 Introduction and Background

The COVID-19 pandemic spread to the United States beginning in January 2020, which was when the the first few cases were identified. To this day, over 9 million people have been infected with coronavirus.

Collective models, including SIR, SIRS, SEIR, SIRD model, have been proposed to understand the evolution of pandemics. Specifically, these models divide the total population into three groups, Susceptible individuals, Infected individuals and Recovered individuals and track the change in their population.

For our model, we decided to work with Prompt 1, which asked us to track the U.S. population during the COVID-19 pandemic. Our main goal was to improve the SIRS (with vital dynamics) model by introducing new factors or removing, adding some proper assumptions.

## 2 Model Explanation

We built the model based on SIRS (with vital dynamics). We introduced an additional constant ( $d_1$ ) to differentiate between COVID related deaths ( $d_1$ ) and deaths by natural causes ( $d$ ).

Our Modified Model:

$$\begin{cases} \frac{dS}{dt} = -\beta \frac{SI}{N} + \alpha R + bN - dS \\ \frac{dI}{dt} = \beta \frac{SI}{N} - \gamma I - (d + d_1)I \\ \frac{dR}{dt} = \gamma I - \alpha R - dR \end{cases} \quad (1)$$

Here  $S$  stands for susceptible individuals,  $I$  stands for infected individuals,  $R$  stands for recovered individuals.

The parameters are:

$\beta$ : contact rate,

$\alpha$ : "return" rate, that is, the possibility that recovered people become susceptible again,

$\gamma$ : recovery rate,

$b$ : birth rate,

$d$ : normal death rate,

$d_1$ : COVID related death rate.

Notice that  $\frac{dN}{dt} = \frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = (b - d)N - d_1I$  reflects the change in population over time.

For this model we make the following assumptions:

- Total population is not fixed (birth and death rates are considered).
- Pandemic is long term.
- No migration during the pandemic due to mobility restrictions.
- Birth, death, infection, recovery, and return rates are all constant parameters.
- Infection, recovery, and return rates are the same for each individual.

The total population has suffered drastic changes due to the deaths from the virus, which is why birth and death rate are incorporated into the model. It's very clear that the pandemic is not going to end overnight, so the model is used to predict populations over an extended period of time. To make the model more specific, the parameters can be adjusted based on a variety of factors, including but not limited to age, vaccination status, season, laws, and variants. Although we didn't demonstrate this in our model formulation, we'll further explain such factors in the simulation section. Considering the fact that we are almost two years into the pandemic, migration in and out of the country is a lot less relevant to the spread within the country, and thus it is ignored in this model.

### 3 Theoretical investigations of the model

First we scale the equations in model (1) by dividing all variables with the total population at time  $t$  ( $N(t)$ ):  $s := \frac{S}{N}, i := \frac{I}{N}, r := \frac{R}{N}$  ( $0 \leq s, i, r$ )

$$\begin{cases} \frac{ds}{dt} = -\beta \cdot si + \alpha \cdot r + b - d \cdot s = -(\beta \cdot i + d)s + (\alpha \cdot r + b) \\ \frac{di}{dt} = \beta \cdot si - \gamma \cdot i - (d + d_1) \cdot i = (\beta \cdot s - \gamma - d - d_1)i \\ \frac{dr}{dt} = \gamma \cdot i - \alpha \cdot r - d \cdot r = \gamma \cdot i - (\alpha + d)r \end{cases} \quad (2)$$

Now each variable represents the proportion of susceptible, infected, recovered individuals in the total population.

### 3.1 Equilibrium points analysis

There are two equilibrium points (constant solutions to the equation system):

$$Point1 : \begin{cases} s = \frac{b}{d} \\ i = 0 \\ r = 0 \end{cases} \quad Point2 : \begin{cases} s = \frac{1}{\beta}(\gamma + d + d_1) \\ i = \frac{1}{\beta} \frac{(\alpha+d)[d(\gamma+d+d_1)-\beta b]}{\alpha\gamma-(\alpha+d)(\gamma+d+d_1)} \\ r = \frac{\gamma}{\beta} \frac{d(\gamma+d+d_1)-\beta b}{\alpha\gamma-(\alpha+d)(\gamma+d+d_1)} \end{cases}$$

Since the exact values of equilibrium points depend on parameters and the signs of RHS functions of the differential equation system depend on the coupling of other variables, we cannot analyze their stability here.

### 3.2 Change in the proportion of susceptible individuals

The change in the proportion of susceptible individuals depends on both recovered individuals ( $r$ ) and infected individuals ( $i$ ).

- (a)  $s > \frac{\alpha \cdot r + b}{\beta \cdot i + d} \Rightarrow \frac{ds}{dt} < 0$ , the proportion of susceptible individuals decreases.
- (b)  $s < \frac{\alpha \cdot r + b}{\beta \cdot i + d} \Rightarrow \frac{ds}{dt} > 0$ , the proportion of susceptible individuals increases.

The more the recovered individuals and the less the infected individuals, the faster the proportion of susceptible individuals starts to increase.

### 3.3 Change in the proportion of infected individuals

The change in the proportion of infected individuals depends on susceptible individuals ( $s$ )

- (a)  $s > \frac{\gamma - d - d_1}{\beta} \Rightarrow \frac{di}{dt} > 0$ , the proportion of infected individuals increases.
- (b)  $s < \frac{\gamma - d - d_1}{\beta} \Rightarrow \frac{di}{dt} < 0$ , the proportion of infected individuals decreases.

At first ( $s = 1, i = r = 0$ ), the number(proportion) of infected individuals is increasing. Compared with the original SIRS model with vital dynamics ( $\frac{\gamma - d - d_1}{\beta} < \frac{\gamma - d}{\beta}$ ), our model says that due to the death caused by COVID-19, it takes longer for the infected people to start decreasing.

### 3.4 Change in the proportion of recovered individuals

The change in the proportion of recovered individuals depends on infected individuals ( $i$ ).

- (a)  $r < \frac{\gamma \cdot i}{\alpha + d} \Rightarrow \frac{dr}{dt} > 0$ , the proportion of recovered individuals increases.
- (b)  $r > \frac{\gamma \cdot i}{\alpha + d} \Rightarrow \frac{dr}{dt} < 0$ , the proportion of recovered individuals decreases.

At first ( $s = 1, i = r = 0$ ), the number(proportion) of recovered individuals is increasing. The more the infected individuals, the longer time it takes for the recovered people to decrease.

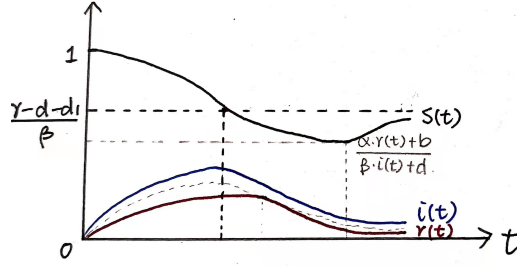


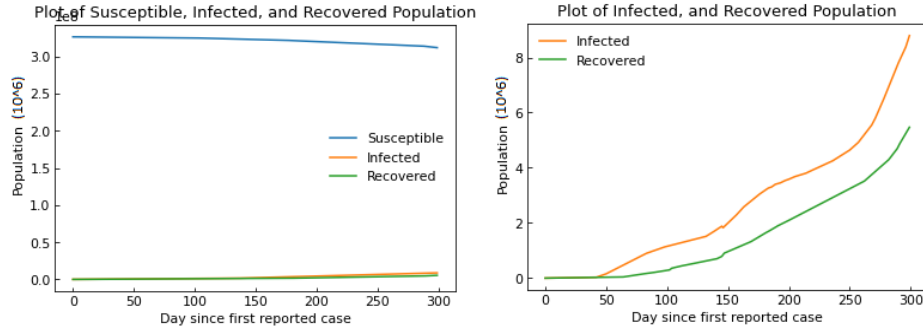
Figure 1: One possible case of the evolution in  $s(t), i(t), r(t)$

### 3.5 Graphic intuition

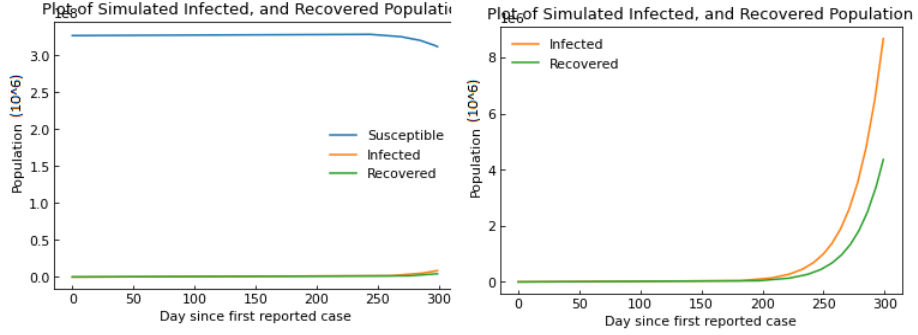
Recall that we assume that at the start of pandemic, everyone is susceptible ( $s = 1$ ), and accordingly there's no infected or recovered individuals ( $i = r = 0$ ). We draw the above graph to demonstrate one possible case, where both infected and recovered individuals reach their maximum while susceptible individuals touch the minimum.

## 4 Visualizations and Simulations

Based on actual data recorded in the US, we first visualize the number of Susceptible, Infected, Recovered people over time (in days) in the following graphs.



After designing the model, we use Python to calculate the results. Here is a graph of the number of Susceptible, Infected, Recovered people over time (in days) base on our SIRS model.



The parameters we use to build our model and simulate the data are:

- $\alpha = 0.1$  (return rate)
- $\beta = 0.148$  (contact rate)
- $\gamma = 0.071$  (recovery rate)
- $b = 0.03/365$  (yearly rate divided by day)
- $d = 0.015/365$  (yearly rate divided by day),
- $d_1 = 0.03$  (COVID-19 death rate)

We numerically simulate the population trajectory with Python's odeint package. We start the simulation with the initial condition  $[326,687,489, 9, 3]$ , which is the first data point in the actual dataset. By manually tuning the parameters, we have obtained the following simulated trajectories that fits the general shape and magnitude of the real data. However, our model is not powerful enough to capture the detailed infection dynamics that results in separate waves. Instead, we have just a single large wave in the simulated trajectory.

We base all parameters except for  $\alpha$  and  $\beta$  on publicly available statistics on Covid-19 in the US. We make a guess on the return rate  $\alpha = 0.1$ , and adjust the contact rate  $\beta$  so that the scale and shape of the simulated trajectory best match with the actual data.

One problem with our model is the unrealistic contact rate of 14.8 percent. Yet this high of a contact rate is needed to put us at the right numbers on day 300. This unreasonably high contact rate is likely due to the discrepancy between the total number of infected cases at a given point vs the reported number of infected cases. If the actual number of cases is much higher on day 0 compared to our starting point, we can have a lower and more reasonable exponential coefficient and still arrive at around the same numbers on day 300.

## 5 Conclusion and Summary

Overall the model is effective but needs improvement. The simplicity of the model is a flaw, as there are many assumptions made that do not apply to the

real spread of the pandemic. The model assumes that the parameters apply to all individuals. Thus, for different groups of people (age, vaccine status, etc.) the parameters need to be adjusted. The model is too general to accurately depict the entire population. Future research may want to look into other external factors such as seasonality since weather can affect the spread of the virus.

## References

- [1] Class Lecture Notes 10/11 and 10/13
- [2] Calafiore, Giuseppe C., Novara, Carlo, and Corrado Possieri. “A Modified SIR Model for the COVID-19 Contagion in Italy”. arXiv.org. Published 2020 Mar. 31, <https://arxiv.org/pdf/2003.14391.pdf>
- [3] Antonopolus, Chris G., Cooper, Ian, and Argha Mondal. “A SIR model assumption for the spread of COVID-19 in different communities”. Chaos, Solitons, and Fractals. Published 2020 Jun. 28, <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7321055/>
- [4] Ajbar, Abdelhamid, Alqahtani, Rubayyi T., and Mourad Boumaza. “Dynamics of an SIR-Based COVID-19 Model With Linear Incidence Rate, Nonlinear Removal Rate, and Public Awareness”. Frontiers. Published 2021 May 13, <https://www.frontiersin.org/articles/10.3389/fphy.2021.634251/full>
- [5] External dataset: <https://raw.githubusercontent.com/nytimes/covid-19-data/master/us-states.csv>