Modeling COVID-19 using the SIIR Model and Vaccine-Modified SIIR Model

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Introduction

Throughout history, there have been constant threats to the species of human beings from infectious diseases. Some prevalent names include smallpox, the plague, flu, AIDS, and more recently, COVID-19. The spread of COVID-19 has had major negative repercussions to many industries including healthcare, social systems, and the economy generally. Epidemiologists model infectious diseases to understand how they are transmitted in human populations and to inform important decisions and findings for governments to follow.

While there have been many models to gauge the behavior of diseases in populations, a new mathematical model called the SIIR model has been constructed and used by Tomochi and Kono to take into account factors specifically affecting the modeling of COVID-19. This model is a time-based model which includes several key components:

- $S(t)$: Susceptible population
- $I_1(t)$: Presymptomatic population (infectious)
- $I_2(t)$: Asymptomatic population (infectious)
- $R_1(t)$: Symptomatic population (quarantined)
- $R_2(t)$: Recovered population (non-infectious)
- $R_3(t)$: Fatalities due to COVID-19 (non-infectious)

Each of these components are connected together by the relationships shown in Figure 1 from Tomochi and Kono:

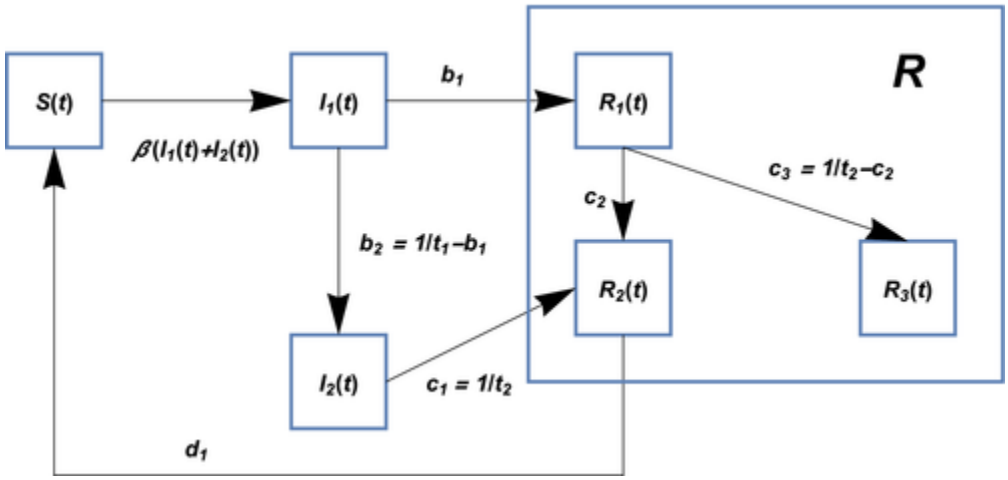


Figure 1. Flow diagram of different populations in a community with COVID-19 present. $S(t)$ represents the susceptible population, $I_1(t)$ represents the presymptomatic population (infectious), $I_2(t)$ represents the asymptomatic population (infectious), $R_1(t)$ represents the symptomatic population (quarantined), $R_2(t)$ represents the recovered population (non-infectious), $R_3(t)$ represetns fatalities due to COVID-19 (non-infectious).

Some interesting differences between the SIIR model above and previous models are the number of variables accounted for with respect to COVID-19. Since COVID-19 can be transmitted to a person who has already had it (whose antibodies have worn off), some amount of the R2 population goes back into the S population. The incubation period and other characteristics of COVID-19 are accounted for by the model parameters which will later be discussed. While this model builds off of previous models and depicts a more accurate representation of the spread of COVID-19 in a population, it does not take into account certain factors such as vaccination. In this report, I will be exploring the SIIR model as the authors have layed it out and add to this model the factor of immunization to see the effects that it has on a population's spread of COVID-19.

Modeling Approach

The SIIR modeled by Komochi and Kono include the following differential equations:

$$\frac{dS(t)}{dt} = \; - \beta S(t)(I_1(t) + I_2(t)) + d_1 R_2(t),$$

$$\frac{dI_1(t)}{dt} = \beta S(t)(I_1(t) + I_2(t)) - (b_1 + b_2) I_1(t),$$

$$\frac{dI_2(t)}{dt} = b_2 I_1(t) - c_1 I_2(t),$$

$$\frac{dR_1(t)}{dt} = b_1 I_1(t) - (c_2 + c_3) R_1(t),$$

$$\frac{dR_2(t)}{dt} = c_1 I_2(t) + c_2 R_1(t) - d_1 R_2(t),$$

$$\frac{dR_3(t)}{dt} = c_3 R_1(t),$$

where β represents the probability a person that is susceptible to the disease will be infected, b_1 and b_2 coefficients represent the bifurcation of presymptomatic individuals transitioning into quarantined individuals (R_1) and asymptomatic individuals (I_2) respectively. c_1 represents the rate at which asymptomatic individuals (I_2) transition into recovered individuals (R_2) and is the inverse of the onset period. c_2 represents the rate that quarantined individuals (R_1) transition to recovered individuals (R_2). c_3 represents the rate quarantined individuals (R_1) transition to the deceased population (R_3). Finally, d_1 represents the rate at which a recovered individual transitions back to a susceptible individual, which is the inverse of the antibody duration (unique to this model).

There are a few assumptions that this model makes which are not accurate of the real world. One is that it assumes infectious populations are evenly distributed throughout the population. However, in the real world, we know that there are "hot-spots" where COVID-19 is more easily spread due to a high population density. Another assumption is that all humans in the population are equal throughout time. However, we know that COVID-19 is a bigger problem to those with risk factors including old age,

obesity, and other conditions. Thus, int reality there is a distinction between those with risk factors and those without and this distinction is c_3. Although these simplifications make the model simpler, they do not fully account for all possible variables that may influence the phenomenon. Additionally, assumptions were made when selecting parameter values for the model. The b and c parameters are all based off of t_1 and t_2 which are the number of days of the incubation period and the disease onset period respectively.

For the base model, the researchers used the following parameters: $N = 1, t_1 = 5, t_2 = 17,$ $\beta = 0.2, b_1 = \frac{0.3}{t_1}, b_2 = \frac{1}{t_1} - b_1, c_1 = \frac{1}{t_2}, c_2 = \frac{0.8}{t_2}$, and $c_3 = \frac{1}{t_2} - c_1$. Two separate d_1 were simulated (0.001 and 0.003) as well as the initial conditions of 0.04% of the population being presymptomatic and 99.96% being susceptible. I believe these parameters were selected due to their resemblance to the COVID-19 pandemic.

Findings

When the base model was simulated by the researchers, they obtained the following curves:

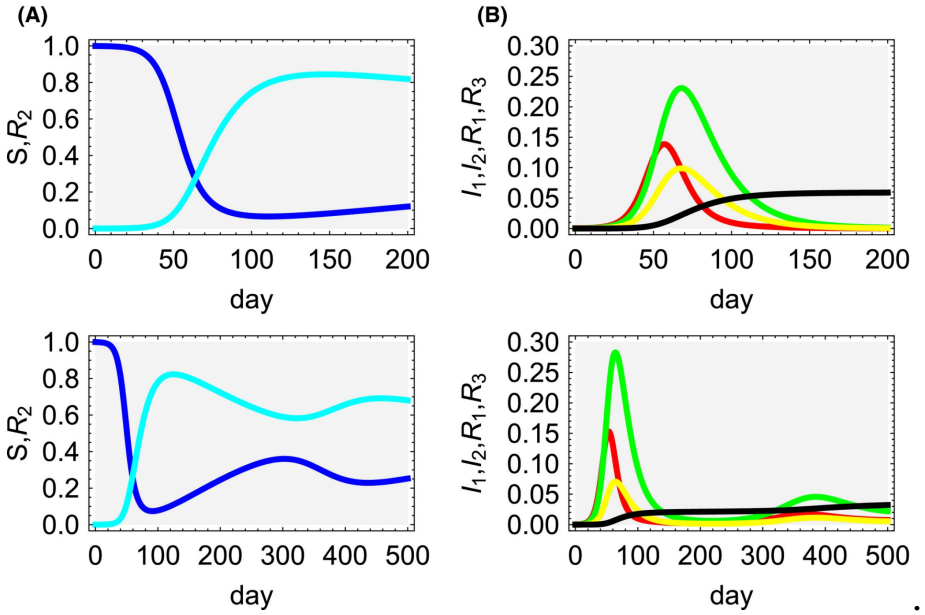


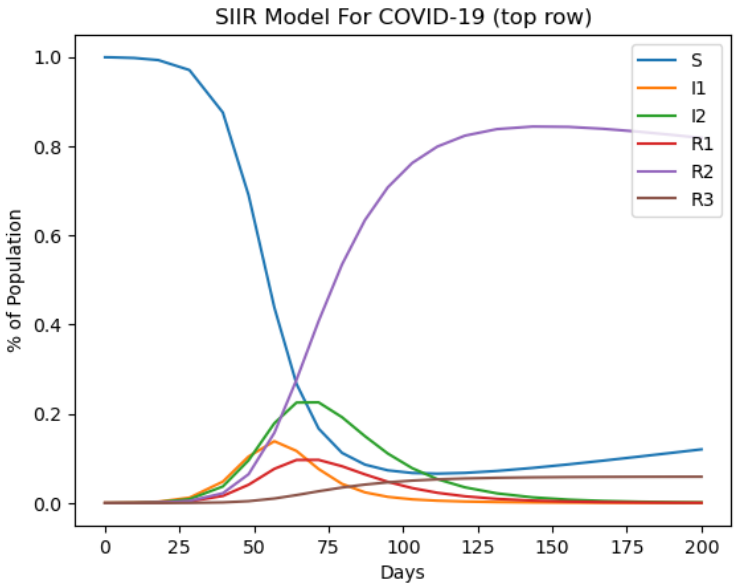
Figure 2. Top two charts represent $d_1 = 0.001$ and the bottom two charts represent $d_1 = 0.003$. S(t) (blue) and recovered population with antibody $R_2(t)$ (cyan). The presymptomatic population $I_1(t)$ (red), asymptomatic population $I_2(t)$ (green), symptomatic and quarantined population $R_1(t)$ (yellow), and fatalities $R_3(t)$ (black).

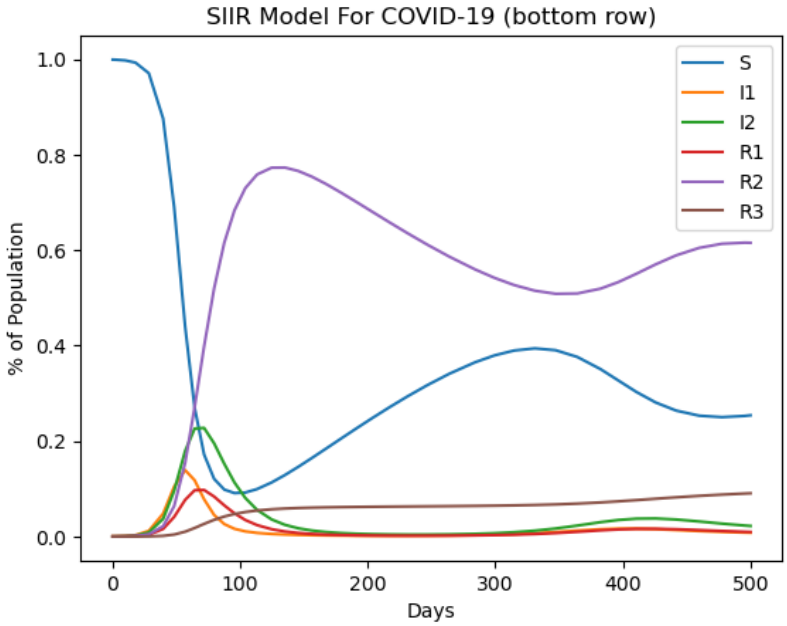
The general phenomenon pictured makes sense as we see a rise in the recovered population (cyan) over time and less susceptible (blue). There is an increasing number of fatalities caused by the illness (black) as well as peaks in similar times for most of the populations. It is worth noting that increasing d_1(decreasing duration/effectiveness of antibodies) leads to periodic peaks in those that are infected and recovered as seen in the bottom row where $d_1 = 0.003$ whereas the top row had $d_1 = 0.001$. The d_1 parameter sets the SIIR model apart from other models as we can see these sorts of expected phenomenon like the periodic peaking in the real world. As for fatalities, we see the largest

increase at the beginning of the pandemic and it starts to equilibrate like the other populations as time passes.

Results

After coding the SIIR model into python and solving the ODEs, the following two graphs were obtained which try to replicate the graphs the authors had along with using the same parameter values.





As seen in the graphs, the general behaviors are consistent to the graphs the researchers published. One interesting difference is the percentage of fatalities were different for the bottom row ($d_1 = 0.003$). The value I obtained at the end of 500 days was a fatality percentage of 9.065% while the researchers seemed to have gotten a value closer to 5%. Having said this, the curve has the same shape and similar time in peak rate of increase. The behaviors of the curves make sense and the justification of the curves the researchers got also apply to the curves I created.

New Findings

While the SIIR model does a great job of modeling COVID-19, it does not take into account vaccination. I believe that this is a crucial variable as we would be able to see the effects vaccination has on the population system above and governmental authorities can optimize the recommended rate of an individual getting vaccinated with respect to cost of the vaccine. To take this new parameter into account, the differential equations for $S(t)$ and $R_2(t)$ are modified as shown below:

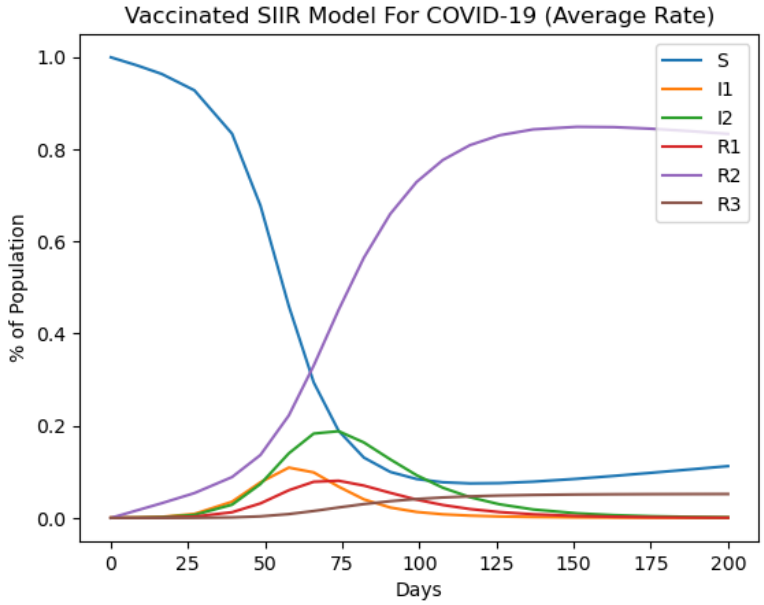
$$\frac{dS(t)}{dt} = -\beta S(t)(I_1(t) + I_2(t)) + d_1 R_2(t) - v_1 S(t),$$

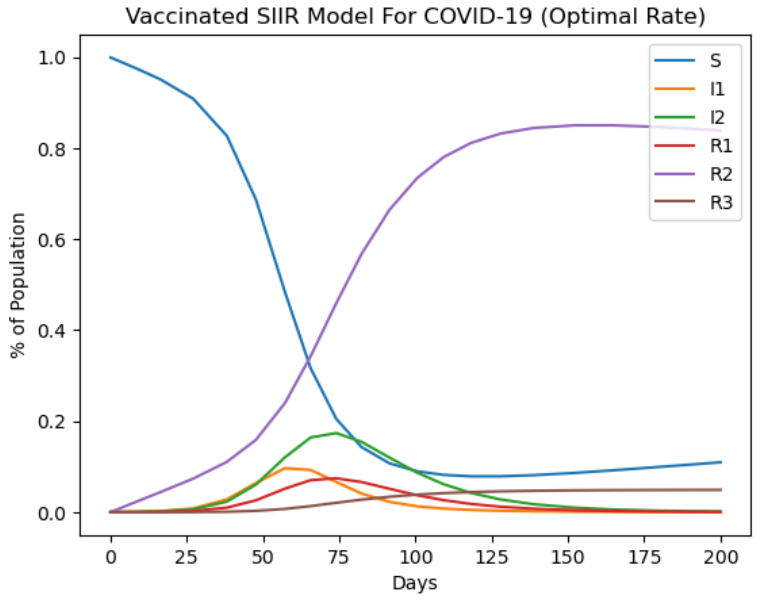
$$\frac{dR_2(t)}{dt} = c_1 I_2(t) + c_2 R_1(t) - d_1 R_2(t) + v_1 S(t).$$

Here, v_1 is the vaccination rate of the population per day. This modified model assumes that only the susceptible population $S(t)$ get vaccinated and the rate that vaccinated people transition back to susceptible people is the same as the rate of those who recovered from the disease and have the antibodies.

Two different rates of v_1 were tested. The first is the average global rate of vaccination from December 16th, 2020 to April 24th, 2023 (assuming global population ~8 billion). It is important to note though that vaccination rate is not steady throughout time in the real world, many members of the population got it as soon as they could and general booster vaccination rates have been low as time

progressed. The other v_1 rate is the optimal rate as found by researchers at Yale and UNC-Charlotte which is once a year. Making the addition of vaccinations to the model, we arrived at these results:





To compare the effect of vaccination on the population, we can use the fatality percentage after 200 days from the first produced chart (without vaccination), and the two above. Without vaccination and all other variables held constant, fatality percentage is about 5.9%. At the average rate of vaccination, the fatality percentage is about 5.2%. Finally, at the optimal rate, the fatality percentage drops to

approximately 4.9%. As the information shows, it's very important for populations to get vaccinated for COVID-19 as they can decrease ~20% of all deaths. Having said this, the patterns of the populations have not significantly changed from the non-vaccinated model.

Conclusion

The SIIR model is an adapted model of previous infectious disease population models and it does well to model population patterns of diseases like COVID-19. While it has been an improvement on other models, the SIIR model does not take into account every important variable to model infectious diseases. Within this paper, I added a vaccination parameter to the SIIR model to better understand how different populations change throughout time with the introduction of vaccines and it has been shown that they play a vital role in the containment and lethality of a disease within a population. While it is optimal for populations to get vaccinated as much as possible (not considering health ramifications of consistent high frequency vaccinations), it is an endeavor that would be highly cost inefficient. Thus a possible future direction and a question posed to the reader would be to take the results from the vaccine adjusted model and model the payoff of saving a life from COVID-19 to find the optimal rate of human vaccinations for COVID-19.

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