COVID-19 Epidemic Modeling with SIR

Mitchell Kelly*
University of Florida Department of Physics
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1. INTRODUCTION

The Susceptible-Infectious-Removed (SIR) model is a simplistic approach to epidemic modeling that classifies individuals into three groups, where their relative population sizes can be monitored over time [1]. Each letter of the acronym SIR represents the specific classification a person in a population will have. Susceptible individuals are at risk of contracting the disease of study if they encounter someone who is infectious, and infectious people eventually recover where they are labeled as removed. Once an individual becomes a part of the removed population, they cannot contract the disease again which is analogous to having permanent protective immunity against the disease [1]. Each transition has a rate governed by irreversible, autocatalytic chemical reactions,

$$S + I \xrightarrow{\beta} 2I \tag{1}$$

$$I \xrightarrow{\gamma} R \tag{2}$$

where β is the incidence rate of infection, and γ is the recovery rate [1]. Eq. 1 describes the process of a susceptible and infectious person interacting, resulting in a new infectious person upon its completion. Eq. 2 illustrates how an infectious individual becomes removed at rate γ, but it should be noted that $1/\gamma$ is the average duration of infectiousness for said individual [1].

The basic SIR model also has an analogous coupled differential equations representation of dynamical behavior, and each equation describes how the respective population of susceptible, infectious, and removed individuals vary over time. The three differential equations are

$$\frac{dS}{dt} = -\frac{\beta}{N}SI \tag{3}$$

$$\frac{dI}{dt} = \frac{\beta}{N}SI - \gamma I \tag{4}$$

$$\frac{dR}{dt} = \gamma I \tag{5}$$

where S, I, and R are the populations of each SIR model classification, and N is the total population of the environment ($N = S(t) + I(t) + R(t)$) [1]. Eqs. 3-5 are better suited for rate equation analysis, whereas Eqs. 1,2 are more useful for stochastic simulations of a population battling a novel virus.

Rate equation analysis and stochastic simulations of COVID-19 with the basic SIR model can lead to a better understanding of the dynamics of the pandemic; however, modifying the original model for loss of immunity and vaccination provides a more realistic treatment of it. The combined model has the capability to determine how often a population should get booster vaccination doses. The basic SIR model will be stochastically simulated via the Gillespie algorithm and analyzed with rate equations for parameters significant in 2023. Additionally, the SIR model will be generalized twice: the addition of immunity loss, and vaccination with loss of immunity. Rate equation analysis will be conducted with both modified models, and the question regarding booster frequency will be answered.

*Electronic address: mitchellkelly@ufl.edu

2. COVID-19 SIR MODEL SIMULATIONS

An essential quantity that characterizes diseases illustrated by the SIR model is the basic reproduction number,

$$\mathcal{R}_0 = \frac{\beta}{\gamma} \tag{6}$$

defined as the susceptible-to-infectious replacement number when a single infectious person is introduced to an entirely susceptible population [1]. If $\mathcal{R}_0 S(0) > 1$, then $I(t)$ initially increases, resulting in an epidemic, but if $\mathcal{R}_0 S(0) < 1$, then $I(t)$ decreases, preventing an epidemic [1]. For COVID-19, Eq. 6 can range from 1.5-6.68 depending on geographical location and public policy [2]. A basic reproduction number of 3 will be taken to simulate the original SIR model. COVID-19's span has been minimized by country-wide vaccination efforts, yet masking is sparse, making it more likely to spread the virus upon contact with susceptible people. The rough average value of 3 intends to encapsulate both contrasting components described formerly. Moreover, the average period of infectiousness of COVID-19 is estimated to be 10 days, so γ equals 0.1 days^{-1} [3]. Solving for β in Eq. 6, we get 0.3 days^{-1}. Both β and γ are now determined for their subsequent stochastic simulation and rate equation analysis.

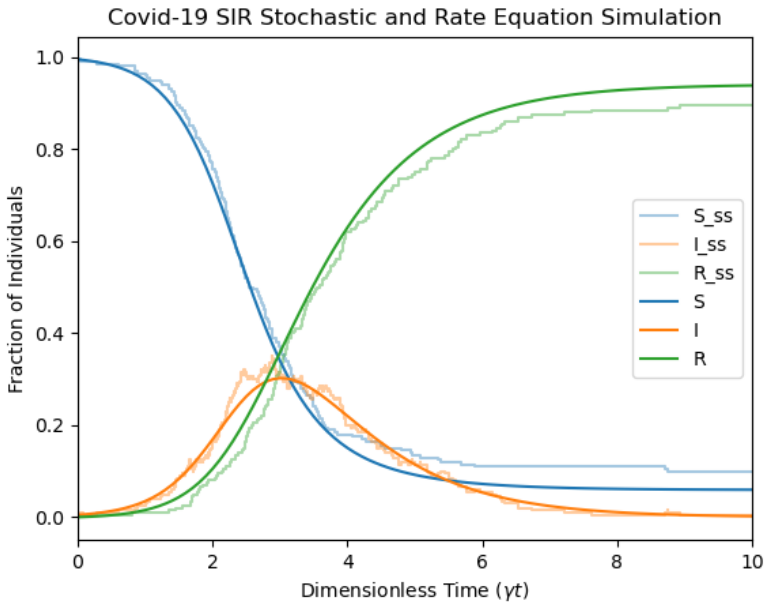

FIG. 1: SIR model stochastic and rate equation simulations from Eqs. 1-5 for relevant COVID-19 parameters where 'ss' stands for stochastic simulation.

Fig. 1 shows the results of both the stochastic simulation and rate equation trajectories for a population size of $N = 200$ initially comprising 199 susceptible individuals and 1 infectious individual. As expected from predictions regarding basic reproduction number, $I(t)$ began increasing which resulted in a surge of infectious individuals (i.e. an epidemic). Consequentially, Fig. 1 shows a decreasing $S(t)$ and increasing $R(t)$ from susceptible individuals transitioning to infectious and then ultimately removed. It should be noted that the concavity of $S(t)$ switches around the 2.5 time mark, and the steady-state solution stabilizes to a non-zero constant. As the number of susceptible people decreases, Eqs. 1 and 3 slow down in response to the lack of 'reactants' or people. Eventually, all members of the population become either removed or susceptible because the steady-state solution of $I(t)$ is zero, signaling the end of the epidemic. Although the stochastic simulations have random fluctuations deviating from the rate equations,

they generally follow the same track and exhibit the same critical behavior. The basic SIR model recreates the characteristics of a novel outbreak of COVID-19 in a community of people without prior immunity.

3. SIR MODEL WITH IMMUNITY LOSS

To incorporate the loss of immunity into the basic SIR model a new reaction where removed individuals become susceptible again is necessary. Specifically an additional reaction,

$$R \xrightarrow{\lambda} S \tag{7}$$

where λ defines the rate at which immunity is lost, can modify the SIR model appropriately. In the same formalism as $1/\gamma$, $1/\lambda$ represents the average duration of immunity to a disease, and for COVID-19 this is estimated as 183 days ($\approx$ 6 months) [4]. Eq. 7 adds a new component to differential equations 3 and 5, where the new coupled differential equation system is,

$$\frac{dS}{dt} = \lambda R - \frac{\beta}{N} SI \tag{8}$$

$$\frac{dI}{dt} = \frac{\beta}{N} SI - \gamma I$$

$$\frac{dR}{dt} = \gamma I - \lambda R. \tag{9}$$

With $\lambda = 1/183$ days^{-1} and the rate constant values defined in the previous section, rate equation trajectories were produced for the same population size and composition as before.

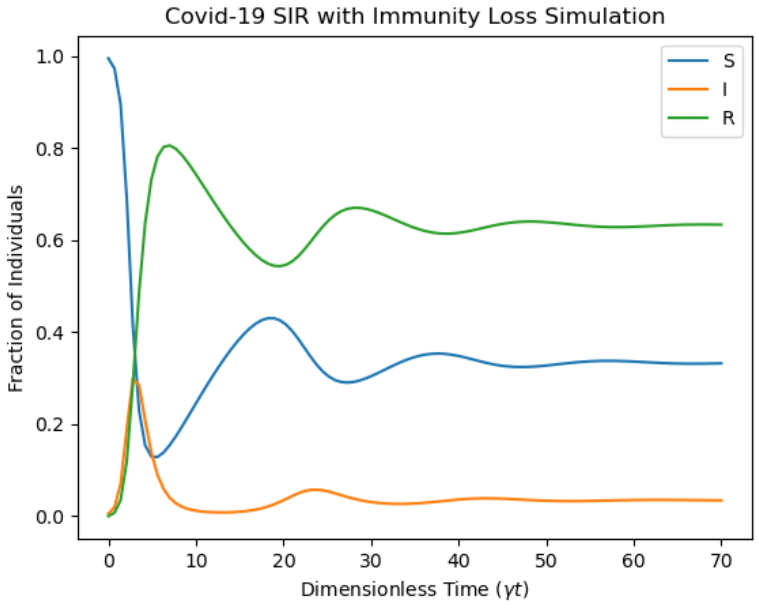

FIG. 2: COVID-19 SIR model rate equation trajectories governed by Eqs. 4, 8, and 9 and associated parameters.

Fig. 2 illustrates the impact of Eq. 7 by its seemingly turbulent trajectories prior to the steady state. Unlike Fig. 1, the removed population eventually decreased in response to the removal of immunity to COVID-19 over time. Once a significant increase in $S(t)$ occurs, a tiny growth of infectious individuals is observed, where these humps can be seen around the 25 and

45 time marks of Fig. 2. The steady-state solution of $I(t)$ is non-zero, albeit small, in this modified SIR model, so variants of COVID-19 have a chance to develop. If the steady-state solution of infectious individuals was zero, then the virus would be eradicated at some point in its duration. Another modification to the model is required to make the steady-state solution of the infectious population zero. Vaccination counteracts the effects of immunity loss, where an ideal booster dose frequency can be achieved.

4. SIR MODEL WITH IMMUNITY LOSS AND VACCINATION

The inclusion of vaccination in the already modified SIR model is equivalent to the reversal of immunity loss. An individual possesses a rate at which vaccination or immunity to COVID-19 is granted,

$$S \xrightarrow{\nu} R \tag{10}$$

where ν is the rate at which vaccination occurs. Similarly to $1/\gamma$ and $1/\lambda$, $1/\nu$ represents the average time between subsequent booster doses. The ideal value of ν was determined via rate equation trajectory simulation of

$$\frac{dS}{dt} = \lambda R - \frac{\beta}{N} SI - \nu S \tag{11}$$

$$\frac{dI}{dt} = \frac{\beta}{N} SI - \gamma I$$

$$\frac{dR}{dt} = \nu S + \gamma I - \lambda R \tag{12}$$

where $\pm\nu S$ is the new modification to Eqs. 8 and 9.

Rate equation trajectories were generated for 100 different values of ν ranging from 1/280 to 1/10, and their steady-state infectious population value was recorded. The optimal ν was determined at the transition where $I(t)$ became less than one. A single 'whole-number' person was assumed to be the minimum number of infectious individuals required to keep COVID-19 alive, so a ν causing $I(t)$ to be slightly lower than one was sought after. ν was numerically determined to be 0.00933 days^{-1}, and taking its inverse led to the ideal booster frequency: every 107.2 days or 3.52 months. To confirm the accuracy of the ideal ν, rate equation trajectories were simulated and plotted using Eqs. 4, 11, 12, COVID-19 parameter values, and population size used in previous sections.

Fig. 3 depicts the impact an optimized booster dosage schedule can have on a population combating a novel COVID-19 epidemic. The initial spike of an increasing $I(t)$ is observed in Fig. 3, but it levels out to its steady-state solution similar to Fig. 1 with a faster rate. The infectious population's steady-state solution graphically appears to be zero, proving the ideal ν altered $I(t)$ correctly from numerical predictions. The trajectories of $S(t)$ and $R(t)$ oscillate similarly to Fig. 2, yet they approached their steady-state solution faster from the addition of vaccination. The quick stabilization towards the steady-state solution of each trajectory in Fig. 3 comes from vaccination balancing the loss of immunity. The counteracting effect is not absolute, resulting in some unstable oscillatory behavior, yet it makes the coupled differential equation system mimic Eqs. 3-5 to a greater degree (where λR and νS are negligible).

The optimal ν was also determined analytically by setting Eqs. 4, 11, and 12 to zero to determine the infectious population's steady-state equilibrium value. Usage of the population constraint, $N = S(t) + I(t) + R(t)$, allowed for the aforementioned conditions to be applied, where

$$I^* = \frac{N\left[1 - \frac{\gamma}{\beta} - \frac{\gamma\nu}{\lambda\beta}\right]}{(1 + \frac{\gamma}{\beta})} \tag{13}$$

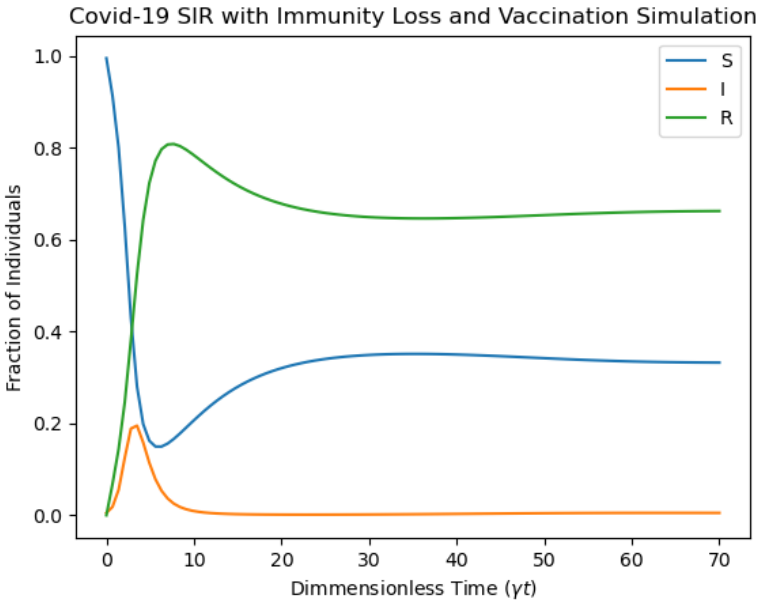

FIG. 3: COVID-19 SIR model rate equation trajectories governed by Eqs. 4, 11, and 12 and associated parameters with numerically determined optimal ν.

is the general expression for the infectious population equilibrium value under the SIR model including vaccination and loss of immunity. When Eq. 13 was set to 0.999 (all other parameters defined previously), ν was determined to be 0.00934 days^{-1}. Corroboration between the numerical and analytical values is evident, and their small difference was caused by limitations with numerical simulations.

5. CONCLUSIONS

The SIR Model and its extensions described the dynamics of the COVID-19 pandemic for isolated populations lacking a substantial removed population. Ultimately, it was determined that a ν of 0.00933 days^{-1} was necessary to make the infectious population effectively go to zero when a $\mathcal{R}_0$ of 3 and λ of 1/183 days^{-1}. Every stochastic and rate equation simulation depended heavily on parameters β,γ,λ, and ν, and any change in these rates could lead to drastically different results. For example, using a larger $\mathcal{R}_0$ with the SIR model would directly lead to a different ideal ν and so on. On the notion of ν, the average period of immunity has an even greater impact on it. The literature suggests that certain vaccines have higher COVID-19 immunity percentages for a given time frame, but pinpointing this value is an arbitrary assessment at best [4]. The λ chosen for this study does not consider partial immunity or immunity granted naturally in the environment, which is what a more sophisticated model should aspire to represent while producing meaningful results. To better simulate real-life conditions, a more advanced SIR model should include birth and death rates into its coupled differential equations, as opposed to a stagnant population. An additional modification to the preexisting SIR model would be to include a population group that has been exposed to COVID-19 but cannot infect susceptible individuals until a period has passed between the susceptible and infectious phases. Despite its elementary principles and guidelines, the SIR model helped

to characterize what constitutes an epidemic and how best to combat it globally.

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