Study of the Effect of Innate Immunity & Fixed-Rate Vaccination on Pandemics

Yifei Deng & Jerry Yao

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Contents

1 Introduction

The SIR model is commonly used as a simulation of the spread of disease. The governing mathematical equations of this model focus on the change of susceptible (S), infected (I), and recovered (R) population. Based on this model, we are interested in studying how immunity plays a role during pandemics. In order to study this question, we examine two cases. In the first case, we assume that a certain proportion of people are inherently immune to the disease. By changing this proportion (V_p), we study (1) the change of total infection, (2) the change of time that infection is the greatest, and (3) the herd immunity effect. In the second case, we assume that a certain proportion of susceptible people started to get vaccinated starting from a certain point during the pandemic. By changing this proportion (V_r), we study (1) the change of total infection and (2) the change of time that infection is the greatest. Besides the two cases, we also made a video that visualizes the change of S,I,R as the disease typically becomes more severe.

2 Equations

2.1 The Original Model

In this section, we will thoroughly explain the governing equations that we used while designing our models. We will begin with the equations used in the basic SIR model, which is used in the varying infectivity study. The equations describe how the numbers of susceptible, infected, and recovered people change over time.

The variables, such as S, I,and R, are all functions of time t. We assume there is no newborn or death so that the sum of all variables should always add up to $N, \forall t, N \in k$. The governing equations in the original model are as followed:

$$\frac{dS(t)}{dt} = -a\frac{I(t)}{N}S(t) \tag{1}$$

$$\frac{dI(t)}{dt} = a\frac{I(t)}{N}S - bI(t) \tag{2}$$

$$\frac{dR(t)}{dt} = bI(t) \tag{3}$$

$$S(t) + I(t) + R(t) = N \tag{4}$$

We observe that the equations are composed of two basic terms: $a\frac{I}{N}S$ and bI. The constant a is going to be called the infectivity of the disease in this essay. a is calculated as followed:

$$a = a_0 P_{trans} \tag{5}$$

a_0 is the number of encounters a typical person would make each unit time. P_{trans} represents the probability of transmission given an encounter. Since transmission would happen only if one meets an infected person, $a_0 P_{trans}$ is multiplied by the probability of encountering an infected person I/N. Therefore, as shown in the first equation, the change of S is $-a\frac{I}{N}$ for a small increase in t. At the same time, I increases by $a\frac{I}{N}$ for a small increase in t.

The constant b is the recovery rate. $1/b$ is the average time that one infected people take to recover. We assume the probability of recovery is the same no matter how long this person has been affected. Therefore, I would change by $-bI$ for a small increase in t. At the same time, R increases by bI for a small increase in t.

$\frac{a}{b}$ is defined as the reproduction number. Please recall that a is the rate at that one infected person directly infects other people assuming every other people are susceptible. $1/b$, the average time that one infected people take to recover, represents the duration that one infected person is able to cause infections. Therefore, $\frac{a}{b}$ is the number of infections that an infected person can cause. A pandemic would only happen when $\frac{a}{b}$ is greater than 1. In our studies, $\frac{a}{b}$ is approximately 2.

2.2 Model for the Study of Innate Immunity

In this study, we take innately immune people's V into account. (Please note that the V in this and the V in the following fixed-rate vaccination study, though have the same name, refer to different things.) Different from the S,I, and R in the original model, V is not considered as a function of t, but a constant instead. Therefore, equation (1)(2)(3) are not affected by V, the only change is that now N become the sum of S, I, R and V. The governing equations of this study are as follows:

$$\frac{dS(t)}{dt} = -a\frac{I}{N}S(t) \tag{6}$$

$$\frac{dI(t)}{dt} = a\frac{I(t)}{N}S - bI(t) \tag{7}$$

$$\frac{dR(t)}{dt} = bI(t) \tag{8}$$

$$S(t) + I(t) + R(t) + V(t) = N \tag{9}$$

2.3 Model for the Study of Fix-rate Vaccination

In this study, we included the vaccinated people V. Here V is a function of time. Therefore, if we have $Vr * N$, a constant number of vaccination received by susceptible people each unit time t_u starting from the moment Vs, change in $V(t)$ can be viewed as a piece-wise function of t:

$$dV(t) = \begin{cases} Vr * N & \text{if } t = Vs + kt_u (k \geq 0) \\ 0 & \text{if } t \neq Vs + kt_u (k \geq 0) \end{cases} \tag{10}$$

Then,

$$V(t) = \int_0^{tmax} dV(t)dt \tag{11}$$

These equations, together with the following equations are the governing equations for this study:

$$\frac{dS(t)}{dt} = -a\frac{I(t)}{N}S(t) - dV(t) \tag{12}$$

$$\frac{dI(t)}{dt} = a\frac{I(t)}{N}S(t) - bI(t) \tag{13}$$

$$\frac{dR(t)}{dt} = bI(t) \tag{14}$$

$$S(t) + I(t) + R(t) + V_I(t) = N \tag{15}$$

3 Numerical Method

At the beginning of our study, the initial state is known, meaning $a, b, S(0), I(0), R(0)$, and $V(0)$ are known. Additionally, the equations derived based on the SIR model quantified the rate of change of these variables $\forall t$. In this case, if we set the time step reasonably small (Δt), we are able to approximate the $S(0), I(0), R(0)$, and $V(0)$ for each t within its domain step by step by using the value of the functions at $t = 0$ and their first order derivatives. This is also called Euler's method.

For example, in the study about fixed-rate vaccination, we would see $\forall t \in [0, tmax)$:

$$\frac{S(t + \Delta t) - S(t))}{\Delta t} = -a\frac{I(t)}{N}S(t) - dv(t) \tag{16}$$

$$\frac{I(t + \Delta t - I(t))}{\Delta t} = a\frac{I(t)}{N}S(t) - bI(t) \tag{17}$$

$$\frac{R(t + \Delta t - R(t))}{\Delta t} = bI(t) \tag{18}$$

Please also note:

$$S(t+\Delta t) + I(t+\Delta t) + R(t+\Delta t) + V(t+\Delta t) = S(t) + I(t) + R(t) + V(t) \tag{19}$$

$$V(t) = \sum_{i=0}^{t} dV(i) \tag{20}$$

4 Validation

The first study involves the change of S,I,R while t and the proportion of innately immune people in the population V_p varies. We set dt to be $\frac{1}{24}$ day, i.e. 1 hour, and V_p to be 0.005. Under this condition, we observe from the graph that the functions appear to be smooth. Additionally, no changes happen to the shape of the graph when we set dt, V_p to be smaller. As verified, dt and V_p are small enough to produce valid results.

In the second study (see Results and Discussion **??**), we observe how the result of the pandemic was changed if the number of vaccinated people per unit time, i.e.$dvp * N$, varies. We set $dt = 1/24$ day and $dvp = 0.001$. Under this condition, we observe from the graph that the functions appear to be smooth. Additionally, no changes happen to the shape of the graph when we set dt, dvp to be smaller. As verified, dt and V_p are small enough to produce valid results. It is worth noting that we discovered with all other parameters unchanged, change in N affects the shape of the graph. According to our model when $N \approx 2000$, the maximum number of infection, $Imax(dvp)$, and the time when this happen, $t_{Imax}(dvp)$, are constants. When $N \approx 30000$, the graph of $Imax(dvp), t_{Imax}(dvp)$ starts decreasing in an oscillating manner as dvp increases. Eventually, we set $N = 10000000$, so that the graphs are smooth and the shape of the graphs remains unchanged as N becomes even larger.

5 Interesting Aspects of the Code

5.1 Interesting Codes in the Study of Innate Immunity

The result of a pandemic is the set of the states of S, I, R at different t. In order to examine the result of a pandemic within a specific innately immune proportion V_p, we need to create a set of pandemics of different V_p. Therefore, we created a for-loop inside another for-loop (Please see comments after %):

```
for step = 1:(stepmax+1)
    V = (step-1) * dvp * N;
    % For each step, we have a different (step-1)*dvp = Vp
    ...
    for clock = 1: clockmax
        tsave(clock+1) = clock * dt;
        % now we examine the state of the pandemic at t=clock*dt
        %under a specific Vp
         ...
    end
end
```

5.2 Interesting Codes in the Study of Fixed-Rate Vaccination

5.2.1

Similar to what was explained in the previous part, we need to examine the result of a pandemic under a certain fixed vaccination rate V_r and the state of the pandemic $\forall t$ and $\forall V_r$.

```
 for Vr = 0.000:dvp:Vpmax
    ...
    Vrsave(column) = Vr;
    % for each loop, the vaccination rate is set to be Vr

    for clock = 1: clockmax
        tsave(clock+1) = clock * dt;
        ...
    end
    ...
end
```

5.2.2

```
 for step = 1:(stepmax+1)
    [Imaxsave(step), clockImaxsave(step)] = max(Isave(step,:));
end
```

5.2.3

Here is how we implanted the vaccination plan. $Vnewsave$ is an array that records the number of newly vaccinated people at t. Vs is the moment when vaccinations start, which is set to be day 50. $Vr * N$ represents the number of people being vaccinated.

```
for clock = clock:(clockmax) % for the whole pandemic
        if clock*dt < Vs % when t = clock*dt is below Vs=50
            Vnewsave(column,clock) = 0; % No new vaccinated people
        else
            if mod(clock*dt,1)==0 % when the next day is reached
                Vnewsave(column,clock) = Vr * N; % new vaccinated people = Vr * N
            else % meaning we haven't reach the next day yet
                Vnewsave(column,clock) = 0; % new vaccinated people = 0
            end
        end
    end
```

6 Results and Discussion

6.1 The Study of Innate Immunity

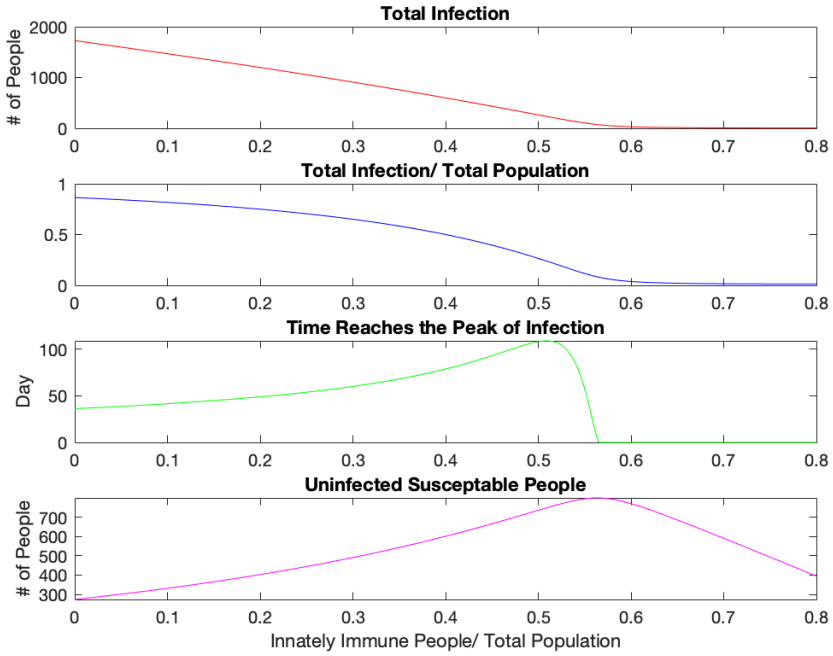

Figure 1: Result of the Study of Innate Immunity: The horizontal axis of the 4 subplots all represent the ratio of the number of people vaccinated at t_0 to the total population N, i.e.Vp.

In the deterministic model we built, we have the following assumptions: the total population $N = 1 \times 10^7$ people; it takes 7 days for a patient to recover, so $b = \frac{1}{7}$; the reproduction number is 2, and the infectivity $a = 2 * \frac{1}{7} = \frac{2}{7}$. We observe the pandemic in its first 500 days, and dt is set to be 1 hour. We assume that there are 3 people infected initially. We studied the relationship between V_p and the following four dependent variables:

(1) Total Infection: The total number of people who got infected at the end of the pandemic, as shown by Figure 1, decreases as V_p increases. When N is large ($N = 1 \times 10^7$ in this case), the graph appears to be linear. And the slope is roughly -3000. It means that the total number of people who got infected at the end of the pandemic decreases by 300 when V_p increases by 0.1.

(2) Total Infection / Total Population: When no people are inherently immune to the disease, the total infection proportion is 0.86. While V_p increases,

the dependent variable decreases. When V_p gets close to 0.6, no pandemic happens.

(3) Time Reaches the Peak of Infection: The time it takes for the infected population to reach its maximum increases as V_p increases from 0 to 0.5, but it rapidly decreases when V_p exceeds 0.5. The reason for the decrease in t when I is the greatest is that pandemic won't happen for V_p is larger than 0.55.

(4) Uninfected Susceptible People: This quantity is the total population minus the sum of the infected & vaccinated population, i.e. $N - I_{total} - Vtotal$. Its value reflects how many people who were not vaccinated did we protect using vaccination, and therefore can be used to study the herd immunity effect. This value reaches the peak when V_p is around 0.6, and starts to decrease when V_p continues to increase.

6.2 The Study of Fixed-Rate Vaccination

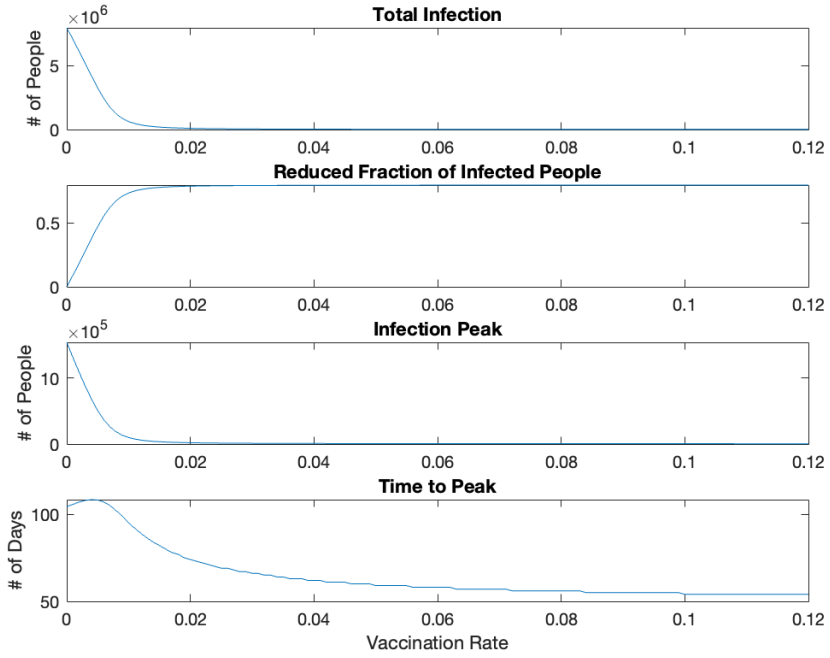

Figure 2: Result of the Study of Fixed-Rate Vaccination: The horizontal axis of the 4 subplots all stand for the vaccinate rate. Its product with the total population stands for the number of newly vaccinated people each day

We built a deterministic model and have the following assumptions: the total population $N = 1 \times 10^7$ people; it takes 7 days for a patient to recover, so $b = \frac{1}{7}$; the reproduction number is 2, and the infectivity $a = 2 * \frac{1}{7} = \frac{2}{7}$; there were initially 3 infected people; we looked at the situation of the first 200 days with each time step equal to 1 hour. In the first 50 days, no one gets vaccinated. Every day after the 50th day, $N * V_p$ people are vaccinated. V_p is called vaccinate rate, which is the parameter we want to study. It determines how many people we vaccinate per day after the 50th day, and we increase V_p from 0 to 0.12 with each increment equal to 0.001. We studied the relationship between the vaccination rate and the following four dependent variables:

(1) Total Infection: The total number of people who got infected at the end of the pandemic decreases rapidly as the vaccination rate increases from 0 to 0.02.

(2) Reduced Fraction of Infected People: This variable is equal to the difference between the number of infected people when the vaccination rate is 0 and the number of infected people when the vaccination rate is not 0 divided by the total population N. It is the fraction of the people we protected using vaccination. It increases and gradually enters a steady state as the vaccination rate increases.

(3) Infection Peak: The maximum number of the infected population decreases as the vaccination rate increases.

(4) Time to the Peak of Infection: As V_p increases, the time it takes to reach $Imax$ overall decreases. However, we found that, interestingly, the curve showed a slight increase before it decreases.

6.3 Additional Findings

While validating the model that we created, we created a video regarding the change of a on the result of the pandemic. In this video, $b = \frac{1}{7}$ and the reproduction number increases from 2 to 5 with each increment = 0.2. The infectivity a increases from $\frac{2}{7}$ to $\frac{5}{7}$ with each increment $b = \frac{1}{35}$. We find that as a increases, $Imax$ increases, and t at which the infected population to reach its maximum decreases.The link to the movie is https://youtu.be/MXbOug5erQM

7 Conclusions

In the Study of Innate Immunity, the more people that are innately immune to the disease, the less severe the pandemics would be. According to our model, we suggest that $V_p \approx 0.55$ could be a threshold that can prevent pandemics from happening. This can explain why herd immunity could happen: if roughly 60% of the population recovered after being infected (here we assume they are permanently immune to the disease), the pandemic would end. The numerical equations also support this conclusion. Looking at the equation of $\frac{dI}{dt}$, I changes by $a\frac{I(t)}{N}S$ for every time step. The increase of V_p reduces S, thereby ending the pandemic. Please note that our graph shows that as V_p approaches 0.8,

the number of uninfected susceptible people decreases. This is not a bad thing because as V_p become greater than 0.6, the total number of infection approaches 0. This means no pandemic would happen. No wonder no herd immunity effect would happen.

In the Study of Fixed-Rate Vaccination, we find that although vaccination always reduces the total infection rate, different intensities of vaccination (number of vaccines) can affect the pandemic differently, especially at the time when the pandemic is the most severe. As shown in the last graph, if the fixed vaccination rate is small, then the time when the pandemic is the most severe would be postponed. In other words, people may experience a longer stage of pandemics until I reaches its peak. However, the peak would be smaller. When the fixed-vaccination rate is larger, not only the peak would become smaller, but the time at which the infection is the most severe would also be reduced.

8 References

Three class notes were referenced:

Peskin, Charles. (2021, February 25). Notes on Deterministic and Stochastic Simulation Methods for Epidemic Modeling. Retrieved March 3, 2023, from (Epidemic Modeling PDF)

Peskin, Charles. (2020, May 9). The SIR Epidemic Model. Retrieved March 3, 2023, from (SIR Model PDF)

Peskin, Charles. (2012, April 9). An Endemic Disease Model and its Application to Malaria. Retrieved March 3, 2023, from (EDM & Malaria PDF)