Applications of the SIR Model of Different Diseases

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1 Abstract

The Susceptible-Infected-Removal (SIR) model is widely used in epidemiology and public health to estimate the population's size in each category, to explain changes in the proportion of people who need medical attention during an epidemic, and to evaluate how well policies are working while the epidemic is in progress. While retaining the basic facts of the classical model, we have explored and discussed application of this model. In this study, we extend the simple model proposed by Kermack and McKendrick in 1927, which we non-dimensionalized three differential equations to explore the relationship between the parameters and the threshold of disease transmission. We use continuous and discrete mathematical modeling to investigate how changes in disease transmission rates and mortality rates affect the rates of change in our healthy, sick, and dying populations. Our result shows the ratio of death rate and number of infected people at the beginning of the epidemics determines the trend of the epidemic.

2 Introduction

2.1 Background and History of SIR

It is generally agreed that the history of infectious disease models began with Daniel Bernoulli's studies on smallpox vaccination in one of his articles in 1760. Ronald Ross, William Hamer, and others started working on epidemic disease models in the early 20th century, which marked the beginning of the development of genuinely deterministic mathematical modeling of infectious illnesses [4]. This model has made a significant contribution to the study of infectious disease dynamics as well as to the field of public health. Three coupled non-linear ordinary differential equations make up the SIR model, which lacks an explicit formula solution. However, we may glean a significant deal of knowledge about the answers using calculus [4]. The idea divides people within the epidemiological range of an infectious disease into three groups: Class S, Susceptible, refers to people who do not have the disease but lack immunity and are susceptible to infection following contact with an infected person; Class I, Infectious, refers to people who have developed an infectious disease that can be transmitted to members of Class S; People who are isolated or immune as a result of those who have recovered from the illness and are immune are referred to as Class R, Removal [1]. The SIR model and various modified models (SI, SIRS, SEIR) have been widely used in simulations of the dynamic transmission of various infectious diseases [2]. For example, the spread of monkey-pox, smallpox, and the familiar COVID-19 virus. In this paper, we will introduce a SIR model and related examples in disease spreading.

We are going to compare the continuous and discrete SIR model and explore change of parameters affect the trends of the epidemic.

2.2 Model Formulation

2.2.1 SI Model

Assume we have a population of N people facing some virus outbreak. Denote N is the size of the population; Suppose the virus will not lead to any death, so N will remain constant, but infected people will not recover from it, so we only consider two categories of individuals: $I(t)$ is the number of infected individuals; $S(t)$ is the number of susceptible individuals. And at any time t, $I(t)+S(t) = N$ which equals the total population. Suppose susceptible individuals get infected as they meet any infected individuals. So, the rate of infected population changes according to

$$\frac{dS}{dt} = -rSI \tag{1}$$

$$\frac{dI}{dt} = rSI \tag{2}$$

where $r > 0$ is a constant of proportionality.

By the property of discrete Markov chain [1], we can transform of differential equations to difference equations. Since the number of infections on a certain day is only related to the

[1]Discrete-time Markov chain, is a stochastic process that goes through a transition from one state to another in the state space. The process requires the property of "memorylessness": the probability distribution of the next state can be determined only by the current state, and the events preceding it in the time series are irrelevant.

number of infections on the previous day. We can express the situation on the n^{th} day by the following difference equation:

$$S_n = S_{n-1} - rS_{n-1}I_{n-1} \tag{3}$$

$$I_n = I_{n-1} + rS_{n-1}I_{n-1} \tag{4}$$

2.2.2 Modified SI Model - SIR Model

Different from the SI Model, we assume the virus can be fatal, and individuals can recover from it and once people recover, they will not be infected again. Hence, people who died and recovered are removed from the contagion dynamics. So, based on the SI Model, we further denote: $R(t)$ is the number of individuals removed from the dynamic; λ is the disease transmission rate; v is the recovery rate. Where λ and v are positive constants. Therefore, we can have the following system of non-linear ODEs, for the most basic SIR Model:

$$\frac{dS}{dt} = -\lambda SI \tag{5}$$

$$\frac{dI}{dt} = \lambda SI - vI \tag{6}$$

$$\frac{dR}{dt} = vI \tag{7}$$

Since N remains constant, i.e $R = N - S - I$, the system can be reduced to a system of two equations, (5) and (6). Similar to the previous SI Model, we can express the situation

on the n-th day by the following different equations:

$$S_n = S_{n-1} - \lambda S_{n-1} I_{n-1} \tag{8}$$

$$I_n = I_{n-1} + \lambda S_{n-1} I_{n-1} - v I_{n-1} \tag{9}$$

$$R_n = R_{n-1} + v I_{n-1} \tag{10}$$

3 SIR Modelling

We focused on one SIR modeling of an Epidemic from **Nonlinear Dynamics and Chaos**, written by Steven H. Strogatz [3]. We will be solving this model in continuous approach and discrete approach:

In pioneering work in epidemiology, Kermack and McKendrick (1927) proposed the following simple model for the evolution of an epidemic. Suppose that the population can be divided into three classes: $x(t)$ is the number of healthy people; $y(t)$ is the number of sick people; $z(t)$ is the number of dead people.

Assume that the total population remains constant in size, except for deaths due to the epidemic. (That is, the epidemic evolves so rapidly that we can ignore the slower changes in the populations due to births, emigration, or deaths by other causes.)

Then the model is:

$$\frac{dx}{dt} = -kxy \tag{11}$$

$$\frac{dy}{dt} = kxy - ly \tag{12}$$

$$\frac{dz}{dt} = ly \tag{13}$$

where k and l are positive constants which k is the infectious rate and l is the rate of death. Since we can ignore the slower changes in the populations due to births, emigration, or deaths by other causes, we assume the total population will remain the same and let N denote the total population, i.e. the change of the population will be zero respect to time

$$\frac{dN}{dt} = \frac{dx}{dt} + \frac{dy}{dt} + \frac{dz}{dt} = 0 \tag{14}$$

Since we cannot find a exact solution to a non-linear system, we need to nondimensionalized the system by rescaling. Based on (11) and (13) and let $x(0) = x_0$ be the initial condition, we know that

$$x(t) = x_0 \cdot e^{\frac{-kz(t)}{l}} \tag{15}$$

Since we have (11) and (13), we can rewrite our equation to be

$$\frac{dz}{dt} = l(N - z - x_0 e^{(\frac{-k}{l})z(t)}) \tag{16}$$

Now we can reduce equations to non-dimensionalized form. Let $u = \frac{kz}{l}$ and $z = \frac{l}{k}u$ and we know $\frac{du}{dz} = \frac{k}{l}$ and $du = \frac{k}{l}dz$, thus we can rewrite (16) as

$$\frac{du}{dt} = (kN - lu - (x_0k)e^{-u}) \tag{17}$$

Let $\tau = (x_0k)t$ where (x_0k) is some constant, then based on (17) we have

$$\frac{du}{d\tau} = (\frac{N}{x_0} - \frac{l}{x_0k}u - e^{-u}) \tag{18}$$

Let $a = \frac{N}{x_0}$ and $b = \frac{l}{x_0k}$, so we know that $a \geq 1$ and $b > 0$, also rewrite (18) to be

$$\frac{du}{d\tau} = (a - bu - e^{-u}) \tag{19}$$

We can determine the number of fixed points by setting $\frac{du}{d\tau} = 0$. If $a > 1$, we have only one valid stable fixed point. We can plot the u-t graph to see if it is consistent with our assumption.

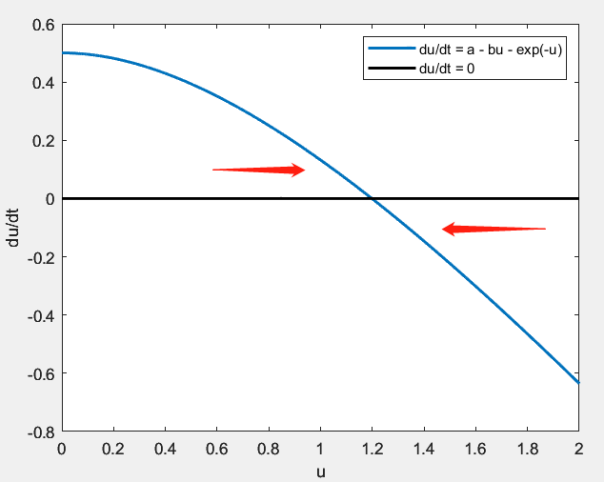


Figure 1: $\frac{du}{dt}$ vs u graph

Let's find the maximum value of $\frac{du}{dt}$, we first find the second derivative of u and set equal to zero.

$$\frac{d^2u}{dt^2} = -l\frac{du}{dt} + x_0k\frac{du}{dt}e^{-u} = 0 \tag{20}$$

Solve (28), we get

$$u = ln(\frac{x_0k}{l}) \tag{21}$$

Which means when $u = ln(\frac{x_0k}{l})$, $\frac{du}{dt}$ is maximum. Similarly, set $\frac{d^2z}{dt^2} = 0$ and $\frac{dy}{dt} = 0$, after solving those two equations, we find the rate of change of death and the number of infected individuals reaches the maximum at the same time.

Now we can convert our equations from continuous to discrete. We will use (8) (9) (10) to

change our differential equations to difference equations.

$$x_n = x_{n-1} - kx_{n-1}y_{n-1} \tag{22}$$

$$y_n = y_{n-1} + kx_{n-1}y_{n-1} - ly_{n-1} \tag{23}$$

$$z_n = z_{n-1} + ly_{n-1} \tag{24}$$

The discrete difference equations are very intuitive. After we have obtained these two models we can discuss our results from these two models and compare each other.

4 Results Overview

Let us now discuss one of the results we obtained based on the above calculations. We are able to rewrite equation (17) as

$$\frac{du}{dt} = kx_0(a - bu - e^{-u})$$

$$\frac{d^2u}{dt^2} = kx_0\frac{du}{dt}(e^{-u} - b)$$

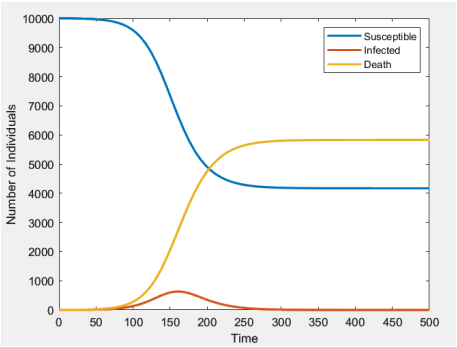
Note that we have 0 people die at the beginning, i.e. $t = 0$, so $z(0) = 0$, which also implies $u(0) = 0$. When $t = 0$:

$$\frac{du}{dt} = kx_0(a - 1)$$

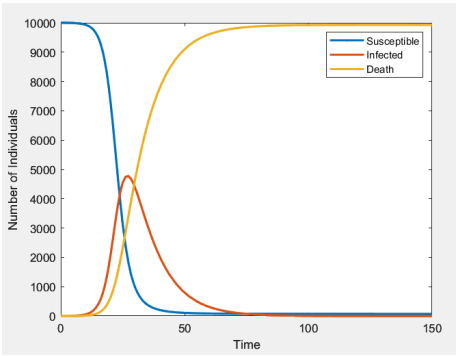
$$\frac{d^2u}{dt^2} = kx_0(a - 1)(1 - b)$$

Let $a \geq 1$, then $\frac{du}{dt} > 0$ when $t = 0$. u is increasing when $t = 0$. There are different results depending on the value of b. Since $b > 0$, we want to discuss $b < 1$, $b = 1$, and $b > 1$.

When $b < 1$, $\frac{d^2u}{dt^2} > 0$ means $\frac{du}{dt}$ is increasing at $t = 0$. There is a peak for $\frac{du}{dt}$ because $u = -\ln(b) > 0$ when $b < 1$. In other words, there is a maximum point for u when $t_{peak} > 0$. We use the numerical method in Matlab to plot the graph of x(Healthy/Susceptible/Blue), y(Sick/Infected/Red), and z(Dead/Death/Yellow) versus time since we were not able to get the precise solution for this non-linear system. Below is the graph using the initial conditions of $N = 10000$, $y_0 = 1$, and $l = 0.1$:



(a) $b = \frac{2}{3}$



(b) $b = \frac{1}{5}$

Figure 2: Continuous SIR Model for $b < 1$

This condition of $b < 1$ ($l < kx_0$) means the death rate is very low, but the epidemic does not stop because the frequency of virus transmission is still high. From Figure 2 (a), since $b = \frac{2}{3}$, we know our death rate (yellow line) and infected rate (red line) grow slower. The number of infected is smaller than the death number even when the infected number of people reaches its maximum. After $t = 250$, three lines stays at the same values, which

means the rate of change of death eventually goes to 0.

From Figure 2 (b), since $b = \frac{1}{5}$, we see that the infected number of people (red line) is larger than the death number of people (yellow line) before two line intersect. We also see the infected number of people reaches its maximum value quicker than the death number of people. Three lines stays at same value after t is approximately 150. By comparison of (b) to (a), we see three lines in (b) moves faster than (a), they took less time to reach the stage that their rate of change of susceptible/infected/death is 0.

When $b > 1$, $\frac{d^2u}{dt^2} < 0$ means $\frac{du}{dt}$ is decreasing at $t = 0$. Also, there is no positive solution for $u = -\ln(b)$ because $b > 1$. Therefore, our peak of u happens when $t = 0$, i.e. $t_{peak} = 0$. When $b > 1$ ($l > kx_0$), the death rate is higher the infectious rate. In other words, the epidemics is in control and would disappear short time. We use the same method, initials, and a different k value to obtain the following graph:

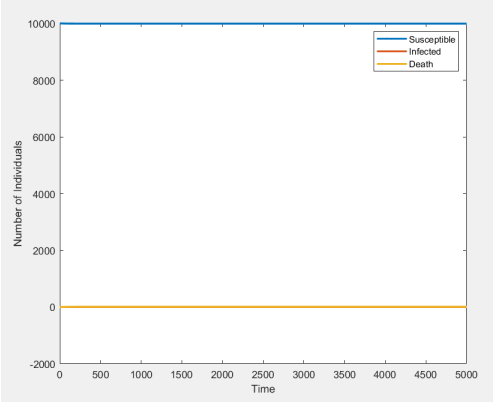


Figure 3: Continuous SIR Model for $b = 1.11 > 1$

We see that the infected number of people (red line) and death toll (yellow line) lies in x-axis (there is no infected people and no one die) in Figure 3, thus the susceptible number of people remains the same.

When $b = 1$, the peak of u still occurs at $t = 0$ because $u = -\ln(b) = 0$. We expect our infectious rate and death rate is similar to each other. And the epidemics would disappear in a short time. We use same technique to obtain the graph of $b = 1$:

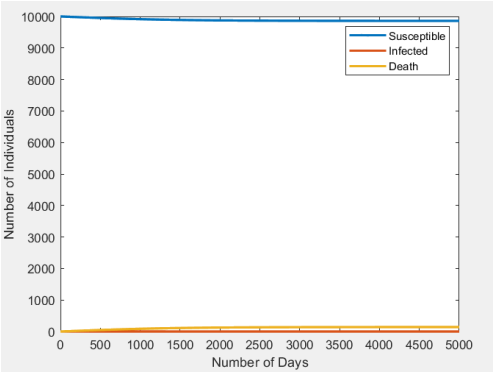


Figure 4: Continuous SIR Model for $b = 1$

From Figure 4, the rate at number of infectious people increases is the same as the death rate because $b = 1$ implies $l = kx_0$. This is the threshold value.

We use the same technique but with discrete equation to model:

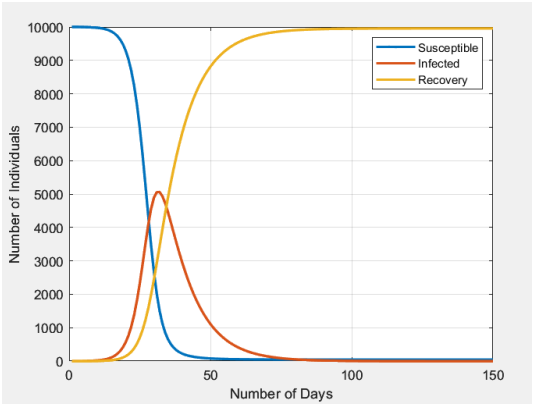


Figure 5: Discrete SIR Model for $b = 0.2$

From Figure 5, we see the discrete SIR model is identical to Figure 2b. We are able to obtain SIR model in continuous and discrete approach.

In summary, $b = \frac{l}{kx_0}$ is rate of l (the death rate) and kx_0 (the infectious rate $\times$ healthy/-susceptible number of people at beginning of epidemic). If $b < 1$, the epidemic would not stop but the death rate is relatively low. If $b \geq 1$, the epidemic is controllable but the death rate is relatively high. In particular, $b = 1$ is the threshold value.

5 Discussion of the Model

Different from the basic SI model, the SIR introduces an absolutely significant new variable, $R(t)$, the individuals who are "removed" from the contagion dynamics, which makes the model more realistic. Although it is still not good enough to predict the real-world situation, it already provides much better simulation than the SI model for the infectious diseases such as Measles, Monkeypox, and COVID-19, etc. In addition, there is also a more advanced

model that is constructed based on the SIR, namely the SEIR model, which introduces $E(t)$, the individuals exposed to the virus but in the incubation period for now, we will not talk about that in detail.

From the result we got previously, parameter b was defined as $b = l/(kx_0)$, where l is the death rate, x_0 is the initial number of healthy people in the beginning of the epidemics, and k is the infectious rate. The value of b determines the trend of the epidemics:

- Case 1, $b < 1$: $l < kx_0$, the death rate is low, but the infectious rate of the virus is high, the epidemics start.
- Case 2, $b > 1$: So, $l > kx_0$, the infected individuals die very soon or the infectious rate is low, the epidemics will be controllable and disappear in short time.
- Case 3, $b = 1$: So, $l = kx_0$, the death rate is equal to the infectious rate, the epidemics will also be controllable.

In general, as $x_0 \leq l/k$, the diseases will not spread. Therefore, in order to avoid epidemics, in addition to improving hygiene and health care, making the threshold l/k large enough, another way is to lower x_0, which can be done, for example, through vaccination. Ignoring the initial value of infected individuals, y_0, let r_0 be the initial number of the individuals who are "removed" from the contagion dynamics, so we have $x_0 = 1 - r_0$. So, the condition which the diseases will not spread, $x_0 \leq l/k$, can be expressed as $r_0 \geq 1 - l/k$. Hence, the spread of diseases can be stopped as long as the proportion of immunizers at the initial moment, r_0, meets the inequality above through herd immunity.

6 Conclusions

In this paper, we introduced the susceptible-Infected-Removal Model of disease, namely the SIR model. Assume the total population remains constant, the model suggests that given the initial condition $x(0) = x_0$, with the passage of time, the number of susceptible individuals $x(t)$ began to monotonically decrease, the number of infected individuals y(t) first reached the peak, and then fell until it was reduced to zero, and the number of recovered individuals (or the death) increased monotonically. There exists a threshold b, such that if $b < 1$, the epidemics start; otherwise, the disease will be controllable.

This SIR model has improved and made things a lot more interesting than the basic SI model. To improve the model further, we can introduce another variable, the exposed: $E(t)$, to simulate the incubation period, which was ignored in the SIR model. Even more complicated, we can assume the exposed can also transmit the virus to others, so we can introduce new constants of infectious rate to turn a healthy susceptible into an exposed or infected. In summary, the SIR model of disease provides us a simple but relatively more accurate way to simulate an epidemic outbreak, giving us a basic principle to prevent and reply to the infectious virus by increasing the proportion of r_0, the individuals with immunity.

7 References

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