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Using the SIR Model as a Guideline for Vaccination during an Infectious Disease

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Abstract: In this paper, we discuss and analyze the well-known Susceptible-Infected-Recovered (SIR) Model to address the following questions: (Q1) What total proportion of the population will get infected? (Q2) What proportion of the population should be vaccinated in order to suppress the epidemic? To answer these questions, we discuss and analyze and the SIR model and its variations to predict the outcome of an epidemic and any measures needed to suppress the outbreak of the disease.

MSC: 92B05.

Keywords: SIR Model, Mathematical Modeling, Infectious Diseases, Vaccination.

1. Introduction

Mathematics has played a role in various fields of science, such as physics, chemistry and astronomy, for a long time. Some of the earliest models date back to the Ancient Greeks. Epidemiology has adapted these mathematics to predict the future of an outbreak using numerical simulations and models. These models, along with data analysis and experimentation, still provide scientists with guides to understand real-life phenomena. One such model is the Susceptible-Infected-Recovered (SIR) model. The SIR model is used to simulate simple cases of outbreaks and to predict the proportion of the population that will get infected. In this article, we will be exploring the SIR model and its applications to determine what proportion of the population will get infected and to determine what proportion of the population must be vaccinated in order to subdue the epidemic.

The calculations produced by this model are not, however, a perfect representation of the reality; they simply give us an approximation of the magnitude of the outbreak so that we can take appropriate measures, such as a vaccine. Since the model could result in some error, further experimentation and data collection should be used complementary to the model to improve accuracy. We are not the first to study and discuss these epidemiological models, so we suggest the reader to consult the references to learn more about the subject.

This article is organized as follows:

- In Section 2, we will explain the model and its variations that are used to determine a result.
- In Section 3, we will numerically simulate the model in order to identify its behaviour.

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- In Section 4, we will analyze the numerical simulations in order to produce meaningful conclusions.
- In Section 5, we will discuss the conclusions of the model and how it can be applied to a real-life situation.

2. The SIR Model

In the SIR model, the total population, denoted by N, is generally constant. Each individual in the population can fall under one of three categories: susceptible (S), infected (I), or recovered (R). In this context, a recovered individual has also developed immunity. An individual can move from one category to another. For example, a susceptible individual can become infected. However, an individual cannot belong to two categories at the same time. Thus,

$$S + I + R = N$$

The rate at which I changes, $\frac{dI}{dt}$ depends on S and I. Thus, we can define:

$$\frac{dI}{dt} = f(S, I)$$

For $(S, I) > (0, 0)$, if S increases, $\frac{dI}{dt}$ increases. Likewise, as I increases, $\frac{dI}{dt}$ increases. Thus, $f(S, I)$ is an increasing function of both S and I. However, for $(S, I) = (0, 0)$, $\frac{dI}{dt} = 0$. I does not change because there are no infected individuals to pass on the disease and there are no susceptible individuals to receive the disease.
With this, we can define our model. Let us first consider a scenario in which recovery does not take place. The simplest case of the SIR model is as follows:

$$f(S, I) = \beta SI; \quad for \quad \beta > 0$$

Here, $R = 0$, so $S + I = N$. Thus,

$$f(S, I) = \beta I(N - I)$$

The solutions to this polynomial is $I = 0$ and $I = N$. Considering that $f(S, I) = \frac{dI}{dt}$, this shows that the rate at which susceptible individuals become infected does not change when the number of infected individuals is 0 or N. However, it can be observed that $I = 0$ is an unstable fixed point while $I = N$ is a stable fixed point. Therefore, if $I > 0$, the number of infected individuals will approach N over time. Since it is evident that susceptible individuals become infected, S and I must be the opposite of each other. Thus, we can define this model for S:

$$\frac{dS}{dt} = -\beta SI$$

Let us now consider recovery. Assuming that recovered individuals (R) do not develop immunity to the disease, recovered individuals are again susceptible. Let us define g as the rate at which infected individuals recover. This rate g depends only on I. Since a greater I gives a greater g, g is an increasing function of I. Thus,

$$\frac{dR}{dt} = g(I) = \gamma I; \quad for \quad \gamma > 0$$

As more individuals recover, the number of infected individuals decreases. Thus, we can modify equation 1 to get:

$$\frac{dI}{dt} = f(S, I) - g(I)$$

Since recovered individuals have not gained immunity, $R = 0$. Thus, $S + I = N$.

$$\begin{aligned}\frac{dI}{dt} &= \beta I(N - I) - \gamma I \\ &= \beta I(N - \frac{\gamma}{\beta} - I)\end{aligned}$$

The solutions to this modified polynomial is $I = 0$ and $I = N - \frac{\gamma}{\beta}$. Like before, if $I > 0$, the number of infected individuals will rise, but will now approach $N - \frac{\gamma}{\beta}$ for some constant $\frac{\gamma}{\beta} > 0$. Let us now introduce immunity. Assuming individuals that recover develop immunity, recovered individuals are no longer susceptible. Therefore, $R > 0$ and it is no longer true that $S + I = N$. Therefore,

$$S \geq 0,\ I \geq 0 \text{ and } S + I \leq N$$

Therefore, the values of S and I is contained in the following region: Let us review the three equations:

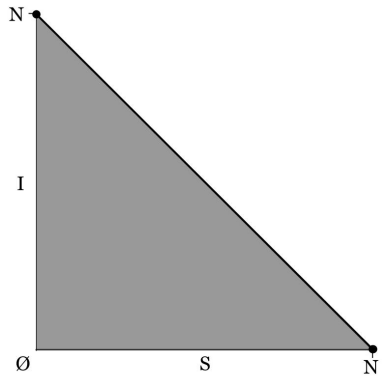

Figure 1. **The set of possible values of S and I is contained in this region.**

$$\begin{aligned}\frac{dS}{dt} &= -\beta SI \\ \frac{dI}{dt} &= \beta SI - \gamma I \\ \frac{dR}{dt} &= \gamma I\end{aligned}$$

Let us consider a point in time near the start of the outbreak. For time $t = 0$, $S \approx N$ and $I \approx 0$. Thus,

$$\frac{dI}{dt} = \beta NI - \gamma I = (\beta N - \gamma)I$$

We can say that if $\beta N - \gamma > 0$, $\frac{dI}{dt} \approx (\beta N - \gamma)I > 0$. But if $\beta N - \gamma < 0$, then $\frac{dI}{dt} \approx (\beta N - \gamma)I < 0$. Keep in mind that I cannot be negative, since it is impossible to have a negative number of infected individuals. Now, let us define $\frac{dS}{dt}$ as $f_1(S, I)$ and $\frac{dI}{dt}$ as $f_2(S, I)$.

$$\begin{aligned}\frac{\partial}{dS} f_1(S, I) &= -\beta I \\ \frac{\partial}{dI} f_1(S, I) &= -\beta S \\ \frac{\partial}{dS} f_2(S, I) &= \beta I \\ \frac{\partial}{dI} f_2(S, I) &= -\beta S - \gamma\end{aligned}$$

Let us define a matrix A of these partial derivatives as follows:

$$A = \begin{bmatrix} -\beta I & -\beta S \\ \beta I & \beta S - \gamma \end{bmatrix}$$

We are primarily concerned with the point $(S, I) = (N, 0)$, because this is at the start of the outbreak. This point is a fixed point, or an equilibrium point for a differential equation. This fixed point can be either stable or unstable. In our context, a stable fixed point will cause the number of infected individuals to approach 0 and an unstable fixed point will cause a surge in the number of infected individuals. For the point $(S, I) = (N, 0)$,

$$A = \begin{bmatrix} 0 & -\beta N \\ 0 & \beta N - \gamma \end{bmatrix}$$

We can determine whether this fixed point is stable or unstable by finding the eigenvalues of the matrix. If the eigenvalues are greater than 0, then the fixed point is unstable and if the eigenvalues are less than 0, then the fixed point is stable. The eigenvalues of the matrix are 0 and $\beta N - \gamma$. From this, we can say that the fixed point is stable when $\beta N - \gamma < 0$ or when $\frac{\beta}{\gamma} N < 1$ and thus, we do not have an epidemic. To determine how many individuals will get infected, we can solve for I in terms of S. Notice that the equations for $\frac{dI}{dt}$ and $\frac{dS}{dt}$ do not contain R, so let us solve the system of these two equations.

$$\frac{dI}{dS} = \frac{\frac{dI}{dt}}{\frac{dS}{dt}} = \frac{\beta IS - \gamma I}{-\beta IS} = -1 + \frac{\gamma}{\beta S}$$

Integrating with respect to S yields:

$$I = -S + \frac{\gamma}{\beta} ln(S) + C$$

Using this equation, various values of $\frac{\gamma}{\beta}$ can be tested to observe the outcome. By finding the maximum value of this function, we can determine how many individuals will get infected.

3. Numerical Simulation

Now that we have a general set of solutions to the previous differential equation, we can test various values of $\frac{\gamma}{\beta}$ to observe the outcome. Keep in mind that the graphs start from the right side when $\frac{S}{N} = 1$ and $\frac{I}{N} = 0$ and move leftward. These graphs are not in terms of t.

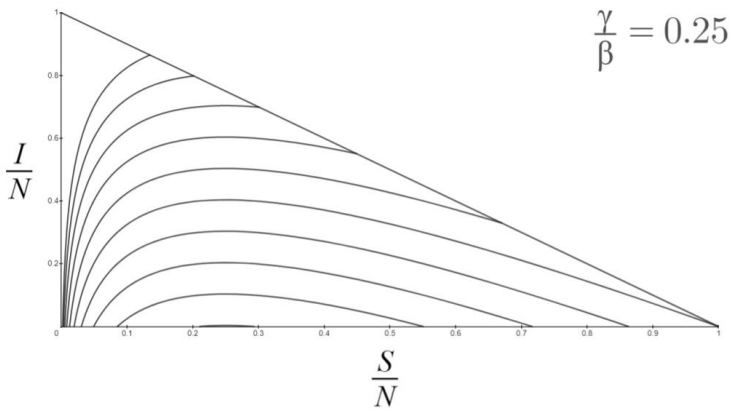

Figure 2. **With a $\frac{\gamma}{\beta}$ value of 0.25**

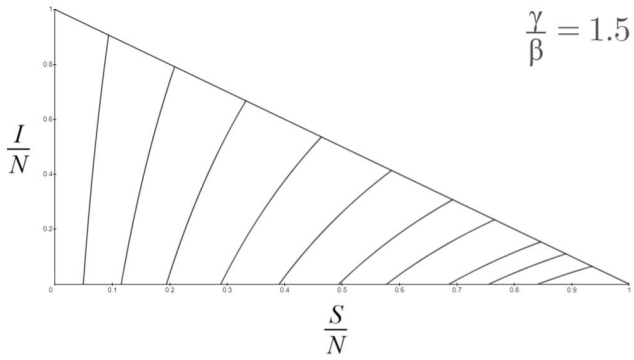

Figure 3. **With a $\frac{\gamma}{\beta}$ value of 1.5**

The following graphs show the percent of the population in each of the three groups in terms of time.

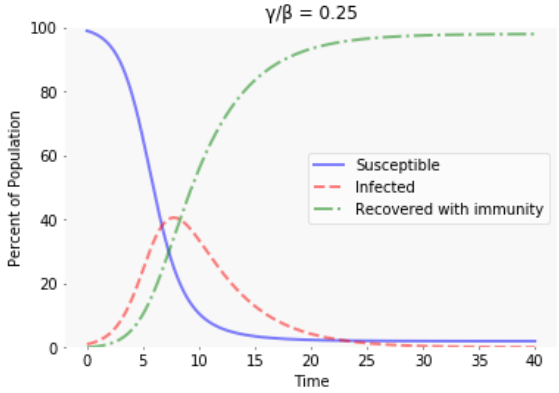

Figure 4. **With a $\frac{\gamma}{\beta}$ value of 0.25**

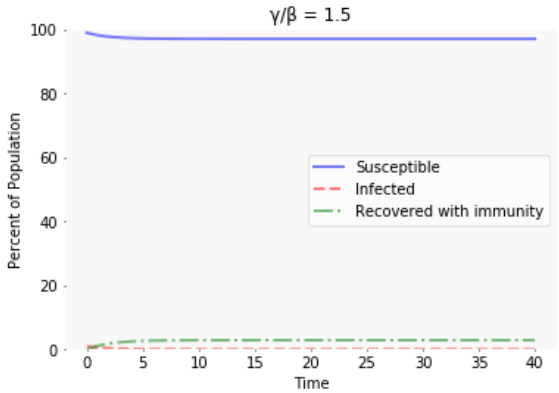

Figure 5. **With a $\frac{\gamma}{\beta}$ value of 1.5**

4. Analysis of Numerical Simulation

Previously, we have solved for I in terms of S. Using this equation, we can find the maximum value to determine how many individuals will get infected. We have the function:

$$I = -S + \frac{\gamma}{\beta} ln(S) + C$$

To find the maximum value of this function, we can find the critical points by setting its derivative equal to 0.

$$\frac{dI}{dS} = -1 + \frac{\gamma}{\beta S} = 0$$
$$S = \frac{\gamma}{\beta}$$

This shows us that the maximum number of individuals will be infected when $S = \frac{\gamma}{\beta}$. Since $S = N - I$, the number of individuals who will get infected is $I = N - \frac{\gamma}{\beta}$. Suppose we have a vaccine. All individuals who receive the vaccine cannot get infected, so they are considered recovered and immune. So if we vaccinate some proportion, q, of the population, it is effectively reducing the pool of susceptible individuals from $S = N$ to $S = (1-q)N$. What proportion q should be vaccinated in order to prevent an epidemic?

We have determined that there is no epidemic when $\frac{\beta}{\gamma}N < 1$ without a vaccine. With a vaccine, N becomes $(1-q)N$, so we do not have an epidemic when:

$$\frac{\beta}{\gamma}(1-q)N < 1$$
$$\frac{\beta}{\gamma}N - 1 < \frac{\beta}{\gamma}Nq$$
$$1 - \frac{\gamma}{\beta N} < q$$

This tells us that we must vaccinate at least $1 - \frac{\gamma}{\beta N}$ of the population. For example, if $1 - \frac{\gamma}{\beta N} = \frac{2}{3}$, then we must vaccinate at least $\frac{1}{3}$ of the population.

5. Conclusion

At the beginning of the article, we posed two questions:

(1). What proportion of the population will get infected over the course of the epidemic?

(2). What proportion of the population must be vaccinated in order to prevent the progress of an epidemic?

By using and analyzing the SIR model, we have been able to answer these two questions. To determine how many individuals will get infected, we solved for I in terms of S. We then found the maximum value of the antiderivative of this new function. This value tells us the total number of infected individuals due to an epidemic given $\frac{\gamma}{\beta}$ and the size of the population.

We have also determined that a vaccine would decrease the pool of susceptible individuals from $S = N$ to $S = (1-q)N$. From this, we have concluded that we must vaccinate at least $1 - \frac{\gamma}{\beta N}$ of the population in order to prevent the progress of an epidemic.

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