The SIR Model of Disease Spread

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1 Introduction

The SIR model is a classical model of disease transmission within a population. It can be modified to account for several important population dynamics, such as death rate, immigration or birth rate, recovery, and immunity - but even the most basic model has powerful public health applications. Here we examine the most basic model, a good starting point for further study. We assume disease spread depends on population size; infection is instantaneous; no one is resistant to the disease at the start; immunity, once gained, is permanent; and that the disease is not fatal.

The SIR model works by placing all individuals in the population into one of three classes at any given time: individuals susceptible to disease, infected individuals, and “removed” individuals. The removed class counts those individuals that are not infected and not susceptible; in other words, immune, quarantined, or dead individuals. The class is significant; in other SIR model variants, it can account for both permanent or temporary immunity acquired from vaccination or from having the disease. Again, however, we choose to use the simplified model where immunity (or lack of susceptibility) is permanent, and describe the recovery rate as the parameter $\sigma$. Our assumption is a reasonable one for diseases like flu, for which vaccines have been developed only recently and which generally do not afflict an individual more than once in the course of an epidemic. Individuals may move from one class to another; for example, an individual may move from the infected class to the removed class upon recovery. Thus the model accounts for the interdependency of the different classes within the population.

The SIR model can be modified to account for change in overall population over time; here, however, we look at a model with a constant population. This assumption is reasonable for low mortality epidemics which run their course
much faster than a human population can reproduce.

2 Fundamental Equations

The fundamental relation of the SIR model is the following:

\[ N = S(t) + I(t) + R(t) \] (1)

where \( N \) is the total population size, taken to be constant; \( S(t) \) is the size of the susceptible population; \( I(t) \) is the size of the infected population; and \( R(t) \) is the size of the removed population.

The derivative of this equation is also useful. It articulates that, given a constant population size, the rates of change of the three sub-classes must cancel each other out.

\[ \frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0 \] (2)

3 Law of Mass Action

The SIR model assumes that individuals within the population follow the law of mass action, that is, they come into contact with one another randomly. The likelihood at which an infected individual comes into contact with any other members of the population is described by the fixed parameter \( c \). The likelihood that the disease is actually transmitted is described by the parameter \( a \). By multiplying \( a \) and \( c \), we can collapse these two constants into a single constant disease transmission rate, \( r \). However, it is important to note the separate components of \( r \) when it comes to disease spread more generally. The law of mass action assumes that the transmission of disease depends on population size. While this is reasonably true for many diseases, such as the flu,
it is inappropriate for others, such as sexually transmitted infections. Diseases that follow alternate transmission patterns are beyond the scope of this paper, however.

The SIR model is perhaps best articulated with a diagram. See Figure 1.

4 Rate Equations

With the preliminary assumptions and structure of the model in place, let us delineate the actual equations.

\[
\frac{dS}{dt} = -acS(t)I(t) \quad (3)
\]

\[
\frac{dI}{dt} = acS(t)I(t) - \sigma I(t) \quad (4)
\]

\[
\frac{dR}{dt} = \sigma I(t) \quad (5)
\]

Let us make some general observations. The effective disease transmission, \( ac \), and the recovery rate, \( \sigma \), are both assumed to be greater than zero. As we can see, the rate of change of the susceptible population, \( \frac{dS}{dt} \), is by definition

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negative. Therefore, the maximum number of susceptible individuals is found at time 0, so $S_{\text{max}} = S_0$. We can see that those individuals that get infected get moved from the susceptible class to the infected class; the infected class consists of those individuals less those that recover; and the removed class consists of those that recover.

The SIR model is a system of three nonlinear differential equations, and is therefore not possible to solve explicitly. However, the system can be solved numerically to differing degrees of accuracy, and that is more than sufficient for understanding the model and using it in the staging of interventions.

5 Setting Initial Conditions

We can move forward by setting initial conditions. We define time 0 as the moment the potential epidemic starts. We assume that the number of susceptible individuals and infected individuals are both greater than zero; otherwise, disease spread would not be possible. If we assume no one is immune to start with, then we can set the value for the removed population equal to 0 at time 0. In other words,

$$S(0) = S_0 > 0, \ I(0) = I_0 > 0, \ R(0) = 0.$$  \hspace{1cm} (6)

If we know the values for $ac$, $\sigma$, $S_0$, and $I_0$ - and health officials very well might have accurate figures for well-known diseases such as flu - then we can see whether the infection spreads and the maximum number of individuals we can expect to be infected. If we want to find the rate of change in the infected population at time zero, we substitute the initial values into the equation:

$$\frac{dI}{dt}_{t=0} = rS_0I_0 - \sigma I_0$$  \hspace{1cm} (7)
Thus the rate of change in the infected population at time 0 is greater than zero when \( rS_0I_0 > \sigma I_0 \) which can be simplified in the following steps:

\[
\begin{align*}
    rS_0I_0 & > \sigma I_0 \\
    rS_0 & > \sigma \\
    S_0 & > \frac{\sigma}{r}
\end{align*}
\]  

(8)
(9)
(10)

So the rate of change in the infected population will be positive (the number of infected will increase) when the relative removal rate (the recovery rate \( \sigma \) over the infection rate \( r \)) is less than the initial susceptible population \( S_0 \). In this situation the disease spreads.

The converse is also true: \( \frac{dI}{dt} = 0 < 0 \) when the relative removal rate is greater than the initial susceptible population, \( S_0 \). This can be determined using a similar analysis to the one above. In this situation, the disease dies out and the epidemic does not ensue. The importance of \( S_0 \) is called the threshold phenomenon.

6 Maximum Number of Infected, \( I_{max} \) and Solution Curves

We can also look at when \( \frac{dI}{dt} = 0 \), which is when \( S_0 = \frac{\sigma}{r} \). When \( \frac{dI}{dt} = 0 \), there is an inflection point in the graph of \( I(t) \); we find the local maximum. The value for \( I \) when \( \frac{dI}{dt} = 0 \) is therefore the maximum number of infected individuals, \( I_{max} \). After this point, the disease will peter out. Naturally, the graph is different for different values of \( S_0 \) and \( I_0 \), but the only singularities (points where a function is not analytic) are found at \( I = 0 \). Since \( I = 0 \) is not meaningful in concrete terms to the study of the spread of disease, we need not
be concerned with these singularities.

A graph of the solution curves illustrates this phenomenon. See Figure 2.  

We can find the equation for these curves by dividing the rate of change of the infected population by the rate of change of the susceptible population.

\[
\frac{dI}{dS} = \frac{(-rSI - \sigma I)}{rSI} = -1 + \frac{\rho}{S}
\]  

(11)

where \( \rho = \frac{\sigma}{r} \). We can integrate this equation to find

\[
I + S - \rho lnS = constant = I_0 + S_0 - \rho lnS_0
\]  

(12)

Since we know $I_{\text{max}}$ occurs when $\frac{dI}{dt} = 0$ and when $S_0 = \rho$, and since $R(0) = 0$, we can rearrange and substitute this equation to find $I_{\text{max}}$, the maximum number of individuals we expect to be infected at any point in the course of the epidemic.

$$I_{\text{max}} = I_0 + S_0 + \rho \ln \rho - \rho - \rho \ln S_0$$

$$I_{\text{max}} = N - \rho - \rho \ln \frac{\rho}{S_0}$$

This figure is useful for public health officials in estimating the severity of the epidemic and how best to mitigate it. At the worst point in the epidemic, what is the highest number of sick individuals we can expect to have? Will we have enough medical personnel? How will this impact the economy of the community? $I_{\text{max}}$ can begin to help answer some of these questions.

7 Maximum Susceptible and Total Infected

In a similar vein, we can also analyse the equations to find the maximum number of individuals who are susceptible, but never get the disease. (Remember, we are assuming no one has immunity at time 0.) We can find this number using the two basic equations for $\frac{dS}{dt}$ and $\frac{dR}{dt}$, (3) and (5) respectively, and dividing the first by the second, as follows.

$$\frac{dS}{dR} = \frac{-r}{\sigma} = \frac{-1}{\rho}$$

We can separate the equation and integrate to find:

$$\ln S = \frac{-R}{\rho}$$

8
and exponentiate to find

\[ S = S_0 e^{-\frac{R}{\rho}} \]  

(17)

Since we know from our graph of solutions that I(t), the number of infected individuals, goes to 0 and time t goes to infinity, then we can find the value of S as time t goes to infinity. The total population, \( N = S(t) + I(t) + R(t) \) and if \( I(\infty) \) is 0 then \( R(t) = N - S(\infty) \). We can substitute this equation into the formulation above.

\[ S(\infty) = S_0 e^{\frac{-R(\infty)}{\rho}} \]  

(18)

\[ S(\infty) = S_0 e^{\frac{-(N - S(\infty))}{\rho}} \]  

(19)

\( S(\infty) \), then, is the positive root of this equation. Naturally, it is greater than 0, and it is also less than \( \rho \) (we can tell this from looking at the graph of the solutions). Given this, then, we can say that the total number of individuals we can expect to be infected over the entire course of the epidemic, found in the following equation:

\[ I_{total} = I_0 + S_0 - S(\infty) \]  

(20)

Looking at this equation even without the derivation, we see that the equation is quite intuitive.

8 Conclusion

In summary, the SIR family of models are powerful and flexible tools for understanding the spread of disease and staging public health interventions. Even the most basic of these models, such as what was examined here, can give us crucial figures. We can find whether the epidemic even occurs, the maximum number of infected individuals at any point in time and hence the severity of the
epidemic, and the total number of individuals who get sick over the course of the epidemic. The assumptions within the model, such as the law of mass action (indicating that disease spread is proportional to the population), the complete lack of immunity at the beginning of the epidemic, instantaneous infection (no latency period), and the short duration of the disease relative to lifespan, are limiting but nevertheless reasonable for diseases such as flu. Furthermore, the SIR model can be modified to account for these factors, and many such variants have been developed and explored.
Bibliography


