

# Chapter 2

## Simple Epidemics and SIS Models

### 2.1 Introduction

Next I analyze some formal models of epidemics. In all of these initial models I make some simplifying assumptions that will aid with the introductory analysis. Later in the chapter and in subsequent chapters I will generalize the models to make them more realistic. Further by the end of these introductory sections you will be prepared to make additional assumptions and generalizations on your own in exactly the same framework introduced here. However I want to point out that making simplifying assumptions in these early chapters, does not make these models invalid or of no use. Often times simple models can reveal a great deal about the dynamics of interest in the spread of an epidemic. Further the solution concepts that I use in these simple introductory models will also apply to more complicated models.

I have two goals in this chapter: One is to introduce the reader to an SI model or what is sometimes called a simple epidemic. I will use this model to introduce the concept of an epidemic threshold, the level at which an epidemic will “take off” and grow in a population. Second, I will introduce the general SIS model framework and discuss the concept of the reproduction number and an epidemic steady state.

### 2.2 The First Model: A Simple Epidemic

To begin I start with the simplest possible dynamic model of an epidemic, an SI model. I want to monitor the number of individuals in the population who are infected with the disease of interest. Again I will use the variable  $t$  to denote the time period. I use  $N_t$  to denote the total size of the population in period  $t$ . In this first model, I have two categories, those that are susceptible to being infected by the disease, denoted by  $S$ , and those that are infected (and infective), denoted by  $I$ . I label the number of those infected in period  $t$  as  $I_t$  and the number susceptible in period  $t$  as  $S_t$ . where  $I_t + S_t = N_t$ . Individuals go from being susceptible to a

disease to being infected and once infected, they never recover and remain in the population forever. Thus the progression of the disease from the standpoint of an individual is susceptible–infected or SI.

Assume that  $N_t = N$  for all  $t$ . In other words there is a constant population size. Further assume that all the people in the population are the same people from period to period. Note that these are two different assumptions. One example where  $N_t$  is constant but with turnover in the population would be if there were equal birth and death rates in the population. In this example, the population size would be constant but some of the people in the population would be different each period. For now I ignore this and assume that there is a constant unchanging population.

Individuals potentially move from the susceptible to the infected group when a susceptible person comes in contact with an infected person. What counts as a contact varies with the disease. Sometimes diseases are transmitted through sexual contact or are carried in blood as in HIV. In other cases one only needs to be near a person as the disease is carried via the air we breath as in SARS or influenza. In addition even if you come in contact with someone it is not always guaranteed that the disease will be transmitted. For instance only a small fraction of sexual contacts between an infective and a susceptible person result in the transmission of HIV. I denote the probability of a contact between a susceptible and an infected person resulting in transmission of the infectious disease to be  $\alpha$ .

Suppose there are  $I_0$  infected individuals in the initial period of the model. In epidemics we are interested in how the disease will spread. Thus what we really want to know in many cases is how many infected individuals there will be in the next period. In other words we want to know  $I_1$ , and then  $I_2$  and then .... We want to know how the spread of the disease will progress.

I begin by looking at the transition from period 0 to period 1. In period 0 there are  $I_0$  infected individuals. Call this the state of the system at time 0. New individuals get infected by coming in contact with members of the infected population. Assume that each infected person contacts  $\gamma$  non-infected people in each period. Thus the number of possible new infections is  $\gamma I_0$ . But not all of the contacts result in an infection. As stated above, suppose that only  $\alpha$  percent of contacts result in an infection. Thus each infected individual results in  $\gamma\alpha$  new infections in the subsequent period. Now write out an equation that describes this process:

$$I_1 = I_0 + \gamma\alpha I_0 = (1 + \gamma\alpha)I_0 \quad (2.1)$$

Now write the equation for period 2:

$$I_2 = I_1 + \gamma\alpha I_1 \quad (2.2)$$

This is the same equation but with different time subscripts. Now substitute Eq. 2.1 into Eq. 2.2 to get:

$$I_2 = (1 + \gamma\alpha)I_0 + \gamma\alpha((1 + \gamma\alpha)I_0) = (1 + \gamma\alpha)^2 I_0 \quad (2.3)$$

Similarly, write the following for  $I_3$  and onward. In general the following equation describes the general solution of the model:

$$I_t = (1 + \gamma\alpha)^t I_0 \quad (2.4)$$

The number of people currently infected in period  $t$  is 1 plus the product of the contact and transmission parameters raised to the power  $t$  multiplied by the initial size of the infected population.

Note that the epidemic will always grow until the entire population is infected as long as both  $\gamma > 0$  and  $\alpha > 0$ . In the simple SI model the only long run outcome is for all individuals in the population to become infected.

Now, change the model slightly. In the previous model once an individual was infected she remained there forever. The only transition in the model was from category S to category I. Now, instead, assume that once infected each individual in the population returns to the susceptible population after one time period. This is a new modeling transition, where agents can go from susceptible to infected and back to susceptible again. With this new assumption the basic equation describing out model becomes:

$$I_{t+1} = I_t + \gamma\alpha I_t - I_t = \gamma\alpha I_t \quad (2.5)$$

Again, trace through the beginning of an epidemic by starting with period 1 and finding  $I_1$ :

$$I_1 = I_0 + \gamma\alpha I_0 - I_0 = \gamma\alpha I_0 \quad (2.6)$$

Again, iterating forward leads to:

$$I_2 = \gamma\alpha I_1 = (\gamma\alpha)^2 I_0 \quad (2.7)$$

Or, more generally:

$$I_{t+1} = (\gamma\alpha)^t I_0 \quad (2.8)$$

This equation has more interesting possibilities. Let us analyze how this system will behave by looking at the number of infected persons in period  $t$  where  $t$  is far into the future. In other words  $t$  is large, say 1,000. Suppose that there is one infected person in the initial period and that  $\gamma$  is 5 and  $\alpha$  is 0.1. Will there be many people infected or a few at period 1,000? Note that  $\alpha\gamma = 0.5$ . So we expect that there will be  $0.5^{1000}$  people infected in period 1,000. You can check on your calculators if you like but this is a VERY small number, essentially 0. What if we increase  $\alpha$  to 0.3? Now we get  $1.5^{1000}$ , a VERY big number! What happens if  $\alpha$  is 0.2? We get  $1^{1000} = 1$ . Lets try one more, let  $I_0$  be 1,000,000 and  $\alpha$  be 0.19. Thus in period 1,000 we would have  $(0.19 * 5)^{1000} * 1,000,000 = 0.95^{1000} * 1,000,000$  which again is essentially 0.

What you have probably already noticed is that if  $\alpha\gamma < 1$  the number of infected individuals decreases to 0 very rapidly; the disease disappears. If  $\alpha\gamma > 1$  the

number of infected individuals keeps increasing; the disease spreads throughout the population. This is sometimes called the *epidemic threshold*. Now what does this really mean? How can we interpret this result? If the number of contacts multiplied by the transmission rate is less than one this means that each infected person infects less than one person on average. So, the number of infected individuals will decrease. It is like the reproduction and population models you may have studied in biology class, if each person has less than one offspring the population will die out. But if the average number of offspring is greater than one the population will grow. Just like our model when the average number of people infected is greater than one; the disease continues to spread to a larger and larger fraction of the population. Thus we reach the epidemic threshold whenever greater than one person is infected by each infected person.

The model of this section has some weaknesses that we will correct in the next section. But the main point of the model is that we can understand most of what is going on if we look at just a couple parameters in the model. And, from a public policy standpoint if we can alter those parameters we can control an epidemic. As an example, if we can limit the number of contacts of infected people with non-infected people so that we are below the epidemic threshold we can end the epidemic. Further, it may not take a large action to break free of an epidemic if we are near the epidemic threshold. Suppose that each infected individual in a population has 11 contacts with susceptible individuals and the transmission rate is 0.10. We would be above the epidemic threshold and the epidemic would grow very quickly. After 100 time periods there would be nearly 14,000 individuals infected. But, if we could decrease the number of contacts by just 1, to 10, the epidemic would stabilize. And, if we were able to decrease the number of contacts to 9 the epidemic would die out quickly as well. (If we decreased the contacts to 9 at period 100 it would take less than 50 periods for the number of infected individuals to drop to less than 100 and by period 190 there would be less than one individual infected on average.) The lesson here is that sometimes even large epidemics can be precariously balanced at the edge of eradication. On the other hand, sometimes it can take only a small nudge to turn a small public health issue into a very large one.

### 2.3 A Full SIS Model

I kept the model of the last section overly simplistic in order to introduce some key ideas. First, I used difference equations to study a diffusion process. And second, I introduced some key parameters that will be used throughout the book. In this section I more fully develop the SIS model to a form that one is likely to encounter in policy and research discussions of diseases that fit the SIS framework.

First, in the final model of the last section I assumed that each contact of an infected individual was with a non-infected, or susceptible, individual. It is more realistic to assume that the number of susceptible contacts is a function of the

number of susceptible persons in the population. Second, I assumed that each infected person was fully recovered after one time period. This may be true if I am measuring time in weeks or months, but it probably isn't true for some diseases if I am measuring time in days or shorter intervals. Thus I would like the model to allow for the possibility that it takes multiple time periods for someone to move from the infected group back to the susceptible group.

I can do this in the following way. First define two new state variables that will measure the percentage of the total population that are susceptible and infected. Let  $i_t = I_t/N_t$  be the percent of the population that is currently infected. Define  $s_t = S_t/N_t$  as the percent of the population that is currently susceptible. I also define a new parameter  $\kappa$  that measures the percent of the population that recovers from a disease each period. Thus if the time to recover is 3 time periods then  $\kappa = 1/3$ . This means that one-third of the population should recover each period on average.<sup>1</sup>

I am now ready to write a system of equations that will describe the full SIS model of epidemics:

$$I_{t+1} = I_t - \kappa I_t + \alpha \gamma s_t I_t \quad (2.9)$$

$$S_{t+1} = S_t + \kappa I_t - \alpha \gamma s_t I_t \quad (2.10)$$

In these equations  $\kappa I_t$  individuals recover each period and thus leave the infected group and re-enter the susceptible group and  $\alpha \gamma s_t I_t$  individuals enter the infected group and leave the susceptible group. Notice that the change in the infected group always equals the change in the susceptible group when there is a constant population. Thus  $S_t + I_t = S_{t+1} + I_{t+1} = N$  if the population is constant.

Equivalently write these equations using the proportion state variables:

$$i_{t+1} = i_t - \kappa i_t + \alpha \gamma s_t i_t \quad (2.11)$$

$$s_{t+1} = s_t + \kappa i_t - \alpha \gamma s_t i_t \quad (2.12)$$

Now, with these equations written, use them to understand the epidemic threshold in the SIS model. First ask the question: when will the number of infected individuals be increasing? Intuitively we can reason through this process by just looking at the equations. If more people flow into the infective state than flow out this means that the level of infective individuals is increasing. If the opposite is true (more flow out than in) the level of infective individuals is decreasing. Thus the epidemic threshold is determined by whether  $\kappa i_t > \alpha \gamma s_t i_t$  or  $\kappa i_t < \alpha \gamma s_t i_t$ .

If  $\kappa > \alpha \gamma s_t$  this means that more individuals leave the infective state than enter it. Thus the level of the disease is decreasing. If  $\kappa < \alpha \gamma s_t$  this means that more

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<sup>1</sup> It may seem that this is a weird assumption since it may be that there are different numbers of people infected in each period. Thus different numbers of people should recover each period. I will show in a moment that if the model reaches steady state this assumption will be valid.

individuals enter the infective state than leave it. Thus the level of the disease is increasing. Another way to write this inequality is:  $\frac{\alpha_i s_t}{\kappa}$ . This is the epidemic threshold for the SIS model. If this fraction is greater than one the level of infective individuals increases (more than one susceptible individual is infected by each infective individual). If it is less than one the level of infective individuals decreases (fewer than one susceptible individual is infected by each infective individual.)

Closely related to the epidemic threshold is the concept of the *reproduction number*. By the analysis above, note that each infected individual is expected to reproduce  $\frac{\alpha_i s_t}{\kappa}$  new infections in the population. This number is critical in the beginning of an epidemic. If the reproduction number is not above one then an epidemic never occurs. Further, because we are often interested in this number at the beginning of an epidemic, we are often interested in this value when most of the population is susceptible, in other words when  $s_t$  is near one. In this case  $\frac{\alpha_i s_t}{\kappa} \approx \frac{\alpha_i}{\kappa}$ . Epidemiologists refer to this number as the reproduction number in the population and following convention I write it as  $R_0 = \frac{\alpha_i}{\kappa}$ .

If we move away from the initial period of an epidemic, we notice that one thing different about this model compared to our previous one is that one of our state variables enters the equation for the epidemic threshold,  $s_t$ . If  $\frac{\alpha_i s_t}{\kappa} > 1$  the disease spreads and the number of susceptible individuals decreases. Thus the fraction gets smaller in the next period. If  $\frac{\alpha_i s_t}{\kappa} < 1$  the disease begins to die out and the number of susceptible individuals increases. Thus the fraction gets bigger in the next period. For those of you who have taken economics courses this reasoning may sound familiar. It may sound like a process that is working its way toward an equilibrium. In fact, that is exactly what we will see in many cases here. The lack of susceptible individuals slows the epidemic when there are many infective individuals; and many susceptible individuals increases the spread of the epidemic when there are few infective individuals. The number of available hosts (or susceptible individuals) introduces negative feedback into the SIS model.

What would be the case where the disease reaches equilibrium? By this I mean the number of susceptibles and infectives is in steady state; both are constant proportions of the population. This would be the case if  $\frac{\alpha_i s_t}{\kappa} = 1$  or, rearranging,  $s_t = \frac{\kappa}{\alpha_i}$ . This would define a steady state of the system where  $s_t$  and  $i_t$  are constant in all periods moving forward in time.

## 2.4 Steady State

The first full model of epidemics can be analyzed a little more formally by looking at the steady state of our system of equations. Again, for those of you who have taken previous economics courses you may think of a steady state as an equilibrium: a situation where a system is not changing. In this model think of a steady state as a condition or set of conditions where our state variables,  $I_t$  and  $S_t$ , do not

change from period to period; they are constant. To find the steady state, find a solution to the system of equations above where  $S_t = S_{t+1}$  and  $I_t = I_{t+1}$ . One way to do this is to drop the time subscript on our equations above and solve for  $s$  and  $i$ . Thus look for a solution to the following set of equations:

$$i = i - \kappa i + \alpha \gamma s i \quad (2.13)$$

$$s = s + \kappa i - \alpha \gamma s i \quad (2.14)$$

To solve these equations first rewrite Eq. 2.13 as:

$$\kappa i = \alpha \gamma s i \quad (2.15)$$

which can then be written as:

$$\bar{s} = \frac{\kappa}{\alpha \gamma} \quad (2.16)$$

This is the steady state value of the proportion of the population that is susceptible. It is the same equation as we found above from our intuitive understanding of the epidemic. Further, because we know that  $s_t + i_t = 1$ , we know that the steady state value of the infected proportion of the population is  $i_t = 1 - s_t$  or:

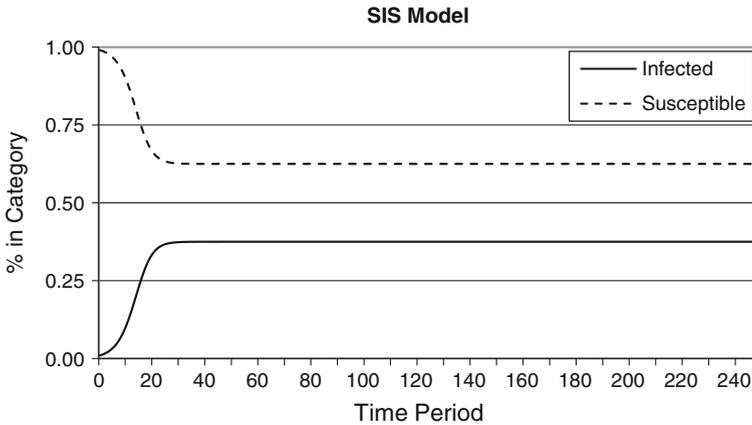
$$\bar{i} = 1 - \frac{\kappa}{\alpha \gamma} \quad (2.17)$$

Note the intuitive properties of the comparative statics of these equations. As the number of contacts of an infected person or the transmission probability increases the number of susceptible individuals decreases (and the number of infected individuals increases). As the time to recover increases (meaning  $\kappa$  decreases) the number of susceptible individuals decreases (the number of infected people increases.)

Next we will cover some simple examples to view how parameter changes affect these outcomes and to check our analytical predictions of steady state values of susceptible and infective individuals in the population.

## 2.5 Computational Implementation

One of the advantages of using simple models and difference equations (instead of differential equations) for introducing these topics is the ease of incorporating the model into a simple spreadsheet program like Excel. One can simply input the set of equations above into the spreadsheet, plug in some parameters of interest, and view the outcome of the models. In this subsection I present some graphs displaying these outcomes. To start note that the only time that  $\alpha$  and  $\gamma$  appear in the equations above is as the product  $\alpha \gamma$ . To simplify notation combine these two parameters into one parameter  $\beta$ . To start suppose that  $\kappa = 0.5$  and  $\beta = 0.8$ . This



**Fig. 2.1** Simple SIS model with  $\beta = 0.8$  and  $\kappa = 0.5$

means that each infected person recovers in two time periods on average (again you may think of a time period as perhaps a day) and each infected person potentially contacts and infects an average of 0.8 persons per time period. We also need to specify an initial fraction of the infected population. Because an epidemic usually begins with a small set of infected individuals, let us choose this value to be  $i_0 = 0.01$ .

In Fig. 2.1 you see that the fraction of infected individuals in the population increases quickly up to 37.5 % of the population. This is exactly the steady state level that we expect,  $1 - \frac{\kappa}{\beta} = 1 - \frac{0.5}{0.8} = 3/8$  infected individuals. Also note that this level does not depend on the fraction of infective individuals in period 0. The steady state is determined only by the infection and recovery parameters of the model.

Now let us see how the parameters affect the steady state level. To start, increase the recovery rate of the model,  $\kappa$ , to 0.6, for example, and the steady fraction of infected individuals drops to 1/4 of the population. Increase  $\kappa$  further to 0.7 the steady state fraction drops further. Increase the level of  $\kappa$  far enough, we go below the epidemic threshold and the steady state level of infective individuals drops to 0; the disease disappears. This happens exactly where the ratio  $\frac{\kappa}{\beta} = 1$  or when  $\kappa \geq \beta$ . Thus, the steady states of the model depend only on the ratio of  $\beta$  and  $\kappa$ .

Similarly one can increase or decrease the size of the steady state fraction of infective individuals by changing  $\beta$ . If I return to the  $\kappa = 0.5$  and increase  $\beta$  to 1.0 I increase the steady state level of infective individuals in the population to 50 %. Or if I decrease  $\beta$  to a level of 0.5 or less I pass below the epidemic threshold and the epidemic disappears.

The SIS model is simple in the sense that one of two things happens, either the system is above the epidemic threshold, converges to a steady state and stays there, or the system is below the epidemic threshold, and the system remains at a steady state with no infective individuals in the population. As we will see in the next chapter, SIR models can have more complicated behavior.



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