

## 1.1 Population Models

## 1.2 Spread of a disease in a community

I ask you to model the spread of a disease in a community. This is clearly very vague. What important questions must be asked? Here are some of the important questions to ask in order to model the process:

- How many people are in the community? say  $N$
- Is the community isolated?
- How many people are currently sick? Say 1 person is sick, so that we have the initial number of susceptible as  $N - 1$ .
- Is the disease deadly? suppose you answer YES
- Is there a vaccination? suppose you answer NO
- How do people get sick? suppose you answer—via contact/ interaction
- Are there people immuned to the infection? suppose you answer NO, and assume that once infected, you get sick.
- Is the community on lockdown to restrict move and avoid people interaction—NO, people are allowed to interact and there is homogeneous mixing.

Of course, you may have many more questions.

Now we develop the model:

Here we will consider only two distinct population, the healthy (susceptible) and the sick (infective). Call this model the SI epidemic model.

We will model the spread of the disease using Compartmental modelling. In this model, no birth and no death.

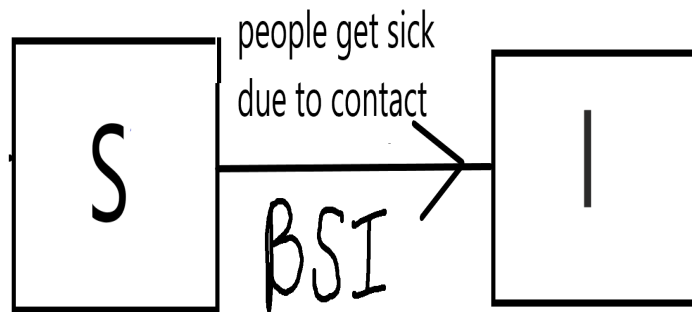


Figure 1: susceptible individuals become infected

We know that

$$I(0) = 1, \quad S(0) = N - 1. \quad (1.1)$$

The community is therefore isolated. The infection spread when healthy people catch the disease from sick people. When a healthy person comes into contact with a sick person, sometimes the healthy person gets sick. Notice that when two healthy people or two sick people come into contact, there will be no new infection since healthy people cannot infect and sick people cannot become sick again.

Let  $S(t)$  be the number of healthy people at time  $t$ . Let  $I(t)$  be the number of sick people at time  $t$ . Denoting the total population by  $N$ , we see that  $N = S + I$ . Each person can only

move from the susceptibles to the infectives compartment. Thus, as the number of susceptibles decreases, the number of infectives will increase with time.

In the SI model, once a susceptible person becomes infected, he or she will remain infective forever. This applies to epidemics with no immunity, e.g., AIDS.

How fast does a disease spread? This is a question that depends not only on how many sick people there are, but also on how many healthy people there are to get infected. It is easy to think that, no matter how many people are healthy, if there is a large amount of infectives, then there are more people to infect the susceptibles. What is being overlooked here is that, due to the closed population  $N$ , as more people become sick, fewer people can become sick. Thus, with a diminishing healthy population, it will be harder for the infectives to find a susceptible whom they can infect. Therefore, the rate of infection is not only proportional to the number of infectives but also to the number of susceptibles. Infact, the rate of infection is proportional to the product of the two groups  $S(t)$  and  $I(t)$ . That is,

$$\text{Infection rate} = \beta(N)S(t)I(t), \quad (1.2)$$

where  $\beta(N)$  is the proportionality constant, known as the effective contact rate per susceptible, and depends on the population size.

The effective contact rate,  $\beta(N)$ , is a product of two separate constants.

Let  $c(N)$  be the number of contacts made by a susceptible person per unit time (e.g. per day). Note that these contacts are not necessarily sufficient for transmission of the disease.

Let the probability of a susceptible getting infected for every contact made with an infective be  $p$ . Thus, the number of contacts which is sufficient for transmission per susceptible per time is

Then,

$$\beta(N) = cp$$

From the flow diagram, it is clearly seen that the governing equations are given by

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

Let  $\beta(N) = \beta N$ ,  $\beta \in \mathbb{R}$ , then

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

$$\frac{dI}{dt} = \beta SI$$

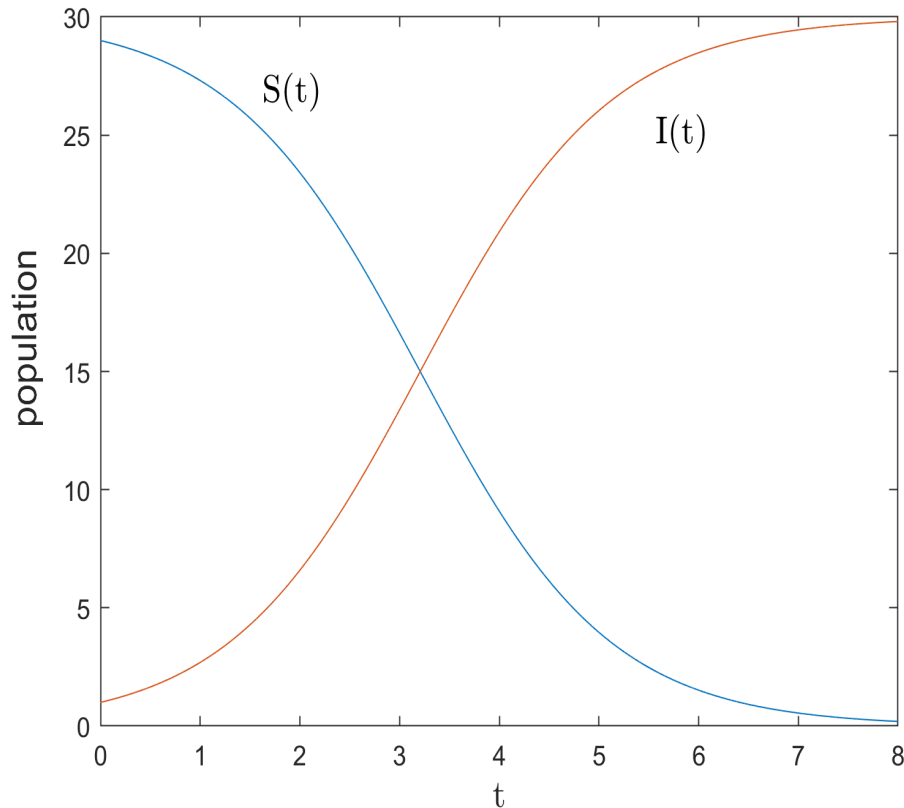


Figure 2: SI model with  $\beta = 0.035$

If you look where each curves starts at time zero, we see there are 29 susceptibles and one infective initially. This is because the spread of a disease can not start unless at least one person is spreading it. Figure 2 also tell us when people are becoming sick the fastest: this happens when there is an equal amount of sick and healthy people. On the graph, the maximum rate of infection is where the slope is the steepest, at the inflection point, at  $t = 4$ .

Another thing we can see from the graph of the SI model is that the infectives curve asymptotically approaches the total population,  $N$ , from below. Similarly, the susceptibles curve decays to zero. Notice that, in this model, the epidemic never ends.

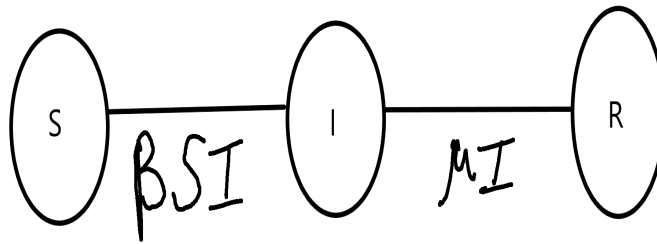
A more realistic model is the SIR model also called the Kermack-Mckendrick SIR model. This

model accounts for three distinct populations: the healthy (Susceptibles), the sick (Infectives), and the recovered (Removeds). In 1927, Kermack and McKendrick proposed a system of differential equations for the SIR model.

Model subdivides total population at time  $t$ , denoted  $N(t)$  into susceptible  $S(t)$ , infected  $I(t)$  and recovered  $R(t)$  compartments.

Thus

$$N(t) = S(t) + I(t) + R(t)$$



$$\frac{dS}{dt} = -\beta S(t)I(t)$$

$$\frac{dI}{dt} = \beta S(t)I(t) - \mu I(t)$$

$$\frac{dR}{dt} = \mu I(t)$$

$\beta$  is the average number of contacts an infective makes per unit time.  $1/\mu$  is the mean duration of infectivity.

In the SIR model, recovered individuals can no longer infect susceptibles nor can they become infected themselves. The initial conditions are the same as in the SI model, with zero recovered individuals at the beginning. The total population is the sum of the three distinct populations:  $N = S + I + R$ . Here the infection rate is still proportional to the product of the susceptible and infective populations, but the removal rate is proportional to the infective population.

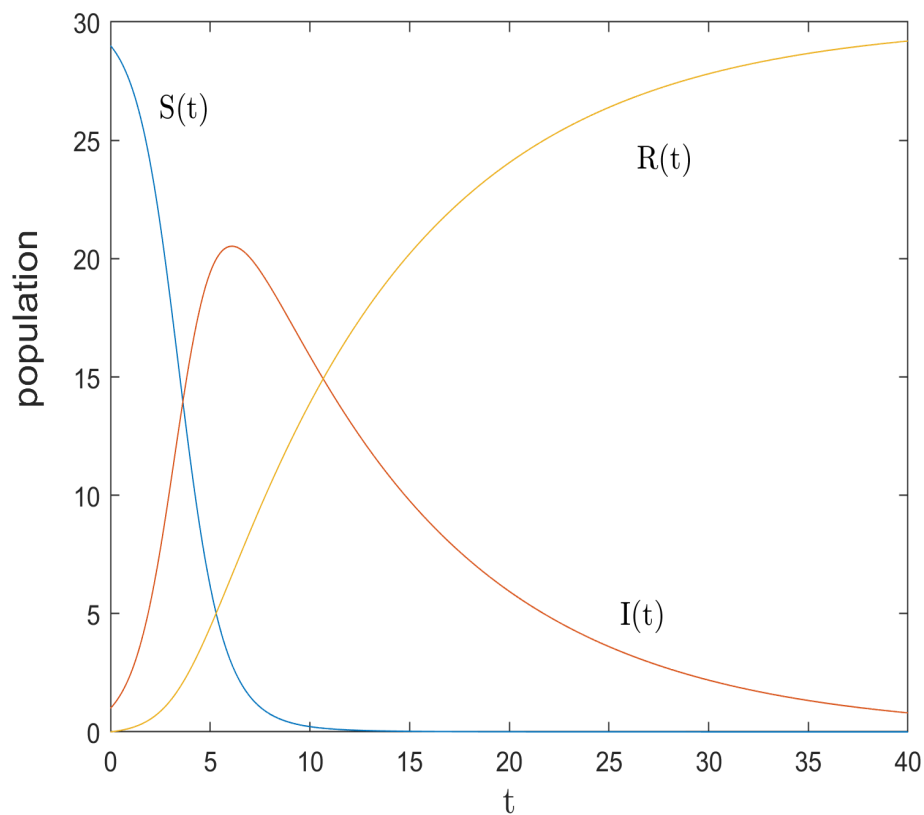


Figure 3: SIR model with  $\beta = 0.035$  and  $\mu = 0.1$

In Figure 3, the graph of  $S(t)$ ,  $I(t)$  and  $R(t)$  are shown. Initially, there are 29 susceptibles, one infective and zero recovered individuals. And as time evolves, we see how the number of susceptibles goes to zero while the number of infectives rises up to a peak and then begins to drop.

Summary of results from SIR model:

- The SIR model explains the rapid rise and fall in the number of infected patients observed

during an epidemic of a pandemic

- Epidemics (or pandemic) comes and go without affecting every member of the community. Thus,  $S_0 - S_\infty > 0$

Basic reproductive number

Suppose that at time  $t \leq 0$ , all individuals were susceptible. That is,  $S(0) = N$ .

Hence, at  $t = 0$ , one infected individual will infect  $\beta S(0) = \beta N$  susceptible individuals per unit time.

Since an infected individual remains infectious for an average period of  $1/\mu$ , then

$$\mathfrak{R}_0 = \beta S(0) \frac{1}{\mu}.$$

Note that  $\beta$  measures the effective contact rate, and  $1/\mu$  is how long people remain infectious.

The values of  $\beta$  and  $1/\mu$  can be obtained by fitting a given data of infected people to the mathematical model.

Note that

- $dS/dt < 0$  for all  $t$
- $dI/dt > 0$  if and only if  $S(t) > \mu/\beta$ , for which  $\mathfrak{R}_0 > 1$
- That is,  $I(t)$  increases so long as  $S(t) > \mu/\beta$ . But since  $S(t)$  decreases for all time,  $I(t)$  ultimately decreases and approaches zero.
- If  $S(0) < \mu/\beta$  (for which  $\mathfrak{R}_0 < 1$ ), then the population  $I(t)$  decreases to zero (no epidemic).
- If  $S(0) > \mu/\beta$  (for which  $\mathfrak{R}_0 > 1$ ), then the population  $I(t)$  first increases to a maximum (attained when  $S(t) = \mu/\beta$ ), and thereafter, decreases to zero (outbreak of epidemic).

Using rigorous mathematical analysis, it is found that

$$\frac{\beta}{\mu} = \frac{\log(S(0)/S_\infty)}{K - S_\infty}$$

where

$$0 < S_{\infty} < K$$

and  $K$  is the total population at time  $t = 0$ .

meaning that a part of the population escapes infection.

Conclusion: Thus,  $\mathfrak{R}_0$  can be estimated from the above relation.

In any equation, every term must have the same units. In other words, we cannot add something measured in metres with another quantity measured in seconds, for example.

In this example,

- $[P] = \text{people}$
- $[I] = \text{people}$
- $[t] = \text{time}$

Now, find the units of  $\alpha$ ,  $\beta$ ,  $\rho$  and  $k$ .

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## Exercise 1

1. In the SIR model, solve the equations for  $I$  and  $S$  subject to  $I(0) = 1$ ,  $S(0) = N - 1$ . Provide plots in Mathematica. Experiment with different parameter values for  $\alpha$ ,  $\beta$ ,  $\rho$ , and  $N$ .

NB: I have used the continuum approximation. Do you foresee any issues with this?

2. Suppose a vaccination is now available. People in  $S$  get vaccinated at a rate of  $\nu S$ . Rewrite the governing equations for this scenario and plot your results in Mathematica. Finally, compare the two models.

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