5.2. THE SIR MODEL OF INFECTIOUS DISEASES

Let’s consider a population in which a contagious disease is spreading. We assume that the modeling time scale is short, and for simplicity we assume the population size, *N*, is constant. That is, we ignore births, disease-unrelated deaths, immigration, and emigration. The population consists of three groups:

*Susceptible group*: those who may catch the disease are not currently infected.

*Infected group*: individuals who are currently infected with the disease and are contagious.

*Removed group*: individuals who are no longer infectious. They are either recovered, acquired immunity, or have died.

The SIR model is a simple model of the spread of contagious disease that uses the three classes *susceptible*, *infected* and *removed* (or *recovered*). The individuals of the population in the SIR model progress through the three classes in order, as illustrated in Figure 5.8.

A susceptible individual remains a susceptible or becomes infected; an infected individual stays infected for a period of time until recovered or died and removed; and a removed individual is not going to be a susceptible or infected individual.

We will use the following notations:

*Sk* = susceptible population at the end of time period *k*.

*Ik* = infected population at the end of time period *k*.

*Rk* = removed population at the end of time period *k*.

Our assumption that the population under consideration is constant can be translated into

(5.19) for all nonnegative integers *k*

We need to develop equations to calculate *Sk*, *Ik*, and *Rk*.

A susceptible individual becomes infected when that individual contacts an infected individual and the disease is transmitted to the susceptible individual. The number of infected individuals depends on the frequency of the interactions between susceptible and infected individuals. It is reasonable to have the product *SkIk* represent the possible number of encounters between susceptible and infected individuals. Note that we assume there is a homogenous interaction among the susceptible individuals and infected individuals. However, not every interaction between an infected individual and a susceptible individual will result in infecting the susceptible individual. Let’s use *α* to represent the probability that the interaction between a susceptible individual and infected individual will result in a new infection. Consequently, the number of susceptible individuals who become infected as a result of interaction with infected individuals is *αSkIk*. This number is subtracted from the number of susceptible individuals and added to the number of infected individuals; *α* is called the ***infection rate*** or the ***transmission coefficient***. Therefore the dynamic of susceptible individuals can be modeled by the following difference equation:

(5.20)

During the time period *k*, the number of infected individuals will increase by *αSkIk* and will decrease by the infected individuals who have recovered or die. We will use *β* to represent the fraction of infected individuals who recover or die and consequently will be removed from the infected class; *β* is called ***recovery* *rate*** or ***removal rate***. Therefore, the dynamic of infected class can be represented by the following difference equation:

(5.21)

Because the number of infected individuals is decreased by *βIk*, the number of removed individuals is increased by the same number. Consequently, the dynamic of the removed class is represented by the following difference equation:

(5.22)

The SIR model is represented by the following system of difference equations (5.19) to (5.22):

**5.2.1. Exploration 1**

Consider the SIR model equations 5.19 to 5.22 for the spread of influenza among the students of a small college dorm with a population of 100 with the parameters: *α* = 0.005 and *β* = 0.1. Assume that 1 student returns to the college at the beginning of the spring semester infected with influenza. Calculate *Sk*, *Ik*, and *Rk* for *k* = 1, 2, … , 50 days; graph *Sk*, *Ik*, and *Rk* vs. *k* on one coordinate system; and describe the three graphs.

***Discussion***

The following is a MATLAB function called **SIR** to calculate *Sn*, *In*, and *Rn* and graph them vs. *n*. The function accepts the parameters **i\_rate, r\_rate, I0, N,** and **t** , where

**i\_rate** = the infection rate (transmission coefficient *α*).

**r\_rate** = removal (recovery or death) rate *β*.

**I0** = the initial number of infected persons *I*0.

**N** = total population.  
**t** = number of iterations.

**function [T, S, I, R] = SIR(i\_rate, r\_rate, I0, N, t)**

% Function input (parameters):

% i\_rate = infection rate

% r\_rate = recovery rate

% I0 = initial number of infected individuals

% N = total number of population

% t = time

% Function output:

% T = sequence of time

% S = sequence of susceptible individuals

% I = sequence of infected individuals

% R = sequence of recovered individuals

**T = 1:t;**

**S = zeros(1, t);**

**I = zeros(1, t);**

**R = zeros(1, t);**

**S(1) = N - I0;**

**I(1) = I0;**

**R(1) = 0;**

**for k = 2:t**

**S(k) = S(k-1) – i\_rate \* S(k–1) \* I(k-1);**

**I(k) = I(k-1) + i\_rate \* S(k–1) \* I(k-1) – r\_rate \* I(k–1);**

**R(k) = R(k-1) + r\_rate \* I(k–1);**

**end;**

**plot(T, S, ‘k.’, T, I, ‘ko’, T, R, ‘k\*’);**

**hold on;**

**plot(T, S, ‘k’, T, I, ‘k’, T, R, ‘k’);**

**hold off;**

**xlabel(‘Time n in days’);**

**ylabel(‘S(n), I(n), and R(n)’);**

**legend(‘Susceptible’, ‘Infected’, ‘Recovered’);**

To call the function SIR with the parameters *i*\_rate = 0.005, *r*\_rate = 0.1, I0 = 1, N = 100, and *t* = 50 days, write the code

**> > [T, S, I, R] = SIR (0.005, 0.1, 1, 100, 50);**

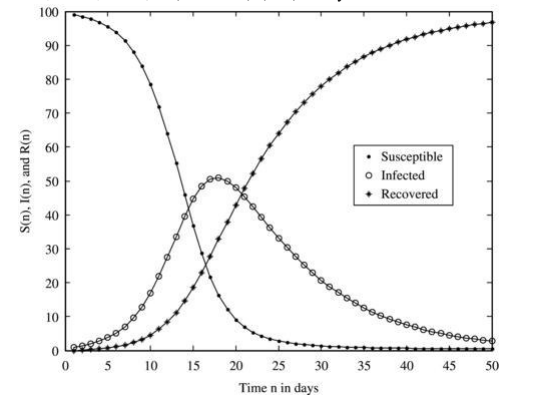
The graphs of *Sn*, *In*, and *Rn* vs. *n* with *n* = 0, 1, 2, … , 50 are shown in Figure 5.9.

The graphs show that the following:

* The number of infected persons increases and then decreases. The peak value of infected persons is about 51, and it occurs on day 17—that is *I*17 = 51. We have *I*50 ≅ 2.
* The number of susceptible persons is decreasing, and it reaches approximately 1 at day 31, that is, *S*31 ≅ 1.
* The number of recovered persons is increasing, and we have *R*50 ≅ 97.

In the exercises you will investigate the effect of the system parameters and the initial values on the behavior of the model.

FIGURE 5.9. Time-series graphs of a SIR model. Graphs of susceptible, infected, and recovered populations *Sn*, *In*, and *Rn* respectively vs. time, *n*, in days. The populations are modeled by the system of difference equations: *Sk* + 1 = *Sk* - 0.005*SkIk*, *Ik* + 1 = *Ik* + 0.005*SkIk* - 0.1*Ik*, and *Rk* + 1 = *Rk* + 0.1*Ik* with *I*0 = 1, and *k* = 1, 2, … , 50 days.



**5.2.2. Transmission Coefficient and Recovery Rate**

How are the transmission coefficient and recovery rate determined? This is an interesting question. Because the recovery (removal) rate *β* is the portion of infected persons removed each time period, the value of *β* depends on the duration of time a person stays infected. In general,

(5.23) .

For example, if the average duration of a certain flu infection is 10 days, then *β* = 1/10 = 0.1.

Knowing the initial number of infected persons, *I*0, and the number of infected persons at time period 1, the transmission coefficient, *α*, can be determined using equation (5.20). Equation (5.20) with *k* = 0 is *S*1 = *S*0 - *αS*0*I*0, where *αS*0*I*0 is the number of newly infected persons in time period 1. The parameter *α* is determined from the following equation:

Number of new infected persons in time period 1 = *αS*0*I*0

so

Because *S*0 = (*N* - *I*0), we have

(5.24)

For example, if the total population is 100 and the initial number of sick persons is 2 and the number of newly infected persons on day 1 is 3, we get

.

Note that equation 5.24 is a simple method for determining *α*, but if the number of newly infected persons in time period 1 is not accurate, then *α* is not accurate.

In addition to the SIR model, we will discuss one similar model of the spread of contagious diseases.

**Exercise 5.2**

In Exercises 1–7 consider the SIR model represented by equations 5.19 to 5.22 with given parameters. For each exercise, investigate the model by graphing *Sn*, *In*, and *Rn* vs. *n*. Describe the model behavior and the effect of the values of the parameters. Let the total population be *N* = 100.

1. Recovery rate > infection rate (e.g., *α* = 0.01, *β* = 0.1, *I*0 = 1).
2. Recovery rate < infection rate (e.g., *α* = 0.01, *β* = 0.008, *I*0 = 1).
3. Recovery rate = 0 (e.g., *α* = 0.01, *β* = 0, *I*0 = 1).
4. Recovery rate = infection rate (e.g., *α* = 0.01, *β* = 0.01, *I*0 = 1).
5. Similar to Exercise 1 but *I*0 = 3—that is, recovery rate > infection rate (e.g., *α* = 0.01, *β* = 0.1, *I*0 = 3).
6. Similar to Exercise 2 but *I*0 = 3—that is, recovery rate < infection rate (e.g., *α* = 0.01, *β* = 0.001, *I*0 = 3).
7. Recovery rate >> infection rate (e.g., *α* = 0.001, *β* = 0.1, *I*0 = 1).