

S-I-R Model of Epidemics

Part 1

Basic Model and Examples

Revised September 22, 2005

1. Introduction

■ Description of the Model

In this notebook, we develop in detail the standard S-I-R model for epidemics. For the integration of the nonlinear differential equations, we use the package DynPac. Although some familiarity with DynPac is assumed, brief descriptions of some DynPac commands are given as they are used. The integrations in this notebook also can be done easily with the *Mathematica* function NDSolve.

Much of our presentation is tied to the specific example given in section 3, an influenza epidemic in a British Boarding School, and for that example we follow the treatment given by J.D. Murray (**Mathematical Biology I, An Introduction**, p. 325-326, Springer-Verlag, 2002).

The S-I-R model was introduced by W.O. Kermack and A.G. McKendrick ("A Contribution to the Mathematical Theory of Epidemics," Proc. Roy. Soc. London **A 115**, 700-721, 1927), and has played a major role in mathematical epidemiology. A summary of the model and its uses is given by Murray. In the model, a population is divided into three groups: the susceptibles S , the infectives I , and the recovered R , with numbers s , i , and r respectively. The total population is

$$n = s + i + r . \quad (1)$$

The susceptibles are those who are not infected and not immune, the infectives are those who are infected and can transmit the disease, and the recovered are those who have been infected and are immune (recovered or dead). In the simple form of the model considered here, we assume that the recovered are permanently immune. We also assume that the whole event is of sufficiently short duration that we may ignore natural births and deaths during the epidemic. Finally, we ignore any subdivisions of the population by age, sex, mobility, or other factors, although such distinctions are obviously of importance.

■ Differential Equations and Parameters of the Model

The basic differential equations are as follows:

$$\frac{ds}{dt} = -asi , \quad (2)$$

$$\frac{di}{dt} = \alpha si - \beta i, \quad (3)$$

$$\frac{dr}{dt} = \beta i, \quad (4)$$

These equations describe the transitions of individuals from S to I to R. By adding the three equations, we show easily that the total population n is constant. We will call the parameter α the transmissivity and the parameter β the recovery rate. The term αsi is a standard kinetic term, based on the idea that the number of encounters per unit time between susceptibles and infectives will be proportional to the numbers of each. The transmissivity α is determined by both the encounter frequency and the efficiency with which the disease is transmitted per encounter. In later notebooks, we will look more closely at the problem of estimating α . We will see later that there are advantages to formulating the problem in terms of population fractions rather than total population. For example, it is obvious that if a given population is placed into a much larger area, the encounter rate will decrease and α will decrease. A proper formulation in terms of fractions will give a transmissivity independent of total population in the first approximation. For the present, we continue with the formulation in terms of total populations. We will not be concerned further in this notebook with the estimation of α from first principles.

The interpretation and estimation of β is more straightforward. We now show that β^{-1} is the average duration of the infection. Consider the special case of no new infections, so that equation (3) reduces to $di/dt = -\beta i$. Then $i(t) = i(0)e^{-\beta t}$. The number of infectives recovering in time $(t, t + dt)$ is $|di| = |(di/dt)dt| = i(t)\beta dt = i(0)\beta e^{-\beta t} dt$, and this is the number of infectives with infection durations in the range $(t, t + dt)$. The average duration t_{avr} is then the average of t with this as a weighting function, hence

$$t_{\text{avr}} = \frac{\int_0^{\infty} i(0) \beta e^{-\beta t} t dt}{\int_0^{\infty} i(0) \beta e^{-\beta t} dt} = \frac{1}{\beta}. \quad (5)$$

We may treat the three equations given by (2) - (4) as a set of two equations in s and i (equations (2) and (3)). After these equations are solved for s and i , we may calculate r from equation (1).

■ Conditions for an Epidemic

In epidemiology, the word "epidemic" has a technical meaning: it is a situation in which the number of infectives increases from the initial value. The condition for an epidemic follows directly from equation (3): di/dt will be positive whenever

$$s > \beta/\alpha. \quad (6)$$

Thus for given α and β there is a critical number of susceptibles for an epidemic, and if s_0 is the initial number of susceptibles, then the condition for an epidemic is $s_0 > \beta/\alpha$. There is a simple interpretation of equation (6). A given infective will, on the average, be infectious for a time $1/\beta$. The number of susceptibles infected by one infective per unit time is αs . Hence the total number of infections produced by one infective is $\alpha s/\beta$, and for an event to qualify as an epidemic, this number must exceed 1, which gives condition (6). The parameter appearing here,

$$R_0 = \alpha s_0/\beta, \quad (7)$$

is called the reproduction ratio of the epidemic.

It is somewhat surprising that the number of initial infectives does not play a role in determining whether there is an epidemic. Of course other aspects of the epidemic will depend on the number of initial infectives -- especially the time of the

peak of the epidemic. The peak of the epidemic is the time of maximum number of infectives. We see from equation (3) that this will occur when $s = \beta/\alpha$ -- that is, when the reproduction ratio is 1.

■ Equilibrium and Stability

It is easy to show that the equilibrium states of equations (2) - (4) are those states in which $i = 0$, and $s = s_*$, where s_* is any positive constant. Thus the equilibria are non-isolated. A formal stability analysis by linearization yields two eigenvalues: 0, and $\alpha s_* - \beta$. If the condition for an epidemic is satisfied, this second eigenvalue is positive and the equilibrium is unstable. If the second eigenvalue is negative, there is no conclusion about the stability from the linearization because of the zero eigenvalue. However, it is obvious that the equilibrium is not strictly stable even in that case, because any perturbation with non-zero i will lead to a situation in which s decreases and therefore does not return to s_* .

Stability isn't really the primary issue in this model. We are much more interested in the time course caused by the introduction of some infectives, and in the final asymptotic state of the system. Some typical questions of interest are: (1) How many susceptibles become infected? (2) What is the peak number of infectives? (3) When does the epidemic peak? (4) How does the time course depend on the initial number of infectives? Before attempting to answer these questions in any generality, we look at an example, in which the model results are compared with observations of a flu epidemic. Before doing that, we define the system for DynPac so that we may carry out the integrations in the example.

2. Defining the Equations for DynPac

In much of what follows, we will be integrating equations (2) - (4) numerically. In this section, we define the equations for DynPac. We start by defining the state vector, the parameter vector and the slope vector.

```
In[329]:=
  setstate[{s, i}];
```

This tells DynPac that the two state variables are s and i .

```
In[330]:=
  setparm[{α, β}];
```

This tells DynPac that the "official" system parameters are α and β .

```
In[331]:=
  slopevec = {-α * s * i, α * s * i - β * i};
```

This defines the slope vector of the equations for DynPac.

We also define an initial time t_0 , a time step h , and the number of time steps $nsteps$. For the events studied here, we use days as the time unit. These parameters may be adjusted later as we work through other examples. The choices below take us out to 25 days with 20 time steps per day.

```
In[332]:=
  t0 = 0.0;
```

```
In[333]:=
  h = 0.05;
```

```
In[334]:=
  nsteps = 500;
```