2.6. Interacting Populations and SI Model of Epidemiology

In this section we consider a model of the spread of a disease. This model illustrates a common method of modeling the interaction of two populations.

The SI Model. We consider the spread of a disease in a population. (The model will be the same if, instead of a disease, we imagine the spread of a rumor or a joke.) To develop a set of differential equations that model the spread of the disease, we must make some assumptions:

(1) The size of the population, N, remains fixed.
(2) The size of the population is large enough that the error made by approximating $1/(N-1)$ with $1/N$ is small. (As a percentage, this error is $100/N$, so, for example, when $N = 10000$, the error is 0.01 percent.)
(3) We consider just two classes of individuals: those who have the disease and are infective, and those who do not have the disease but are susceptible to it. Each individual is in one of these two classes. (In this model, no one is immune, and once an individual has the disease, the individual remains infective.)
(4) We assume that the disease spreads through interactions between pairs of individuals, and these interactions are random. (Our model will not attempt to deal with the geographic spread of the disease. It will only look at the total number of individuals infected within the given population.) An *interaction* is modeled as making a random selection of two individuals from the population. If one is susceptible and one is infected, the susceptible *might* become infected. We let c be the fraction of susceptible-infective (SI) interactions that actually result in the spread of the disease ($0 < c \leq 1$). (We can think of the units of c as *the average number of infections per SI interaction.*)
(5) The rate of interactions within the population is constant. We let γ be the interaction rate, with units of *number of interactions per unit time.*

Let $I(t)$ be the number of infectives at time t, and let $S(t)$ be the number of individuals who are susceptible. By assumptions (1) and (3), we have

$$S + I = N. \tag{2.44}$$

Given an initial number of infectives $I(0)$, we would like to know what will happen to $I(t)$. We will use the assumptions to formulate differential equations that model this process.

If we pick two people at random from the population, what is the probability that one is susceptible and the other is infected? The probability of picking a susceptible person is S/N, and the probability of picking an infective is I/N. (Assumption (2) allows us to assume that these events are independents. If we really chose a susceptible with our first random selection, then the probability that the second individual will be an infective is $I/(N-1)$. Since N is large, we can approximate this by I/N.) The probability that two random people will consist of one susceptible and one infected is

$$2\left(\frac{S}{N}\right)\left(\frac{I}{N}\right) = \frac{2}{N^2}SI. \tag{2.45}$$

This expression gives the average number of SI interactions per interaction. By assumption (5), the quantity $\frac{2\gamma}{N^2}SI$ gives the average number of SI interactions per

unit time, and then by assumption (4), the average number of infections per unit time is

$$\frac{2c\gamma}{N^2}SI. \tag{2.46}$$

This quantity determines the rate at which $I(t)$ is increasing. For convenience, let

$$r = \frac{2c\gamma}{N^2} \tag{2.47}$$

Then the equation for $I(t)$ is

$$\frac{dI}{dt} = rSI. \tag{2.48}$$

We have just two classes of individuals, the infectives and the susceptible, so any gain in I must result in an equal loss in S. Thus

$$\frac{dS}{dt} = -rSI. \tag{2.49}$$

Equations (2.48) and (2.49) constitute a *system of differential equations.* Many dynamical processes are modeled with systems of differential equations; we'll see many more in this course. In fact, this is a *nonlinear* system. Typically, nonlinear systems that arise in the real world can not be solved analytically. It turns out that this particular system can be solved.

First, we check that the total population remains constant by adding these two equations. We find

$$\frac{dS}{dt} + \frac{dI}{dt} = 0 \tag{2.50}$$

and integrating from 0 to t gives

$$S(t) + I(t) = S(0) + I(0). \tag{2.51}$$

The initial population was N, so we have $S(t) + I(t) = N$. This means we can replace S in (2.48) with $N - I$ to obtain

$$\frac{dI}{dt} = r(N - I)I. \tag{2.52}$$

This is just another version of the logistic equation, with carrying capacity N. If $I(0) > 0$, $I(t)$ will approach the equilibrium N as $t \to \infty$. Thus, this simple model predicts that eventually everyone will become infected, no matter how small the initial population of infectives.

Many models of physical, social, or biological systems involve interacting populations. We consider another example, in which we model the interaction of a predator and its prey.

A Predator/Prey Model. Let $x(t)$ be the population of, say, mice in a forest, and let $y(t)$ be the population of foxes. Suppose that the mice are an essential component of the foxes diet; without mice, the foxes will eventually starve. That is, we assume that when there are no mice, the differential equation for the fox population is

$$\frac{dy}{dt} = -\mu y \tag{2.53}$$

where $\mu > 0$.

We also assume that, in the absence of foxes, the mice population grows according to a logistic equation:

$$\frac{dx}{dt} = rx\left(1 - \frac{x}{K}\right) \tag{2.54}$$

where r is the small population per capita growth rate of the mouse population and K is the carrying capacity of the mouse population (in the absence of foxes).

We model the interaction of these populations with assumptions similar to those of the SI model. (However, in this case the total size of the population does not remain constant.) In particular, *the rate of interactions between mice and foxes is proportional to the product of the populations.* We modify equations (2.53) and (2.54) as follows:

$$\begin{aligned}
\frac{dx}{dt} &= rx\left(1 - \frac{x}{K}\right) - k_1 xy \\
\frac{dy}{dt} &= -\mu y + k_2 xy
\end{aligned} \tag{2.55}$$

The constants $k_1 > 0$ and $k_2 > 0$ determine how the interactions affect the mouse and fox populations, respectively. Since the foxes eat the mice, interactions results in a loss for $\frac{dx}{dt}$. The foxes, on the other hand, benefit from the interaction. Unlike the SI model, the cofficients k_1 and k_2 are not equal; we do not assume that each mouse is converted to a fox one-for-one. The parameter k_2 determines how much benefit results from a fox capturing a mouse. For example, if k_2 is small, the foxes each have to catch many mice in order to improve the growth rate by a significant amount.

We can interpret these equations in terms of the per capita growth rates of the mice and foxes. For the mice, the per capita growth rate is

$$r\left(1 - \frac{x}{K}\right) - k_1 y, \tag{2.56}$$

and we see that increasing y lowers the per capita growth rate of the mice. The per capita growth rate of the foxes is

$$-\mu + k_2 x. \tag{2.57}$$

This shows that in order for the fox population to grow, the mouse population must be larger than μ/k_2.

Unlike the SI model, we can not reduce the system of differential equations (2.55) to a single equation. We will learn more about the analysis of systems of differential equations in later chapters.