Population Dynamics of Infectious Diseases (SIR)

**Objective:** To model the progression of epidemics for diseases of different infectivities and to determine the effects of isolation and prior vaccination.

**Discussion:**

Population dynamics models are based on the same principle as accounting. If you want to know your daily cash total, you could count it every day. Or you could keep track of your income and expenditures and use them to update your daily totals. This is the principle used for epidemic models. We classify people according to their current status, such as Infectious or Recovered, and use update formulas to calculate daily changes in the class counts. In disease models, as in most population models, the class count need not be an integer. This sounds horrible, but it isn’t when you realize that models are not meant to give “correct” answers. Class counts in the real world depend on chance; for example, the number of new infections might be 7 one day and 5 on each of the next 2 days. If the model assumes that the number is the same every day, we would use 5.67, which is an average of 7, 5, and 5. When studying a model, focus on the general trends, not the specific numbers.

Parameters are quantities that are fixed in any given scenario but can vary among different scenarios. The most important parameter in epidemic modeling is the *basic reproductive number*, denoted as (and usually read as “R zero”). This quantity is the average number of secondary infections caused in a fully susceptible population by one infected person over the duration of that person’s illness. If the basic reproductive number is less than 1, the disease cannot propagate because the average person recovers before infecting anyone else. This is what happened with many strains of influenza, which has a seasonal basic reproductive number that is low in the summer. The most infectious human disease is measles, with a basic reproductive number estimated at 12-18.

**Notation and Assumptions:**

Disease models can vary greatly in complexity. In this module, we consider the prototype epidemic model, called the SIR model because the population is divided into three classes: Susceptible, Infectious, and Removed. It is a good model to learn about first because it is relatively simple, and therefore easier to study, and yet its behavior illustrates that of more complicated models.

The basic SIR model has only two processes that change the class counts: transmission and recovery. A schematic diagram is helpful to show how the new infections and recoveries change the class counts. Transmissions increase I and decrease S, while recoveries increase R and decrease I.

transmissions

recoveries

R

I

S

1. Suppose infectious individuals create an average of *b* new cases per day in a population where all *N* individuals are susceptible. Then *I* infectious individuals would combine to create *bI* new cases per day. If the population is not wholly susceptible, then the expected number of new cases would be *bI\*S/N*, where *S/N* is the fraction of encounters that are with susceptibles.

Total new infections = average new cases per infective if everyone else is susceptible (*b*) \* number of infectives (*I*) \* fraction of contacts who are susceptible (*S*/*N*)

We define a parameter *B*=*b/N* so that we can write the new infection count per day more simply as *BSI*. This quantity gets subtracted from *S* and added to *I* every day.

1. Suppose *T* is the average amount of time an individual is infectious. We can reasonably assume a fraction 1/*T* of infected individuals recover in any given day. Thus, the change in class counts is *gI*, where *g*=1/*T*.

It is convenient to define a quantity *p* to be the fraction of infectious individuals who do NOT recover on a given day. Clearly *p*=1-*g*, and then *pI* is the number of infectious individuals who will still be infectious on the following day.

We will include one additional process: isolation of infected individuals. This is one of several tools that can be used to modify the course of an epidemic. Other processes could be included, but we want to look at the simplest reasonable model.

Mathematical models have a lot of parameters, making it difficult to decide how to study their results. One way to reduce the number of options is to give some of the parameters fixed values. The total population is not particularly important, as it is best to report results in terms of percentages. We’ll take a total population of 10000, which is just slightly larger than the number of people on the largest cruise ship. The infectivity parameter is very important, but it is difficult to determine from data. Instead, we will consider to be the principal measure of infectiousness and use it to calculate the infectivity from the relationship .

We also need to specify the initial populations. To do this, we’ll let *f* be the fraction of the population that is initially infectious and let *v* be the fraction that is initially immune (this provides a way of introducing prior vaccination into the model).

**Governing Equations:**

**Eq. 1: Parameters**

, , ,

**Eq. 2: New Infections**

where and are the populations of the Susceptible and Infected classes, *N* is the total population, is the infectivity (the average number of new infections per day caused by one infected individual in a fully susceptible population), and is defined for convenience.

**Eq. 3: Recovery / Death**

where  is the average time an individual spends in the infected class. With *T*=10, one tenth of infectious individuals will move to the removed class each day.

**Eq. 4: Isolation**

where *p*=1-*g* represents the fraction of today’s infected class who are still contagious tomorrow and *q* is the fraction of symptomatic individuals who are put into isolation. The formula assumes that symptoms appear in the third day of infectivity: the factor is the number of individuals who have been infected for at least three days, and therefore symptomatic, and a fraction *q* of these are isolated.

**Eq. 5, 6, 7: Population Updates**

where *n* is the current time and *p*=1-*g* is defined to combine and into one term.

**Eq. 8, 9, 10: Initial Conditions**

where *f* is the fraction of the population that is initially infected and *v* is the fraction of the population that is initially immune.