SEIR Student Notes

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 $\mathcal{R}_0$ (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 standard SEIR epidemic model, so called because the population is divided into four classes: Susceptible, Exposed (latent),[1] Infectious, and Removed. It is a better fit to COVID-19 than the simpler SIR model, but it is a little too simple to capture all of the important features of COVID-19, such as asymptomatic cases. Nevertheless, its results are qualitatively similar to those of a COVID-19 model and it is much easier to understand.

The basic SEIR model has only three processes that change the class counts: infection, incubation, and recovery. A schematic diagram is helpful to show how these processes change the class counts. The new infections increase E and decrease S, the incubations increase I and decrease S, and the recoveries increase R and decrease I.

[1] The term "Exposed" is misleading. These are individuals who are already infected, not merely exposed, but who cannot yet spread the disease. It is better to describe this class as "Latent", but we retain the symbol E because it is the mathematical convention.

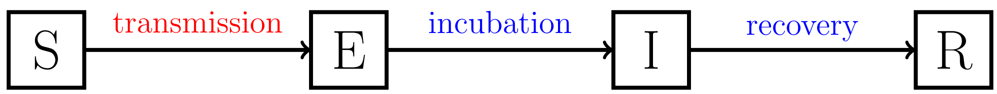

Figure 1: The SEIR epidemic model.

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.

$$\begin{aligned}\text{transmission rate} &= \text{rate per infective if everyone else is susceptible}(b)\\ &\quad * \text{number of infectives } (I) * \text{susceptible fraction } (S/N).\end{aligned}$$

   We define a parameter $\beta = b/N$ so that we can write the rate as

$$\text{transmission rate} = \beta SI. \tag{1}$$

   This rate is part of the overall rate of increase for E and the overall rate of decrease for S.

2. Suppose T_L is the average amount of time an individual is latent. We can reasonably assume a fraction $1/T_L$ of latent individuals become infectious per day. We define $\eta = 1/T_L$. Then the rate is

$$\text{recovery rate} = \eta E. \tag{2}$$

   This rate is part of the overall rate of increase for I and the overall rate of decrease for E.

3. Suppose T_I is the average amount of time an individual is infectious. Then a fraction $1/T_I$ of infectious individuals recover in any given day. With $\gamma = 1/T_I$, the rate is

$$\text{recovery rate} = \gamma I. \tag{3}$$

   This rate is part of the overall rate of increase for R and the overall rate of decrease for I.

The Finished Model

The assumptions lead to the differential equations

$$\frac{dS}{dt} = -\beta SI, \tag{4}$$

$$\frac{dE}{dt} = \beta SI - \eta E, \tag{5}$$

$$\frac{dI}{dt} = \eta E - \gamma I, \tag{6}$$

$$\frac{dR}{dt} = \gamma I. \tag{7}$$

Parameters

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; by taking it to be 1 we will be reporting all class counts as fractions of the total population. The infectivity parameter is very important, but it is difficult to determine from data. Instead, we will consider $\mathcal{R}_0$ to be the principal measure of infectiousness and use it to calculate the infectivity from the relationship $\mathcal{R}_0 = bT_I$.

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). We also need to specify the fraction of the population that is initially latent. This could be left as a separate parameter, but it is better to calculate it from some basic assumptions, with the result (see the homework questions) that the initial ratio of E to I is given by

$$k = \frac{\gamma - \eta + \sqrt{(\eta - \gamma)^2 + 4\eta\beta N}}{2\eta}. \tag{8}$$

Modeling Isolation

The simplest means for moderating the course of an epidemic is to isolate individuals known to be infectious. This can be problematic when the disease typically has a presymptomatic period. In order to address questions about isolation, we need to expand our model. Rather than let it get too complicated, we'll omit the Latent class, instead assuming that the newly infected are presymptomatic infectives. We also make two additional simplifying assumptions:

1. Isolation happens immediately for a fraction q of patients who show symptoms. For additional simplicity, we assume that isolation completely controls transmission.

2. Everyone with the disease is eventually symptomatic, with an average presymptomatic duration of $T_P < T$ days, where T is the average total duration of infectivity.

These assumptions require several changes in the SEIR model.

1. We need to partition the Infectious class into two subgroups: Presymptomatic and Unisolated.

2. Newly infected individuals go into class P.

3. There is a symptom development process that removes individuals from class P at a rate σP, where $\sigma = 1/T_P$.

(a) A fraction q of the individuals removed from class P are isolated. These people are still infected, but they can no longer trasmit the disease; hence, they move directly to class R, leading to an increase in R at rate $q\sigma P$.

(b) The remaining individuals removed from class P move into class U, increasing U at rate $(1-q)\sigma P$.

4. There is still a recovery process, this time moving individuals from class U to class R. The rate is γU, where $\gamma = 1/(T - T_A)$ is the reciprocal of the mean time spent in class U.

For simplicity, we also eliminate the latent class.

These additional features yield the SPUR model:

$$\frac{dS}{dt} = -\beta S(P+U), \tag{9}$$

$$\frac{dP}{dt} = \beta S(P+U) - \sigma P, \tag{10}$$

$$\frac{dU}{dt} = (1-q)\sigma P - \gamma U, \tag{11}$$

$$\frac{dR}{dt} = q\sigma P + \gamma U. \tag{12}$$