COVID-19 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. This module uses a somewhat complicated model designed to capture some of the nuances of COVID-19. Models are designated by acronyms representing the classes. Our COVID-19 model is SEAIHRD: Susceptible, Exposed (latent),[1] Asymptomatic, (symptomatic) Infectious, Hospitalized, Recovered, and Deceased.
   Figure 1 displays the compartment diagram that represents our COVID-19 model. The diagram is based on a set of assumptions about the processes that move individuals among the classes.

1. Susceptible individuals become exposed at a rate proportional to the susceptible population count S and an 'effective infectivity' count X. Where the infectious class I is the only class capable of transmitting the disease in an SEIR model, the COVID-19 model has different categories of infectives with different levels of infectivity, which contribute to the effective infectivity in different ways (see below).

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[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.
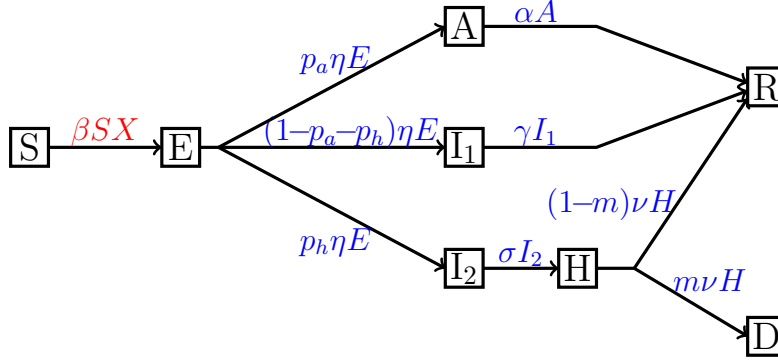
Figure 1: The SEAIHRD epidemic model.

2. Exposed individuals become infectious at rate ηE; a fraction p_a of these become asymptomatic, a fraction p_h eventually become hospitalized, and the remainder become symptomatic but never hospitalized.

3. Asymptomatic individuals gradually recover at rate αA.

4. Group I_1 infectives gradually recover at rate γI_1.

5. Group I_2 infectives become hospitalized at rate σI_2

6. Hospitalized individuals recover or die of the disease, with total rate νH. A fraction m of these individuals die.

7. Recovered individuals are immune for long enough that we can ignore possible loss of immunity.

8. Birth and deaths from unrelated causes are sufficiently small over the course of the epidemic that they can be ignored.

These assumptions lead to the differential equations

$$\frac{dS}{dt} = -\beta SX, \tag{1}$$

$$\frac{dE}{dt} = \beta SX - \eta E, \tag{2}$$

$$\frac{dA}{dt} = p_a \eta E - \alpha A, \tag{3}$$

$$\frac{dI_1}{dt} = (1 - p_a - p_h)\eta E - \gamma I_1, \tag{4}$$

$$\frac{dI_2}{dt} = p_h \eta E - \sigma I_2, \tag{5}$$

$$\frac{dH}{dt} = \sigma I_2 - \nu H, \tag{6}$$

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$$\frac{dR}{dt} = \alpha A + \gamma I_1 + (1 - m)\nu H, \tag{7}$$

$$\frac{dD}{dt} = m\nu H, \tag{8}$$

To complete the model, we need to define the quantity X that represents the number of individuals of class I needed to match the total infectivity of the actual population distribution. It is here that the complexity of COVID-19 dynamics is seen. A significant number of additional assumptions are needed.

1. A fraction p_c of class I are identified by a positive test. These confirmed cases have decreased infectivity because they are put into isolation.[2]

2. Similarly, a fraction p_{ca} of class A are confirmed cases through testing. We expect $p_{ca} = 0$ in the absence of contact tracing.

3. The infectivity of each unconfirmed symptomatic infective is 1 (without loss of generality because there is the additional rate constant β in the transmission rate formula).

4. Asymptomatics, confirmed infectives, and hospitalized infectives have infectivities of f_a, f_c, and f_h (all less than 1) relative to that of unconfirmed symptomatic infectives.

5. There is a 'contact factor' δ that represents the level of risk from the average person's sum total of encounters, relative to normal. This parameter can be used to represent both physical distancing, which decreases the rate of encounters, and wearing of masks, which decreases the risk of each encounter. It is applied to unconfirmed infectives, both symptomatic and asymptomatic, but not to confirmed infectives.

With these assumptions, the effective number of infectives is

$$X = \delta\left[f_a(1 - p_{ca})A + (1 - p_c)I\right] + f_c(p_c I + p_{ca}A) + f_h H, \quad I = I_1 + I_2. \tag{9}$$

Parameters

Our model has 17 parameters, making it difficult to decide how to study its 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. We'll take most of the other parameters to be best estimates, but we'll allow 6 parameters to be specified for each scenario so that their effects can be studied:

1. δ is a contact factor that represents the effect of physical distancing. A value of 1 means that there is no physical distancing, and a value of 0.5 means that contact rates for individuals (not isolated ones) are half of normal.

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[2]The word 'quarantine' is incorrect here, as it refers to the isolation of individuals who have *not* tested positive, generally done because of known exposure–these individuals could be in any of classes S, E, A, I, or even R.

2. p_C is the fraction of symptomatic individuals who are confirmed cases. Roughly speaking, this parameter is a measure of how much testing is being conducted. A value of 0.1 means that only 10% of symptomatic patients are tested and diagnosed.

3. p_{CA} is the fraction of asymptomatic individuals who are isolated (confined). This parameter serves as a measure of contact tracing, since that is the only reasonable way to find asymptomatic carriers.

4. t_2 is the initial infection doubling time, which is the best way to measure the rate of spread. Values of 3 to 5 days have been reported.

5. H_0 is the initial hospitalized population per 100,000. We'll generally take this to be 1. Initial values of the other infectious classes and the latent class are calculated from this value and the doubling time.

6. V is the fraction of the population that is initially immune. This is 0 for scenarios that begin at first exposure of a community. Including this parameter allows the model to be used to investigate herd immunity, which is the reduction of the spreading power of the disease caused by having a relatively large fraction of the population consist of people who cannot get the disease because they have acquired immunity or been vaccinated.

Outcomes

The model simulations generate a large amount of data. In order to understand the model predictions, we need to identify a small number of outcomes to report. For example, rather than reporting the requirements for ventilators, ICU beds, and total hospital beds, just one of these quantities can serve to represent the stress on the health care system. The programs report three key outcomes:

1. The percentage of people still susceptible at the end of the scenario. This is important because it measures the overall risk to society if physical distancing were to end.

2. The population that dies of COVID-19 during the scenario (which we can express as a total number for the United States and as a percentage of the population).

3. The maximum number of patients who require hospitalization per million people. This is important because the most immediate threat of a serious illness is the capacity of the health care system to treat all patients who need professional care. For reference, the average number of hospital beds in the United States is about 0.28% of the population. Of course this number varies by locality, so the model predicts dire consequences if the number of patients requiring hospitalization comes close to the number of hospital beds.

The programs also give visual representations of the results.