Workshop on models of an epidemic

The classic model of an epidemic focuses on populations of individuals: those who are Susceptible to infection with a disease, those who are Infected and are infectious with the disease and those who have Recovered from the disease and are immune to further infection. The classic model is really a family of models called "SIR models" after Kermack and McKendrick (1927)[1]

The sizes of the populations of susceptible (S), infected (I), and recovered (R) individuals are the variables of the model. We will assume they are related by the transitions:

S → I at a rate proportional to I. The rate constant depends on the frequency of interpersonal contacts and the ease with which the pathogen is transmitted.

I → R at a rate dependent on the clearance of the pathogen from a typical individual.

The task of this workshop is to model the system using the continuous deterministic approach, the stochastic probability distribution approach, and an individual agent approach.

1. For the continuous deterministic approach, we can describe our model as a system of ODEs:

$$\frac{dS}{dt} = -\frac{a}{N} IS$$
$$\frac{dI}{dt} = \frac{a}{N} IS - bI \qquad (1)$$
$$\frac{dR}{dt} = bI$$

where N=S(t)+I(t)+R(t) is the total population.

Use ode45 in Matlab (or a similar function in Python) to solve this system. Let us use a=2ln(2)/week so that the initial doubling time of the infected is 1 week and b=ln(2)/week so that the half life of an infected state is one week as well. Use the following initial condition: S=999; I=1; R=0; (hence N=1000), and integrate over t=[0 20] in unit of weeks;

Think about how you may understand the qualitative behavior of the solution. For example, what do you expect the initial growth of the infected to be like (linear, quadratic, or exponential)? And at what population of the Susceptible do you expect the number of the Infected to decrease? The latter result, known as herd immunity, forms the basis of a general theory of vaccination policy.

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[1] Kermack, W.O. and McKendrick, A.G. "A Contribution to the Mathematical Theory of Epidemics." Proc. Roy. Soc. Lond. A 115, 700 - 721, 1927.

The value a/b is known as the basic reproduction number or R_0 and can be interpreted as the number of people an infected individual can infect before she or he recovers without immunity or intervention. Our choices of a=2ln(2)/week and b=ln(2)/week give a R_0 of 2, broadly suitable for the seasonal influenza. For COVID-19, R_0 is estimated to be between 2 and 3 (again without social distancing)[2], and some new variants of the virus are found to have R_0 values 50% higher. Hold the value of b the same, change a to produce different R_0 values to explore its effect.

2. Follow what we did for the probabilistic population model, consider the conditional probability of the populations of Susceptible and Infected at time t+h given their populations at time t for a time interval h small enough that only one infection or recovery event can happen. Modify the code that we used in that class and in HW#2 to model the epidemic. This is often called the Reed-Frost model.

To start, figure out what should the probability of having an event per unit time be for the probabilistic model to be consistent with the continuous deterministic model in the limit of large population. Also note that S→S-1 and I→I+1 are the same event and need to be determined by the same random number. The same is true for I→I-1 and R→R+1. In fact, like in the stochastic population model discussed in class, you can use the same random number and three buckets to determine how the infected population will evolve and determine the evolution of the other two categories by consistency.

3. Check consistency between the deterministic and the probabilistic approaches.

4. We can also model the spread of infectious diseases by representing each individual in the population explicitly. A separate discussion of the individual agent model is on the course webpage, along with the codes. Use them to model the epidemic as well.

5. Discuss the pros and cons of the different approaches.

6. Make a list of the different ways that mathematical modeling was used in the fight against the COVID-19 pandemic.

[2] Kucharski, A. J. *et al. Lancet* 20, 553–558 (2020).