MATH495.3 (CRN 13695)

Laboratory # 7: SIR Model

1 Part 1: Developing the model

Just as we have studied a one dimensional discrete model and a one dimensional continuous model (Logistic equation), we can also have multi-dimensional discrete models and continuous models. In Laboratory # 6 we constructed a multi-dimensional discrete model in the form of age-classifications. This week, we will examine a very well known continuous model of infectious diseases. Instead of classifying the states in age classes, we will split up the population in terms of the progression of the disease.

Let S(t) be the density of susceptible individuals at time t, I(t) be the density of infected individuals at time t, and R(t) be the density of recovered individuals at time t. Our model will have three differential equations, one for each of these populations.

We assume that new infections occur at a rate proportional number of interactions between susceptible and an infected individual. If there are not many susceptible individuals, you shouldn't see a large influx of new infections. Similarly, if there are not many infected individuals, there shouldn't be many new infections. Hence the number of interactions is assumed to be proportional to the product of the densities of susceptible and infected population, *SI*. We further assume that β is the rate of infection. We introduce a term $-\beta SI$ in the *S* equation and a corresponding term $+\beta SI$ term in the *I* equation, since contact leading to infection occurs infected individuals move from the susceptible to the infected class.

Next, we assume that the recovery of the infection is proportional to the number of infected individuals. Let γ be the recovery rate. Therefore, we introduce a term $-\gamma I$ in the *I* equation and a term $+\gamma I$ in to the *R* equation since on recovery individuals move from the infected to the recovered class.

We assume that the natural death rate in the population is δ and introduce $-\delta S$, $-\delta I$, and $-\delta R$ in to the *S*, *I*, and *R* equations, respectively. We also assume there is an additional, disease-specific death rate μ , so add a $-\mu I$ term to the *I* equation.

So far so good. Finally, we assume that the total population is held constant, i.e. that $\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0$. Additional terms are added to the *S* equation to ensure constant population.

The differential equations we will consider are:

$$\frac{dS}{dt} = -\beta SI - \delta S + \delta (S + I + R) + \mu I
= -\beta SI + \delta (I + R) + \mu I,
\frac{dI}{dt} = \beta SI - \gamma I - \delta I - \mu I,
\frac{dR}{dt} = \gamma I - \delta R,$$
(1)

We will use the following values for the parameters.

Parameter	Numerical Value	Interpretation
β	0.008	Infection rate
δ	0.1	Natural death rate
γ	0.3	Recovery rate
μ	0.1	Disease-specific death rate

Table 1: Parameter Values for SIR Model, units of β , δ , γ , and μ are (years)⁻¹.

Using the values given in Table 1, and the initial conditions of S(0) = 599, I(0) = 1, R(0) = 0, find the numerical solution to the SIR model in 20 years. Recall the way you did this for the Logistic equation. This time, the subfunction defining the ODE system will be a vector: dx(1) = _____, dx(2) = _____, and dx(3) = _____. You do not need to make the parameters as inputs to the function, just hardwire the values in to the subfunction. Please title your plot, label both axes, and include a legend defining which lines are *S*, *I*, and *R*. Copy the plot and your code in a Word document.

2 Part 2: *R*₀

There is a biological index known as R_0 for this model. It is defined as the number of secondary infection produced from a single infected individual in a wholly

susceptible population. It is analyzed primarily as a threshold. If $R_0 < 1$, then the new infection in the population can not be sustained. If $R_0 > 1$, then the new infection can produce more that one secondary infection, and the infection will persist in the population.

While this is a nice biological definition, its mathematical construction can be difficult. Furthermore, sometimes there are cases which $R_0 < 1$ yet the disease persists in the population. For our model, R_0 is mathematically defined as:

$$R_0 = \frac{\beta S^*}{\gamma + \mu + \delta} \tag{2}$$

where S^* is the number of susceptibles at an equilibrium where there is no infection. A point such as S^* is called a disease-free equilibrium (DFE).

- 1. Show that [599,0,0] is a DFE for the system by plotting the solution in time using these initial conditions. Copy your titled and labeled plot in a Word document.
- 2. What is R_0 for the above DFE?
- 3. If you introduce infection by using the initial conditions [599,1,0], you will get the same plot you turned in from Section 1. Is the threshold nature of R_0 consistent with the trajectory? Please explain.
- 4. In general, if I = R = 0, what is/are the DFE(s) for *S*? Remember that a point x^* is an equilibrium of a differential equation if $\frac{dx}{dt}(x^*) = 0$
- 5. Now, let's consider the DFE [49,0,0]. What is R_0 for this DFE? If you introduce infection by using the initial conditions [49,1,0], do you expect the infection to persist in the population? Answer why or why not, and include a (titled and labeled) plot that confirms your assertion. You will need to plot the trajectory for more than 20 years (300 years would be convincing).
- 6. Now, with the same DFE of [49,0,0], introduce 20 infected individuals and simulate. Did anything change? Is this what you would expect given the value of R_0 ? Explain what happened using the biological definition of R_0 , and include the (titled and labeled) plot in your results.
- 7. What is the value of S^* that will produce $R_0 = 1$? That is, if S^* is below this value, the infection should not persist, but if S^* is above this value,

the infection should persist. Now examine the solution trajectories from Question 6. About what year did the infection start to increase? In light of the critical S^* , explain why the infection began to increase in that year.

8. In light of the exercises, explain how R_0 may not be sufficient to tell you whether the infection will persist in the population.