Infectious Disease Dynamics: understanding the spread of disease using an SIR Model

Marking – 10 points per question, 30 points total.

Introduction: Developed by Kermack and McKendrick (1927), the SIR Model is commonly used to model the spread of disease by contact by calculating the number of Susceptible, Infected, and Recovered individuals in a fixed population, where:

$$S \longrightarrow I \longrightarrow R$$

There are a number of assumptions that must be held for this model to be appropriate:

1) fixed population size;
2) no intraspecific variation in disease susceptibility;
3) disease transmission is equally likely for individuals in a population;
4) all individuals are considered "susceptible" until they have become "infected". Once an individual is a member of the "infected", the only way out of the group is to become "recovered". Once an individual has "recovered", they are then immune;
5) No inherited immunity.

Our notation of the SIR Model is as follows: $S(t)$ = number of susceptible individuals at time t, $I(t)$ = number of infected individuals at time t, and $R(t)$ = number of recovered individuals at time t. Based on our assumptions described above, the population size (N) consists of:

$$S(t) + I(t) + R(t) = N$$

The change in the number of susceptible individuals as:

$$\frac{dS}{dt} = -\beta S(t)I(t)$$
$$\frac{dI}{dt} = (\beta S(t) - k)I(t)$$
$$\frac{dR}{dt} = kI(t)$$

where β is the transmission coefficient and k is the recovery rate.

Exercise 1. In R, run a simulation demonstrating the dynamics of the SIR Model over 100 time steps where $k = 50$, $\beta = 0.05$, the initial number of susceptible individuals = 10000, the number of initial infected individuals = 1, and 0 initially recovered individuals. To discretize the derivatives of Equations 1, 2, and 3, we will be using an Euler approximation:

Equation 1.1: $S(t) = -\beta * S(t-1) * I(t-1) * d_t + S(t-1)$
Equation 2.1: $I(t) = \big(\beta * S(t-1) * I(t-1) - k * I(t-1)\big) * d_t + I(t-1)$

Equation 3.1: $R(t) = k * I(t-1) * d_t + R(t-1)$

where $d_t = 0.001$ is the discretization interval. Plot all three population categories over time in one figure. Remember to connect the points over time, label your axes, and create a legend. Describe the trends for each population category within the model. Are the trends as you expected? Why or why not? Does the number of infected individuals peak? If so, when?

Hint:

#Parameters

- ➤ k<-50;
- ➤ b<-0.05;
- ➤ dt<-0.001;

#Timescale of simulation

- ➤ T<-100;

#Vector for each class

- ➤ S<-numeric(T); I<-numeric(T); R<-numeric(T);

#Initial conditions

- ➤ S[1]<-10000; I[1]<-1; R[1]<-0;

#Simulation

- ➤ for(t in 2:T){

```
    S[t]=-b*S[t-1]*I[t-1]*dt+S[t-1]
    I[t]=(b*S[t-1]*I[t-1]-k*I[t-1])*dt+I[t-1]
    R[t]=k*I[t-1]*dt+R[t-1]
```

    }

#Plot results

- ➤ TT<-seq(1,T)
- ➤ plot(TT,S,xlab="Time(days)",ylab="Abundance",type="l",ylim=c(0,10000));
- ➤ lines(TT,I,lty=2);
- ➤ lines(TT,R,lty=3);

Hint: For the following exercises, the R code will be very similar to the code in Exercise 1

Exercise 2. Next you will be testing the theory of a host density threshold. Recall in class that we discussed the idea that parasites or pathogens have a greater chance of encountering a suitable host when there are a greater number of hosts within a given environment. This implies that the Net Reproductive Value (R_0; the number of secondary infections generated by a single infection in a completely susceptible host population) is dependent on host density.

In our SIR Model, if we assume that for the host population (N), that $I = 1$ and $S \approx N$, the rate at which susceptible individuals become infected is $\beta SI = \beta N$. The Net Reproductive Value (R_0) is therefore $= \beta N/k$.

Calculate R_0 for the simulations performed in Exercise 1. Record your answer. What does this value imply for the prevalence of the disease?

The Critical Host Density Threshold (N_C), or the host density in which a disease is unable to successfully transmit and become an epidemic, occurs when $R_0 = 1$. Calculate N_C for the simulations performed in Exercise 1. Record your answer. How much larger is the initial population size (N) than the critical host density threshold (N_C)?

Visualizing N_C can provide a much better understanding. Let's run some simulations to see how changing the host density (N), and therefore R_0, impacts our SIR Model dynamics. Perform calculations of the number of Susceptible, Infected, and Recovered individuals over 100 time steps where $k = 50$, $\beta = 0.05$, and $d_t = 0.001$. However, this time produce 6 individual graphs where initial Recovered numbers = 0, initial Infected numbers = 1, and initial Susceptible numbers = 5000, 4000, 2000, 1001, 1000, and 500. Calculate R_0 for each scenario and report your findings.

How do the patterns change as you alter N? Although probably not visually apparent, how do the graphs with initial S values of 1001 and 1000 differ?

Exercise 3. Trying to control the spread of disease has become an increasingly important challenge for wildlife biologists. Within our simple SIR Model, recall that below the critical host density threshold (where $R_0 = 1$), disease is unable to spread. In Exercise 2, we altered the host population size (N) in order to bring R_0 below this critical threshold. This represents the situation where transmission is dealt with through culling and/or partial vaccination. However, in reality we can also drop R_0 by reducing β or increasing k.

For this exercise, we will imagine that we are studying a hypothetical lake fish population threatened by disease. For this exercise, you will come up with a plausible alternative disease control scenario to reduce R_0 below 1. Here, you will need to think about how you would be able to alter β, k, and/or N in the wild. In this instance, culling the population to less than 1000 individuals is something that local anglers will not allow.

Again we will run our model over 100 time steps where $k = 50$, $\beta = 0.05$, and $d_t = 0.001$, and an initial population size of 10000 Susceptible individuals, 1 Infected individual, and 0 Recovered individuals.

Holding the other parameters constant, how far would you have to increase k to meet the N_C? Plot a series of 4 simulations demonstrating how changes in k alter the SIR dynamics. One of your plots should be at the critical host density threshold, and the other 3 should provide figures to show how the shapes of the relationships change.

Likewise, holding the other variables constant, how far would you have to decrease β to meet the N_C? Again, provide a series of 4 simulations demonstrating how changes in β alter the SIR dynamics. Similarly, provide one plot at the critical host density threshold and 3 to show the changing dynamics.

Finally, describe your own individual strategy where you alter all three parameters to eradicate the disease in the population. How could these parameters be met?

References

Kermack, W.O., and McKendrick, A.G. 1927. A contribution to the mathematical theory of epidemics. Proceedings of the Royal Society of London. Series A, Containing Papers of a Mathematical and Physical Character. 115(772):700–721.