

# EEB319 Lab 7: Infectious Disease Modeling

Name:

Lab Section:

This week, we'll learn how to use SIR models to understand the spread of disease.

**Marking:** Each question is worth 10 points, for a total of 30 points.

## 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:

$$S \rightarrow I \rightarrow R$$

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, infected, and recovered/removed individuals can be represented by the following system of ordinary differential equations:

$$\begin{aligned}\frac{dS}{dt} &= -\beta SI \\ \frac{dI}{dt} &= (\beta S - k)I \\ \frac{dR}{dt} &= kI\end{aligned}$$

Where  $\beta$  is the transmission coefficient, and  $k$  is the recovery rate.

## Exercise 1

Run a simulation demonstrating the dynamics of the SIR Model over 100 time steps where  $\beta = 0.05$ ,  $k = 50$ , the initial number of susceptible individuals = 10,000, the initial number of infected individuals = 1, and the initial number of recovered/removed individuals = 0. To discretize the derivatives of Equations 1, 2, and 3, we will be using an Euler approximation such that:

$$\begin{aligned}S_t &= -\beta S_{t-1} I_{t-1} dt + S_{t-1} \\ I_t &= (\beta S_{t-1} I_{t-1} - k I_{t-1}) dt + I_{t-1} \\ R_t &= k I_{t-1} dt + R_{t-1}\end{aligned}$$

Where  $dt = 0.001$  is the discretization interval. Plot all three population categories over time in one figure. Remember to label your axes, differentiate your compartments, and create a legend.

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## Parameters

## Time

## Empty vectors and initial conditions

## Model simulation via for loop

## Plotting
```

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?

Type your answer here.

## 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  $S \approx N$  and  $I = 1$ , 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 at 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  $\beta = 0.05$ ,  $k = 50$ , and  $dt = 0.001$ . However, this time, produce 6 individual plots where the initial number of susceptible individuals = 5000, 4000, 2000, 1001, 1000, and 500, the initial number of infected individuals = 1, and the initial number of removed/recovered individuals = 0. Calculate  $R_0$  for each scenario and report your findings.

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## Calculating R0 for above simulation

## Calculating Host Density Threshold (NC) for simulation above

#### New simulations! ####
## Parameters

## Time

## Model simulation via for loop (HINT: You can use a nested loop to do all 6 simulations in one chunk of code...)
)

## Calculating R0

## Plotting
```

How do the patterns change as you alter  $N$ ? Although probably not visually apparent, how do the plots that begin with 1001 and 1000 susceptible individuals differ?

Type your answer here.

## 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  $\beta$  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  $\beta$ ,  $k$ , 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  $\beta = 0.05$ ,  $k = 50$ , and  $dt = 0.001$ , with an initial population size of 10,000 susceptible individuals, 1 infected individual, and 0 removed/recovered individuals.

Holding the other parameters constant, how far would you have to decrease  $\beta$  to meet the  $N_C$ ? Plot a series of 4 simulations demonstrating how changes in  $\beta$  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 population dynamics change.

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

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

Type your answer here.

## 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.