Dynamic Models in Biology
Computer Lab: Epidemiology model

The modeling of infectious diseases and their spread is an important part of mathematical biology, part of the field of mathematical epidemiology. Modeling is an important tool for gauging the impact of different vaccination programs on the control or eradication of diseases. Modeling is also essential for predicting the transmission of disease in populations. For example, during the Ebola epidemic in 2014, the US Centers for Disease Control used a mathematical model of susceptible and infected populations to predict the course of the epidemic: how bad would it be? They also used the model to plan possible strategies for intervention: how much would we have to reduce the transmission rates to control the epidemic and even to make the number of infected decline to zero?

In this lab, based in part on notes from Eduardo Sontag at Rutgers University, you will investigate a model of susceptible and infected populations and try to see if you can control an epidemic!

SIR model

The classical work on epidemics dates back to Kermack and McKendrick, in 1927. We will study their SIR model without "vital dynamics" (births and deaths). To explain the model, let us think of a flu epidemic, but the ideas are very general. In the population, there will be a group of people who are *Susceptible* to being passed on the virus by the *Infected* individuals. At some point, the infected individuals get so sick that they have to stay home, and become part of the *Removed* group. Once they recover, they still cannot infect others, nor can they be infected since they developed immunity. Individuals belong to this group as long as they remain immune. The numbers of individuals in the three classes will be denoted by S, I, and R respectively, and hence the name "SIR" model. The model assumes that these numbers can be modeled as real numbers. Non-integers make no sense for populations, but it is a mathematical convenience and therefore often used (recall the rabbit vs. sheep and the spruce budworm models).

The model equations are given by:

$$\begin{aligned}\dot{S} &= -\beta SI + \gamma R \\ \dot{I} &= \beta SI - \nu I \\ \dot{R} &= \nu I - \gamma R.\end{aligned}$$

The transmission of disease is increased with both more Susceptibles and more Infected individuals, hence the nonlinear term βSI. The parameter β is the transmission rate. It is an important parameter that can be manipulated with measures to prevent spread of disease and make infected people less likely to infect others.

The parameter γ is the rate of loss of immunity among the Removeds. When they lose immunity they become Susceptible again.

The ν parameter gives the rate of transitioning from the Infected to the Removeds group. A low value of ν would indicate that onset of disease is slow so that Infecteds may spread disease more prior to falling sick enough to become Removeds.

You may be thinking "Hey, this is a 3-dimensional model and we have only learned about 1- and 2-dimensional systems in class". Well, since this model assumes no births and deaths, the total population size is constant and given by the conservation equation $N = S+I+R$. This means that R can be written in terms of S and I as an algebraic (rather than a differential) equation: $R = N - S - I$. The SIR system can therefore be rewritten as:

$$\begin{aligned}\dot{S} &= -\beta SI + \gamma(N - S - I) \\ \dot{I} &= \beta SI - \nu I,\end{aligned}$$

i.e., a 2-dimensional system.

Matlab file
The Matlab program `SIR_lab3.m` uses our usual `ode45` solver to numerically integrate the SIR model. Go through the matlab file and make sure you understand what it does.

Fixed points
We'll start out by examining the system when $N = 2$ and $\beta = \gamma = \nu = 1$. Verify that the fixed points of the system are $(S^*, I^*) = (2, 0)$ and $(1, \frac{1}{2})$.

Use linearization to classify the dynamics close to the fixed points. To do so, first verify that the Jacobian is

$$J = \begin{bmatrix} -I - 1 & -S - 1 \\ I & S - 1 \end{bmatrix}$$

Then, compute the eigenvalues of the fixed points. To do so in Matlab, for the fixed point $(S^*, I^*) = (2, 0)$, first evaluate the Jacobian at that fixed point:

```
S = 2;
I = 0;
J = [-I-1 -S-1; I S-1];
```

and then compute the eigenvalues:

```
lambda = eig(J)
```

response 1

Matlab should return $+1$ and -1 in this case. What type of fixed point is $(S^*, I^*) = (2, 0)$?

Classify the fixed point $(S^*, I^*) = (1, \frac{1}{2})$. redefine S and I, use eig(J) to compute lambda, response 2

Quiver plots

Use `quiver` to display the velocity vectors. Make sure the `quiver` plot is consistent with your results regarding the dynamics close to the fixed points. quiver plot and fixed points classification

Numerical simulation at last!

Run the `SIR_lab3` program. A physically realistic initial condition may be a situation where the majority of the population is Susceptables and a few are Infecteds and Removeds. The initial condition `y0 = [1.8; 0.1];` in the program is a reflection of this situation. Explain the dynamics. Is there an epidemic? response 4

response 3

Vary the initial conditions to obtain a phase portrait. Does the phase portrait agree with your results from the linerization? plot a ode45 phase portrait response 5

Increased transmission rate

As stated above, the parameter β is an important parameter as it sets the rate of disease transmission. What do you think will happen to the model dynamics if you increase β? Try it: run the model with, e.g., a value of 2 for β. What happened with this change? Was your prediction right? response a prediction, and try beta=2, and describe the figure, say if it is right

Disease prevention try beta=0.5, and say if it works

An epidemiologist comes up with a method to reduce β to 0.5. Run simulations to find out if this prevents/stops an epidemic.

Immunization

Another epidemiologist comes up with a new vaccine against the disease. Immunization essentially permanently removes a certain proportion of individuals from the population, decreasing N. Say that half the population receives the vaccine and the vaccine is 100% efficient. Run simulations to find out if this vaccination program prevents/stops an epidemic. 0.5 N and see what happened

Other measures for disease prevention certain actions that change v and y, and test it

Can you think of other interventions to reduce the spread of the disease? Maybe changing ν or γ? Come up with a suggestion and test it in your model.