Lab Activity # 1 - Susceptible-Infectious-Recovered (SIR) models

Numerical Solvers

We often rely on numerical solvers to numerically integrate differential equations. Because of the complexity of many systems of differential equations, these numerical solvers allow us to solve complex differential equation systems that may not be solvable symbolically, or are high dimensional. In this lab we will be using <code>solve_ivp</code>, which is a part of <code>scipy.integrate</code>, to solve ODE systems related to epidemic models. You can read the documentation for <code>solve_ivp</code> at <code>https://docs.scipy.org/doc/scipy/reference/generated/scipy.integrate.solve_ivp.html.</code>

solve_ivp takes the differential equation as a function, a tuple containing the start and end time, and an array with the initial conditions as arguments, and returns a bunch object containing the solution and other information. We can solve the following system of differential equations with the following code.

$$\begin{cases} y_1'(t) = y_2(t) \\ y_2'(t) = \sin t - 5y_2(t) - y_1(t) \end{cases}$$
$$y_1(0) = 0, y_2(0) = 1, t \in [0, 3\pi]$$

```
import matplotlib.pyplot as plt
import numpy as np
from scipy.integrate import solve ivp
# define the ode system as given in the problem
def ode(t, y):
    return np.array([y[1], np.sin(t) - 5*y[1] - y[0]])
# define the t0 and tf parameters
t0 = 0
tf = 3*np.pi
# define the initial conditions
y0 = np.array([0,1])
# solve the system
sol = solve ivp(ode, (t0,tf), y0)
# plot y 1 against y 2
plt.plot(sol.y[0],sol.y[1])
plt.xlabel('$y 1$')
plt.ylabel('$y 2$')
plt.show()
```

Recall that the SIR model describes the spread of an epidemic through a large population. It does this by describing the movement of the population through three phases of the disease: those individuals who are susceptible, those who are infectious, and those who have been removed from the disease. Those individuals in the removed class have either died, or have recovered from the disease and are now immune to it. If the outbreak occurs over a short period of time, we may reasonably assume that the total population is fixed, so that S'(t) + I'(t) + R'(t) = 0. We may also assume that S(t) + I(t) + R(t) = 1, so that S(t), I(t), and R(t) represent the fractions of the population that are susceptible, infectious, and recovered, respectively.

From the discussion earlier in this module, you saw that the differential equations which model the populations in the model are given by

$$\frac{dS}{dt} = -rSI$$

$$\frac{dI}{dt} = rSI - aI$$

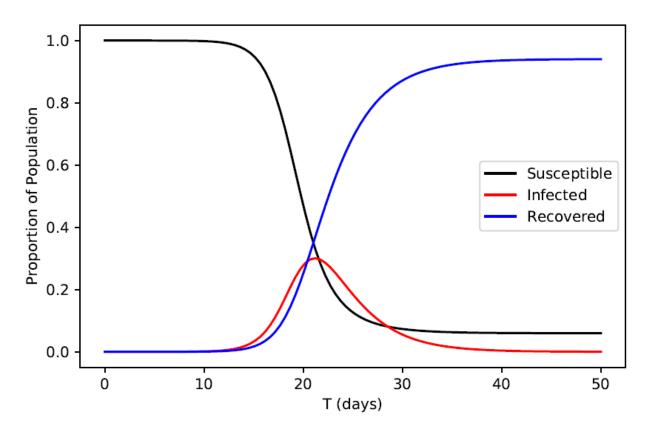
$$\frac{dR}{dt} = aI$$

Problem 1. Suppose that, in a city of approximately three million, five people who have just become infectious have recently entered the city carrying a certain disease. Each of those individuals have one contact each day that could spread the disease, and an average of three days is spent in the infectious state. Find the solution of the corresponding SIR equations using <code>solve_ivp</code> for fifty days, where each time period is half a day, and plot your results. Use the percentages of each state, not the actual number of people in the state.

At the peak of the infection, how many in the city will still be able to work (assume for simplicity that those who are in the infectious state either cannot go to work or are unproductive, etc.)?

Hint: Use the t-values parameter in $solve_ivp$ to pass in an array of t-values. Also, assume that your b value is equal to 1.

Compare your plot to the figure below.



SIR is an effective model for epidemic spread under certain assumptions. For example, we assume that the network is what's called "fully mixed". This implies that no group of members of a network is more likely to encounter each other than any other group. Because of this assumption, we should not use SIR to model networks we know to be poorly mixed. In fact, we should be clear in stating that almost no network is truly fully mixed; however, this model is still effective for networks that are reasonably well mixed. In the next

problem we will be using SIR to model data from the recent Covid-19 outbreak. To adhere to the "reasonably well mixed" criteria, we will be using only data from one county at a time.

Problem 2. On March 11, 2020, New York City had 52 confirmed cases of Covid-19. On that day New York started its lockdown measures. Using the following information, model what the spread of the virus could have been, using <code>solve_ivp</code>, if New York did not implement any measures to curb the spread of the virus over the next 150 days:

there are approximately 8.399 million people in New York city, the average case of Covid-19 lasts for 10 days, and each infected person can spread the virus to 2.5 people. Also, assume your b value is equal to 0.1.

Plot your results for each day.

- 1) At the projected peak, how many concurrent active cases are there?
- 2) Assuming that about 5% of Covid-19 cases require hospitalization, and using the fact that there are about 58,000 hospital beds in NYC, how many beds over capacity will the hospitals in NYC be at the projected peak?

Variations on the SIR Model

The SIS model is a common variation of the SIR model. SIS Models describe diseases where individuals who have recovered from the disease do not gain any lasting immunity. There are only two compartments in this model: those who are susceptible, and those who are infectious. Here, f is the rate of becoming susceptible again.

The basic equations are given by

$$\frac{dS}{dt} = -rSI + fI$$

$$\frac{dI}{dt} = rSI - fI$$

Another alteration we can make to the SIR model is to add a birth and death rate. In the equations below we are assuming that the natural death rate together with the death rate caused by the disease is equal to the birth rate. This model is given by

$$\frac{dS}{dt} = \mu(1 - S) - rSI$$

$$\frac{dI}{dt} = rSI - (a + \mu)I$$

$$\frac{dR}{dt} = aI - \mu R$$

where μ represents the death rate and equal birth rate, noting that any new person born is born into the susceptible population.

If we combine the last two variations we made on the SIR model we come to this formulation, which is an SIRS model. This SIRS model allows the transfer of individuals from the recovered/removed class to the susceptible class and includes modeling of the birth and death rates.

$$\frac{dS}{dt} = fR + \mu(1 - S) - rSI$$

$$\frac{dI}{dt} = rSI - (a + \mu)I$$

$$\frac{dR}{dt} = -fR + aI - \mu R$$

Problem 3. There are 7 billion people in the world. Influenza, or the flu, is one of those viruses that everyone can be susceptible to, even after recovering. The flu virus is able to change in order to evade our immune system, and we become susceptible once more, although technically it is now a different strain. Suppose the virus originates with 1000 people in Texas after Hurricane Harvey flooded Houston, and stagnant water allowed the virus to proliferate.

According to WebMD, once you get the virus, adults are contagious up to a week and kids up to 2 weeks. For this lab, suppose you are contagious for 10 days before recovering. Also suppose that on average someone makes one contact every two days that could spread the flu. Since we can catch a new strain of the flu, suppose that a recovered individual becomes susceptible again with probability f=1/50. The flu is also known to be deadly, killing hundreds of thousands every year on top of the normal death rate. To assure a steady population, let the birth rate balance out the death rate, and in particular let $\mu=0.0001$. Lastly, assume your b value is equal to 1.

Using the SIRS model above, plot the proportion of population that is Susceptible, Infected, and Recovered over a year span (365 days).