

MATH 226  
Assignment 14: Project Two

*A Mathematical Model for the COVID-19 Pandemic*

**Introduction** The classic SIR model (see notes from Class 7) was developed in the 1920's and 1930's. It has proven to be very useful in studying the dynamics of infectious diseases. The model yields the extremely important Threshold Theorem of Mathematical Epidemiology.

The SIR model partitions the population into three groups: Susceptibles, Infectives, and Removeds. The *Susceptibles* ( $S$ ) are those persons who are currently uninfected, but may become infected. The *Infectives* ( $I$ ) are those who are currently infected and capable of spreading the infection. The *Removeds* ( $R$ ) are persons who have had the disease and are dead, or have recovered and are permanently immune, or are isolated until death, recovery, or permanent immunity occur. A susceptible person might remain so or become infective through contact with an infected individual. An infective may stay infective or could enter the removed category.



The numbers of persons,  $S$ ,  $I$ , and  $R$ , in each category change with time. We will study mathematical models that attempt to discover how these numbers fluctuate with respect to time, denoted as usual by  $t$ , and with respect to each other.

There are just a few fundamental assumptions of the SIR model:

- 1) The rate of change of the susceptible population depends on the number of contacts between the Susceptible and the Infectives as well as the transmission rate (not every contact results in a Susceptible becoming infected). The SIR model posits that the number of contacts at any time is jointly proportional to the two populations.
- 2) The rate at which Infectives become Removeds is proportional to the number of Infectives.

The model also assumes that initially there are no removeds and that the time period of the epidemic is sufficiently short that we can regard the total population as constant.

Mathematically, the SIR model is a system of three first order differential equations:

$$S' = -\beta S I \quad \text{for some positive constant } \beta$$

$$I' = \beta S I - rI \text{ for some positive constant } r$$

$$R' = r I$$

with initial conditions  $S(0) = S_0, I = I_0, R(0) = 0$   
(The primes ' denote differentiation with respect to  $t$ )

An important consequence of the SIR model is the Threshold Theorem: If  $S_0 < \frac{r}{\beta}$ , then the number of infectives decreases monotonically to 0 while if  $S_0 > \frac{r}{\beta}$  (the threshold), then the number of infectives will initially increase but later will decrease monotonically to zero. The number of susceptibles will approach a positive limiting value as time increases.

Epidemics can then be prevented, or controlled, by ensuring that the susceptible population is pushed below the threshold by such means as vaccination or quarantine.

One drawback of the SIR model is that we can not solve the system of differential equations to obtain explicit formulas for  $S, I$  and  $R$  as functions of  $t$ . We shall study the SIR model in greater depth later in the course.

**A Solvable Model.** One of the major assumptions of the SIR model is that the rate at which the Susceptible population changes is jointly proportional to the  $S$  and  $I$  populations. It assumes then that if the number of Infectives doubles, then the number of contacts between Susceptibles and Infectives will double. There is a similar increase if the Susceptible population doubles. Our model for the COVID19 epidemic you will investigate changes this assumption: we maintain the idea that larger populations of Susceptibles and Infectives will produce more contacts, but not quite so dramatically .

The differential equations for this model are:

$$S' = -\beta \sqrt{S} \sqrt{I} \text{ for some positive constant } \beta$$

$$I' = \beta \sqrt{S} \sqrt{I} - r\sqrt{I} \text{ for some positive constant } r$$

$$R' = r \sqrt{I}$$

with initial conditions  $S(0) = S_0, I(0) = I_0, R(0) = 0$   
and  $S(t) + I(t) + R(t) = N(t)$  is the total population.

### ***Part 1: Deriving Conclusions from the Model***

1. In a sentence or two, explain why the Susceptible population can not increase and the Removed population can not decrease.
2. Show the equations of this model imply that the total population remains constants.  
[Hint: add them up.]

3. Show that the number of Infectives can increase only when the number of Susceptibles exceeds  $\frac{r^2}{\beta^2}$  and that infected population decreases when the susceptible population drops below  $\frac{r^2}{\beta^2}$ . Thus this model also exhibits a threshold phenomenon.
4. Use the Chain Rule (or another argument) to show that the relationship between  $S$  and  $I$  satisfies the differential equation
 
$$\frac{dI}{dS} = \frac{r}{\beta} S^{-1/2} - 1$$
5. Solve the differential equation in Exercise 4 to show that  $I$  is a function of  $S$  of the form  $I = 2 \frac{r}{\beta} \sqrt{S} - S + C$  for some constant  $C$ .
6. Show that  $C = I_0 + S_0 - 2 \frac{r}{\beta} \sqrt{S_0}$
7. Let  $S^* = \frac{r^2}{\beta^2}$ . Show that we can write the relationship between  $I$  and  $S$  at every instant as  $(*) I(t) + S(t) - 2\sqrt{S^*S(t)} = I_0 + S_0 - 2\sqrt{S^*S_0}$
8. The *basic reproduction number* is  $R_0 = \frac{S_0}{S^*}$ . Explain why the disease will die out if  $0 < R_0 < 1$  while an epidemic will occur if  $R_0 > 1$ . [We can interpret  $R_0$  as the number of additional infections induced into a susceptible population by a single infective individual.]
9. Suppose  $S_0 > S^*$  so an epidemic does occur. We are interested in the largest number  $I_{max}$  of infected people we will ever see; that's when the medical system will experience maximum stress on its staff and facilities. Show that  $I$  reaches its maximum when  $S = S^*$ . Use this fact and equation (\*) of Exercise 7 to show  $I_{max} = I_0 + (\sqrt{S_0} - \sqrt{S^*})^2$
10. When the epidemic has run its course, there will be no infectives; that is,  $I_\infty = \lim_{t \rightarrow \infty} I(t) = 0$ . We seek  $S_\infty = \lim_{t \rightarrow \infty} S(t)$ , the number of Susceptibles who never succumbed to the disease. Explain why  $S_\infty < S^* < S_0$ .
11. Show that  $S_\infty = S^* \left[ 1 - \sqrt{\left( \frac{\sqrt{S_0}}{\sqrt{S^*}} - 1 \right)^2 + \frac{I_0}{S^*}} \right]^2$  [This calculation involves a fair amount of algebra but nothing very advanced].
12. Finally, determine that the total number of individuals who were ever infected is  $I_0 + S_0 - S_\infty$ .

## Part 2: Investigate in *Maple* or MATLAB

Let's construct a *Maple* representation of this model an experiment with it. The usual way to stipulate the first differential equation of the model in *Maple* would be to write something like

$$\text{Ode1} := S'(t) = -\text{beta} * \text{sqrt}(S(t)) * \text{sqrt}(I(t))$$

but this will not quite work because *Maple* reserves the symbol *I* for its way to represent the pure imaginary *i*. You can replace *I* by something else, say *Infectives* or *INF*. I used the letter *J* so my equations look like

$$\text{Ode1} := S'(t) = -\text{beta} * \text{sqrt}(S(t)) * \text{sqrt}(J(t))$$

$$\text{Ode 2} := \text{beta} * \text{sqrt}(S(t)) * \text{sqrt}(J(t)) - r * \text{sqrt}(J(t))$$

*Maple* displays the differential equations as

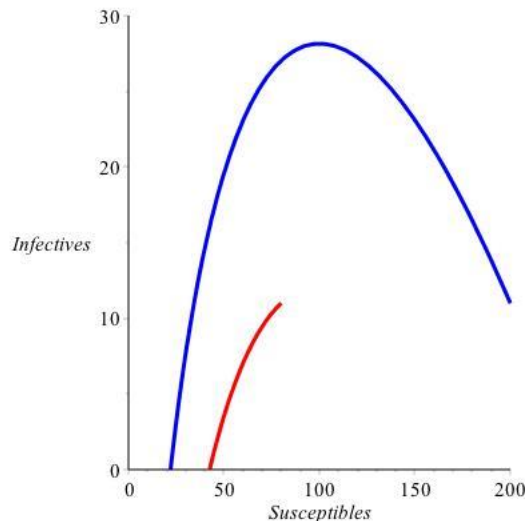
$$D(S)(t) = -\beta \sqrt{S(t)} \sqrt{J(t)}$$

$$D(J)(t) = \beta \sqrt{S(t)} \sqrt{J(t)} - r \sqrt{J(t)}$$

13. Now you can use the *DEplot* command to see what the solutions might look graphically.

I suggest using  $\beta = .03$  and  $r = 0.3$  with  $J(0) = 11$  and  $S(0) = 200$ .

You should get a picture that looks something like:



where the blue curve is the trajectory in the Susceptibles-Infectives plane. Note that there are still a positive number of Susceptibles left when the number of Infectives drops to 0. The red curve illustrates the situation when  $S(0) = 80$ . You should generate these two cases. You should also display the graphs of Susceptibles and Infectives each as functions of  $t$ . The graph of Infectives as a function of  $t$  should look a lot like the ones you are seeing on TV.

See *ProjectTwoEpidemic.pdf* for relevant MATLAB commands.

- From the graphs, estimate  $S_\infty$  and the maximum number of Infectives at any time. Do these estimates match what you found in your earlier work?
- Choose some other interesting values for  $\beta, r$ , and the initial number of Susceptibles and Infectives. Report on your results.

### Part 3: Convert To a Solvable Linear Model

One of the nicest features of this model is that it is possible to obtain the exact solutions of the differential equations so that we will have explicit formulas for the numbers of Susceptibles, Infectives, and Removeds as functions of  $t$ .

The technique is to make a change of variables to obtain an equivalent system of **linear** differential equations.

In particular, let  $u = \sqrt{S} = s^{1/2}$ , and  $v = \sqrt{I} = I^{1/2}$

- Show that these substitutions yield the equivalent system

$$u' = -bv, \quad v' = bu - s$$

$$\text{where } b = \frac{\beta}{2} \text{ and } s = \frac{r}{2}$$

- Write this system in the form  $\mathbf{X}' = A\mathbf{X} + \mathbf{w}$  where  $X = \begin{pmatrix} u \\ v \end{pmatrix}$   $\mathbf{w} = \begin{pmatrix} 0 \\ -s \end{pmatrix}$ .

What does the 2 by 2 matrix  $A$  look like?

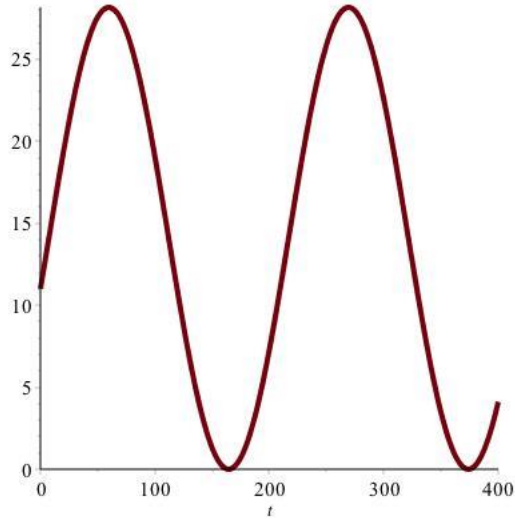
- Show that the eigenvalues of  $A$  are purely imaginary and find the general solution to the homogeneous system  $\mathbf{X}' = A\mathbf{X}$ .

- Verify that the solution for  $v(t)$  is 
$$v(t) = \sqrt{I_0} \cos(bt) + \left( \sqrt{S_0} - \frac{S}{b} \right) \sin(bt).$$

- What is the formula for  $u(t)$ ?

- Since  $v = \sqrt{I}$  and  $u = \sqrt{S}$ , it is tempting to set  $I = v^2$  and  $S = u^2$  to get solutions to the original model. This would not be quite right as the

solution for  $v(t)$  in (19) exhibits oscillatory behavior. Verify that the graph of  $v^2$  will look something like the picture below for our example:



22. Discuss why your earlier analysis of the model rules out a graph like the one above for the number of Infectives.
23. When the number of Infectives reaches 0, it remains there forever. Thus we amend our model to stop at the time  $t^*$  when  $I(t^*) = 0$ . Show that  $v(t^*) = 0$  when  $t^* = \frac{1}{b} \left( \pi - \arctan \left[ \frac{\sqrt{I_0}}{\sqrt{S_0 - \frac{s}{b}}} \right] \right)$ . Rewrite this expression for  $t^*$  in terms of  $\beta$  and  $r$ .
24. Compute  $t^*$  for some different choices of the parameters  $\beta$ ,  $r$ ,  $I_0$ , and  $S_0$ . For the suggested values of  $\beta$  and  $r$ , show that if the initial number of Infectives is 11, then  $t^*$  is about the same for  $S_0 = 2450$  (the Middlebury student body) as it is for  $S_0 = 335$  million (the U.S. Population) or 7.8 billion (world population). How does the estimate of  $t^*$  change if the initial number of Infectives is only 1? For the suggested parameter values, the pandemic should end within 7 months.
25. Show that limiting value of  $t^*$  as  $S_0$  increases without bound, for any choices of  $\beta$ ,  $r$ , and  $I_0$ , depends only on  $\beta$ ; that is, find the duration of the epidemic as  $\lim_{S_0 \rightarrow \infty} \frac{1}{b} \left( \pi - \arctan \left[ \frac{\sqrt{I_0}}{\sqrt{S_0 - \frac{s}{b}}} \right] \right)$  in terms of  $\beta$ .

26. We hear a lot of "flattening the curve" for this COVID-19 pandemic by lowering the transmission rate; that is, making  $\beta$  smaller by limiting contacts among people by social distancing and quarantines. From your work on (25) and earlier problems, show that decreasing  $\beta$  increases the duration of the pandemic but lowers the maximum number of Infectives at any one time.

#### **Part 4: Modify The Model**

There are many ways this model could be made more realistic. For example, it assumes that the total population stays fixed during the pandemic. In the real world, there are births and there are deaths from other causes than the disease.

The model also treats Removeds as a single group, but for many purposes, you might want to distinguish between those who recovered from the diseases and those who died from it. Our model assumes that after you have recovered, you have immunity from the disease and cannot be infected again. We don't actually know if recovery from COVID-19 gives lifelong immunity or not to everyone. A certain percentage of Recovereds might rejoin the Susceptibles.

There are also diseases for which there is are intermediate states between Susceptible and Infective. In the Infective state, you are not only sick but you can pass the disease on to others. There may be an intermediate stage, such as occurs for some people with COVID-19 where there would test positive for the virus but do not exhibit any symptoms yet are able to infect others. There could also be states for individuals who have the virus but are not yet infective to others.

There are a myriad of other variations of epidemic models that could be formulated and studied.

Choose a modification or two of our model that you believe makes it more realistic and investigate the consequences for the dynamic behavior of the system. Generally speaking, the more realistic the model, the less we are

able to say about it *analytically* but we can certainly use *Maple* to do computer simulations.

In another direction, you might determine better estimates for the values of  $\beta$  and  $r$  from recently published/posted data. You could also test the validity of the model for a particular state or nation for which reliable data is available.

This final part of the project provides opportunities for you to be more creative. You might generate some important new insight into the COVID-19 pandemic.