COVID-19 SIR Model

S. Roiz
e-mail: samuel.roiz.123@my.csun.edu

Aug. 14th, 2020

Contents

1 Introduction

A powerful virus hits us in November of 2019. It is called the COVID-19 which stands for CO as the corona, VI for the virus, and D for the disease. The COVID-19 began in Wuhan, China, and spread like a wildfire. It eventually reached the United States. It spread dramatically and the United States did not do anything about it until a death happened in the states. The United States finally had its first death case on February 29th of 2020. This death shocked the United States and had its people panicking. Research and data started its journey on keeping data for the COVID-19 cases. As you can see, that is why the data does not start until early March. For this project, I want to use ODE to show to the people that it can be used on dramatic events.

2 Model

I will be using the SIR Model and SIRS model to display my solution of the project.

2.1 SIR Model and SIRS model

Mckendrick and Kermack used the SIR model in 1927. They said it was mainly used to determine when its recovery of affection or disease, virus, etc. The model consists of three parts. First is S for the number of susceptible. Second is I for the number of infectious and deceased. Thirdly, R is for the number of recovered or immune or deceased individuals. As time goes by, the number of people in each of these groups changes. The amount of susceptible people is highest at the start of the virus. Most people are not affected yet. So those who are not affected by the virus are known as the susceptible group. The infected group will start the lowest and will rise later on like a snowball rolling down the hill because it will eventually break out and have a higher rate of passing on to people. We are going to use these variables to create a SIR model. Our variable of t (t) is going to be measured in days. S() is going to be the number of susceptible individuals. With susceptible individuals depending on its day of (t), it will be written as S(t). I() is the number of infectious individuals and I(t) is the number of infectious individuals with depending on the time of day. We have R stand for removed individuals where the number of individuals that either deceased or recovered. So removed individuals variable on a day will be R(t).

2.2 Formula of SIR Model

There are models, but they are all duplicates from the main SIR model. The SIR model I am going to use is not going to ignore the vital dynamics. Some models ignore the vital dynamics especially if the outbreak is short and not fatal. However, the COVID-19 has been an outbreak for months and is fatal.

So here are the variables that I am going to use for my equations...

$S = S(t)$	amount of susceptible individuals r
$I = I(t)$	amount of infected individuals
$R = R(t)$	amount of removed individuals
$s(t) = S(t)/N$	susceptible over the population
$i(t) = I(t)/N$	infected over the population
$r(t) = R(t)/N$	recovered over the population

We will have an equation that determines the growth of the differential equations to see which is growing when the other is decreasing.

s(t) + i(t) + r(t) = 1

It graph should look something like this.

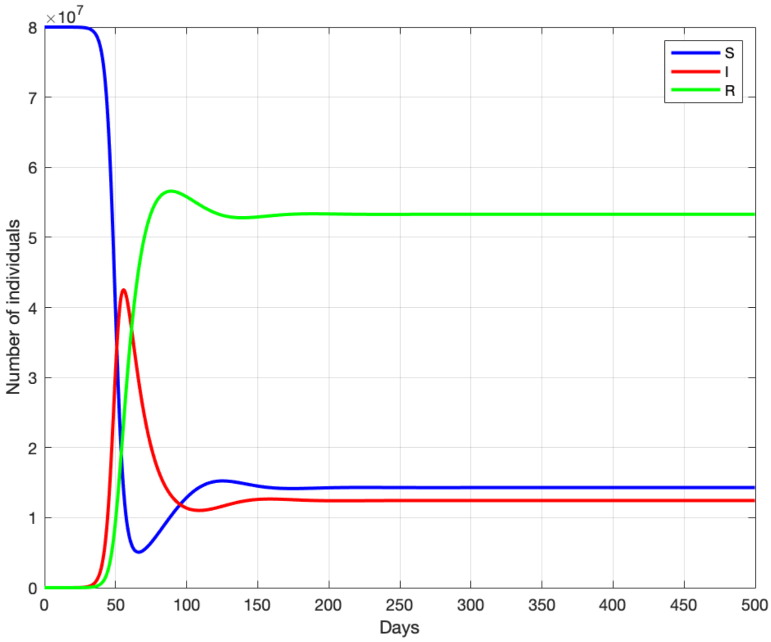

Figure 1: Example of s(t),i(t), r(t)

2.2.1 Susceptible Equation

Now we have equations for each variable. First is the Susceptible Equation. The rate of change of the susceptible individuals over time can be expressed as ds/dt. The negative sign demonstrates the rate of change is consistently negative since it is continually decreasing. will utilize the boundary, β, to display the chance that an infectious individual will transmit the COVID to a susceptible individual. It relies upon the probability that an irresistible individual interacts with a helpless individual and the pace of sickness transmission per contact.

$ds/dt = -\beta * s(t) * i(t)$

So depending on the number of βit affects the curve. If $\beta$is large, the infection will spread faster and the amount of susceptible individuals reduces. If $\beta$is small, the flatter curve will show that its disease spread slows down. So if the larger β, the more the curve drops.

2.2.2 Removed Equation

Now we have a rate that is for removed. It is known as γ. Since those who die and recover are removed from the removed group, that is when γcomes in. We will take the average number of days it takes for individuals to recover from the virus is contrarily corresponding to γ.

$\gamma = 1/n$

Now, we need $\gamma$and removed group together to make our second equation that depends on the given time and the amount of γ. It will be positive since it is the recovery/removed group and should be higher depending on its day.

$dr/dt = \gamma * i(t)$

The graphs below display how the difference in each value of γcan affect the removed curve. If the $\gamma$is large, people recover very quickly and more from the infectious group to the removed group. This means that the virus could die out before infecting the entire population if treated properly. So, if the larger value of $\gamma$is meant fewer people will catch the infection.

GRAPH

2.2.3 Infectious Equation

The infectious equation is based on the βrate and γrate. We will take the infection group and susceptible group to see how much people are going to be infected. While the other side is going to calculate the number of people removed and to see if it has more people removed.

$di/dt = \beta * i(t) * s(t) - \gamma * i(t)$

GRAPH

3 Solution/Results

I will be using the SIR model as I explained above to show the COVID-19 impacting California and New York. To see if they both are at the same rate because they both started with the COVID-19 at a different time. We will start the dates on March 1st since that is when the COVID-19 data has started.

3.1 California

3.1.1 Susceptible Equation

ds/dt = -β*s(t)*i(t)

Based COVID-19 research, the R0 for COVID-19 is approximately 5.7. The average for recovery time is 14 days, so using R0 = β/ $\gamma$for N = 1. The population of California is 39,937,500, but rounded up is to 40 million. Now we can solve 5.7 = (40,000,000 * β)/ (1/14).
β= 5.7/560,000,000
Then Solve for β... which is β= 9.975*10^{-9}

3.1.2 Removed Equation

di/dt = β*i(t)*s(t) - γ*i(t)

γ= 1/n

Based COVID-19 research, the gamma for COVID-19 is approximately 14 days to recover or die. So our gamma of n is going to be 14. We already found $\beta$from the susceptible equation.

γ= 7/100 relatively close to 1/14

3.1.3 Infectious Equation

di/dt = β*i(t)*s(t) - γ*i(t)

We have all of the information we have to plug in the numbers.

3.1.4 California Graph Results

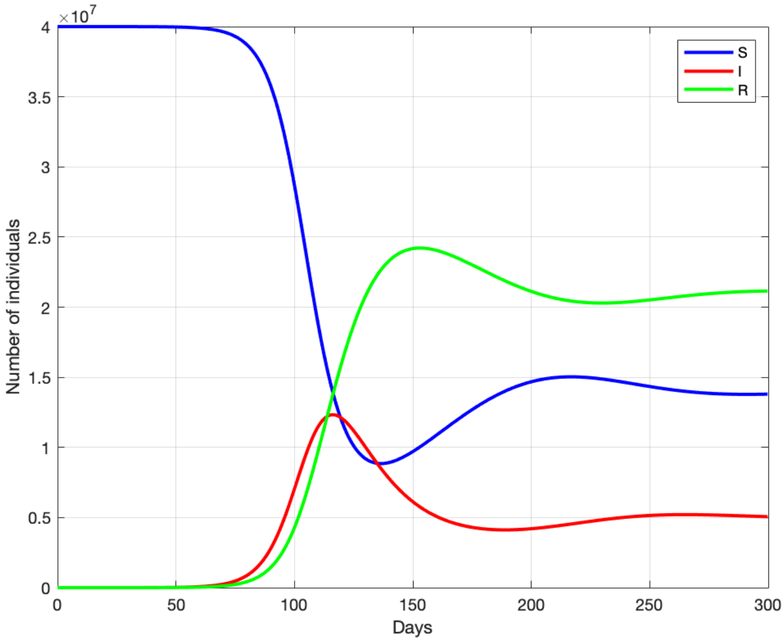

Figure 2: California Graph

3.2 New York

3.2.1 Susceptible Equation

Based COVID-19 research, the R0 for COVID-19 is approximately 5.7. The average for recovery time is 14 days, so using R0 = β/ γfor N = 1. The population of New York is 19,440,500, but when rounded up is 19.441 million. Now we can solve 5.7 = (19,441,000 * β)/ (1/14). β= 5.7/272,174,000. Then Solve for βwhich is β= 2.094*10^{-9}.

However, New York has a denser population of a number of 412.8 (number of people per square mile). California is 253.7 mi^2. New York has almost double of California, so we are going have to adapt β.

3.2.2 Removed Equation

di/dt = β*i(t)*s(t) - γ*i(t)

γ= 1/n
Based COVID-19 research, the gamma for COVID-19 is approximately 14 days to recover or die. So our gamma of n is going to be 14. We already found βfrom the susceptible equation.
γ= 7/100 relatively close to 1/14

3.2.3 Infectious Equation

di/dt = β*i(t)*s(t) - γ*i(t)

From the Removed Equation and Susceptible Equation, we have all of the time information we need.

3.2.4 New York Graph Results

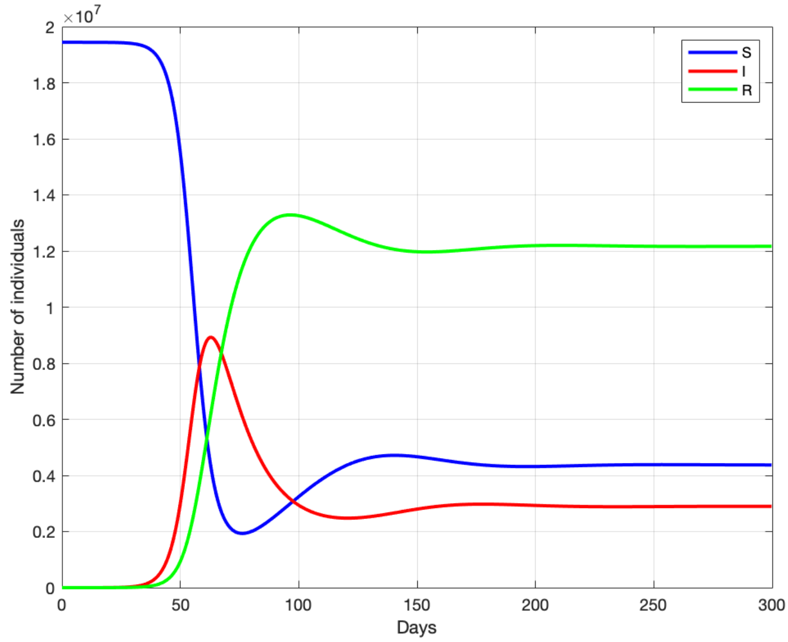

Figure 3: New York Graph

4 Discussion

The two graphs show us a difference in how the COVID-19 impacted the states. California had a slower rate and it took a while to get it is susceptible affected by the COVID-19 as it took up to 60 to 67 days to show the response from the COVID-19. To reach its peak of infected individuals, it took hundred-fourteen days. Then it reduced to an average of 500,000 infected Individuals after 250 days. The removed individual's highest peak is up to 24 million people at one-hundred-fifty days. It is more than the infected which shows somewhat positively, but remember some of those are deaths. After around 250 days for California, it shows the stability of the susceptible individuals at a population of 13,750,000. For New York, it had a faster rate as it infected a lot of susceptible individuals within day 25 through day 74. It was very steep because of the dense population. They are all very tight together, so it had a higher rate of spreading from one to another. The highest peak of infected individuals happens between 63 and 64 days. California's highest infected individuals were at 114 days which shows a huge difference between New York and California COVID-19. It tells us that they both had different rates and how the density population can play a huge factor.

5 Discussion

The project was somewhat a success. The success I saw is that I understood mainly was what each variable mean and do. I could see the changes in how the graph would be if you tweak a variable number differently. For example, if I tweaked the population which is N. Its graph would look different because there are more or fewer people so the rate could be higher or lower since it lacks or has a more density population. That was my biggest success. My other success could be is getting the graph done because if you look up the COVID-19 by the states, it is accurate. The population is what has not made it successful. I had my rate too harsh where it actually made the graph have not that many susceptible individuals. It was more of a prediction after 157 days. The SIR model is a predict, but with accuracy, if the rate does not change. So, if California or New York rate changed because of a cure or an incident, the graph will definitely be off after 157 days. The reason why I am saying 157 days is that counting from today is March 1st. If I had to do the project again, what would I do differently? I would try to learn about R0. In the SIR model, they talk about the R0 and I did not talk about it because I had a lack of information on what it does. It plays a huge role in the model.

References

[1] Abou-Ismail, Anas.
Compartmental Models of the COVID-19 Pandemic for Physicians and Physician-Scientists. ncbi.nlm.nih.gov. NCBI, 4 Jul. 2020. Web. 19 Aug. 2020. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7270519.

[2] The New York Times.
California Coronavirus Map and Case Count. The New York Times, The New York Times, 1 Apr. 2020, www.nytimes.com/interactive/2020/us/california-coronavirus-cases.html.

[3] The New York Times.
California Coronavirus Map and Case Count. The New York Times, The New York Times, 1 Apr. 2020, www.nytimes.com/interactive/2020/us/california-coronavirus-cases.html.

[4] Bhargava, Hansa D.
Coronavirus Recovery: Rate, Time, and Outlook. WebMD, WebMD, 7 Aug. 2020, www.webmd.com/lung/covid-recovery-overview.

[5] Smith, David, and Lang Moore.
The SIR Model for Spread of Disease - The Differential Equation Model. The SIR Model for Spread of Disease - The Differen-

tial Equation Model — Mathematical Association of America, Dec. 2004, www.maa.org/press/periodicals/loci/joma/the-sir-model-for-spread-of-disease-the-differential-equation-model.

[6] Joshua McGee (2020). fitVirusCV19v3 (COVID-19 SIR Model) (https://www.mathworks.com/matlabcentral/fileexchange/74676-fitviruscv19v3-covid-19-sir-model), MATLAB Central File Exchange. Retrieved August 19, 2020.

[7] Abou-Ismail, Anas. Compartmental Models of the COVID-19 Pandemic for Physicians and Physician-Scientists. Sn Comprehensive Clinical Medicine, Springer International Publishing, 4 June 2020, www.ncbi.nlm.nih.gov/pmc/articles/PMC7270519.

[8] Smith, David, and Lang Moore. The SIR Model for Spread of Disease, Dec. 2004, www.maa.org/book/export/html/115606.