Computational Modelling of SARS-Cov-2

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Introduction

SARS-Cov-2, commonly known as COVID-19, is a coronavirus that was first reported in Wuhan, China in November 2019 and has since spread throughout the world. The virus has caused a major pandemic, resulting in over 700 million cases worldwide and 6 million deaths worldwide, severely disrupting everyday life and disrupting the economies of countries. To understand how this virus spreads throughout a population, I aim to use a Susceptible - Infectious - Recovered (SIR) model, which is commonly used to model infectious diseases. I will be using CPGLOT to visualize each curve and understand how changes in parameters can impact the spread of COVID-19 throughout a population.

Method

The SIR model contains 3 ODEs:

$$\begin{array}{lcl} \frac{dS(t)}{dt} & = & -\beta S(t) \frac{I(t)}{N} \\ \frac{dI(t)}{dt} & = & \beta S(t) \frac{I(t)}{N} - \gamma I(t) \\ \frac{dR(t)}{dt} & = & \gamma I(t) \end{array}$$

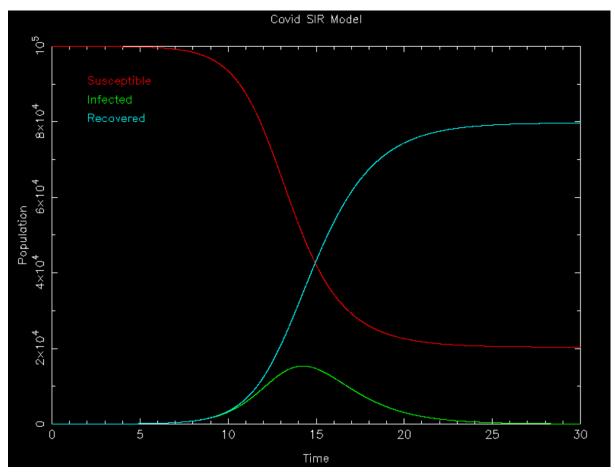
Equation 1 represents the rate of change of susceptible (S) people with respect to time, equation 2 represents the rate of change of infected (I) people with respect to time, and equation 3 represents the rate of change of recovered (R) people with respect to time. Variable β represents the transmission rate, and γ represents the recovery rate. Lastly, N represents the total number of individuals or sample size,

which is calculated by S+I+R=N. For the best approximation, I chose to code each ODE using the runge-kutta method.

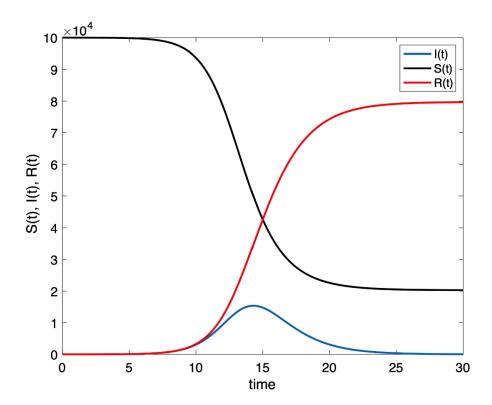
Tests

To test the accuracy of my SIR plot, I chose to compare my plot with several other SIR plots from reliable online sources, given the same parameters. The x-axis represents the amount of time in days, while the y-axis represents the total population.

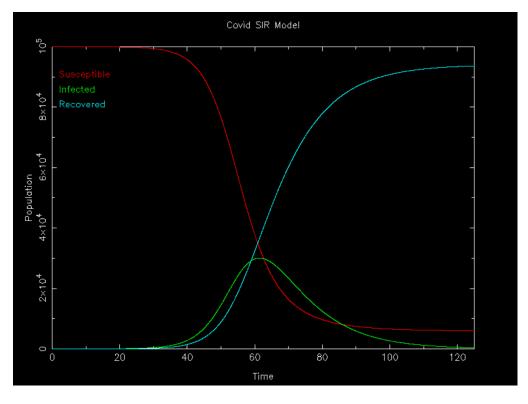
In a research paper by Francois G Schmitt, the SIR plot has parameters beta = 1.5, gamma = 0.75, and initial conditions population (N) = 100000, infection rate (I) = 2, recovery rate (R) = 2, so therefore S = N-I-R = 99996.



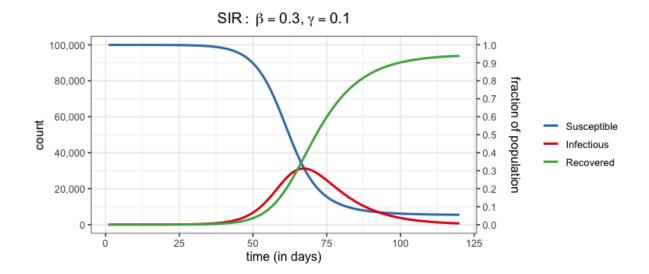
Compared with the original SIR plot, it appears to be accurate:



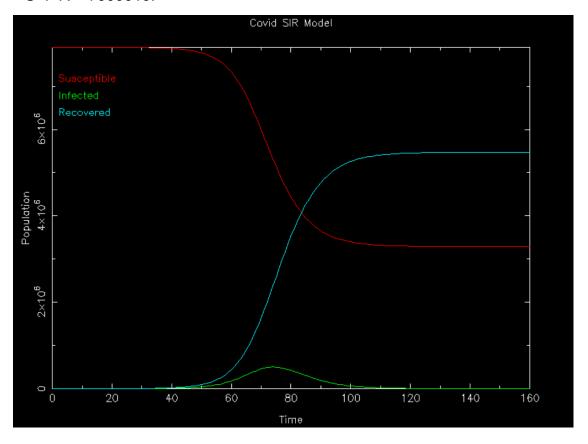
To further test the accuracy, I will compare with a SIR plot by Michael Porter that has parameters beta = 0.3, gamma = 0.1, and initial conditions N = 100000, S = 99999, I = 1, and R = 0.



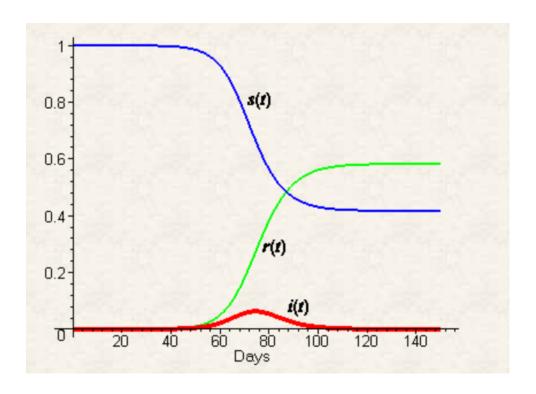
Again, compared with the actual SIR plot, it appears to be accurate:



Doing one more test with a 3rd source, that has a SIR plot with parameters beta = 0.5 and gamma = 0.33, and with initial conditions S = 7900000, I = 10, R = 0, and N = S+I+R = 7900010.



Compared to the original SIR plot, it is once again accurate.



Therefore, it appears that the SIR plot is working as expected.

Results

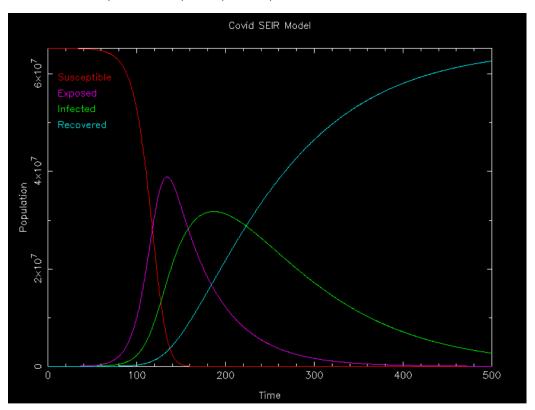
As an extension of the SIR model, I decided to do an SEIR model, which contains 4 equations and is given by the following equations:

$$\begin{array}{lcl} \frac{dS(t)}{dt} & = & -\beta S(t) \frac{I(t)}{N} \\ \frac{dE(t)}{dt} & = & \beta S(t) \frac{I(t)}{N} - \alpha E(t) \\ \frac{dI(t)}{dt} & = & \alpha E(t) - \gamma I(t) \\ \frac{dR(t)}{dt} & = & \gamma I(t) \end{array}$$

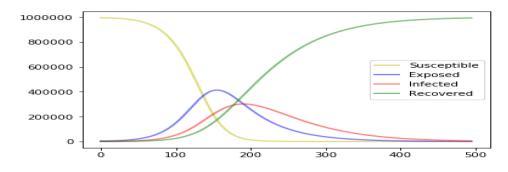
This time we have an additional ODE, where equation 2 represents the rate of change of exposed (E) people with respect to time, and equation 3 is now a bit different, with the addition of the E initial condition affecting its formula. The variable

 α represents the infection rate and now N = S+E+I+R. The benefit of using the SEIR model is that it is a bit more realistic than using the SIR model as people who are exposed to the virus usually do not get infectious right away, so this ODE helps to rectify that.

Once again, I chose to code the SEIR model using runge-kutta and plotted with the x-axis representing days and the y-axis representing the total population. To compare the accuracy of the model, I compared my model with another SEIR model, given parameters beta = 0.5, alpha = 0.02, and gamma = 0.01, and initial conditions N = 65260000, E = 5000, I = 0, R = 0, and S = N - E - I - R = 65255000.

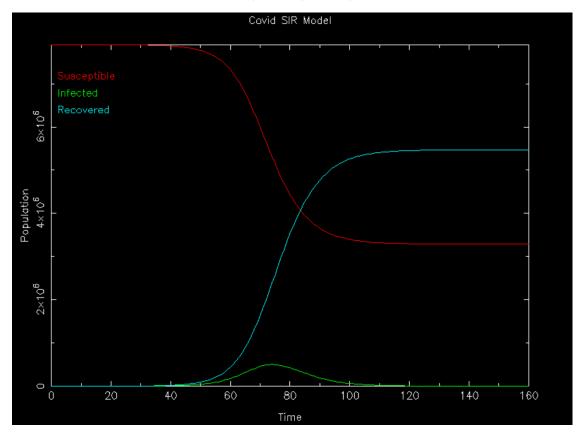


The model appears to be similar compared to the original:

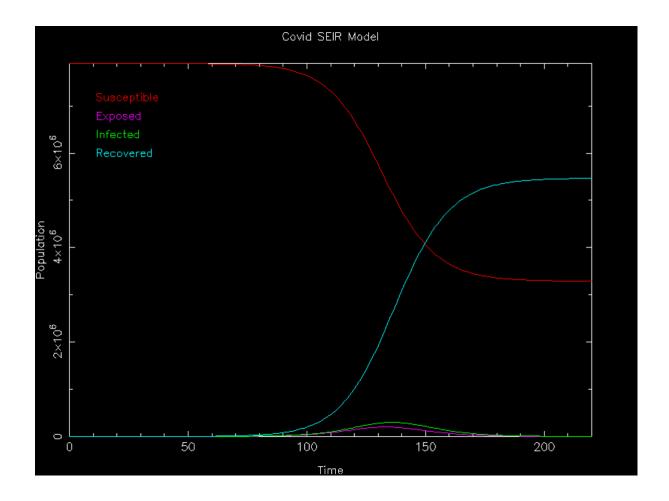


To test the differences between the SEIR with the SIR model, I chose to compare my SEIR model to my SIR model given the same parameters. However, I will change the new infection rate (α) in the SEIR parameters to see how the plots differ.

Compare the original SIR plot with parameters beta = 0.5 and gamma = 0.33, and with initial conditions S = 7900000, I = 10, R = 0, and N = S + I + R = 7900010.

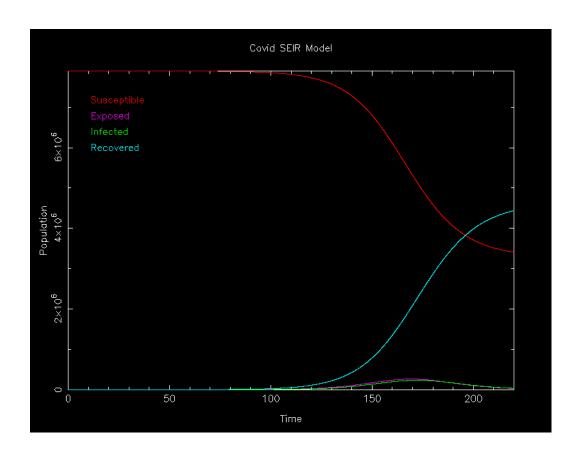


Now, giving the SEIR plot the same parameters, and in addition to setting E = 0 and the infection rate (α) = 0.5, the plot tells a different story.

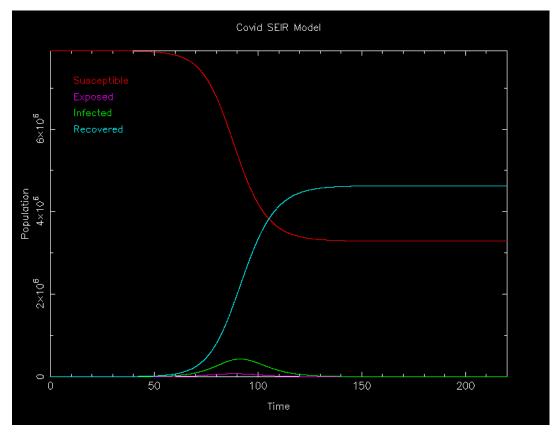


Now, with this added equation in the SEIR model, it shows that it takes longer for COVID-19 to spread, with the virus spreading around 100 days in, whereas compared to the SIR plot, the virus started spreading around 60 days in. Also, we see that the infection line does not go as high, with the exposed ODE influencing how the infected line is calculated and graphed.

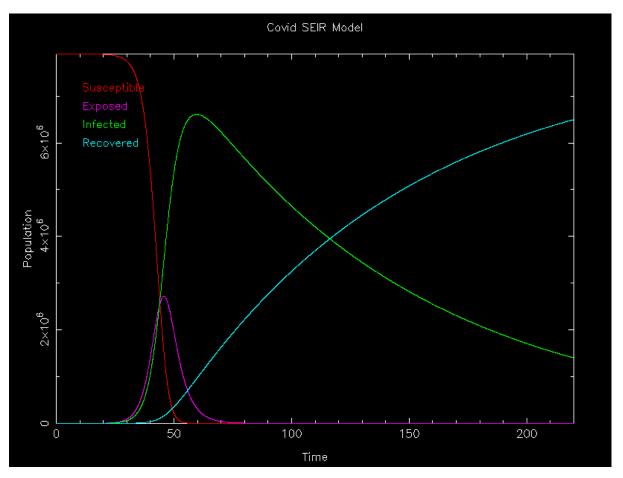
In changing the infection rate to different values, some interesting observations arise. When setting the infection rate (α) to a lower rate, such as 0.1, it takes longer for COVID-19 to start spreading, and for the most part, there are more people exposed to the virus than infected by the virus.



However, if the infection rate (α) is high, such as 2.0, COVID-19 begins to spread at an earlier rate and there are more people infected, as shown below:



When testing different values for the other parameters and initial conditions for the SEIR plot, more patterns emerge. For example, a higher transmission rate (0.8) and low recovery rate (0.01) with an infection rate (0.02) results in COVID-19 spreading throughout the population faster, but taking longer for the population to recover from the virus.



Conclusion

In conclusion, using the SIR and SEIR models represents an effective way of understanding the spread of COVID-19. Depending on the parameters, patterns begin to emerge. For example, in the last plot, we can see how a high transmission rate results in the virus spreading quickly throughout a population and that a low recovery rate results in the population recovering slowly from the virus.

Despite these models proving effective, telling the whole story behind COVID-19 is a lot more complicated than just using a simple SIR and SEIR plot, and there are so many factors to take into consideration, not to mention the change in parameters and initial conditions can give many surprising results. For example, if we take into consideration a population that is vaccinated vs a population that is not vaccinated, there will certainly be different results, or comparing the spread of COVID-19 in a country that has had quarantine restrictions versus other places that have not had any restrictions. For example, a group of scientists in China used a susceptible, unquarantined infected, quarantined infected, confirmed infected (SUQC) model to help understand the spread of COVID-19 in China. This model clearly has different factors but could tell a better story than a SIR or SEIR plot of the spread of COVID-19.

For future work, I would like to use more factors to extend the SEIR plot further to understand more about the spread of COVID-19. Another factor that is of interest is modeling different variants of the virus, as some variants have proven to be stronger than others. Another factor that would be of interest is to compare models of a population that is vaccinated with a population that is not vaccinated, as each model would certainly tell a different story.

Modelling COVID-19 or any virus is always difficult to do, as there are so many factors to take into consideration. With more and more research being done, we will continue to better understand the best measures to take whenever the next major pandemic happens.

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