

MA391 Project: COVID-19 Model Write Up

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Introduction

Coronavirus. This one small pathogen has taken the entire world's 'normal' routine and thrown it out the window. People are losing money, jobs, relationships, planned trips, even the ability to go back home because of the international response to this virus. Coronavirus or more accurately referred to as COVID-19 due to the existence of many coronaviruses, is a pneumonia like virus with respiratory symptoms, and before it was classified officials already were comparing it to SARS and the bird flu that also originated from wildlife markets similar to the market in Wuhan that COVID-19 came from (NY Times). This disease was officially reported as a local epidemic in Wuhan on December 31st, and on January 22nd the United States reported its first case (Wuhan Municipal Health and Health Commission; CDC). Since then, in just over 10 weeks the US has reported up to 213,144 cases (CDC). Modeling this disease is crucial for understanding the best way to mitigate its effects, and understanding governments can respond to minimize transmissions, deaths, and flatten the infected individuals curve.

Defining Variables

To model COVID-19 and other viruses that spread through a population a SIR model is typically used with certain assumptions (Bauch). This acronym stands for Susceptible, Infected, Recovered and refers to the 3 states that people in a population could be regarding the virus. The model reported is a SIRD model, because it accounts for Deaths. In our model below, the differential equations $S'(t)$, $I'(t)$, $R'(t)$, and $D'(t)$ calculate the rate of change for the susceptible, infected, recovered, and dead population, respectively. The model's coefficients are used to account for the interactions between two populations and correct the rates of change to behave as expected. α corrects the interaction between the susceptible and infected population to determine how many more susceptible people will become infected for that week. β controls the number of people who move from infected to recovered from the illness, and the ω coefficient represents those infected by the illness who die.

Assumptions

In order to model a disease this infectious and complex a few assumptions have to be made. There are two categories for assumptions: theoretical and numerical. The theoretical assumptions are the ones that allow modelers to simplify the virus' spread in a way that is modelable numerically. Theoretical assumptions for our COVID-19 model are that each individual infected is equally infectious, only person to person contact can transmit the disease, that is, no one can get it from an infected surface, initially no quarantine measures, all cases resulted from one 'patient zero' and not multiple infected travelers, and all people in the population are equally

likely to come into contact with each other. The numerical assumptions are the ones that we base the model off of given the simplified or ideal situation established by the theoretical assumptions. These assumptions are that the virus has an r_0 (“r naught”) of 2.2, meaning that each infected individual will infect 2.2 other individuals (I_i). Also it is assumed that the virus incubates for 5.2 days and infected individuals have the disease for 2 weeks (I_i). Because the virus can be transmitted regardless of symptoms, individuals are contagious for 2.74 weeks. The estimated death rate for COVID-19 is 3.4%, so it is estimated that 96.6% of infected individuals recover (WHO).

The Model

For our ‘SIRD’ model, we used the following system of equations:

$$S'(t) = -\alpha S(t)I(t)$$

$$I'(t) = \alpha S(t)I(t) - \beta I(t) - \omega I(t)$$

$$R'(t) = \beta I(t)$$

$$D'(t) = \omega I(t)$$

With initial point $x_0(S(0), I(0), R(0), D(0)) = (330534135, 1, 0, 0)$ because 330,534,135 is the US population. We based the coefficients off of the data found and assumptions we made from our research. Alpha is the interactions coefficient, beta is the recovery coefficient, and omega is the death coefficient.

$\alpha = 2.2 * 1/330534135$, because when multiplied by the initial $S(0)$ and $R(0)$ populations it generates 2.2 new infected individuals which is based on the r_0 of COVID-19.

$\beta = .966/2.74$, because it represents COVID-19’s 96.6% recovery rate divided by the average length of being contagious which is 2.74 weeks (5.2 days of incubation and 2 weeks of symptoms).

$\omega = .034/2.74$, because it represents the 3.4% chance of death divided by 2.74 weeks of the average disease course.

To model this disease spread, we used a ‘path’ algorithm to recursively run the current population (starting at x_0) through the differential equations above, and added the resulting change in population to the previous population point to generate x_1 , our estimate of the population one week in advance. These resulting estimates would be run through multiple times to predict the long term spread of COVID-19.

Accuracy of the Model

The number of current COVID-19 cases in the US is projected by the CDC to be 213,144, and our model has that number of cases occurring between weeks 11 and 12 from January 22nd, and we are currently just past week 10. However, if any cases were not reported in the beginning, all it would take to advance our model by one week and accurately place the infected number of individuals in the 200,000s is an extra 2 cases. Because the infected estimate is only off by one week, or two cases, our model is very accurate up to today. This error also could be explained if there were 3 independent 'patient zeros' that infected the US, not just one individual.

It must be noted that cases will not continue to skyrocket from this point going forward. United States quarantine and social distancing measures have been enacted to 'flatten the curve' and spread out the timeline of the disease. We modeled this by having a secondary model that starts at week 13 (the week where infected individuals reach the 200,000s) and goes forward with a halved interaction coefficient α_2 to reduce the effectiveness of infection by 50%. When comparing the two models, the change brings the curve down by reducing the original 215 million case peak at week 19 to a 114 million peak during week 25. This model was included to show how quarantine measures to reduce the number of interactions between sick and susceptible groups literally 'flatten the curve,' which is shown when graphing the number of sick individuals of each model and comparing them in **Appendix A**.

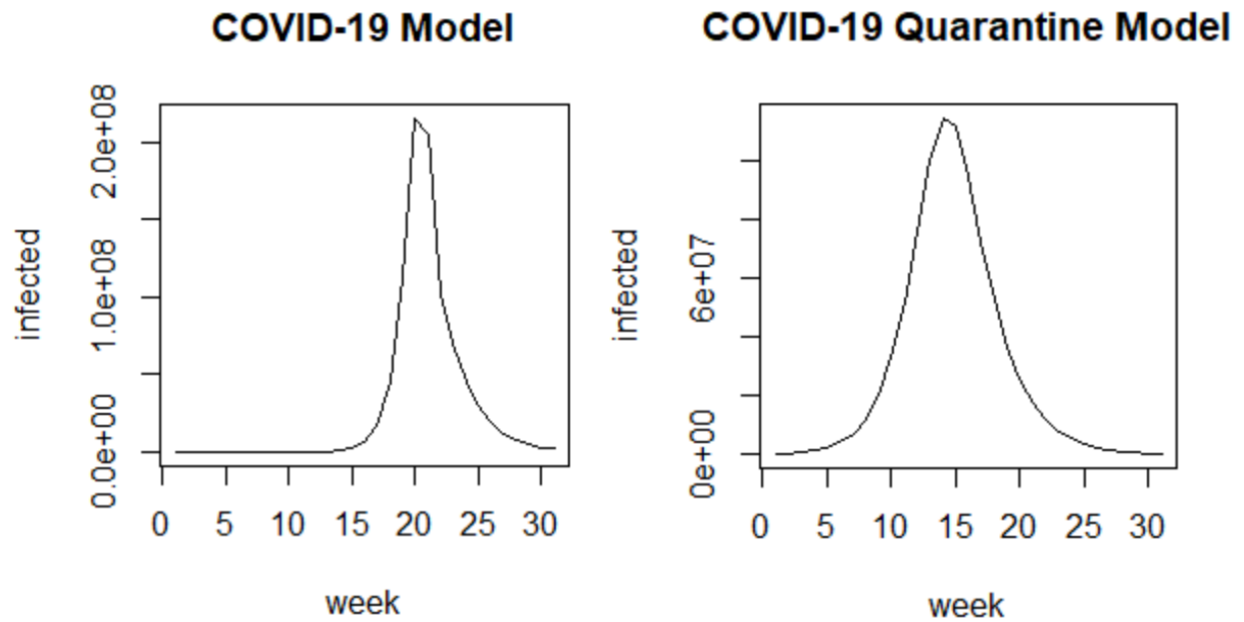
Annotated Bibliography

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APPENDIX A



The Quarantine Model starts at week 12 of the COVID-19 model with initially 269,000 cases, and models how the quarantine would push the peak back from week 19 to week 25 and reduce the number of peak cases also by 100 million cases, close to $\frac{1}{3}$ of the US population! Social Distancing works!