Amath383 Term Paper - Modeling the Spread of COVID-19

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Abstract

The coronavirus, COVID-19, has spread all over the world, causing more than 22,000,000 infected people and many deaths. The mathematical mode, SIR, is useful when we predict the development of the disease. We introduce the SIR model and apply this basic model to develop two mathematical models for the spread of the coronavirus disease 2019(COVID-19). The two models take into account the known characteristics of this disease, as the existence of asymptomatic infected individuals and symptomatic infected individuals. In particular, the second model considers the possibility of a second infection happening on recovered individuals. In this project, we simulate two models by numerical analysis and estimate the development and prediction of the impact of COVID-19.

Introduction

Coronavirus disease 2019(COVID-19) is an infectious disease caused by the novel SARS coronavirus-2 (SARS-CoV-2), a virus closely related to the SARS virus. The virus appears highly transmissible from human to human pathogen which causes a wide spectrum of clinical manifestations in patients with COVID-19[1]. The rapid spread and ensuing public health control measures have led to unprecedented isolation and quarantine of large populations around the world.

In this project, we will derive our model from the SIR model by Kermack and Mckendrick, and discuss the influence of different parameters to the spread of COVID-19.

Formulation of the Mathematical Models

Theoretical Background based on the SIR mode

SIR model is a basic mathematical model applied for virus outbreak first promoted by Kermack and McK- endrick in 1927. The model has been used to predict the development of a variety of diseases, including virus transmission, airborne children disease with lifelong immunity upon recovery[1].

The total population is denoted as N. The model derives three equations relating the susceptible people S(t), the number of people infected I(t), and the number of people who have recovered R(t). In the SIR model, the parameter β denotes the fixed rate that each infected individual contacts with susceptible individuals in order to be sufficient to spread the disease. γ is the fixed rate that infected individuals become recovered. One thing to notice is that it assumes that the size of the total population is fixed. N will not be affected by birth or death.

COVID-19 Model

We intended to formulate a mathematical model to predict the development of COVID-19 in two infection states: the initial state and the second infection state. In the second infection state, we include the possibility that some recovered individuals would get infected again. More specifically, we will model and analyze the development of the

coronavirus outbreak with stimulating different transmission rates between susceptible, infected, death and recovered individuals.

Based on the SIR model, we separate human groups into five sub-populations for our COVID-19 model.

(1) Healthy group(H(t)). This group presents a healthy individual.

(2) Asymptomatic group(A(t)). This group presents individuals who are infected with the COVID-19 but do not show any symptoms.

(3) Symptomatic group(S(t)). This group presents an individual who gets infected and shows symptoms of COVID-19.

(4) Recovered group(R(t)). This group presents an individual who gets covered from COVID-19.

(5) Death group(D(t)). This group presents an individual who died from COVID-19.

First Infection Model

We will start our modeling from dividing the infected groups in the SIR model into asymptomatic and symptomatic groups, and dividing the recovered group in the SIR model into the recovered group and death group. This model only considers the first infection, where the recovered group would not be infected by COVID-19 anymore.

In the first infection stage, using differential equations, the interaction of these dynamics can be captured in the following way:

$$\frac{dH}{dt} = -i_a AH - i_s SH$$

$$\frac{dA}{dt} = (i_a AH + i_s SH) * c_a - rA$$

$$\frac{dS}{dt} = (i_a AH + i_s SH) * c_s - rS - dS$$

$$\frac{dR}{dt} = r(A + S)$$

$$\frac{dD}{dt} = dS$$

Second Infection Model

In our second infection model, we would treat the recovered group® as part of the susceptible group. As a RNA virus, COVID-19 consists of several mutation types, and could cause antibody-dependent enhancement effect[3], a phenomenon in which suboptimal antibodies enhance the virus' ability of entering host cells. Therefore, we assumed that the recovered group would likely have a higher chance of being infected than the healthy group which has never been infected by COVID-19 before[2].

For this reason, we added a parameter to our second infection model, i_si, the ratio of the infection rate of the recovered group versus the infection rate of the healthy group. To demonstrate that the recovered group would have a higher chance of being infected, this parameter should be greater than 1. The improved version of our model looks like this:

$$\frac{dH}{dt} = -i_a AH - i_s SH$$

$$\frac{dA}{dt} = ((i_a AH + i_s SH) + i_{si}(i_a AR + i_s SR)) * c_a - rA$$

$$\frac{dS}{dt} = ((i_a AH + i_s SH) + i_{si}(i_a AR + i_s SR)) * c_s - rS - dS)$$

$$\frac{dR}{dt} = r(A + S) - i_{si}(i_a AR + i_s SR)$$

$$\frac{dD}{dt} = dS$$

Analysis and Results

Obtaining parameter values from real world data

With more than 4 dimensions in our model, finding the fixed points could not help us analyze the model. Hence, we decided to simulate this model for long-term behaviors of this system. We plan to obtain approximated recovered and death rate from real world data, and discuss how different values of the infection rate affects the behaviors of this system.

In order to obtain the approximate value of recover and death rate, we used the datas from https://www.worldometers.info/coronavirus/worldwide-graphs/, and picked several points from the data and calculate the ratio of the growth of recovered group versus the population of infected group, the ratio of the growth of death group versus the population of infected group. Substituting these ratios into our model and simplifying the equations, we obtain the r and d values to be $r = 0.0375$ and $d = 0.0011$, and will use these two values in our further analysis.

The choice of i_a and i_s value

i_a and i_s each represents the infection rate of asymptomatic group and the infection rate of symptomatic group. The values of these parameters are affected by several different conditions, such as patients' range of acuity and their choice of

quarantine options. We will start from $\frac{dA}{dt} + \frac{dS}{dt} = 0.016(A + S)$, which approximately

matches the real world data we collected, and then discuss how different quarantine

choices made by the patient infected the behaviors of our system.

As the asymptomatic group would be less likely to quarantine, we assume that i_a

would be higher i_s, and considering the chance of being asymptomatic is around $\frac{1}{100}$ of

being symptomatic, we set our initial i_a and i_s values to be $i_a = 0.1/P$ and $i_s = 0.055/P$.

Where P stands for the total population. The initial asymptomatic population is set to 10

and the initial symptomatic population is set to 100.

First Infection Simulation

We run our simulation of the first infection model with the population size set to

be 10000, and we simulate 100 days and 365 days to find the behavior of this system.

The resulting graphs are as follows:

First Infection Model 100 days

First Infection Model 365 days
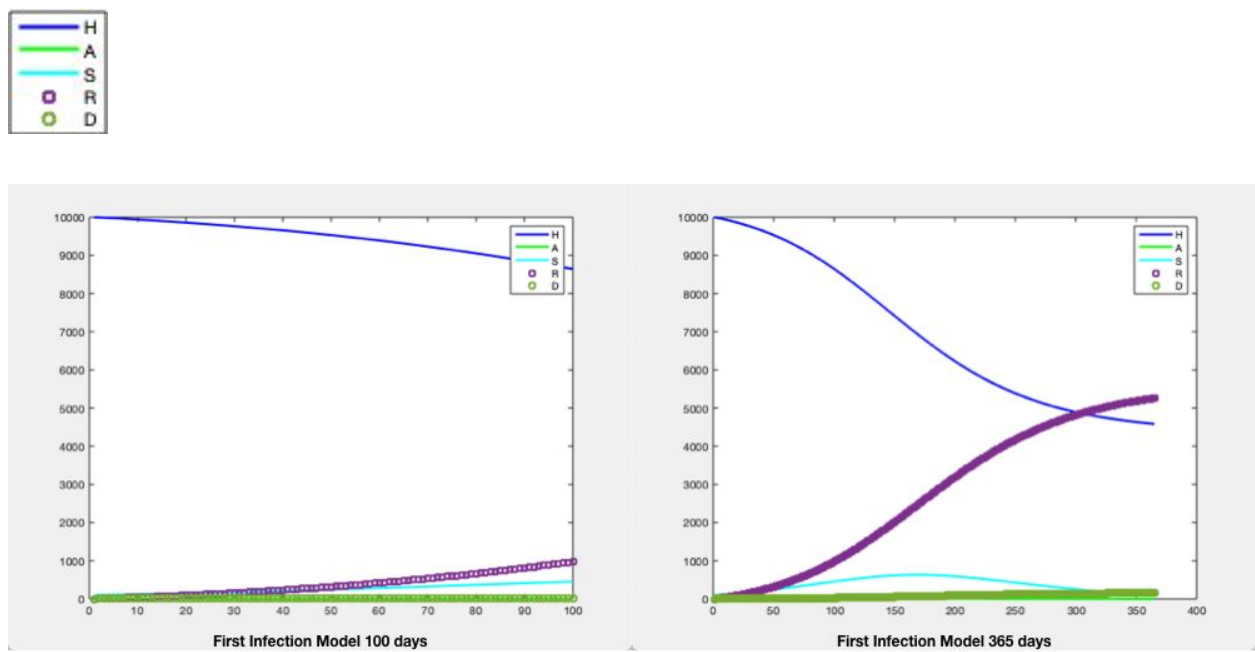
As the parameters we used in this simulation are obtained from real world data, the curves in this graph are similar with the graph generated by real world data, except that recovered population is much higher than the infected population, while these two groups have similar populations in the real world graph, with less than 4 percent difference in the data points we picked. This might be due to the fact that coronaviruses could cause a second infection and we need to take this into account.

Second Infection Simulation

We run our simulation of the second infection model with the population size set to be 10000, and we simulate 100 days and 365 days to find the behavior of this system. The resulting graphs are as follows:

Second Infection Model 100 days   Second Infection Model 365 days
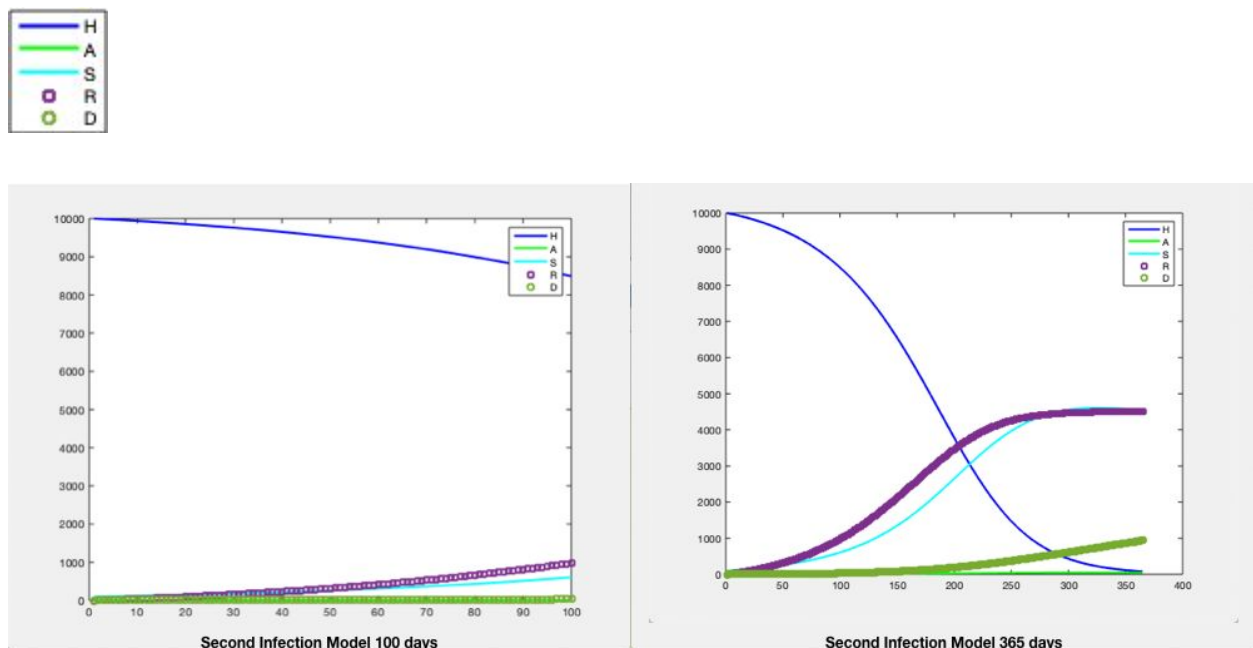
In this simulation, the recovered group and the infected groups are growing at a similar rate, and every curve is almost identical with the real world graph, indicating the

ability of this model to simulate how the disease developed in current conditions.

Therefore, we will use this model to analyze the spread of COVID-19 under different

conditions.

Different quarantine strategies

In our previous simulations, we use i_a and i_s values that approximate the real

world data. However, if people decide to use different quarantine strategies, how would

this system behave? We will discuss the case where quarantines become much more

lenient and everyone has a higher chance of contacting each other.

In this case, we set the i_a and i_s values to be ten times larger, which is the

difference between the gathering requirement between phase 2 and phase 3. The

simulated graph is as follows:

Second Infection Model 100 days

Second Infection Model 365 days
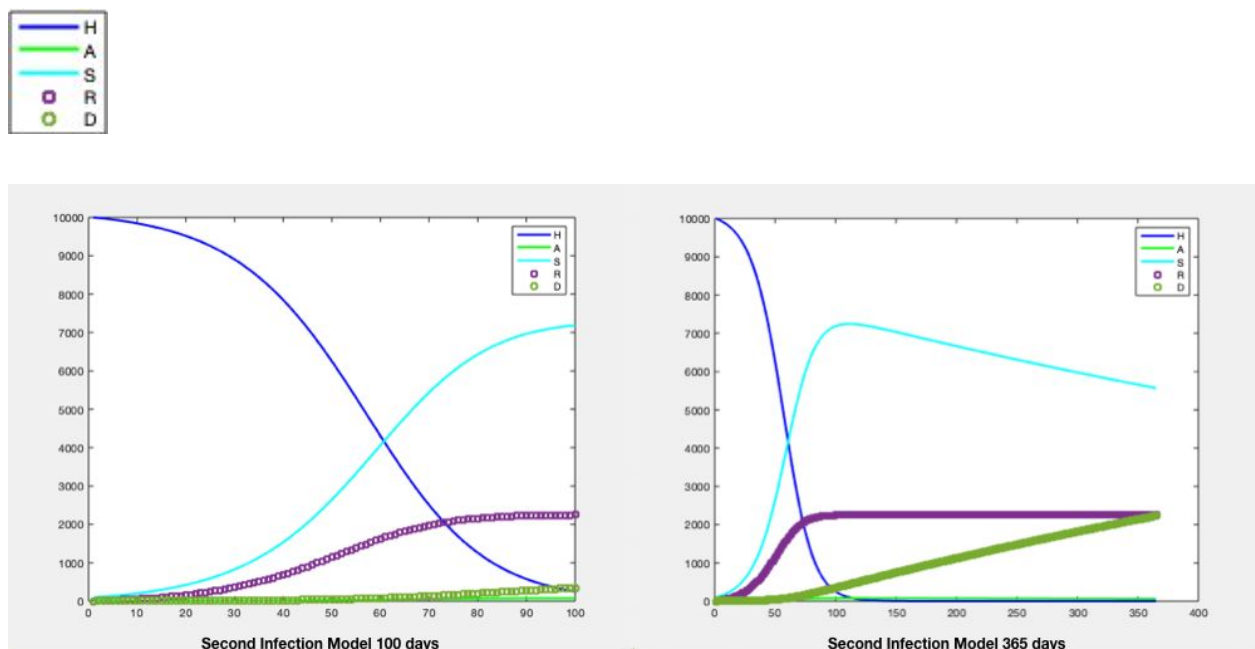
From the graph, we notice that the infected groups(S+A) are growing drastically faster than before, and it only took less than 90 days to infect more than 90% of the total population, and cause far more death(around 25 percent of the total population) in a year. This graph demonstrates the necessity of quarantines, which might have saved billions of lives.

Live with COVID-19

Second Infection Model 100 days   Second Infection Model 365 days
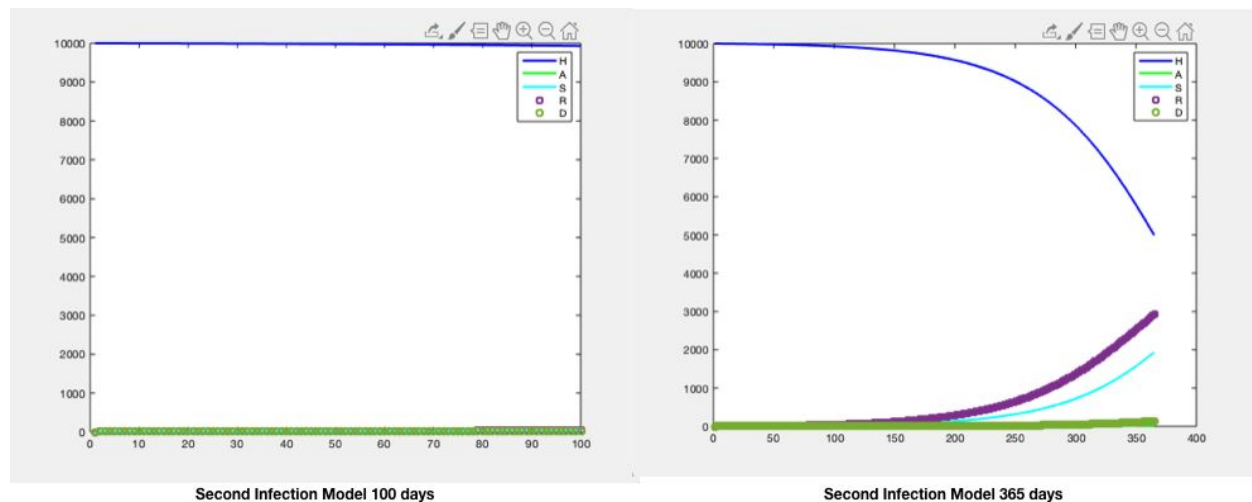
We also wonder, when can we release the quarantine? We then set the initial asymptomatic population to 0 and the initial symptomatic population to 5 to see if it could stop the spread of COVID-19. To our surprise, although it look safe in the first 100 days, the growth of infected group become large after day 150, which indicates the possibility that we have to live we coronavirus in the future as even though the population of infected group become less than 1/2000, it could still come back in around half a year.

Summary and Discussion

Our simulation of the second infection model is very similar to real world data, and has similar growth of all the variables we used. Our analysis is mostly based on this model, and obtained surprising results that shows that we might have to live with COVID-19 in the future as this model shows that it could not diminish itself even with a really low infected population.

There are also some flaws in this model, such as we did not consider the detection of COVID-19 and could thus quarantine them in hospital and thus control the disease.

Reference

[1]SIR and SIRS models — Generic Model documentation. (2020). Retrieved 18 August 2020, from https://idmod.org/docs/emod/generic/model-sir.html

[2]Raoult, D., Zumla, A., Locatelli, F., Ippolito, G., & Kroemer, G. (2020). Coronavirus infections: Epidemiological, clinical and immunological features and hypotheses. *Cell Stress*, https://doi.org/10.15698/cst2020.04.216

[3]Luz, P., Struchiner, C., & Galvani, A. (2010). Modeling Transmission Dynamics and Control of Vector-Borne Neglected Tropical Diseases. *Plos Neglected Tropical Diseases*, *4*(10), e761. doi: 10.1371/journal.pntd.0000761