Spread of Diseases during a Pandemic

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I. Introduction

This project is based on for simulating the spread of multiple diseases during a pandemic. It can be said during a pandemic such as covid 19, a lot of work and effort was given to tracking the spread of the novel coronavirus that had spread all across the world. However, what might be overlooked is that diseases that existed for years are still around during the pandemic as well. It may be said that certain diseases spreading at the same time could affect the spread, infection or even death rate of the disease. Some disease my exacerbate existing problems caused by the main actor of the pandemic, or some diseases may compete with each other instead. All of these may be simulated in a slightly modified SIRD model, where there are multiple S and I factors present in the same time.

II. Related Works

In the paper, "An agent-based approach for modeling dynamics of contagious disease spread" a spatially explicit epidemiological model of infectious disease is proposed for a greater understanding of the disease's spatial diffusion through a network of human contacts. an agent-based modelling approach the integrates geographic information systems (GIS) to simulate the spread of a communicable disease in an urban environment, as a result of individuals' interactions in a geospatial context.

The results of disease propagation simulation indicate that the model is successfully able to generate various scenarios of an outbreak in complex and realistic geographic urban settings by incorporating movement in the agent entities. The addition of mobility allow realistic emulation of daily behaviours of individuals of a population that interact among themselves and that perform stationary activities in fixed spatially located areas after moving from one place to another. The model implemented in this study can be extended to incorporate parameters such as population gender, age, and ethnicity in order to introduce levels of susceptibility in different groups of individuals. Likewise, decisions taken by infected individuals such as stay at home to avoid the contact and spread of the disease can be included. The advantage of the GIS-AB model designed in this study is that any other communicable disease spread can be simulated by simple adjusting the modeled disease timeline and/or the infection model and modifying the transmission process

Another paper talks about the herd immunity against covid 19. The authors wrote this paper with the following question: given a disease with a high rate of non-symptomatic transmission, is contact tracing a useful intervention? One reason for focusing on contact tracing is that it is among the first lines of defence when faced with a new contagious disease; it requires little research overhead compared to pathogen-specific interventions such as vaccines.

present a simple model of the early stages of the spread of COVID-19, which allows us to obtain analytical estimates, as a function of a varying amount of non-symptomatic transmission, of the fraction of the population that needs to participate in a digital contact-sharing network in order to prevent new epidemics. While modeling with various differences from our own became available while we were working on this problem, we feel that our approach has the virtue of making the existence and values of the estimated compliance thresholds transparent. Our estimates for the fraction of the population that needs to own a contact tracing app to avert a COVID-19 epidemic range from 75 percent to 95 percent for R(Theta) = 3, depending on the fraction of asymptomatic transmission, Theta = 20 percent to 50 percent, that takes place. For smaller values of R(Theta) due to social distancing, this fraction is lower.

In another paper in 2020, 3 authors, Claudio, Pedro and Felipe wrote the "FORECASTING COVID-19 PANDEMIC IN MOZAMBIQUE AND ESTIMATING POSSIBLE SCENARIOS", where they simulate the spread and explore methods to stop the spread of the covid 19 virus. They have found that their simulations suggest that a lockdown shows potential for reducing the infection peak height in 28average, ranging from 20 to 36 percent, and can lower the spread while also increasing the amount of recovered individuals. The model they create is an SEIR model (E for exposed). The model treats of populations, therefore these transitions between groups are given by rates of changes in a specific population. Susceptible individuals, denoted by S, become infected through contact with infected (I) or exposed (E) individuals at a rate proportional to the density of infected and exposed [(1 Pexp)(beta)I + Pexp(beta)E]/N, where Pexp is the

percentage of infections caused by the exposed population and (beta) is the infection rate. The exposed population declines as patients become infected by a rate c proportional to the inversion of the incubation period (c = 1/T) , with T being the incubation period. Once inside the infected population, patients now transit to recovered (R) or dead (D) groups through constant rates y and μ respectively. These rates are proportional to the infection fatality rate (IFR)

With regards to open source project, one such project called CovidHunter by Mohammed Alser, Jeremie S.kim, Nour Almadhoun Alser, Stefan W, Tekk and Onur M was published on the February 2021. Their idea for the CovidHunter simulation was to quantify the spread of COVID 19 in a geographical regions ab simulating the average numbers of latest inefections caused by an infected person considering the effect of external factors such as environment conditions, ie climate, temperature, humidity as well as mitigation measures taken by the government to quell the spread. With some emperical data, CovidHunter predicts that reduction of mitigation measures such as lockdown rules, social distancing, etc results in an exponential increase of Covid cases by about 500 percent for a 30 percent reduction of mitigation measures. The authors claim their model is open source, well documented, accounts for weather changes, has a low number of parameters and uses reported covid 19 statistics

Other papers such as that by Parul and Reka simulate different possibilities of the slow lifting of the lockdown by varying the transmission rate as facilities are slowly opened but people follow prevention measures like wearing masks etc. Their model make predictions on the probability and intensity of a second wave of infection in each of these scenarios.

III. Methods

Generally, and SIRD model have 4 main variables, and their respective "change in variable" value, which is S, I, R, D and Change in S, "dS", Change in I, "dI", Change in R, "dR", and Change in D, "dD", respectively. In normal circumstances:

$$dS = -\beta SI \tag{1}$$

This is true for all cases of multiple diseases except for a special case where the secondary disease inhibits the susceptibility of the main disease, but not vice versa. For example, Sickle Cell Anemia is a genetic disease where red blood cells becomes elongated and sickle-like in shape and is able to hold far less oxygen than an health red blood cell. Malaria is another disease that uses red blood cell as hosts to to create more Malarial Pathogens. However, if the afflicted already suffers from Sickle Cell Anemia, then the cell ruptures soon after it is invaded by the Malaria pathogen, preventing pathogen production. In other words, people who are affected by Sickle Cell Anemia are immune to Malaria.

For such a case, Equation (1) can be re-written as follows:

$$dS = -\beta SI - \alpha I2 \tag{2}$$

Where I2 are people infected with Sickle Cell Anemia.

Its worth mentioning that I2 may be followed with its own death rate and recovery rate. However, in case of Sickle Cell Anemia, this secondary disease is not generally fatal nor is it possible to recover from, because this disease spreads via genetics.

However, for other cases, where I2 may be similar to the main disease such as being fatal and can be recovered from, then I2 can have normal coefficients for death and recovery instead of zero.

For a case where the secondary disease worsens the situation of the pandemic, then the total death rate of the disease will be much higher than normal. This can also affect the susceptibility of the main disease.

Our new equations for the death and recovery rate should include both of the diseases:

$$dR = \gamma * I + \gamma 2 * I2 \tag{3}$$

$$dD = \delta * I + \delta 2 * I2 \tag{4}$$

For comparism, here are the old equations for an normal SIRD model:

$$dS = -\beta * S * I \tag{5}$$

$$dS = -\beta * S * I \tag{6}$$

$$dI = \beta * S * I - \gamma * I - \delta * I \tag{7}$$

$$dR = \gamma * I \tag{8}$$

$$dD = \delta * I \tag{9}$$

IV. Results

To start off with, let us first simulate the spread of 2 diseases during a pandemic. Here, the secondary diseases competes the primary one and it worsens the situation of the pandemic. It should be said that both diseases can affect the same person, so the death rate and recovery rate may appear inflated because in the graph because of it (i.e, if one person recovers from the primary disease, but dies from then secondary disease, the both death and recovery values may go simultaneously). For this case, one may assume that the y-axis is multiplied by 2 to get the actual death and recovery values.

From Fig. 1, we can clearly see the effects 2 diseases existing simultaneously during a pandemic can cause. Each disease are set to spread rapidly to infect as many hosts as possible, and each disease have their own lethality and recovery values (both of which simply state their removal).

The infection of the secondary disease and primary disease causes a great increase in death and recovery rates. However, such high values also means that people quickly becomes less susceptible to the disease as well. It is a very rapid rise for R(t) and D(t) and a rapid fall for S(t) but a gradual decline for S2(t) and I2(t).

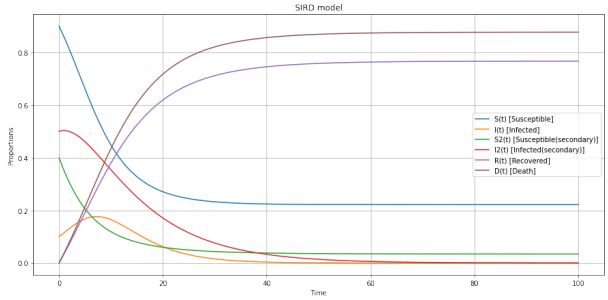

Fig. 1. SIRD model where both diseases worsens the pandemic

Now, let us look at a case where the secondary disease actively inhibits the spread of the primary disease. This simulation is trying to model the case with Malaria and Sickle Cell Anemia(SCA). SCA cannot be easily removed and if a vast majority of people are affected by it, it can act as a cure for Malaria. The following Fig 2 explains the situation.

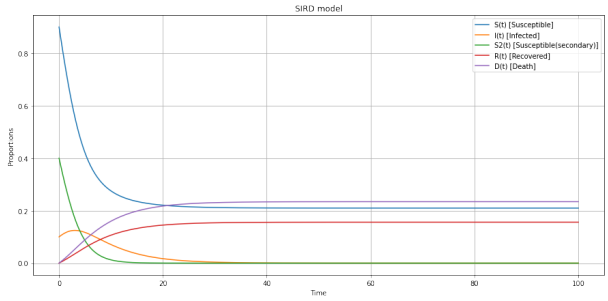

Fig. 2. SIRD model where both diseases worsens the pandemic

Here we can see that the spread and susceptibility of the primary disease falls rapidly. Moreover, the death rate of the Primary disease is very low. This is because the secondary disease itself is not very lethal and it actively prevents the spread if the primary disease, allowing more people to actively recover from it by other means.

V. Discussion

The spread of diseases of this simulation model can simulated more than one disease. However, it should be noted that this greatly increases the complexity of the model as well as decreases the readability of the graph. With this model, we are able to simulate many different cases as there can be a near infinite ways in which 2 or more disease can affect each other. Diseases can complement or compete against each other in more than one way, and can have their own recovery and death coefficients. There are simply far to much variables to account for. For example: disease A may actively inhibit disease B, but it is easier to recover from disease A than it is from B. Therefore, during a pandemic, if A falls to zero, then the susceptibility of B will start rising instead of decreasing to a plateau. This is because when people recover from disease A, they well become vulnerable to disease B. This can be called a delayed action spread of the disease B.

So far, our equations for our model for 2 disease as follows:

$$dS = -\beta * S * I \tag{10}$$

$$dI = \beta * S * I - \gamma * I - \delta * I \tag{11}$$

$$dS2 = -\beta 2 * S1 * I1 \tag{12}$$

$$dI2 = \beta 2 * S1 * I1 - \gamma 2 * I1 - \delta 2 * I1 \tag{13}$$

$$dR = \gamma * I + \gamma 2 * I1 \tag{14}$$

$$dD = \delta * I + \delta 2 * I1 \tag{15}$$

These are for the cases for figure 1. Due to lack of work being in this specific topic, there is not a lot of data where 2 diseases were recorded in the same time and on the same patients. So these equations are not necessarily final. However, they do give a decent representation of how such a situation may look like, and simulations can be made with them. This may be a very important field of study as secondary diseases during a pandemic is often overlooked

VI. Conclusion and Future Work

In conclusion, this project can simulate the spread of more than one diseases during a pandemic. There may be a case where one disease, which is suspected to be the cause of the pandemic, may not necessarily be the only actor in this scene, or may not explain how some deaths are being caused. It may be a case where the disease requires the aid of another disease to actually cause the damage it is doing. Secondary diseases during a pandemic is often overlooked as people are more afraid of the main disease. At the same time, the reverse can also be true, where the secondary disease inhibits the primary disease, and therefore, the primary disease may never be able to spread before it causes severe harm, and be noticed by the people. Who is to say that we didn't get infected by a lethal disease that failed to spread because it could not compete against an existing, non-lethal one? Such a case would go unnoticed.

Future work regarding this simulation can require additional data, especially data where 2 or more diseases are recorded in the same time frame, and on the same patients. That way, accurate estimations based on empirical data can be made. Moreover, it may also improve the equations used on this mode and can greatly improve its accuracy in simulating the given scenario.

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