New mathematical compartment modeling and prevention strategy analysis for the COVID-19

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I. Introduction

Coronavirus has become one of the most frequently used words in 2020 and is still causing an impact in people's life when moving towards 2021. It is undeniably the consequence of the spreading of the coronavirus is tremendous, from the aspect of innumerable deaths to the ineluctable collapse of global economics and international cooperations. Therefore, the most urgent affair is to control the spread of the virus and prevent a second epidemic, although this is what scientists and professions have been doing for the past year — working on vaccines and using existed statistics to calculate R number, before everything, we do not have a complete mathematical model for COVID-19. Mathematical models are useful to understand the behavior of an infection when it enters a community, and it can used to predict the trend of the virus and the effectiveness of vaccines by using differential equations and computational analysis and therefore producing efficient strategies to minimize the impact of COVID-19.

In 1927, W. O. Kermack and A. G. McKendrick created a set of ODEs (ordinary differential equations) — SIR (susceptible, infected, and recovered) epidemic model which is considered under a fixed population, using three compartments to predict statistics. Most of the mathematical models for COVID-19 are based on the SIR model where scientists modified the model catering to characteristics of coronavirus. For example, the SEIR model considered the incubation period and the SIRD model specifies between the recovered (immune) and the deceased (death)[1]. I will discuss the detail of these models in later sections.

Unfortunately, coronavirus statistics are generally expected to be much higher than that predicted in these models, that is why I started to construct my epidemic model based on combinations of the current models. One of the reasons that caused the difference between mathematical prediction and real statistics is coronavirus is an on-going situation in which a lot of up-to-date data need to be used when solving equations. The second reason is with the occurrence of mutations as well as vaccines, new parts of the compartment model need to be introduced. Therefore, in my model, which is called the SEIRI model, I considered the following modifications regarding the basis SIR model where I will discuss in detail in section II:

-The role of natural birth rate and natural death rate played in the model,

-The chance of got second infection directly from the infectious group,

-The incubation period of the virus and the possibility of the people in the incubation period transmit infections to the susceptible people.

-A more precise model of Infectious group includes the symptomatic, asymptomatic; severe, mild cases and the super spreader group,

-The possible effect of the vaccine.

By constructing a set of ODEs regarding the features described above, I successfully obtained trend line graphs using Python, which can be used to predict the tendency of Covid-19, and the time

when the number of infectious will reach maximum. And therefore I gave out prevention strategies for the government and public regarding the results of my epidemic model to prevent further spreading of coronavirus.

The paper is organised as follows: Section II is related to the construction of the model and further mathematical development regarding my epidemic model. Section III is presenting the simulation results by solving the equations in Python. Section IV is concerned with some discussions about strategies draw from the results and further development of the model. Conclusion are presented in section V.

II. Methods

A. SIR model and ODE

In this section, let us recall the SIR model and the set of its ordinary differential equations. The construction of ODEs is described as follows: Rate of change = Positive action term - Negative action term i.e,

$$\frac{dx}{dt} = f(x,t) - g(x,t)$$

From there, we can deduce the equations for the three-compartment SIR model:

$$\frac{dS}{dt} = -\beta SI$$

$$\frac{dI}{dt} = \beta SI - \gamma I$$

$$\frac{dR}{dt} = \gamma I \qquad (1)$$

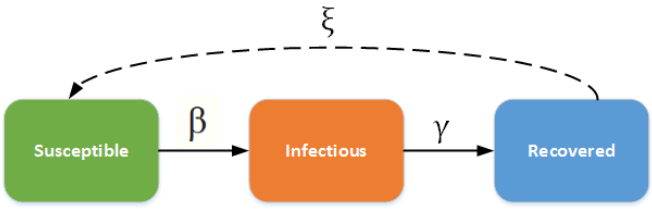

Figure 2.1 (Source: FH Vorarlberg)

where the parameters indicate:
S: the number of susceptible
I: the number of infectious
R: the number of recovered or deceased (or immune) individuals
β: the rate of transmission
γ: the rate of recovery or mortality

From the equations we can deduce the basic reproductive number R_0 which describes the relationship between the number between the rate of transmission and rate of recovery:

$$R_0 = \frac{\beta}{\gamma} \qquad (2)$$

The basic reproductive number is an indicator of the contagiousness of infectious of one single case to the whole population of susceptible. From the equation, we can draw some conclusions about R_0: Higher the basic reproductive number, the faster the epidemic will progress, which also means the smaller the recovery rate γ, the bigger the R_0. The same thing happens when the transmission rate β increase. If the average R_0 in the population is greater than 1, the infection will spread exponentially. On the other hand, the best expectation of the virus is when γ is big while β is small, so R_0 is smaller than 1. As the transmission is slower than the recovery rate, the virus will eventually tend to disappear as every infectious has recovered. (shown in graph 2.2)

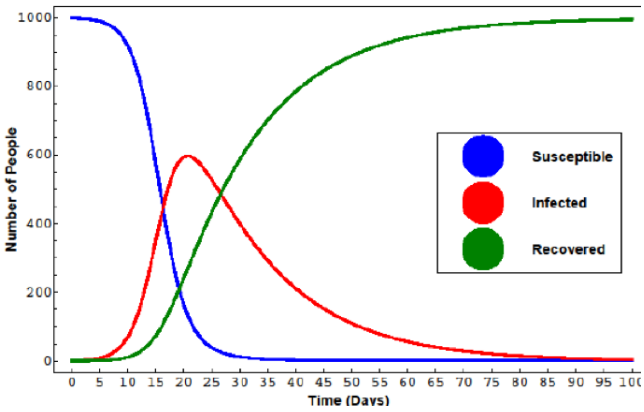

Figure 2.2 (C.M.Macal, To agent-based simulation from System Dynamics, Jan 2011)

Below is a table of the UK R number change from May 2020 to February 2021[2]. We can see from September to November 2020 is the most severe period where the highest R number was reached at around 1.6, which means that, on average, every 10 people infected will transmit virus to almost 16 other people.

Date	UK	
	Lower bound	Upper bound
29-May-20	0.7	0.9
05-Jun-20	0.7	0.9
12-Jun-20	0.7	0.9
19-Jun-20	0.7	0.9
26-Jun-20	0.7	0.9
03-Jul-20	0.7	0.9
10-Jul-20	0.7	0.9
17-Jul-20	0.7	0.9
24-Jul-20	0.7	0.9
31-Jul-20	0.8	0.9
07-Aug-20	0.8	1
14-Aug-20	0.8	1
21-Aug-20	0.9	1.1
28-Aug-20	0.9	1.1
04-Sep-20	0.9	1.1
11-Sep-20	1	1.2
18-Sep-20	1.1	1.4
25-Sep-20	1.2	1.5
02-Oct-20	1.3	1.6
09-Oct-20	1.2	1.5
16-Oct-20	1.3	1.5
23-Oct-20	1.2	1.4
30-Oct-20	1.1	1.3
06-Nov-20	1.1	1.3
13-Nov-20	1	1.2
20-Nov-20	1	1.1
27-Nov-20	0.9	1
04-Dec-20	0.8	1
11-Dec-20	0.9	1
18-Dec-20	1.1	1.2
23-Dec-20	1.1	1.3
08-Jan-21	1	1.4
15-Jan-21	1.2	1.3
22-Jan-21	0.8	1
29-Jan-21	0.7	1.1
05-Feb-21	0.7	1
12-Feb-21	0.7	0.9

Table 2.3

A.1 Modelling SIR model with population change

The premise of the SIR model is assuming the total population is fixed, which is extremely unrealistic for coronavirus where many cases and mutation cases are mainly transported from abroad. Dr. Tom Crawford from Oxford university did a video of constructing a compartment with population change[3], and I think it is significant to mention here. The model itself uses a set of partial differential equations (PDEs), assuming although the Susceptible (S) and the Recovered (R) groups do not move, Infectious group (I) migrated at a random constant rate. I will introduce the derivation of the equations mentioned in Dr. Tom Crawford's video.

Where D is the rate of diffusion in a moving population. The PDEs which allows S, I, and R groups to become dependent on both time t and space x are:

$$\frac{\partial S}{\partial t} = -\beta SI$$

$$\frac{\partial I}{\partial t} = \beta SI - \gamma I + D\frac{\partial^2 I}{\partial x^2}$$

$$\frac{\partial R}{\partial t} = \gamma I \tag{3}$$

Using the method of introducing a new variable y with constant c to make the equations simpler to analyse:

$$y = x - ct \tag{4}$$

From (3) (4) we got:

$$0 = c\frac{dS}{dy} - SI$$

$$0 = \frac{d^2S}{dy^2} + c\frac{dI}{dy} + I(S - \frac{\gamma}{S_0\beta}) \tag{5}$$

Where S_0 is the initial susceptible population.
To find how fast the disease is going to spread, we need to model S = 1 - Q where Q is a small number that changes S over time. Substitutes into (5) using the method of linearisation we get:

$$-c\frac{dQ}{dy} - I = 0$$

$$\frac{d^2S}{dy^2} + c\frac{dI}{dy} + I(S - \frac{\gamma}{S_0\beta}) = 0 \tag{6}$$

Applying phase plane analysis to (6), we can deduce that for the minimal wave speed of transmission to exist, constant $c \geq 2\sqrt{1-\frac{\gamma}{S_0\beta}}$.

Because R_0 is given by β/γ, so c minimum (the lowest transmission rate in Infectious) is given by:

$$c = 2\sqrt{1-\frac{1}{S_0 R_0}} \tag{7}$$

To reach the lowest transmission rate in Infectious, the only way is also minimise R_0. The ways to reduce R_0 are provided in section IV.

B. Constructing SEIRI model

Based on equations of the SIR model, I developed my compartment dynamic model (figure 2. 4) which modified in the manner as introduced in the introduction, where variables and parameters can be found in table 2.5,

$$\frac{dS}{dt} = \mu N - \frac{\beta SI}{N} - vS$$
$$\frac{dE}{dt} = \frac{\beta SI}{N} - \delta E - vE$$
$$\frac{dI}{dt} = \delta E - \gamma I - vI + \alpha R$$
$$\frac{dR}{dt} = \gamma I - vR - \alpha R \tag{8}$$

Parameter	Definition
N	Total population
μ	Nature Birth rate
v	Natural death rate
S	Number of susceptible
E	Number of exposed in incubation period
I	Number of infectious
R	Number of removed
β	Transmission rate
δ	Exposer's infection rate
γ	Recovery rate
α	Second infection rate

Table 2.5 variables and parameters

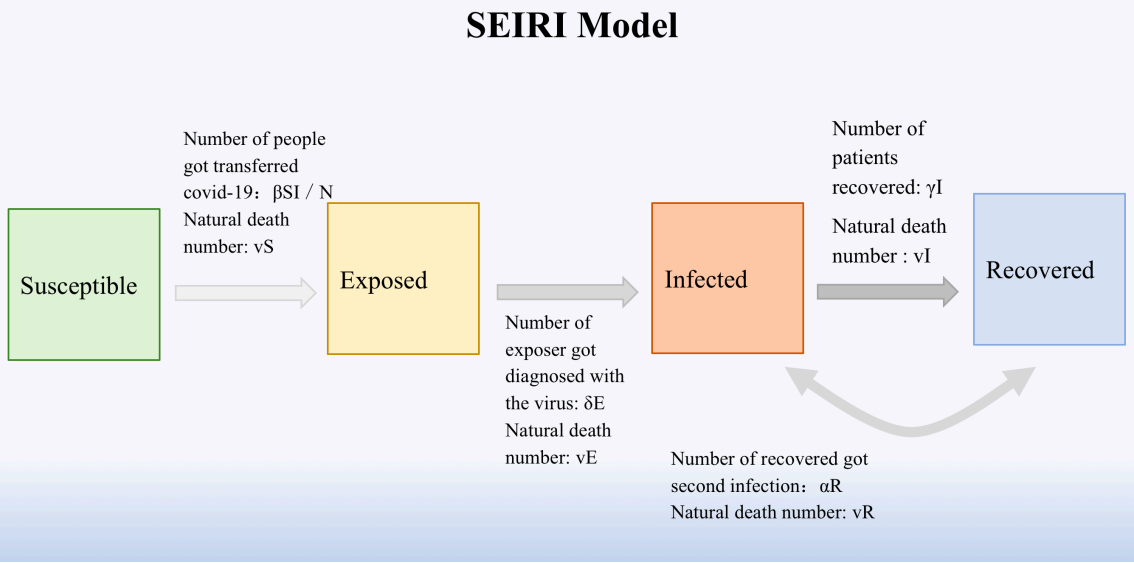

Figure 2.4 SEIRI model

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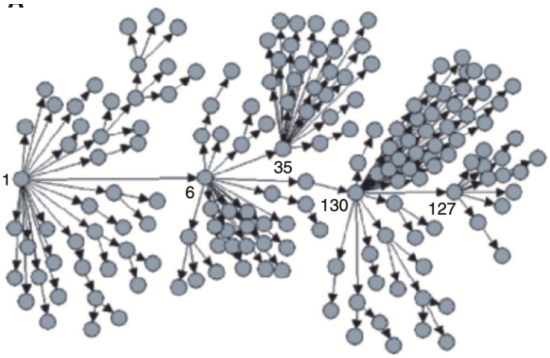
B.1 SEIRI model with specific I stage

In this section, I specify the infectious stage by separating the Infectious group into several compartments to let the model cater to COVID-19 in real-life where the asymptomatic will cause a delay in reporting the number of the infectious when 'coming out of' the Exposed group; the existence of super-spreaders will affect transmission rate (shown in figure 2.6) and therefore have an impact on the R number especially when a super-spreader is an asymptomatic infectious; and identifying between mild and severe cases allow us to have precise prediction and analysis of the recovery rate. I developed this model based on my SEIRI model described in the previous section, which starts from the SEIR model with the asymptomatic compartment to the final one which is consists of eleven compartments (shown from figure 2.8 to 2.11). The infectious model describes the impact of super-spreader and asymptomatic groups; mild and severe cases; and the second infection. New variables and parameters used are introduced in the table on the right.

Premises of this specific infectious model are that I assumed that all symptomatic infections are either mild or severe cases, and all infectious have the possibility of getting a second infection.



[4] Figure 2.6 shows the cluster of a super-spreader is much bigger than a normal infectious, meaning they have the ability of transmitting virus to more susceptible individuals. A example would be in 2020, an Italian marathon runner transmitted the virus to 13 other people (BBC news).

Parameter	Definition
ζ	The possibility of a exposed (E) is a super spreader
ε	Super spreader's transmission rate where ε >> β
η	The possibility of a infectious is symptomatic
θ	The possibility of a infectious is a severe case
μ	The rate of recovery of mild cases
κ	The rate of recovery of severe case where κ<< μ
A	Number of asymptomatics
I'	Number of symptomatics
Su	Number of super-spreaders (infectious)
No	Number of normal spreaders (infectious)
M	Number of mild cases
Se	Number of Severe cases

Table 2.7 new variables and parameters

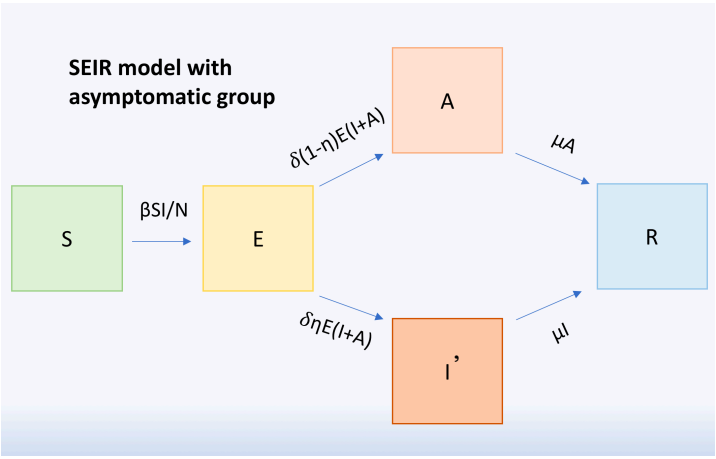


Figure 2.8

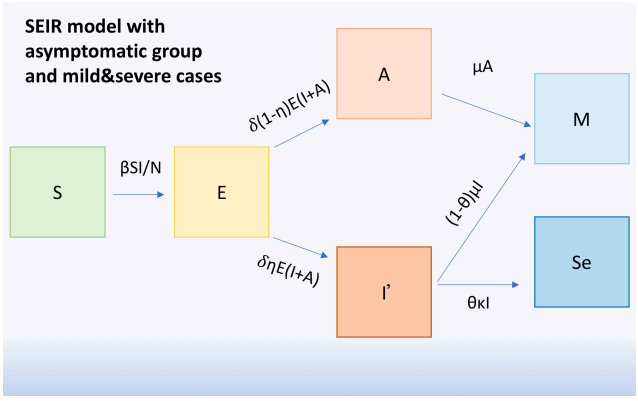


Figure 2.9

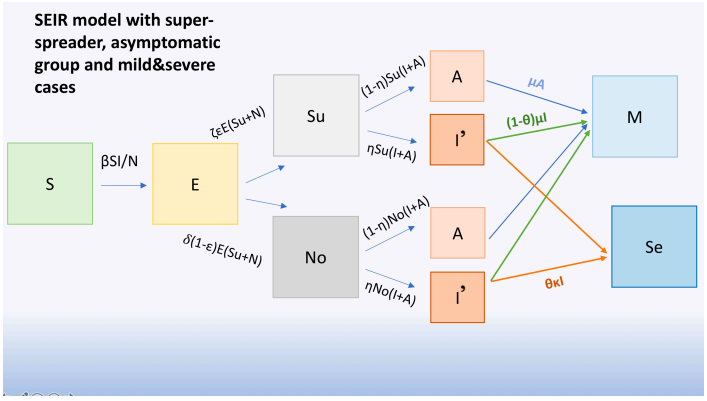


Figure 2.10

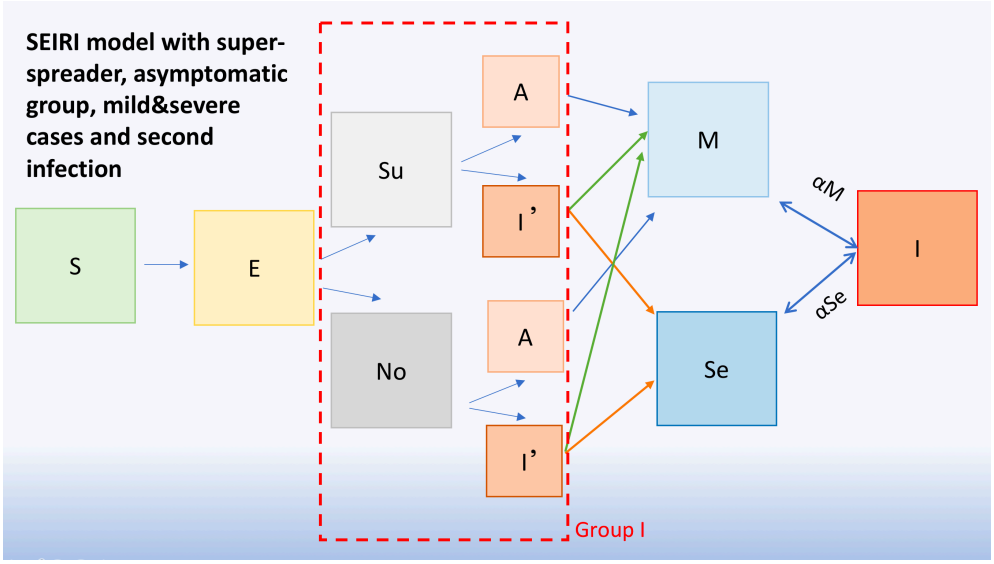


Figure 2.11

Therefore the modified system can be expressed by:

$$\frac{dS}{dt} = \mu N - \frac{\beta SI'}{N} - \nu S$$

$$\frac{dE}{dt} = \frac{\beta SI'}{N} - \zeta\varepsilon E(Su + No) - \delta(1-\varepsilon)E(Su + No) - \nu E$$

$$\frac{dSu}{dt} = \zeta\varepsilon E(Su + No) - \eta Su(I + A) - (1-\eta)Su(I + A) - \nu Su$$

$$\frac{dNo}{dt} = \delta(1-\varepsilon)E(Su + No) - (1-\eta)No(I + A) - \eta No(I + A) - \nu No$$

$$\frac{dA}{dt} = (1-\eta)E(I+A) - \mu A + \alpha M - vA$$

$$\frac{dI}{dt} = \eta E(I+A) - (1-\theta)\mu I - \theta\kappa I + \alpha M + \alpha Se - vI$$

$$\frac{dM}{dt} = 2(1-\theta)\mu I + 2\mu A - \alpha M - vM$$

$$\frac{dSe}{dt} = 2\theta\kappa I - \alpha Se - vSe$$

■

By simplifying, we got:

$$\frac{dS}{dt} = \mu N - \frac{\beta SI'}{N} - vS$$

$$\frac{dE}{dt} = \frac{\beta SI'}{N} - E(Su + No)(\zeta\varepsilon + \delta - \delta\varepsilon) - vE$$

$$\frac{dSu}{dt} = \zeta\varepsilon E(Su + No) - Su(I+A) - vSu$$

$$\frac{dNo}{dt} = \delta(1-\varepsilon)E(Su+No) - No(I+A) - vNo$$

$$\frac{dA}{dt} = (1-\eta)E(I+A) - \mu A + \alpha M - vA$$

$$\frac{dI}{dt} = \eta E(I+A) - (\mu - \theta\mu + \theta\kappa)I + \alpha(M+Se) - vI$$

$$\frac{dM}{dt} = 2\mu(I - \theta I + A) - \alpha M - vM$$

$$\frac{dSe}{dt} = 2\theta\kappa I - \alpha Se - vSe \quad (9)$$

■

C. Vaccination in the model

The UK is the first country to implement vaccinations for everyone. However, coronavirus cases and deaths had still arisen to a peak after one month of the vaccination project. The objective of the model shown in figure 2.12 in this section is to predict the effectiveness of the vaccination and the tendency of COVID-19 with more people being vaccinated over time. To model the vaccination into the compartment model, we need to introduce time dependent equations with the time change.

The number of people vaccinated each day is τ(t), the effectiveness of the vaccination is f where $0 < f \leq 1$.

We have, the first equation in (8) becomes:

$$\frac{dS}{dt} = \mu(t)N - \frac{\beta(t)S(t)I(t)}{N} - v(t)S - f\tau(t), t \geq t_0 \quad (10)$$

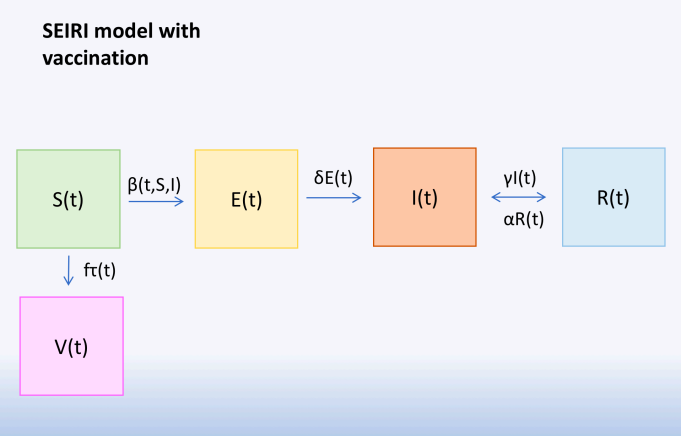


Figure 2.12

III. Results and Analysis

In this section, I will consider the system of (8) which will be solved and demonstrated using Python. The parameter and variable values used are itemised below:

1.Initial population size N_0: 66500000
2.Initial susceptible population S_0: $0.999999N_0$
3.Initial infectious population I_0: 66
4.Initial Exposed and Recovered population E_0, R_0: 0
5.The new birth rate μ: 11.4 per 1000
6.The natural death rate v: 9.3 per 1000
7.Transmission rate β_0: 0.6
8.Infection rate of Exposed δ_0: 0.6
9.Recovery rate γ_0: 0.1
10.Second infection rate α: 0.01
11. Efficiency of the vaccination f: 0.9 [5]

Figure 3.1 to 3.4 below shows a simulation of the spread of the virus over time which I carried out in Python

(code of the full dynamic simulation can be found in the appendix). We can see how an initially all susceptible (blue spots) population, becomes partially exposed (yellow spots) and in which over time will turn into the infectious group (red spots). The number of infectious will keep increasing as the population changes whereas recovery also occurs in the population and eventually all the infectious will turn into the recovery group as time goes by. I did this computational simulation because it makes the process of the virus clearer. However, this simulation is only reliable when we are not considering the second infection or the vaccination and does not tell us any useful information about predicting the trend of the virus.

Figure 3.1, initial condition simulation

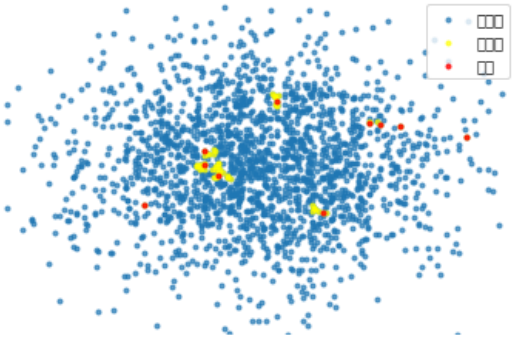


Figure 3.2, appearance of the exposed and therefore infected population

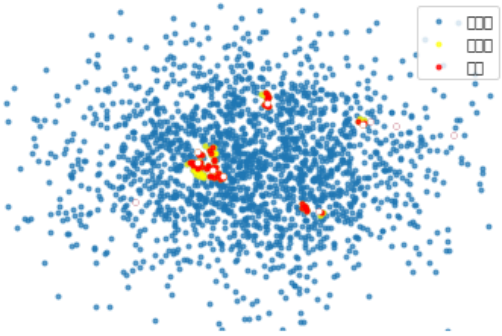


Figure 3.3, the spreading of the virus

Figure 3.4, eventually, every infected individual is recovered

To solve this problem, I compute equation (8) mentioned in Section II to show the results for my mathematical dynamic model. Figure 3.5 below shows my first attempt with the modelling of a purely SEIR model without the consideration of the natural births and deaths, the possibility of a second infection, and the impact of the vaccination. Comparing Figure 3.5 to the existed SIR mode (Figure 2.2), they follow relatively a similar pattern, the number of susceptibles will gradually decrease to 0 while the number of recovery increase. The number of the exposed and infected will first rise to the peak and gradually decrease to 0. However, when we take into consideration of natural birth and death and the chance of a second infection, we get the trend in figure 3.6 where the virus will not disappear but instead decrease to a relatively fixed value at last. Looking at the statistics of COVID-19 spread in China, we can see the epidemic follows a similar path, figure 3.7 shows the active cases cumulation from January 22 to May 25, 2020, where figure 3.8 shows a daily infectious increase from February 2020 to February 7, 2021. Both figures show a similar pattern as predicted in my mathematical model where the peak of the epidemic reached at about 100 days after the first case. After March 2020, the number of infectious started to decrease significantly and maintained a mean daily increase of about 14 cases every day in China now[6].

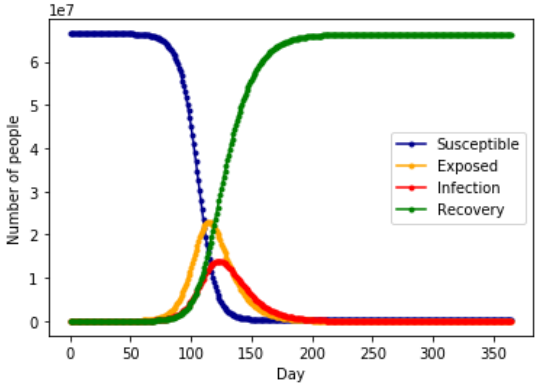


Figure 3.5

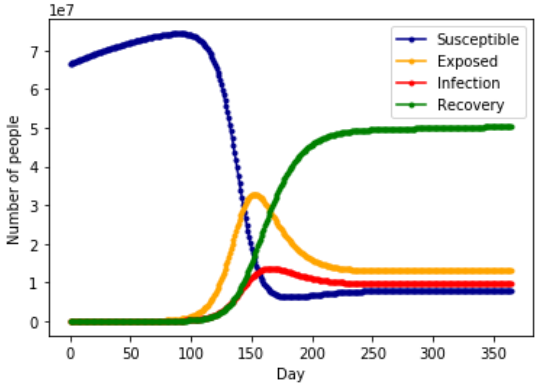


Figure 3.6

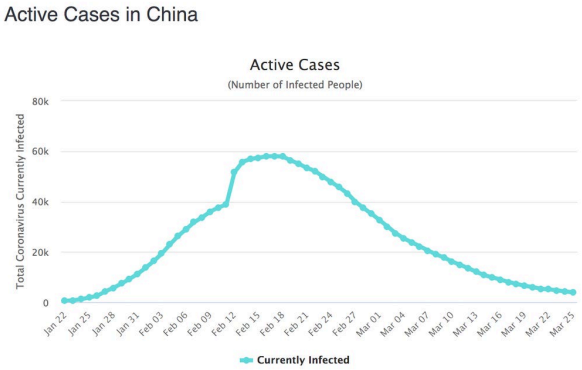


Figure 3.7

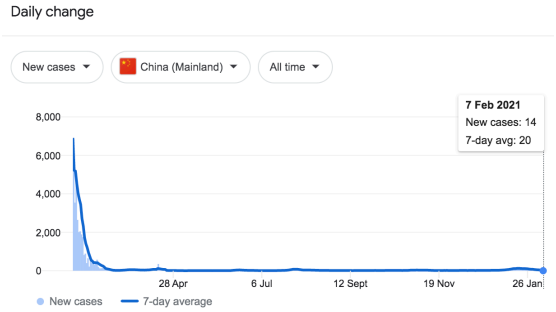


Figure 3.8

When taking vaccination into account, I used the statistics from the UK government as England is the first country to implement a vaccination program and it has been quite successful so far. The United Kingdom began vaccination on December 8 with the Pfizer regime and later with the AstraZeneca vaccine. Since the government suggested that before July 31, all adults in the UK will be vaccinated, which means approximately 80% of the population will become immune and therefore will be subtracted from the S compartment over about 233 days. If assuming the efficiency of the vaccination is 90%, we get the simulation result in figure 3.9. We can see that the impact of efficient vaccination is significant in reducing the number of infectious, which almost halved compared to figure 3.6. However, after a period of time of the epidemic peak, the number of infectious will still stay relatively constant and will decrease again only if everyone is vaccinated.

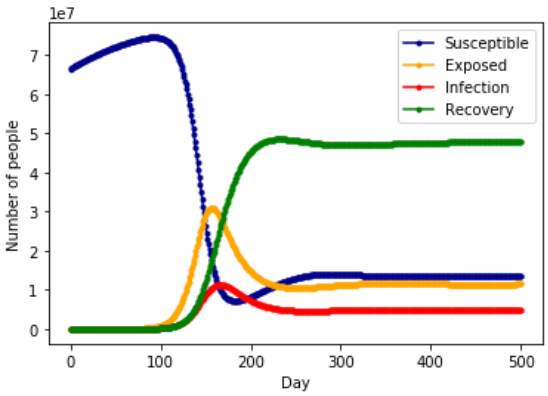


Figure 3.9 demonstrates the simulation of SEIRI model with vaccination modelling. Due to the number of people vaccinated, we can see the number of susceptible decreased rapidly which results in the decrease in the number of infectious. While exposed and recovery line stays at a constant rate. In the modelling, I assumed the number of people being vaccinated everyday is 257000 people (approximately 2 millions of people vaccinated per week [7]).

Overall, this section illustrated and interpreted the results from my SEIRI compartment model. Achieving by this section, we can see how coronavirus evolves with time in a more realistic mathematical model. However, the overall trend of the virus is similar no matter how many new variables (compartments) are taken into account: the number of susceptible and recovered shows a opposite trend, with one tends to 0, the other one will increase to the initial population; the number of exposed and infectious will fist increase to a local maximum and then decrease. We can use these simulation results to estimate the future trend of the virus, the time taken for the epidemic to end, the number of the maximum infectious at a given time, and whether a second peak will come. The model itself is not completely consummate as different assumptions made and different values of the parameter used will give out different

results. However, the aim of mathematical modelling is to apply it to real-life and to optimise current anti-epidemic provisions and strategies. In other words, making this model evolve in the optimal way, which I will discuss in the following section.

IV. Prevention strategy analysis and further development of the model

This section will be consist of the following two parts: the first part is the analysis of the prevention strategy for COVID-19 based on the modelling results, and the second part will be the evaluation and further development of my mathematical model.

A. Prevention strategy analysis

The two significant pieces of information we can derive from figure 3.5, 3.6, and 3.8 are: to optimise the situation of the epidemic, we should either attempt to reduce the crest of the infectious graph, therefore, reducing the number of the maximum infectious, or to delay as much as possible the time which the crest occurs. The reason for the second point is, if the peak occurs at the very start of the epidemic, the government is not prepared, the rapid and vast amount of infectious would consume a large amount of medical resources and therefore when demand exceeds supply, the deterioration of the virus would cause an increase in the number of infected and the death rate. So we need to delay the peak to enable professions to take steps, for example, to find the sources of the virus and therefore produce effective vaccines.

From eq.(7), we see the importance of R_0 in the spreading of the virus, so to reduce the epidemic peak of the COVID-19, public strategies should be mainly focus on reducing the R number. In other words, we need the find valid ways to reduce the transmission rate β and to increase the recovery rate γ. Current provisions such as the enforcement of wearing masks largely decreased the number of infectious as wearing a mask reduces the possibility of potential infectious in a dense population. However, although most countries have the policy of wearing a mask, it is not effective if the mask is not N95 or other respirator masks. In the figure 4.1 below, we can see that normal surgical mask cannot prevent the coronavirus, not to mention that in the UK, most people only wear normal cotton masks and scarfs as face covering. Therefore, in other to reduce the transmission rate to the minimum, promoting citizens to wear proper respirator masks is essential.

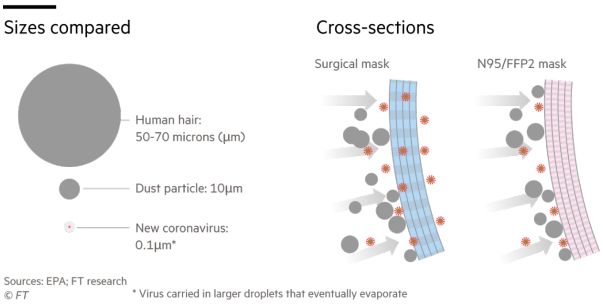


Figure 4.1

The second way to reduce the transmission rate is through effective self-isolation/quarantine periods for the exposed population. The quarantine can diagnose potential infectious or asymptomatic individuals. The UK has have been doing effectively in isolating international travellers, but if the virus gets severe again, stricter regulations like isolation for people commuting from different cities in the UK need to be considered.

To retard the time which an epidemic peak will occur (although it is suggested the peak has already occurred in 2020, it is very likely that under the loosening of the policies and the appearance of various mutations, a second or third epidemic will occur in the future), we need to control or reduce the population in specific regions at a given time, that is, lockdown. From my perspective, regional lockdowns for severely infected areas is more practical and effective than a national lockdown. A whole national lockdown still cannot avoid personnel circulation in a single city and long-term national lockdown would result in an increase in financial deficit and dissatisfaction from citizens. A successful example of effective lockdown is the Wuhan (Hubei province) lockdown in early 2020. Comparing figure 4.2 and figure 4.3, we can find that the number of diagnoses cases is positively correlated with the number of travellers from

Wuhan to other regions of China, which means although the epidemic in Wuhan was severe, the 76-day (just over 2 months) lockdown to a large extent 'saved' other cities and pushed back the peak of the epidemic to a later time when medical resources were relatively sufficient. The implementation of other smaller lockdowns and semi-lockdowns (figure 4.4) had also helped in shortening the time for the epidemic peak.

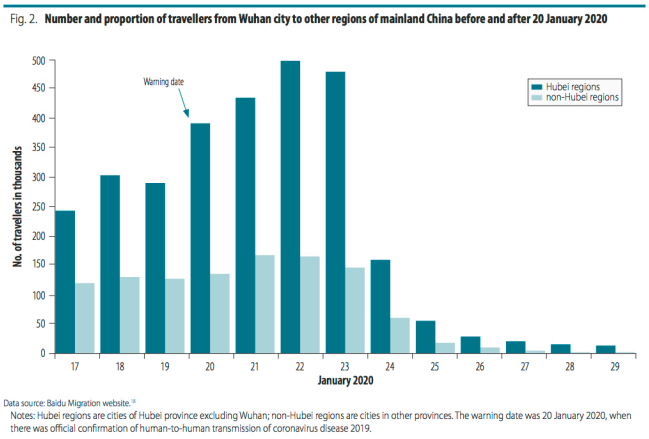


Figure 4.2 shows the proportion of travellers from Wuhan city to other regions of mainland China before and after lockdown in 20 January 2020. We can see the Wuhan lockdown enforcement was very strict and productive. Sources marked on the figure.

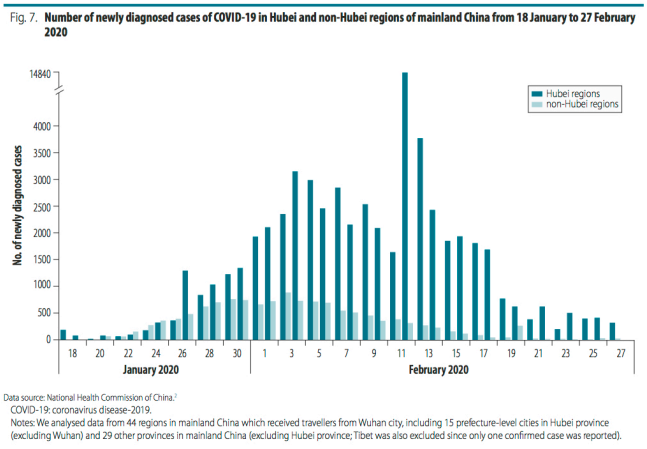


Figure 4.3 shows a comparison between Hubei and non-Hubei newly diagnosed COVID-19 cases from 18 January to 27 February. The number of cases outside Hubei province decreased significantly after the Hubei lockdown on 20 January (the number fist increased can be explained by figure 4.2 as there were still travelers until 28 January and the exposed period can take up to 14 days). [8]

Last but not least, maximising the recovery rate γ is also an indispensable factor in controlling the epidemic. In 2020, there were many shortages of medical resources such as hospital beds and protective suits for doctors. Currently, the global number of infections has decreased compared to

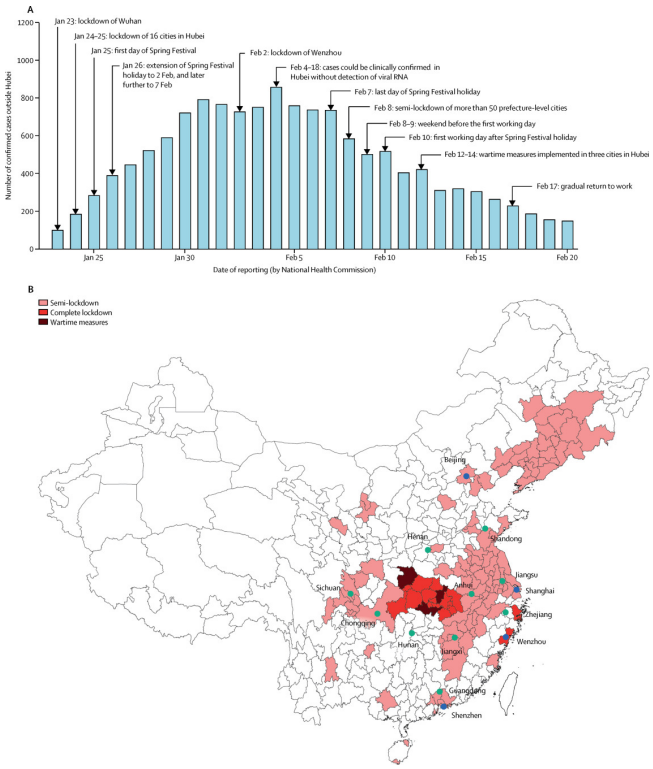


Figure 4.4 shows the relationship between the number of confirmed cases outside Hubei and the lockdown/semi-lockdown. The epidemic in China is relatively tends to end now, looking at the graph, only about 5% of Chinese cities had complete or wartime lockdowns, about 10% had a semi-lockdown, but the epidemic had been controlled successfully. Therefore, a national lockdown might be helpful but not necessary. On the other hand, strictly controlling severe regions is more urgent in order to reduce transmission rate. [9]

last year, however, we should always be prepared for a potential epidemic in the future. The urgent affair for professions and researchers is to identify the characteristics of the various mutations that appeared and their origins, also to increase the efficiency of the vaccinations. The government, on the other hand, should vaccinate as many people as they could and strengthen international cooperations in vaccination and medical resources to remedy the lack of international business due to COVID-19.

Overall, the key to control the epidemic is to control the basic reproductive number R_0 by reducing the transmission rate and increasing the recovery rate, specific strategies suggestions can be seen in this section.

B. Evaluation and further development

In this section, I will evaluate my model mentioned in section II and discuss further development of my compartment model.

Due to time limitation, I did not model eq.(9) in python, which will become an extension when time is allowed.

Besides time shortage, my model has many other aspects which I had not taken into consideration due to the complexity of the mathematical model, but they are essential when modelling the real-life COVID-19. The first one is self-isolation period. As mentioned in section IV.A, self-isolation would affect the transmission rate. As the incubation period is up to 14 days, whether everyone has followed the self-isolation and some patients may have self-recovered in the incubation period need to be taken into consideration.

The second one is that all models' premise is that there is no turnover of personnel. However, a place cannot keep the total population unchanged unless it is a complete lockdown. An overall population circulation should be considered using the population model (i.e logistic growth equation).

The third one is to predict the possibility and size of the second outbreak of coronavirus, we need to introduce delayed differential equations (DDE) into the model. Specifically for coronavirus, a study showed that that every recovered's antibody of the coronavirus may not last forever, which may only last about two to three months[10]. Also under the loosening regulation for quarantine and lockdown, the second outbreak of COVID-19 might be unstoppable.

Last but not least, since the appearance of the mutational COVID-19, we should construct a set of models including the original and the mutation s model, to give out a more complete picture and clearer understanding of coronavirus.

V. Conclusion

In this work, I presented a new mathematical compartment model designed for COVID-19 and suggested some prevention strategies regarding the model simulation and results. My model shows that how a susceptible individual undergoes the process of exposed, infected, and recovered with a chance of a second infection. I had also constructed a more specific model for the infectious group where superspreader, asymptomatic, and mild/severe cases were taken into account. I had also considered the impact of the current vaccination regime on the overall model. This model can be used to predict the future trend of the virus as well as a source from where the prevention strategy could come from. Overall, this paper is devoted to implement the mathematical model into real-life situations to help with analysing coronavirus and provides a way of understanding the basic reproductive number. Future development of this research will be in the area of constructing a more consummate model by considering time and population change and other aspects.

VI. Appendix

The code I wrote for simulation and solving differential equations in Python can be found in the link below:
https://github.com/Stephanieyang0/steph0

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