Plague Inc:
Mathematical Model of Contagions

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1. Abstract

This project is a study about using Mathematical model to simulate the spread of the COVID-19 virus. In our research, we first analyse why we cannot use the existing Mathematical models to simulate the transmission of COVID-19. Then we revise the model based on the biological traits of the virus and related data from authorities. Finally, we use our model to evaluate the effectiveness of different measures to provide an insight of possible ways to fight against the spread of virus.

Some of our objectives are:

1. To find out how COVID-19 spreads.

2. To create a Mathematical model that can simulate the spread of COVID-19.

3. Provide an insight related to the effectiveness of various measures.

Through the research and study conducted, we can give preliminary explanation of how COVID-19 spreads differently from other diseases and what should we revise to set up a proper Mathematical model. Based on our model, we have gathered sufficient evidences to provide the insight related to measures fighting against the transmission of the virus and offer our suggestions to the public and the government in fighting the pandemic.

2. Introduction

2.1 Brief Introduction

Human beings have suffered from contagions since long time ago. From the Black Death in 1346-1353, Spanish Flu in 1918, SARS in 2003, to COVID-19 this year, all these severe contagions caused numerous infected cases and countless deaths all around the world. Why were these contagions able to infect so many people even though we were aware their existence? What measures can be taken to stop the spread of the virus effectively?

This project aims to modify existing Mathematical model related to the spread of various kinds of contagions and create a revised Mathematical model that is proper to be applied for COVID-19 virus specifically to analyse the mechanism of the spread of it. Then, we will try to use the revised Mathematical model to simulate diverse measures that might be taken to fight against the virus and determine their effectiveness.

2.2 Research problems

1. What is the mechanism behind the spread of the COVID-19 virus?

2. How to set up an accurate model that can be applied for COVID-19 specifically?

3. Provide the insight related to the effectiveness of various measures.

2.3 Objectives

1. To find out how COVID-19 spreads.

2. To create a Mathematical model that can simulate the spread of COVID-19.

3. To find effective measures that can prevent the rapid spread of the virus by using the mathematical model.

2.4 Rationales

COVID-19 disease has spread all over the world. Different countries are either experiencing the terrible transmission of the virus among their citizens or have already controlled the situation successfully. However, we notice that the infected cases per day in Singapore at first increased slowly, then rose drastically all of a sudden. Now, the curve of the infected cases per day is flatten gradually. These three periods correspond to three different measures that the Singapore government has taken to prevent the spread of COVID-19. Based on this phenomenon, our group is interested in which measures are effective to fight against the transmission of COVID-19 and hence deciding to research in this area by using Mathematical models.

2.5 Fields of Mathematics

1. Differential equations

2. Functions

3. Statistics

4. Mathematical models

3. Literature Review

3.1 SIR model

Models of disease transmission have been studied from pioneer models of Kermack and McKendrick in 1927. Based on data observed in epidemics such as the Great Plague happened in London in 1665-1666 and cholera happened in London in 1865, a model that assumes that the size of the population is a constant and incubation period does not exist was developed.

This model divides the population into 3 types: The Susceptible, the Infectious, and the Recovered, based on the suggestion that patients are infectious instantaneously after they are infected and recovered patients will never be infected again due to the presence of antibodies.
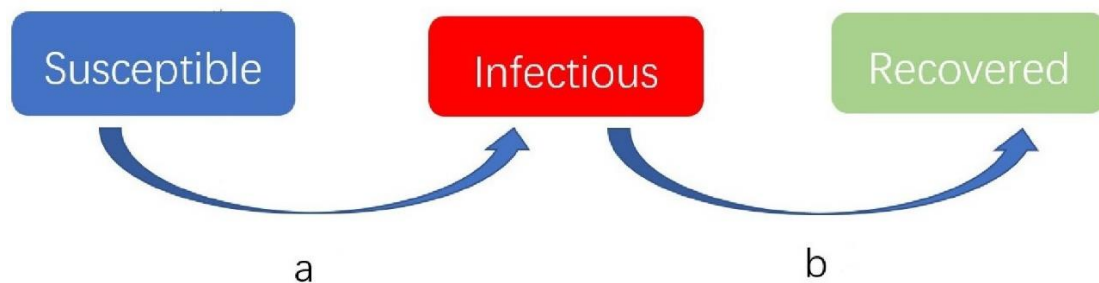

Fig.1 Schematic Diagram of SIR model

We suggest the total population in the area is **P**, which is a constant. We suggest the number of the Susceptible, Infectious and Recovered are **S**, **I** and **R**.

We have **P=S+I+R**.

We have **I** infectious patients, every infectious patient meets **w** people per **t** time, with the possibility of **a** to infect. We suggest the possibility of infectious patients being cured is **b** per **t** time. Since the ratio of the Susceptible to the whole population is $\frac{S}{P}$, we

have the following differential equations:

$$\frac{dS}{dt} = \frac{-waIS}{P}$$

$$\frac{dI}{dt} = \frac{waIS}{P} - bI$$

$$\frac{dR}{dt} = bI$$

The iteration form of these equations is:

$$S_{n+1} = S_n - \frac{waI_nS_n}{P}$$

$$I_{n+1} = I_n + \frac{waI_nS_n}{P} - bI_n$$

$$R_{n+1} = R_n + bI_n$$

This model applies well for diseases without an incubation period like cholera, which provides a basis for the further development of Mathematical models of contagion. However, for contagions with a period of incubation in which patients are infected but not showing symptoms, the assumption of SIR would not simulate the real situation accurately.

3.2 SEIR model

The SEIR model is a modification of the SIR model, which consists of one more group of population E that represents the Exposed.

The model divides the population into 4 types: The Susceptible, the Exposed, the Infectious, and the Recovered, based on the suggestion that a period of time is needed

for an infected patient to show symptoms and have the ability to infect others and recovered patients will never be infected again due to the presence of antibodies.
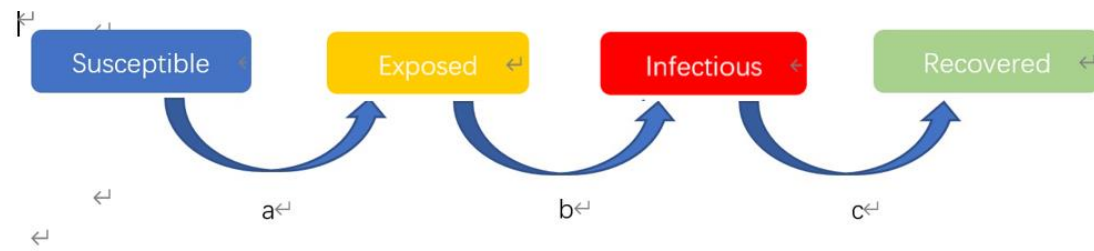

Figure 2 Schematic Diagram of SEIR model

We suggest that the total population in the area is **P**, which is a constant. We suggest the number of the Susceptible, the Exposed, the Infectious and the Recovered are **S**, **E**, **I** and **R**.

We have **P=S+E+I+R**.

We have **I** infectious patients, every infectious patient meets **w** people per **t** time, with the possibility of **a** to infect and the possibility for exposed patients to become infectious ones is **b** per time. We also suggest the possibility of infectious patients being cured is **c** per **t** time. Since the ratio of the Susceptible to the whole population is $\frac{S}{P}$, we have the following differential equations:

$$\frac{dS}{dt} = \frac{-waIS}{P}$$

$$\frac{dE}{dt} = \frac{waIS}{P} - bE$$

$$\frac{dI}{dt} = bE - cI$$

$$\frac{dR}{dt} = cI$$

The iteration form of this equation is:

$$S_{n+1} = S_n - \frac{waI_nS_n}{P}$$

$$E_{n+1} = E_n + \frac{waI_nS_n}{P} - bE_n$$

$$I_{n+1} = I_n + bE_n - cI_n$$

$$R_{n+1} = R_n + cI_n$$

The SEIR model is an accurate simulation of contagions with an incubation period, including AIDS, influenza A and SARS. However, this model simulates the situation where the Exposed are not infectious in incubation period. This may not apply to COVID-19 virus due to the infectibility of its patients in incubation period.

4. Methodology

1. Read up on resources of previous Mathematical models of contagions to understand what the Mathematical mechanism behind the spread of the virus.

2. Explain why previous Mathematical models cannot be applied to COVID-19

3. Analyse data from Singapore and make possible assumptions to create a revised Mathematical model for COVID-19 specifically.

4. Determine the effectiveness of different measures by using the revised Mathematical model and the computer programmes.

5. Use the data we get to tell the public which measure can prevent the transmission of the virus most effectively.

5. Working Progress

5.1 First Stage

After reading enough resources related to the Mathematical model of transmission of the virus and the traits of COVID-19, we realised that simple Mathematical models cannot be directly used.

Most contagions have the following processes of infection: Either Susceptible-Infectious-Recovered or Susceptible-Exposed-Infectious-Recovered. The mechanisms behind these two kinds processes are explained in the Literature Review part, corresponding to SIR model and SEIR model respectively.

Nevertheless, COVID-19 virus does not belong to these two categories of contagions. Different from the other coronavirus SARS, COVID-19 virus presents the infectivity during the period of incubation when patients present no symptoms.

Hence, we need to create a revised Mathematical model that considers this characteristic of COVID-19. We would use a different four-stage-process: Susceptible-Incubated-Infectants-Recovered. In this case, the new patients in the incubation period are able to infect the Susceptible.
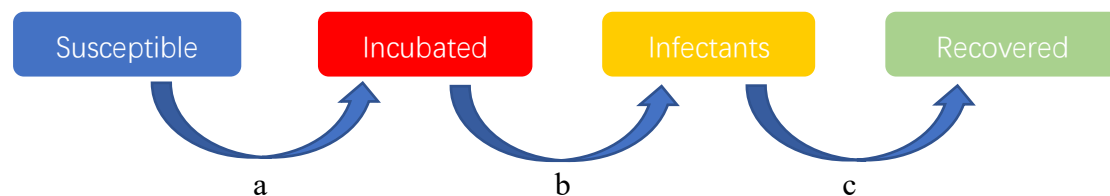

Fig.3 Schematic Diagram of the revised SEIR model

We suggest the total population in the area is **P**, which is a constant. We suggest the number of the Susceptible, Incubated, Infectants and Recovered are **S**, **I**, **F** and **R**.

We have **P=S+I+F+R**.

We have **I** patients in the incubation period, every patient meets **w** people per **t** time, with the possibility of a_1 to infect and the possibility for them to become the exposed is **b** per time. We have **F** exposed patients, every patient meets **k** people per **t** time, with the possibility of a_2 to infect. The possibility of them to be discovered and isolated is **c** per **t** time. Since the ratio of the Susceptible to the whole population is $\frac{S}{P}$, we have the following differential equation:

$$\frac{dS}{dt} = \frac{-wa_1IS}{P} - \frac{ka_2FS}{P}$$

$$\frac{dI}{dt} = \frac{wa_1IS}{P} + \frac{ka_2FS}{P} - bI$$

$$\frac{dF}{dt} = bI - cF$$

$$\frac{dR}{dt} = cF$$

The iteration form of this equation is:

$$S_{n+1} = S_n - \frac{wa_1I_nS_n}{P} - \frac{ka_2F_nS_n}{P}$$

$$I_{n+1} = I_n + \frac{wa_1I_nS_n}{P} + \frac{ka_2F_nS_n}{P} - bI_n$$

$$F_{n+1} = F_n + bI_n - cI_n$$

$$R_{n+1} = R_n + cI_n$$

5.2 Second Stage

Based on the characteristics of COVID-19 and simple concepts of the contagions,

we created a revised Mathematical model for COVID-19 specifically. In the above

equations, the total population **P** is a constant that can be easily obtained, while **w, k,**

$\boldsymbol{a_1}$, $\boldsymbol{a_2}$, **b, c** are constants that need to be calculated. Thus, our next step is to try to find

the constants of these equations as well as further revise the model via two means: Real

data of the history pandemic in Singapore and scientific studies of the COVID-19 virus.

5.2.1 The value of b

First, we study the length of the incubation period of COVID-19 virus in order to

find the value of **b**. As WHO and Chinese scholars have published: The average

incubation period of COVID-19 virus is 5 to 6 days while the mean incubation period

is 5.2 days, with the 95th percentile of the distribution at 12.5 days. Meanwhile, special

cases with 24-day-long incubation periods had also been reported.

Since the records of incubation period were to days, we set **t** as 1 day (24 hours).

We have the equation that given 1 patient being just infected, the possibility of turning

to be "infectants" from "incubated" on a certain day is $\boldsymbol{b(1-b)^{t-1}}$, where **t** denotes

the number of days passed. Hence, we have:

$$\sum_{t=1}^{24} b(1-b)^{t-1} t = 5$$

$$1 - (1-b)^{12.5} = 0.95$$

From second equation, we have b=0.213.

Substitute b=0.213 into the first equation, we have 4.603 on the left-hand side.

This is acceptable as 4.603 is close to 5.

We also examine the value of $(1-b)^{24}$, which is the possibility of the incubation

period that is longer than 24 days, we have:

$$(1 - 0.213)^{24} = 0.003187$$

This value is small enough to be neglected. Hence, it is applicable for us to set the value of **b** per day to be 0.213.

5.2.2 The value of a_1 and w

We use the basic reproduction number of COVID-19 virus to estimate its rate of transmission.

In epidemiology, the basic reproduction number, denoted by R_0, of a contagion can be considered as the expected number of cases directly generated by one case in a population where all individuals are susceptible to infection.

As we aim to set up a time-based dynamic model, we would calculate the average number of infections per patient per day, which is denoted by $\frac{S_n a_1 w}{P}$. Since the percentile of patients in the population is extremely low and the change of S_n is neglectable, we ignore the influence of change of S_n and consider it as a constant.

Based on different studies, the basic reproduction number of COVID-19 varies from 2.2 according to the Chinese scholars to an average of 5.7 according to USACDC. As the latter is more recent and applicable, we take R_0 as 5.7.

Since we assume the possibility for an infectant to infect the Susceptible is equal for every day before isolation, the number of cases directly generated by one case is evenly distributed in every day. Since the definition of basic reproduction number is under the absence of "any deliberate intervention in disease transmission", we shall

consider the expected number of cases in the natural term of infection, which is 3 weeks.

As such, the average number of infection one patient causes in one day is $\frac{5.7}{21} =$ 0.271.

Hence, we consider $\frac{S_n a_1 w}{P}$ as 0.271.

5.2.3 The value of a_2 and k

To simplify the model, we consider $a_2 = k = 0$ in this stage. Due to the education to the public from the Singapore government, this assumption is highly applicable in Singapore's case as after the patients become symptomatic, they would avoid contact with others until being cured. Hence, we may ignore the infection from infectants who are not in the incubation period temporarily. However, we will discard this assumption when we evaluate the effectiveness of various measures of preventing the spread of virus later.

5.2.4 The value of P

Since all Singapore's population reside in the limited area without the personnel flow after the transmission of the virus, we take the population of Singapore as 5,639,000. Hence, we have **P** = 5,639,000.

5.2.5 The modification of the model

Take the values of the constants, we have the following sets of equation:

$$S_{n+1} = S_n - 0.271 I_n$$

$$I_{n+1} = I_n + 0.271I_n - 0.213I_n$$

$$F_{n+1} = F_n + 0.213I_n - cI_n$$

$$R_{n+1} = R_n + cI_n$$

Since we assume the infectants who are symptomatic would not go out and infect others, we may simplify the model by considering **F** and **R** as one category, denoted by **K**. Hence, we have:

$$K = F + R$$

$$K_{n+1} = F_{n+1} + R_{n+1} = K_n + 0.213I_n$$

The final sets of equation would be:

$$S_{n+1} = S_n - 0.271I_n$$

$$I_{n+1} = I_n + 0.271I_n - 0.213I_n$$

$$K_{n+1} = K_n + 0.213I_n$$

5.2.6 Verifying the reliability of the model

We use the real data of the pandemic in Singapore to verify the reliability of the model.

We chose Singapore because of the distribution of Singapore's population firstly. Since all Singapore's population reside in the same limited area without natural boundaries, all citizens could be regarded as one whole population with the same condition of disease transmission, which correspond to our assumption. In big countries like China and America, the boundaries between provinces or states would prevent the

travelling and divide citizens into different populations.

Secondly, when COVID-19 virus started to spread in Singapore, this contagion has been studied considerably well. This resulted in the Singaporean government and society to be highly alarmed about this pandemic. Patients with symptoms would hardly contact other people due to the timely safety measures. This corresponds to the assumption we made that $a_2 = k = 0$.

To verify the model, we first set $I_0 = 1$, which represents the first case in Singapore.

Using C++ language to calculate the value of I_n and K_n, we list some of the output here:

$$I_{30} = 5; \ K_{30} = 15$$
$$I_{60} = 28; \ K_{60} = 99$$
$$I_{75} = 65; \ K_{75} = 234$$
$$I_{90} = 151; \ K_{90} = 551$$

While the real data are:

$$K_{30} = 88$$
$$K_{60} = 1132$$
$$K_{75} = 6498$$
$$K_{90} = 18732$$

Compare the data produced by our model to real data in Singapore, we found that the rate of transmission is much faster in real situation.

This is probably because the imported cases greatly increase the number of

infectants during the early stage of pandemic. To reexamine our model, we would add a "input case variable", denoted by I_i, which represents the average number of import cases in Singapore per day.

Then, we calculated the value of I_i. According to MOH, the total number of import cases till 26 July, 2020 is 673. Noted that some people are tested positive and immediately isolated after arriving in Singapore without any possibility to infect others, we can deduce that the total number of I_i is much less than 673.

Meanwhile, in the first two months of the pandemic, the measure of quarantine was not taken by the government. Hence, the influence of the imported cases should only be counted in these 60 days.

Hence, we have these new sets of equation:

$$S_{n+1} = S_n - 0.271I_n$$
$$I_{n+1} = I_n + 0.271I_n - 0.213I_n + I_i$$
$$K_{n+1} = K_n + 0.213I_n$$
$$(n \leq 60)$$

$$S_{n+1} = S_n - 0.271I_n$$
$$I_{n+1} = I_n + 0.271I_n - 0.213I_n$$
$$K_{n+1} = K_n + 0.213I_n$$
$$(n > 60)$$

After repetitive experiments, we decide to set I_i as 1.6, which provided the closest simulation to the real situation.

Here is part of the data we obtained from the revised model:

$$I_{30} = 119;\ K_{30} = 263$$

$$I_{60} = 768;\ K_{60} = 2471$$

$$I_{75} = 1695;\ K_{75} = 5868$$

$$I_{90} = 4177;\ K_{90} = 14985$$

Graph of no. of infectants confirmed and discharged per day
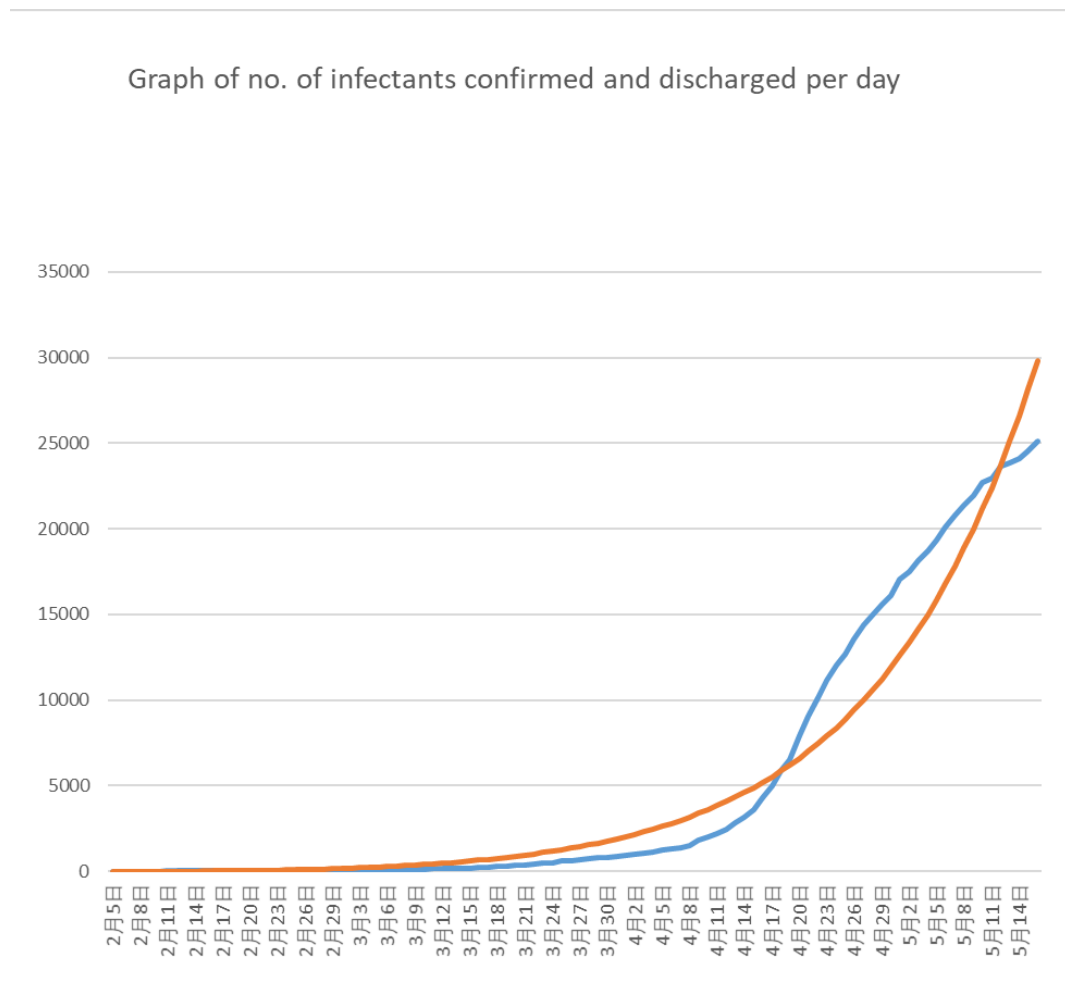
Fig.4 Comparison Diagram between the real data and simulated data

(The blue curve represents the real data; the orange curve represents the simulated data.)

We notice that in the early period of pandemic, due to the deficiency of medial

resources, it is difficult to test every suspected case immediately. Hence, the number of reported cases was less than the actual number of cases. In comparison, in the late period of the pandemic after March, various measures have been taken in the country and the transmission of the virus was slowed down. In the model, however, we did not take the measures into account, causing the curve of simulated data to exceed real data again in the end.

Hence, we set the model as:

$$S_{n+1} = S_n - 0.271I_n$$

$$I_{n+1} = I_n + 0.271I_n - 0.213I_n + 1.6$$

$$K_{n+1} = K_n + 0.213I_n$$

$$(n \le 60)$$

$$S_{n+1} = S_n - 0.271I_n$$

$$I_{n+1} = I_n + 0.271I_n - 0.213I_n$$

$$K_{n+1} = K_n + 0.213I_n$$

$$(n > 60)$$

This is our final Mathematical model to simulate the spread of COVID-19.

As the model provides a rough estimation to the increasing number of cases in Singapore, we might look at the estimated result if no measure was taken in the country. After 150 days' free transmission, the total number of cases K_{150} in Singapore will be 426,734, which is 7.6% of Singapore's total population.

However, because of the presence of diverse effective measures that have been taken in the country for the past few months, the transmission of COVID-19 virus has

been successfully inhibited. The accumulative number of cases to 31 July, 2020 is 51,782 including 5,474 active cases.

5.3 Third Stage

As different measures have played a significant role in fighting against the transmission of COVID-19 virus, we will aim to analyse the effectiveness of different measures that were taken, not taken or possibly be taken in Singapore in the next section. Three main measures are evaluated: Education of COVID-19, isolating patient-related individuals and total ban of going out.

5.3.1 Education of COVID-19

As a current measure, the education of the infectivity of COVID-19 to the public results in the patients to isolate themselves or seek for treatment immediately when they have symptoms after the incubation period. This allows us to consider k, the number of people that patients after incubation period meet as 0. However, this circumstance is not always applicable in other countries around the world, such as America where a number of citizens are not convinced of the seriousness of COVID-19 virus.

What would the situation be like in Singapore if this measure was not taken at the first place? We would reuse the discarded assumption that infectants who are symptomatic would contact with others and cause infection. Since we assume that the possibility of infecting others is the same throughout the 3 weeks of infection, we may simply "extend" the incubation period to simulate the situation that patients with

symptoms would not isolate themselves until treatment.

We add 3, 5 and 7 days to the incubation period which represents patients would

seek for treatment after 3, 5 and 7 days once symptoms appear respectively.

In this case, the model is:

$$S_{n+1} = S_n - 0.271I_n$$

$$I_{n+1} = I_n + 0.271I_n + 1.6 - 0.213I_{n-q} \quad (q = 3, 5, 7)$$

$$K_{n+1} = K_n + 0.213I_n$$

$$(n \leq 60)$$

$$S_{n+1} = S_n - 0.271I_n$$

$$I_{n+1} = I_n + 0.271I_n - 0.213I_{n-q} \quad (q = 3, 5, 7)$$

$$K_{n+1} = K_n + 0.213I_n$$

$$(n > 60)$$

The following is part of the simulated data:

When q=3:

$$I_{30} = 608; \ K_{30} = 927$$

$$I_{45} = 3402; \ K_{60} = 5892$$

$$I_{60} = 18489; \ K_{60} = 32763$$

$$I_{90} = 539095; \ K_{90} = 964798$$

When q=5:

$$I_{30} = 1848; \ K_{30} = 2095$$

$$I_{45} = 21447; \; K_{60} = 25659$$

$$I_{60} = 245915; \; K_{60} = 296452$$

When q=7:

$$I_{30} = 3595; \; K_{30} = 3417$$

$$I_{45} = 69017; \; K_{60} = 67496$$

The results showcase an extremely rapid rate of transmission when the reaction time increases from 3 days to 7 days. When the reaction time is 3 days, the transmission of the virus would reach the uncontrollable stage within 3 months; when the reaction time is 5 days or longer, this disastrous situation would come much earlier.

Not surprisingly, we recognise the importance of the knowledge about the danger of COVID-19 virus and the social responsibility to avoid contact after the presence of symptoms.

5.3.2 Isolating patient-related individuals

Contact tracing and isolating individuals who contacted with confirmed cases in the last 14 days is one of the most significant measures that Singaporean government is conducting to stop the transmission of the virus with the smallest price.

For this measure, we assume once an infectant is identified, all individuals who have contacted with him or her would be immediately isolated, which means all cases directly caused by one case would be unable to infect other individuals the moment the

previous case is identified.

First, we would use our original model to simulate this situation. As our model could not count cases separately based on their related cases, we would use the expected number of potential infectants being isolated by contact tracing after one patient is identified.

The expected number of patients caused by one case could be estimated as:

$S_n a_1 w \times$ average length of incubation period $= 0.271 \times 4.603 \approx 1.247$

In this case, the new sets of equation are:

$$S_{n+1} = S_n - 0.271 I_n$$
$$I_{n+1} = I_n + 0.271 I_n - (0.213 \times 2.247) I_n$$
$$K_{n+1} = K_n + (0.213 \times 2.247) I_n$$

We set the initial number of infectants $I_0 = 10000$. The following are part of the output:

$$I_5 = 3942; \ K_5 = 65563$$
$$I_{10} = 1232; \ K_{30} = 94902$$
$$I_{15} = 385; \ K_{15} = 104067$$
$$I_{46} = 0$$

From the results, we could see that an immediate contact tracing and isolating patient-related individuals can effectively decrease the number of cases in the pandemic. However, the assumption we made is highly ideal because we set the responding

time as 0. In real life condition, making diagnosis and tracing contacts would necessarily take time. In this circumstance, the effectiveness of contact tracing would somewhat decrease.

5.3.3 Circuit Breaker measures

For total ban of going out, the rate of infection would drop to 0, as no individual is allowed to go out and contact with others.

We set the initial number of infectants I_0= 10000. The following are part of the output:

$$I_5 = 3836; \ K_5 = 6164$$
$$I_{10} = 1158; \ K_{10} = 8842$$
$$I_{15} = 350; \ K_{15} = 9650$$
$$I_{38} = 1$$

From the results, it is obvious that the total ban of going out can wipe out all cases more rapidly than any other method. However, recognising the huge side effect of this measure on economy and society, we advise the government to think carefully before taking this measure. Comparing the effect of this measure to contact tracing, we find that a rapid-responding contact tracing is nearly as effective as the total ban of going out with less negativities.

6. Conclusions

In this research paper, we explored the possibility of using Mathematical model to

simulate and predict the transmission of COVID-19 virus, as well as to determine the effectiveness of various measures of fighting against the pandemic.

For how COVID-19 virus spreads, given the fact that COVID-19 virus presents the infectivity during the period of incubation when patients are asymptotic, the SEIR model cannot be used to simulate the transmission of COVID-19 directly. Hence, we aim to set up a revised Mathematical model to simulate the spread of the COVID-19 virus.

For how to create this revised Mathematical model for COVID-19, we firstly modify the SEIR model. Then we use data from authorities to determine the constants in this model. Finally, we use real data from Singapore to further improve the accuracy of the model.

For determining the effectiveness of measures fighting against the transmission of COVID-19, we find that it is crucial for government to educate citizens so that they are fully aware of the infectivity of COVID-19. For the possible measures, total ban of going out would be the most effective method. Nevertheless, a fast-responding contact tracing system could stop the transmission of the virus with similar effectiveness but less negative impacts on the economy and society. Hence, we would like to offer our suggestion to the governments to adopt an efficient contact tracing system if possible, to overcome the challenge with the least cost.

The battle between human beings and the contagions would be everlasting. We hope that our research may help people to have an insight on contagions and the effectiveness of different measures to fight against them. We hope that human beings

will always be the winner of the battle.

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