# **Mathematical modelling of SARS-CoV-2 (coronavirus) Epidemic in South Korea**

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# Content



## <span id="page-2-0"></span>1. Introduction and Research Question

Not only was I infected by SARS-CoV-2 (Covid-19) three times, as a high school student, there were instances where my life seemed to revolve around the coronavirus and the global pandemic. The school was closed for months. Online classes replaced physical learning, and I could only see my friends through the small laptop screen rather than meeting them in person. Moreover, when my family traveled to South Korea during the 2021 summer, we had to stay in a strict quarantine for 14 days and receive mandatory vaccine. My personal experience with coronavirus and its impact to my upbringing has ever since established a lasting interest in the field of epidemiology. Questions like how effective vaccines were in decreasing the rate of transmission of coronavirus still permeate my thoughts when I reflect upon the strict enforcement of vaccination programs in South Korea. Consequently, when I recently encountered a video about the SIR (Susceptible, Infected, and Recovered) model – the most widely used model to simulate an epidemic with a set of differential equations – I was inspired to apply my mathematical knowledge to model the spread of coronavirus in South Korea. I also wanted to use my mathematical model to determine how big of a difference would vaccination have had on reducing the spread of the coronavirus infection in the overall population.

Hence, to explore mathematics behind the spread of coronavirus, this exploration has made the following research question: *"How can a system of differential equations be used to model the coronavirus epidemic in South Korea and the effectiveness of vaccination in reducing the rate of transmission?"*

To answer my research question, I aim to achieve the following goals:

- In the first part of my exploration, I will develop a realistic model for the spread of coronavirus in South Korea. This model will account for distinctive characteristics of coronavirus, including its incubation period, asymptomatic transmission, asymptomatic recovery, and reinfection. To achieve this, I will utilize Euler's method to find numerical solutions to a system of first-order differential equations.
- In the second part of my exploration, I will quantify the efficacy of vaccination in reducing the spread of coronavirus. To achieve this, I will compare the maximum number of infected population and the maximum rate of increase in the infected population during the successive waves of coronavirus outbreak between populations undergoing vaccination and those not undergoing vaccination.

## <span id="page-3-0"></span>2. Background Information and Methodology

As one of the most densely populated country, South Korea was hit hard during the initial spread of SARS-CoV-2 (commonly referred to as coronavirus or Covid-19). Without any vaccine to mitigate the spread of the disease, South Korea initially showed an extreme growth in the number of infected populations (Jeong, 2020). However, its rigorous vaccination program that has started 387 days after the initially confirmed covid case has enabled the country to minimize further spread of the virus and bring the epidemic to its halt (Na, 2023) (Han-joo, 2021). In total, only 0.1% of South Korea's infected population has died from covid, a tenfold lower mortality rate than the global average of 1% (Worldometer, 2024) (Worldometer, 2024). However, would not have coronavirus eventually 'died out' as more people got infected and developed natural immunity against the virus? How significant was vaccination in reducing the number of infected population and decreasing the severity of successive waves of coronavirus? Though there are a variety of factors, such as but not limited to, socioeconomic and political factors that come into play, this exploration will not consider them when modelling the spread of coronavirus in South Korea owing to the sheer complexity in coronavirus's epidemiology.

Before beginning, the epidemiological model that will be developed in this exploration will be grounded upon a set of foundational assumptions. These assumptions and generalizations are needed as the spread of coronavirus in reality is far more complex and influenced even by decisions made at the individual level:

- 1. The entirety of South Korea's population is susceptible to coronavirus. Everyone, regardless of age, gender, health conditions, and lifestyle will have the equal chance of being infected by the virus without any prior immunity against the virus.
- 2. The South Korea's population is distributed with equal population density. In reality, the transmission rate differs by locations since there is more contacts between individuals living in densely populated cities such as Seoul, which contains about 20% of the country's population while covering 0.28% of its landmass, than in rural areas (SEOUL SOLUTION, 2023). However, for the sake of simplicity, this investigation will assume that South Korea's population is distributed homogenously.
- 3. South Korea's total population is constant at 50 million throughout the epidemic and its vital dynamics – the birth and death rates – will be ignored.
- 4. Coronavirus produces identical effect on all infected individuals. This means that the severity and duration of infection, which usually depends on the patient's age and prior health conditions, will be assumed identical.
- 5. There are no external measures such as quarantine and hospitalization being performed to reduce the spread of coronavirus. No preventative measures other than vaccination will be considered in virus transmission to isolate the effectiveness of vaccine.
- 6. Lastly, all parameters concerning the spread of coronavirus will remain constant throughout the epidemic, such as its contractibility and the duration of the disease, unlike in reality where parameters constantly change as the virus mutates.

## <span id="page-4-0"></span>3. Creating a Model for the Spread of Coronavirus in South Korea

#### <span id="page-4-1"></span>3.1 The SIR Model

#### <span id="page-4-2"></span>3.1.1 Introduction to the SIR model

SIR consists of a system of three differential equations that models an epidemic by considering three functions: the susceptible, infected, and recovered population with respect to time. The susceptible population,  $S(t)$ , represents the fraction of South Korea's population that can contract the disease in respect to time t. For instance,  $S(t) = 0.5$  means that 50% of South Korea's population (25 million), is in the susceptible category capable of becoming infected. The infected population,  $I(t)$ , represents the proportion of South Korea's population who have contracted coronavirus and can spread the disease to individuals in the susceptible group. In SIR model, individuals can only leave the infected population by recovering, which is modelled by the recovered population  $R(t)$  that represents the fraction of South Korea's population who have recovered.

The SIR model is defined as the following (Mathematical Association of America, 2024):

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

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

$$
\frac{dR}{dt} = \gamma I
$$

These systems of differential equations show the relationship between the susceptible  $(S)$ , infected  $(I)$ , and recovered  $(R)$  population during an epidemic based on the rate of change of the susceptible population  $\left(\frac{dS}{dt}\right)$ , infected population  $\left(\frac{dI}{dt}\right)$ , and recovered population  $\left(\frac{dR}{dt}\right)$ .

Since South Korea's total population is assumed constant, the rate of change of the susceptible population  $S(t)$ , which is denoted as S, is dependent on one factor – the number of individuals becoming infected every day. For a coronavirus to spread, interaction between the susceptible and infected population is necessary. However, not every encounter between a susceptible and infected individuals results in transmission. Depending on how easily a virus spreads, which is represented by the contractability constant  $\beta$ , the proportion of interaction between the infected and the susceptible population that results in virus transmission varies. For instance,  $\beta = 0.1$ indicates that an infected person will transmit his/her disease to one in every ten susceptible individuals that he/she encounters on average. Consequently, the higher the value of β, the faster the disease spreads from the infected to the susceptible. As the contractability constant  $\beta$ , the susceptible population, and the infected population are always positive, a minus sign is required to indicate how the susceptible population always decreases throughout an epidemic. Hence, the rate of change of the susceptible population dependent on the contractibility and the amount of interaction between the susceptible and infected population can be expressed as:

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

The rate of change of the infected population is dependent on two factors – the number of individuals becoming infected and recovering. The number of individuals becoming infected every day is equivalent to the number of susceptible that decreases every day, which has been defined as  $\beta SI$ . The decrease in the number of infected individuals, however, depends on how many individuals become recovered. Consequently, a new parameter  $\gamma$  must be introduced to represent the proportion of the infected population recovering every day. For instance,  $v = 0.2$ indicates that 20% of the existing infected population will recover every day. Consequently, with  $\gamma I$  representing the proportion of infected that is transferred to the recovered population every day, the overall rate of change of the infected population can be expressed as the sum of the rate of influx of infected patients from susceptible group  $(\beta S I)$  and the rate of outflux of infected patients to the recovered group  $(-\gamma I)$ :

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

Since  $\gamma$  is related to the speed of recovery, it is also worth noting that  $\gamma$  is roughly the reciprocal of the number of days the infection lasts (Mathematical Association of America, n.d.). Consequently,  $\frac{1}{\gamma}$  indicates the duration of the disease, where the lower the value of  $\gamma$ , the longer the disease lasts. For  $\gamma = 0.2$ , the disease would last 5 days.

Lastly, the rate of change of the recovered population is dependent on only one factor – the proportion of the infected population recovering every day, which has been defined as  $\gamma I$ . As SIR model assumes that a recovered individual is immune to the virus, the recovered population will only increase throughout the epidemic and can be expressed as:

$$
\frac{dR}{dt} = \gamma I
$$

#### <span id="page-6-0"></span>3.1.2 Determining constants  $β$ ,  $γ$ , and  $$

To determine the constants  $\beta$  and  $\gamma$ , there is another epidemiological constant that must be defined – the R naught value  $(c)$ . The R-naught value, otherwise known as the contact number, is a parameter for approximating the average number of susceptible individuals that one infected person transmits the virus to before recovering. For instance, a R-naught value of 3 means that one infected person will on average transmit the disease to three susceptible individuals before recovering.

Since  $\beta$  represents the contractability – the proportion of contact between the susceptible and the infected that results in transmission – and  $\frac{1}{\gamma}$  represents the duration of the disease, the Rnaught value for coronavirus epidemic in South Korea's susceptible population can be obtained by finding the product of contractibility, duration of the disease, and the susceptible population as shown in the following equation (Mathematical Association of America, n.d.):

$$
c = \beta \times \frac{1}{\gamma} \times S
$$

$$
c = \frac{\beta S}{\gamma}
$$

But since we assume that the entire population is susceptible to coronavirus at the start of the epidemic except for the initial infected individual that propagates the disease, the fraction of South Korea's population susceptible to the virus at  $t = 0$ , the onset of the epidemic, is:

$$
S(0) = \frac{49,999,999}{50,000,000}
$$

$$
S(0) \approx 1
$$

Consequently, the expression for R-naught can be revised as:

$$
c = \frac{\beta \times 1}{\gamma} = \frac{\beta}{\gamma}
$$

Hence, I will first determine the value of  $\gamma$  using online data about the duration of coronavirus infection and derive the value of  $c$  using the differential equations for the rate of change in the susceptible  $\left(\frac{dS}{dt}\right)$  and the infected  $\left(\frac{dI}{dt}\right)$  population. Subsequently, the expression for the Rnaught (c) will be used to obtain the value of  $\beta$  as unlike the duration of coronavirus  $(\frac{1}{\alpha})$  $\frac{1}{\gamma}$  or the R-naught value which can be derived mathematically, the contractability of coronavirus cannot be determined directly from literature data as it varies by the size of population.

According to Centers for Disease Control and Prevention, the duration of coronavirus infection (the period during which one is contagious) is approximately 10 days (CDC, 2023).

$$
\frac{1}{\gamma} = 10
$$

$$
\gamma = \frac{1}{10}
$$

The expression for R-naught  $(c)$  can be obtained by manipulating the following differential equations (Mathematical Association of America, n.d.):

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

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

Since both differential equations represent the susceptible and infected population in respect to time,

$$
\frac{dI}{dt} \times \frac{dt}{dS} = \frac{(\beta SI - \gamma I)}{-\beta SI}
$$

$$
\frac{dI}{dS} = -1 + \frac{\gamma}{\beta S}
$$

Since  $c = \frac{\beta}{\gamma}$  $\frac{\beta}{\gamma}$ , substituting  $\frac{\gamma}{\beta}$  with  $\frac{1}{c}$  gives:

$$
\frac{dI}{dS} = -1 + \frac{1}{cS}
$$

Now, I will integrate both sides with respect to  $S$  in order to obtain an expression for the infected population  $I(t)$ :

$$
\int \frac{dI}{dS} dS = \int (-1 + \frac{1}{cS}) dS
$$

$$
I = -\int 1 dS + \frac{1}{c} \int \frac{1}{S} dS
$$

$$
I(t) = -S + \frac{1}{c} \ln S + k
$$

where  $k$  is the constant of integration.

At the onset of epidemic when  $t = 0$ , the proportion of South Korea's population susceptible and infected to coronavirus is:

$$
S(0) = \frac{49,999,99}{50,000,000}
$$

$$
S(0) \approx 1
$$

$$
I(0) = \frac{1}{50,000,000}
$$

$$
I(0) \approx 0
$$

Therefore, these initial conditions can be used to determine the constant of integration:

$$
I(0) = -S(0) + \frac{1}{c} \ln S(0) + k
$$
  

$$
0 = -1 + \frac{1}{c} \times 0 + k
$$
  

$$
0 = -1 + k
$$
  

$$
k = 1
$$

If  $\lim_{t\to\infty} I(t)$  represents the proportion of South Korea's population infected at the end of the epidemic,  $\lim_{t\to\infty} I(t) = 0$  since everyone remaining after an epidemic will either belong to the susceptible or the recovered population. We can use this terminal condition to obtain another expression for the constant of integration:

$$
\lim_{t \to \infty} I(t) = -\lim_{t \to \infty} S(t) + \frac{1}{c} \lim_{t \to \infty} \ln S(t) + k
$$

$$
0 = -S_{\infty} + \frac{1}{c} \ln S_{\infty} + k
$$

$$
k = S_{\infty} - \frac{1}{c} \ln S_{\infty}
$$

where  $S_{\infty}$  denotes the proportion of South Korea's population susceptible at the end of the epidemic.

By setting the two expressions for the integration constant determined from the initial and terminal conditions as equal, we can obtain the following expression for the R-naught value:

$$
S_{\infty} - \frac{1}{c} \ln S_{\infty} = 1
$$

$$
\frac{1}{c} \ln S_{\infty} = S_{\infty} - 1
$$

$$
\frac{1}{c} = \frac{S_{\infty} - 1}{\ln S_{\infty}}
$$

$$
c = \frac{\ln S_{\infty}}{S_{\infty} - 1}
$$

Since this expression is independent of time  $t$ , we can assume that the R-naught value is constant throughout the epidemic and only dependent on the proportion of South Korea's population remaining susceptible at the end of the epidemic – those that have not been infected by coronavirus at all.

Of 50,000,000 people living in South Korea, 34,571,873 of them have been infected by coronavirus. Thus, the proportion of South Korea's population remaining in the susceptible category at the end of the epidemic is:

$$
S_{\infty} = \frac{50,000,000 - 34,571,873}{50,000,000} = 0.30856
$$

Consequently, the R-naught value for coronavirus pandemic in South Korea is:

$$
c = \frac{\ln 0.30856}{0.30856 - 1} = 1.7005
$$

Hence, the contractability of the coronavirus in South Korea is:

$$
\beta = c\gamma = 1.7005 \times \frac{1}{10} = 0.17005
$$

$$
\beta \approx 0.170
$$

From these results, it can be concluded that the SIR model predicts every infected patient to transmit coronavirus to approximately 1.70 susceptible individuals before becoming recovered. Furthermore, the contractibility of 0.170 indicates that 17.0% of interactions that infected individuals make with susceptible individuals will result in transmission. Unlike my initial expectation that had predicted coronavirus to spread more rapidly, it was surprising to find that the R-naught value for coronavirus predicted by the SIR model was actually lower than a common flu which has a R-naught value between 2 to 3 (Shabir, 2021).

#### <span id="page-10-0"></span>3.1.3 Graphing the SIR model using Euler's method

Using the value for  $\beta$  and  $\gamma$  determined, the system of differential equations in the SIR model below can produce a rudimentary model for the spread of coronavirus in South Korea.

$$
\frac{dS}{dt} = -0.170SI
$$

$$
\frac{dI}{dt} = 0.170SI - 0.1I
$$

$$
\frac{dR}{dt} = 0.1I
$$

Though it is best to find analytical solutions that expresses the  $S(t)$ ,  $I(t)$ , and  $R(t)$  as functions with respect to time  $t$ , solving a system of differential equations analytically requires much more complex math outside of the IB syllabus. Hence, I have decided to rather use the Euler's method to find numerical solutions that approximate the functions for the susceptible, infected, and recovered populations throughout the coronavirus epidemic.

By denoting the susceptible population at  $t = n$ ,  $S(n)$ , as  $S_n$  where *n* represents the number of days after the onset of the epidemic,

$$
S_{n+1} = S_n + (the change of susceptible population over a day)
$$
  
=  $S_n + \frac{dS}{dt} \times dt = S_n + (-0.170S_n I_n)dt$ 

Thus, this recursive relationship between the susceptible population at  $t = n$  and  $t = n + 1$ (step size of one day) indicates that we can predict the future susceptible population using data from the present susceptible population and the rate of change of the susceptible population over a day. Hence, the with the initial conditions for the susceptible, infected, and recovered populations at  $t = 0$ , the Euler's method allows us to extrapolate the changes of each population category over the course of the epidemic.

The same method has been used to obtain the recursive formula for  $I_{n+1}$  and  $R_{n+1}$ :

$$
I_{n+1} = I_n + (0.170S_nI_n - 0.1I_n)dt
$$

$$
R_{n+1} = R_n + (0.1I_n)dt
$$

As there is one initially infected individual in South Korea's population with everyone else belonging in the susceptible category,

$$
S(0) = \frac{49,999,999}{50,000,000}, I(0) = \frac{1}{50,000,000}, R(0) = 0, dt = 1
$$

Using these initial conditions, the numerical solutions and the representative curves for the susceptible, infected, and recovered populations have been obtained in Excel:



*Figure 1 Using excel spreadsheet to perform Euler's method in extrapolating the SIR model up to 500 days after the onset of epidemic.*



*Figure 2 Modelling the spread of the coronavirus in South Korea using SIR.* 

From the SIR curves modelled in figure 2, it can be noticed that the increase in the infected population results in a rapid decrease in the susceptible population. As one-tenth of the infected population recovers every day, the recovered population increases alongside the rise in the infected population. Since the maximum of  $I(t)$  occurs when the slope of the tangent for  $I(t)$ is zero,

$$
\frac{dI}{dt} = \beta SI - \gamma I = 0
$$

by substituting

$$
\beta SI = -\frac{dS}{dt} \text{ and } \gamma I = \frac{dR}{dt}
$$

it is clear that the maximum infected population occurs when:

$$
-\frac{dS}{dt} = \frac{dR}{dt}
$$

the point at which the rate of decrease of the susceptible population equals the rate of increase of the recovered population.

The curves for susceptible, infected, and recovered population plateau from around day 400, which indicates that the coronavirus outbreak lasts 400 days. This, of course, is not an accurate model of how coronavirus has spread in South Korea, both in terms of the shape of the curves and the duration of the outbreak. Furthermore, simplifying the coronavirus epidemic into individuals who can get infected, are currently infected, and have recovered fails to represent details that characterize coronavirus. Hence, I will develop this SIR model to represent the realistic spread of the virus involving the incubation period, asymptomatic transmission, asymptomatic recovery, and reinfection by incorporating more terms into the system of differential equations in the upcoming sections of the exploration.

#### <span id="page-13-0"></span>3.2 The SEIR model

#### <span id="page-13-1"></span>3.2.1 Introduction to the SEIR model

When you are infected by coronavirus, you do not immediately express the symptoms. For days, you are in an "exposed" state where the virus remains in its incubation period. As the SIR the model fails to distinguish individuals that are sick (infected) from those who have just been exposed, as the first step in tailoring the epidemiological model to coronavirus, I have added the exposed category  $E(t)$ , which represents the proportion of South Korea's population that are exposed to coronavirus but do not experience its symptoms yet. The system of differential equations in the SEIR model is presented below:

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

$$
\frac{dE}{dt} = \beta SI - \delta E
$$

$$
\frac{dI}{dt} = \delta E - \gamma I
$$

$$
\frac{dR}{dt} = \gamma I
$$

The SEIR model shows that when individuals from the susceptible population are infected by people in the infected category, they are first transferred into the exposed population during which the coronavirus is at its dormancy. This can be seen from how the term  $-\beta SI$  that represents the decrease in the susceptible population leads to the increase in the exposed population by  $\beta SI$ .

The proportion of coronavirus in the exposed population that breaks out of its incubation period every day is denoted by the constant  $\delta$ . For instance,  $\delta = 0.2$  indicates that 20% of the exposed individuals become contagious and sick every day, being transferred from the exposed to the infected category. Like how the reciprocal of the contractibility  $(\beta)$  indicated the duration of the disease, the reciprocal of  $\delta$  represents the duration of the incubation period  $(\frac{1}{\epsilon})$  $\frac{1}{\delta}$ ). Consequently, with  $\delta E$  representing the proportion of the exposed population that is transferred to the infected category every day, the overall rate of change of the exposed population can be expressed as the sum of the rate of influx of exposed individuals from the susceptible population ( $\beta$ SI) and the rate of outflux of exposed individuals to the infected category ( $-\delta E$ ):

$$
\frac{dE}{dt} = \beta SI - \delta E
$$

#### <span id="page-14-0"></span>3.2.2 Further development of the SEIR model

Another unique characteristic of coronavirus is that even the exposed individuals undergoing the incubation period can transmit the virus to the susceptible. This characteristic is called asymptomatic transmission, represented by the term  $\epsilon SE$  where  $\epsilon$  denotes the transmission constant that indicates the proportion of the interaction between the susceptible and the exposed population that results in transmission (same principle as the contractibility constant  $\beta$ ). Consequently, the rate of change in the susceptible and the exposed population is also dependent on the interaction between the two groups and the transmission constant  $\varepsilon$ , represented by  $-\varepsilon SE$  and  $+\varepsilon SE$  in  $\frac{ds}{dt}$  and  $\frac{dE}{dt}$ , respectively.

Furthermore, it is also seen in coronavirus infection that a proportion of individuals in the exposed category with a strong immune system overcomes the disease without experiencing the symptoms, recovering without undergoing the infected stage. This direct transfer from the exposed to recovered population is called asymptomatic recovery, represented by  $-\mu E$  and + $\mu E$  in  $\frac{dE}{dt}$  and  $\frac{dR}{dt}$ , respectively, where the constant  $\mu$  denotes the proportion of exposed individuals recovering without becoming infected.

Such tailored SEIR model can be expressed by a system of differential equations presented below:

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

$$
\frac{dE}{dt} = \beta SI + \varepsilon SE - \delta E - \mu E
$$

$$
\frac{dI}{dt} = \delta E - \gamma I
$$

$$
\frac{dR}{dt} = \gamma I + \mu E
$$

#### <span id="page-15-0"></span>3.3 The SEIR+SRS model

#### <span id="page-15-1"></span>3.3.1 Introduction to the SEIR+SRS model

The last step in advancing the model for the spread of coronavirus in South Korea is to incorporate the concept of reinfection. Reinfection is the most important feature of coronavirus that distinguishes it from other viruses where even the individuals who have recovered from the disease once can become susceptible to coronavirus again. As there is no permanent immunity against the coronavirus, the SEIR model must demonstrate how some people in the recovered category are transferred back to the susceptible category over time. I decided to call this transfer from the recovered to susceptible population as the SRS cycle since a susceptible individual who is infected and recovered from the coronavirus can be susceptible and become exposed, and thus infected again.

The transfer from the recovered to susceptible category is represented by  $\omega R$ , where  $\omega$  denotes the proportion of the recovered population becoming susceptible again. Consequently, the susceptible population increases while the recovered population decreases by  $\omega R$  every day, which is illustrated by the term  $+\omega R$  and  $-\omega R$  within  $\frac{dS}{dt}$  and  $\frac{dR}{dt}$ , respectively.

The system of differential equations presented below shows a more realistic epidemiological model that I have created to model the coronavirus epidemic in South Korea:

$$
\frac{dS}{dt} = -\beta SI - \varepsilon SE + \omega R
$$

$$
\frac{dE}{dt} = \beta SI + \varepsilon SE - \delta E - \mu E
$$

$$
\frac{dI}{dt} = \delta E - \gamma I
$$

$$
\frac{dR}{dt} = \gamma I + \mu E - \omega R
$$

The recovered population within the SEIR+SRS model does not discriminate between those who survived or died due to coronavirus. However, I found it unnecessary to create another differential equation involving  $D(t)$  to model the proportion of South Korea's population that has died since coronavirus is a relatively mild disease with a low mortality rate especially in developed countries like South Korea.

#### <span id="page-16-0"></span>3.3.2 Determining the constants  $\delta$ ,  $\varepsilon$ ,  $\mu$ , and  $\omega$

As previously determined from the SIR model,  $\beta = 0.170$  and  $\gamma = 0.1$ .

As the mean incubation period of coronavirus is 6.5 days according to Centers for Disease control and Prevention,  $\frac{1}{s}$  $\frac{1}{\delta}$  = 6.5, meaning that  $\delta$  = 0.15384  $\approx$  0.154 (CDC, 2023).

Though there is not much coughing or sneezing when coronavirus is in its dormancy, the incubation period makes a significant contribution to the asymptomatic transmission since the exposed individuals will continue to interact with the susceptible population without realizing that one has coronavirus. Thus, I will assume the asymptomatic transmission constant  $\varepsilon$  to be equal to the contractibility constant  $\beta$  since the exposed population will interact more with the susceptible population than the infected population, which offsets its reduced transmissibility due to the virus being at its dormant state:

$$
\varepsilon=0.170
$$



*(Population Pyramid, 2022)*

Using South Korea's demographic distribution, I will assume that 50% of people between the age of 15 to 24 – the age where individuals are most physically active – to have the most powerful immune system to undergo asymptomatic recovery. Consequently, even if they have been transmitted, they are transferred from the exposed to recovered category without

experiencing the severe symptoms which the

infected population experiences. Hence, the proportion of the exposed population undergoing asymptomatic recovery is:

$$
\mu = \frac{2.3 + 2.1 + 2.9 + 2.7}{100} \times 50\% = 5\% = 0.05
$$

Finally, literature study indicates that the reinfection rate of coronavirus in South Korea was 0.3% (Jang, 2022). This means that approximately 0.3% of the recovered population enters the susceptible population again every day, resulting in  $\omega = 0.003$ .

#### <span id="page-17-0"></span>3.3.3 Graphing the SEIRD+SRS model using the Euler's method

$$
\frac{dS}{dt} = -0.170SI - 0.170SE + 0.003R
$$

$$
\frac{dE}{dt} = 0.170SI + 0.170SE - 0.154E - 0.05E
$$

$$
\frac{dI}{dt} = 0.154E - 0.1I
$$

$$
\frac{dR}{dt} = 0.1I + 0.05E - 0.003R
$$

With a system of differential equations shown above, the same Euler's method presented in 3.1.3 has been used to obtain the susceptible, exposed, infected, and recovered population curves, approximating the analytical solutions to the SEIR+SRS model. Hence, the recursive formula for  $S_{n+1}$ ,  $E_{n+1}$ ,  $I_{n+1}$ , and  $R_{n+1}$  are:

$$
S_{n+1} = S_n + (-0.170S_nI_n - 0.170S_nE_n + 0.003R_n)dt
$$
  
\n
$$
E_{n+1} = E_n + (0.170S_nI_n + 0.170S_nE_n - 0.154E_n - 0.05E_n)dt
$$
  
\n
$$
I_{n+1} = I_n + (0.154E_n - 0.1I_n)dt
$$
  
\n
$$
R_{n+1} = R_n + (0.1I_n + 0.05E_n - 0.003R_n)dt
$$

The initial conditions for  $t = 0$  are:

$$
S(0) = \frac{49,999,999}{50,000,000}, E(0) = \frac{1}{50,000,000}, I(0) = 0, R(0) = 0, dt = 1
$$

Using these data, the representative curves for the susceptible, exposed, infected, and recovered populations have been obtained in Excel up to day 1457 as it has been 1457 days since  $20<sup>th</sup>$  of January 2020 – the onset of coronavirus epidemic in South Korea – to  $16^{th}$  of January 2024 – the day when this calculation was performed:

$\boldsymbol{A}$	А	B	C.	D	E	F	G	H
1	Day	Susceptible	Exposed	Infected	Recovered		dt.	
2	Ω.	0,99999998	0,00000002	0	0		1	
3	1.	0,99999998	1,932E-08	3,08E-09	1E-09		beta	
4	$\overline{c}$	0,99999997	1,9187E-08	5,7473E-09	2,271E-09		0,17	
5	з	0,99999997	1,9511E-08	8,1273E-09	3,7983E-09		gamma	
6	4	0,99999996	2,023E-08	1,0319E-08	5,5752E-09		0,1	
7	5.	0,99999996	2,1296E-08	1,2403E-08	7,6018E-09		delta	
8	6	0,99999995	2,2681E-08	1,4442E-08	9,8841E-09		0,154	
9	7.	0,99999995	2,4365E-08	1,6491E-08	1,2433E-08		Epsilon	
10	8	0,99999994	2,634E-08	1,8594E-08	1,5263E-08		0,17	
11	9	0,99999993	2,8605E-08	2,0791E-08	1,8393E-08		Mu	
12	10 <sup>1</sup>	0,99999992	3,1167E-08	2,3117E-08	2,1847E-08		0.05	
13	11	0,99999991	3,4037E-08	2.5605E-08	2,5652E-08			
14	12	0.9999999	3.7233E-08	2,8286E-08	2,9837E-08			
15	13	0,99999989	4,0775E-08	3,1191E-08	3,4438E-08		Omega	
16	14	0.99999988	4,4691E-08	3,4351E-08	3.9493E-08		0,003	
17	15	0,99999987	4.9012E-08	3,7799E-08	4,5044E-08			
18	16	0,99999985	5,3771E-08	4,1567E-08	5,1139E-08			
19	17	0,99999984	5,9009E-08	4,5691E-08	5,7831E-08			
20	18 <sup>1</sup>	0,99999982	6,477E-08	5,0209E-08	6,5177E-08			
21	19 <sup>15</sup>	0,9999998	7.1104E-08	5,5163E-08	7,3241E-08			
22	20	0,99999978	7,8064E-08	6,0597E-08	8,2093E-08			
23	21	0,99999976	8,5711E-08	6,6559E-08	9,1809E-08			
24	22	0,99999973	9,4112E-08	7,3102E-08	1,0248E-07			
25	23	0,9999997	1,0334E-07	8,0285E-08	1,1418E-07			
26	24	0,99999967	1,1347E-07	8,8171E-08	1,2704E-07			
27	25	0,99999964	1,2461E-07	9,6829E-08	1,4115E-07			
28	26	0,9999996	1,3683E-07	1,0634E-07	1,5664E-07			
29	27	0.99999956	1,5025E-07	1.1677E-07	1.7364E-07			

*Figure 4 Using excel spreadsheet to perform Euler's method in extrapolating the SEIRD+SRS model. The table shows up to the day 29 but the values until day 1457 have been extrapolated.* 



<span id="page-19-0"></span>3.3.4 Reflecting on SEIR+SRS in modelling the spread of coronavirus in South Korea

*Figure 5 Modelling the spread of the coronavirus in South Korea using the SEIR+SRS model.*



*Figure 6 The close-up visualization of the function* () *modelled using the Euler's method from the SEIR+SRS model.* 

The  $I(t)$  curve modelled by SEIR+SRS illustrates some distinct differences compared to the infected curve of SIR model (figure 2). Compared to the SIR model, there are four "waves" of infection due to the reinfection rate of 0.003. As 0.3% of the recovered population is transferred into the susceptible population, upon reaching its peak at the end of each outbreak, the recovered population begins to fall since there is no more infected population to become recovered. Consequently, the susceptible population rises again as shown in figure 5. When sufficient proportion of South Korea's population becomes susceptible to coronavirus again, the exposed and infected populations increase, initiating the second wave of outbreak. Hence, the element of reinfection establishes the oscillatory relationship between the susceptible and recovered populations, allows the coronavirus to propagate once more among the susceptible population and cause successive waves of coronavirus outbreaks.

Also, it can be noticed that the successive wave of infection becomes milder in its magnitude. In fact, the proportion the exposed and infected population does not rise as rapidly as they did in the preceding outbreaks (figure 5 and 6). This can be explained using the fact that there are less susceptible individuals available to be transmitted after every wave of outbreak. Compared to the onset of epidemic when the entire population was susceptible, the proportion of South Korea's population susceptible at day 525, 883, and 1242 – the start of the second, third, and fourth wave of outbreak when the susceptible population starts to decline – is 0.615, 0.521, and 0.489 according to figure 5. As the increase in the exposed population is dependent on 0.170SI and 0.170*SE*, terms that involve the susceptible population  $S(t)$ , when there is less susceptible population to begin with, there are less individuals available to become exposed to coronavirus. Consequently, there are less people infected since the term responsible for the rise in the infected population,  $0.154E$ , also decreases when the exposed population decreases.

#### Active Cases in South Korea



*Figure 7 A graph recording the real-life data of the infected population throughout coronavirus epidemic in South Korea. Unlike how I have the proportion of South Korea's population as the y-axis, this graph shows the number of individuals on the y-axis instead (Worldometer, 2024).* 

When the  $I(t)$  curve of the SEIR+SRS model (figure 6) was compared to the real-life data that records the number of infected individuals throughout the coronavirus epidemic (figure 7), it was shocking to find that the SEIRD+SRS model manages to predict the most important features of how coronavirus has spread in South Korea. Not only did coronavirus epidemic in South Korea consisted of four successive outbreaks (represented by four peaks in the figure 7) as predicted by the SEIR+SRS model, but my model also managed to predict how the successive waves of outbreak will decrease in their magnitude with less people becoming infected.

Furthermore, the SEIR+SRS model predicts 0.1220, 0.03014, 0.01665, and 0.01317 as the maximum proportion of South Korea's population infected at each consecutive outbreak, which corresponds to 6.10 million, 1.51 million, 0.833 million, and 0.659 million individuals, respectively. Considering how the real-life infected curve indicates the maximum number of infected individuals to be 6.63 million, 2.20 million, 1.22 million, and 0.868 million in the corresponding outbreaks, it can be concluded that though not completely accurate, the SEIR+SRS model can produce a sufficiently realistic prediction of the number of infected population throughout the coronavirus epidemic in South Korea.

However, there are areas where the SEIR+SRS model fall short of. For instance, the  $I(t)$  curve of the SEIR-SRS model fails to accurately model features such as the time interval between successive wave of outbreak or the duration of individual outbreaks. But it must be noted that even the SEIR+SRS model is an extremely simplified model grounded upon numerous initial assumptions like South Korea's homogenous population distribution and assumptions I have made in determining the parameters for my differential equations. Thus, it is inevitable that there are some differences between my model and the actual spread of coronavirus.

Despite the temporal differences of when individual outbreaks have occurred, I believe that SEIR+SRS model is far more successful in modeling the spread of coronavirus in South Korea than the initial SIR model as it entails key characteristics of coronavirus like dormancy, asymptomatic transmission, asymptomatic recovery, and reinfection. Through the oscillatory (periodic) relationship between the susceptible and recovered population, SEIR+SRS models the infected curve that resembles how the infected population has changed in reality. Hence, its strength in correctly predicting the decreasing severity of four successive outbreaks and sufficiently approximating the number of infected individuals at the peak of each outbreak allows me to conclude that the SEIR+SRS a realistic model in representing the spread of coronavirus in South Korea.

## <span id="page-22-0"></span>4. Determining the Effectiveness of Vaccination in Reducing the

## Spread of Coronavirus

#### <span id="page-22-1"></span>4.1 The SEIR+SRS Model with Vaccination

#### <span id="page-22-2"></span>4.1.1 The Significance of Vaccination in SEIR+SRS Model

In the context of epidemiological model, vaccination means transfer from the susceptible to recovered population, becoming immune to the disease without becoming exposed to it. As with the case of coronavirus, however, even the recovered population with immunity can contract the disease again. Still, as the reinfection rate  $(\omega)$  is much lower than the contractability constant for the interaction between the susceptible-infected  $(\beta)$  and susceptible-exposed  $(\varepsilon)$  populations, we can hypothesize that the transfer of the susceptible population to recovered category through vaccination will ultimately decrease the number individuals becoming infected by coronavirus. If vaccination had no pertinent outcome, why would South Korea have had enforced a strict vaccination program to combat the epidemic to begin with? But a question remains: how effective (quantitatively) was vaccination in reducing the spread of coronavirus?

South Korea began distributing the coronavirus vaccine 386 days after the onset of epidemic. If we assume that 50,000 susceptible individuals were vaccinated every day since the arrival of vaccine,  $\frac{50,000}{50,000,000}$  $\frac{30,000}{50,000,000}$  = 0.001 is the proportion of South Korea's population transferred from the susceptible to recovered population every day, irrespective of the time and changes of other population categories. Hence, the element of vaccination can be integrated into the SEIR+SRS model by transferring 0.1% of South Korea's population in the susceptible category to the recovered category every day.

To avoid confusions, a small dot will be placed on top when referring to the population curves that model SEIR+SRS with vaccination. The system of differential equations modelling the spread of coronavirus in South Korea's population undergoing vaccination is presented below:

$$
\frac{dS^{\circ}}{dt} = -0.170S^{\circ}I^{\circ} - 0.170S^{\circ}E^{\circ} + 0.003R^{\circ} - 0.001
$$
  

$$
\frac{dE^{\circ}}{dt} = 0.170S^{\circ}I^{\circ} + 0.170S^{\circ}E^{\circ} - 0.154E^{\circ} - 0.05E^{\circ}
$$
  

$$
\frac{dI^{\circ}}{dt} = 0.154E^{\circ} - 0.1I^{\circ}
$$
  

$$
\frac{dR^{\circ}}{dt} = 0.1I^{\circ} + 0.05E^{\circ} - 0.003R^{\circ} + 0.001
$$

#### <span id="page-23-0"></span>4.1.2 Graphing the SEIR+SRS model with vaccination using the Euler's method

The same recursive equations presented in 3.3.3 were used to obtain the representative curves for the susceptible, exposed, infected, and recovered population without vaccination until  $t = 386$ . From  $t = 387$ , the recursive equations presented below with the 'vaccination term' (−0.001 and +0.001) were used to obtain the representative curves for the susceptible, exposed, infected, and recovered population up until  $t = 1457$ :

$$
S_{n+1}^{\circ} = S_n^{\circ} + (-0.170S_n^{\circ}I_n^{\circ} - 0.170S_n^{\circ}E_n^{\circ} + 0.003R_n^{\circ} - 0.001)dt
$$
  
\n
$$
E_{n+1}^{\circ} = E_n^{\circ} + (0.170S_n^{\circ}I_n^{\circ} + 0.170S_n^{\circ}E_n^{\circ} - 0.154E_n^{\circ} - 0.05E_n^{\circ})dt
$$
  
\n
$$
I_{n+1}^{\circ} = I_n^{\circ} + (0.154E_n^{\circ} - 0.1I_n^{\circ})dt
$$
  
\n
$$
R_{n+1}^{\circ} = R_n^{\circ} + (0.1I_n^{\circ} + 0.05E_n^{\circ} - 0.003R_n^{\circ} + 0.001)dt
$$

<span id="page-24-0"></span>4.1.3 Reflecting on SEIR+SRS with vaccination in modelling the spread of coronavirus in South Korea



*Figure 8 Modelling the spread of the coronavirus in South Korea using the numerical solutions to SEIRD+SRS model with vaccination.*



*Figure 9 The close-up visualization of the function*  $\int$ <sup>*c*</sup>(*t*) *modelled using the Euler's method from the SEIR+SRS model with vaccination.* 

Since vaccine is administered from  $t = 387$ , the infected population is same between the South Korea's population undergoing vaccination and those that does not undergo vaccination during the initial outbreak (from now on, I will refer to South Korea's population undergoing vaccination as 'vaccinated population' and South Korea's population that does not undergo vaccination as 'non-vaccinated population' interchangeably).

Though the SEIR+SRS model with vaccination predicts wrongly by indicating how there will not be a fourth outbreak (there are only three peaks corresponding to three outbreaks as illustrated in figure 9 compared to how there are four peaks in the real-life data shown in figure 7), the model demonstrates how vaccination significantly reduces the magnitude of the second and third outbreaks. The SEIR+SRS model without vaccination predicted  $0.03014$  ( $t = 614$ ) and 0.01665 ( $t = 982$ ) as the peaks for South Korea's infected population at the second and third outbreak, corresponding to 1.51 million and 0.833 million infected individuals, respectively. On the contrary, the SEIR+SRS model with vaccination predicts  $0.008320$  ( $t =$ 733) and 0.005267 ( $t = 1335$ ) as the peaks for South Korea's infected population at the second and third outbreak, corresponding to 0.416 million and 0.263 million infected individuals, respectively. This demonstrates that vaccination decreases the maximum number of infected individuals at the second and third outbreaks by 72.5% and 68.4%, respectively.

## <span id="page-25-0"></span>4.2 Finding the Derivative of  $I(t)$  and  $I^{\degree}(t)$

Though data from Euler approximation allows comparison of the maximum infected population at each consecutive outbreak between vaccinated and unvaccinated population, I cannot compare their maximum rate of increase of the infected population which requires differentiating  $I(t)$  and  $I^{\circ}(t)$  functions which I don't have.

Since I could not solve the system of differential equations analytically, I have initially tried to model the  $I(t)$  and  $I^{\circ}(t)$  by attempting to create functions that best fits the infected curves modelled with the Euler's method. During the modelling process, however, I realized a much more effective alternative to obtain the derivative of  $I(t)$  and  $I^{\circ}(t)$  – using the values extrapolated by Euler's method to approximate the slope of the tangent for  $I(t)$  and  $I^{\circ}(t)$  at every point.

By definition, the derivative of a function  $f(x)$  can be expressed as:

$$
f'(x) = \lim_{\Delta x \to 0} \frac{f(x + \Delta x) - f(x)}{\Delta x}
$$

Consequently, the derivative of the function  $I(t)$  can be obtained by:  $I'(t) = \lim_{\Delta t \to 0}$  $I(t + \Delta t) - I(t)$  $\Delta t$ 

Since  $I'(t)$  is collection of slopes of the tangent at every point in  $I(t)$  when  $\Delta t \to 0$ , to obtain the "correct" derivative (continuous derivative) of  $I(t)$ , the corresponding value for  $I(t)$  must exist for every value of  $t \in \mathbb{R}$ .

However, it is unrealistic to monitor the change in infected population for every real value of . In fact, the population of the infected is recorded and updated every day in reality, like how this exploration has performed the Euler's approximation with  $dt = 1$ . Though the derivative of  $I(t)$  becomes more accurate when the time interval  $\Delta t$  between two measurements becomes smaller, when applying mathematics to model a realistic situation like the spread of coronavirus, it may be sufficient enough to approximate  $I'(t)$  as a discrete derivative by connecting the slope of the tangent for  $I(t)$  at every value of  $t \in \mathbb{N}$  where  $\Delta t = 1$ . Since the slope of the tangent for  $I(t)$  represents the rate of change in the infected population at day t,

$$
I'(t) = \frac{I(t) - I(t - 1)}{t - (t - 1)}
$$

$$
I'(t) = \frac{I(t) - I(t - 1)}{1}
$$

$$
I'(t) = I(t) - I(t - 1)
$$

Hence, the slope of the tangent for  $I(t)$  – rate of change in the infected population – can be calculated by finding the difference between the infected population at day  $t$  and day  $t - 1$ , which is already obtained up to  $t = 1457$  from Euler's approximation performed previously!

By approximating  $I'(t)$  and  $[I<sup>o</sup>(t)]'$  by calculating  $I(t) - I(t-1)$  and  $I<sup>o</sup>(t) - I<sup>o</sup>(t-1)$  using Excel, the following two curves modelling the daily change in the infected population with and without vaccination have been obtained:



*Figure 10 The change in daily infected population modelled by SEIR+SRS model without vaccination.* 



*Figure 11 The change in daily infected population modelled by SEIR+SRS model with vaccination.* 

#### <span id="page-28-0"></span>4.3 Comparing the rate of increase in the infected populations in SEIR+SRS model with

#### vaccination and without vaccination





It is evident that the curves modelling the rate of change in the daily infected populations are respective derivatives for the curves modelling the infected population since they illustrate slopes of tangent in  $I(t)$  and  $I^{o}(t)$ . For instance, considering how the maximum infected population during the first outbreak occurs at  $t = 193$  for both vaccinated and non-vaccinated populations, it makes sense that the rate of change in daily infected population is zero at  $t = 193$  since the slope of the tangent for  $I(t)$  and  $I^{\circ}(t)$  at  $t = 193$  is zero. Also, the maximum rate of increase in the infected population during the first outbreak for the vaccinated and nonvaccinated population corresponds to the maximum point on the curves modelling the rate of change in the daily infected population, occurring at day 177 where  $0.004019 \times 100\% = 0.4019\%$  of South Korea is predicted to get infected over the day. This indicates that the slope of the tangent for  $I(t)$  and  $I^{\circ}(t)$  is steepest at  $t = 177$ , which tells when the infected population was rising the fastest – when the first outbreak was most out of control. Hence, the numerical approximation of the discrete derivate for  $I(t)$  and  $I^{\circ}(t)$  using the data extrapolated from the Euler's method produces an accurate  $I'(t)$  and  $[I<sup>°</sup>(t)]'$  curves.

The second local maximum points for  $I'(t)$  and  $[I<sup>o</sup>(t)]'$  are (574, 0.0003864) and (650, 0.00004904), which indicates that at the peak of the second wave of coronavirus outbreak where the slope of the tangent for  $I(t)$  and  $I^{\circ}(t)$  are at their maximum, 0.03864% of South Korea's population is predicted to become infected without vaccination in contrast to 0.004904% if South Korea's population had been undertaking vaccination since  $t = 387$ . This shows that the rate of individuals becoming infected at the peak of secondary outbreak is expected to decrease by 87.3% with vaccination.

As the third local maximum points for  $I'(t)$  and  $[I<sup>o</sup>(t)]'$  are (915, 0.0001012) and (1202, 0.00001321), when the same comparison is undertaken for the third outbreak, it can be predicted that the vaccination decreases the rate of individuals becoming infected at the peak of the third outbreak by 86.9%.

Hence, it can be concluded that vaccination is extremely effective in reducing the spread of coronavirus in South Korea since according to the  $I'(t)$  and  $[I<sup>o</sup>(t)]'$  curves derived from the  $I(t)$  and  $I^{\circ}(t)$  curves from my SEIR+SRS model, since vaccination not only decreases the number of maximum infected population at every outbreak but also significantly reduces the maximum rate of increase in the infected population for the second and third outbreaks.

## <span id="page-29-0"></span>5. Conclusion

In this exploration, I have investigated how a system of differential equations can be used to model the coronavirus outbreak in South Korea and the effectiveness of vaccination in reducing the rate of transmission.

In the first part of the exploration (from 3.1.1 to 3.3.4), I have attempted to use a system of differential equations to create a realistic model for the spread of coronavirus in South Korea from the onset of the epidemic up until the present day by finding numerical solutions to the differential equations with the Euler's method. Though SIR model has its strength as a generally applicable epidemiological model in simulating the spread of a disease, I realized that the simple interaction between the susceptible, infected, and recovered populations is not enough to represent the unique features of coronavirus. SIR model depicts coronavirus as a disease where individuals become sick immediately after contracting the virus and attain permanent immunity after recovering from it. I have addressed this weakness of SIR model by creating a new differential equation with the exposed category and incorporating the aspect of reinfection where the recovered population can become susceptible again, arriving at the SEIR+SRS model that accurately models the coronavirus epidemic in South Korea as consisting of four successive outbreaks that successively decrease in their magnitude of severity.

In the second part of the exploration (from 4.1.1 to 4.3), I modelled the spread of coronavirus in South Korea's population undergoing vaccination to quantify the effectiveness of vaccination in mitigating the spread of coronavirus. I compared not only the maximum number of infected but also the maximum rate of increase in the infected during the successive waves of coronavirus outbreak between the vaccinated and non-vaccinated population by approximating the derivatives for the infected curves obtained with the SEIR+SRS model with data extrapolated by Euler's method. Within South Korea's population undergoing vaccination, the maximum number of infected individuals in second and third outbreaks decreased by 72.5% and 68.4% compared to South Korea's population not undergoing vaccination, respectively. Furthermore, rate of increase of the infected population at the peak of second and third outbreak decreased by 87.3% and 86.9% as well. This allows me to conclude that though vaccinated individuals can become susceptible to coronavirus again, the direct transfer from the susceptible to the recovered population through vaccination drastically reduces the severity of the second and third outbreaks by decreasing the proportion of susceptible population that can become exposed to the virus. Hence, from this estimation, it can be predicted that vaccination would have served a crucial role in reducing the spread of coronavirus in South Korea.

Hence, this exploration concludes that SEIR+SRS model can effectively represent the spread of coronavirus in South Korea and predicts vaccination to have had crucial role in decreasing the magnitude of successive outbreaks and allowing the epidemic to come to a halt in South Korea.

### <span id="page-31-0"></span>6. Evaluation

Like all mathematical modelling of real-life phenomenon, however, it is extremely difficult to make a perfect representation of how coronavirus has actually spread in South Korea. Although the SEIR+SRS model has its strength in capturing the essential aspects of coronavirus (incubation period, asymptomatic infection, asymptomatic recovery, and reinfection) and extrapolating the change in infected population that matches the real-life infected population data with a high degree of accuracy, the model bases itself from the myriads of assumptions. The model would not have worked if South Korea's 50 million population was distributed unevenly, if hospitalization and quarantine were in effect, or if the contractibility of coronavirus varied throughout the epidemic. As a mathematical model cannot take account for exceptions or outliers, numerous generalizations must be accepted as a premise to predict the outcome of an epidemic, which is why my SEIR+SRS model is ultimately different from the real-life data.

Furthermore, I have utilized Euler's method to circumvent the challenge in finding analytical solutions to the set of differential equations in the SEIR+SRS model. Though Euler's method was efficacious in producing numerical solutions which enabled this exploration to extrapolate the change in susceptible, exposed, infected, and recovered populations throughout the epidemic, numerical solutions are ultimately 'approximations' of the true values. Consequently, using Euler's approximation to model the SEIR+SRS curves and approximate the derivatives for  $I(t)$  and  $I^{\circ}(t)$  by plotting their discrete derivatives pose limitation to the mathematical accuracy of predicting the maximum number of infected and the maximum rate of increase in the infected population using my model. Although the SEIR+SRS model manages to predict the overall trend of the coronavirus epidemic in South Korea, the nature of numerical approximation to differential equations may have introduced errors in predicting the maximum number of infected individuals at each outbreak and temporal differences compared to the real-life data of infected population.

Despite the mathematical limitations of my epidemiological model involving its accuracy, a key takeaway from my exploration is realizing the importance of vaccination in inhibiting the spread of disease. Although vaccination may not "guarantee" permanent immunity, as the increase in exposed and infected populations are both dependent on the susceptible population, it is vital that individuals take vaccination to minimize the interaction between the susceptible and exposed/infected patients. Limiting the spread of virus by decreasing the susceptible population is also a crucial step in establishing a "herd immunity." The "physical barrier" formed by the recovered population surrounding the non-vaccinated individuals allow even those who cannot take vaccines owing to their health conditions to be protected from the virus.

## <span id="page-32-0"></span>7. Further Study

As this investigation has relied upon the Euler's method to circumvent the difficulty in obtaining the analytical solutions, future studies could attempt to solve the system of differential equations in SEIR+SRS model analytically. By obtaining functions that express the susceptible, exposed, infected, and recovered populations with respect to time, the mathematical accuracy of the epidemiological model can increase, thus its validity in modelling the coronavirus epidemic in South Korea.

Alternatively, future studies could also attempt to model the spread of coronavirus with considerations of external factors such as quarantine or hospitalization. This could be attempted by simply adding more terms into existing differential equations or developing new population categories that further specifies which state individuals belong in.

Lastly, future studies could find methods to represent the spread of coronavirus without grounding the epidemiological model to the set of assumptions listed in the background information. Finding methods to incorporate the population's vital dynamics or represent the uneven population distribution across South Korea can further strengthen the validity and applicability of SEIR+SRS model in modelling epidemics.

## <span id="page-33-0"></span>8. Citation

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