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Modelling of the Spread of Pandemic COVID-19 using SEIR Model

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Abstract This research aims to study the basic approach of the mathematical model implemented on the spread of COVID-19 using the Susceptible-Exposed-Infected-Recovered SEIR model. The equilibrium point considered in this study is the disease-free equilibrium point (DFEP), and its stability was investigated. The analysis of the model uses the Next-Generation Matrix method to obtain the basic reproduction number, R_0 which acts as a threshold determining whether an infectious disease will die out quickly or lead to an epidemic. Lastly, the simulation of the SEIR model was carried out using MATLAB. The values of parameters were adjusted to see how it affects the outcome.

Keywords COVID-19; SEIR model; Basic reproduction number; Disease-free equilibrium point; Next-generation matrix.

1 Introduction

Coronavirus disease (COVID-19) is an infectious disease caused by a newly discovered coronavirus. COVID-19 is a highly transmittable and pathogenic viral infection caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), which emerged in Wuhan, China and spread worldwide [1]. As of June 25, 2020, more than 9.46 million people in more than 188 countries and territories tested positive for COVID-19, resulting in 483,247 deaths [2]. As of April 17, 2020, there were 5,251 COVID-19 cases, including 86 deaths and 2,967 cases of recovery reported by the Ministry of Health (MOH) in Malaysia. Selangor had recorded the highest number of confirmed COVID-19 cases (1,338) to date (April 17, 2020) [2].

World Health Organization (WHO) declared a pandemic on March 11, which has spread worldwide [3]. The preliminary guidelines were published on the WHO website with public health care to deal with the pandemic. Countries that were significantly affected by this pandemic are Italy and the USA [4]. Almost all national governments forced people to stay at home and self-isolation. As a result, this disease is growing fast in many countries around the world. The most widely used strategy to control the pandemic is social distancing, self-quarantine, and wearing a facemask. COVID-19 symptoms usually manifest as fever, dry cough, and tiredness. People who are highly vulnerable to COVID-19 are the elderly, young children, pregnant women, and people with chronic diseases [2].

Due to the disease becoming more severe, understanding the dynamics transmission of COVID-19 disease can help prevent and control this epidemic's spreading. Therefore, mathematical models play a significant role in understanding COVID-19 transmission

mechanisms, structures, and features [5]. Currently, COVID-19 is of great concern to researchers, governments, and all people because of the high infection rate and the significant number of deaths. The Susceptible–Infectious–Recovered (SIR) model is widely used to estimate disease transmission, recovery, deaths, and other significant parameters separately for various countries for different, specific regions of high to low reported cases COVID-19 [5]. In addition, mathematical modelling on the spread of COVID-19 has been carried out by [6], which using the Susceptible–Exposed-Infectious–Recovered (SEIR) model and vaccination as parameters in the model. The basic reproduction number, R_0, will be calculated using the Next-Generation Matrix method. When $R_0 > 1$, The epidemic increases exponentially, which means that one infected individual infects more than one individual on average. Meanwhile, when $R_0 < 1$ shows that the disease will surely die out without affecting a large share of the population. Therefore, the research is done in the hope that the SEIR model can be used as a reference model for COVID-19 spread.

2 Formulation of the Model

2.1 SEIR Model

This section discussed the derivation of the extended SIR model for the pandemic of COVID-19. The extended SIR model is called as Suspected-Exposed-Infected-Recovered (SEIR). The SEIR model derivation and the stability analysis of the model will be carried out throughout this section. The SEIR model on the spread of COVID-19 is divided into four compartments, namely Suspected (*S*), Exposed (*E*), Infected (*I*), and Recovered (*R*). *N* is the total population size. Individuals in an infected class can cause other individuals to become infected. The SEIR model is presented schematically in Figure 1. The model is based on the work of Annas S. et al. [6].

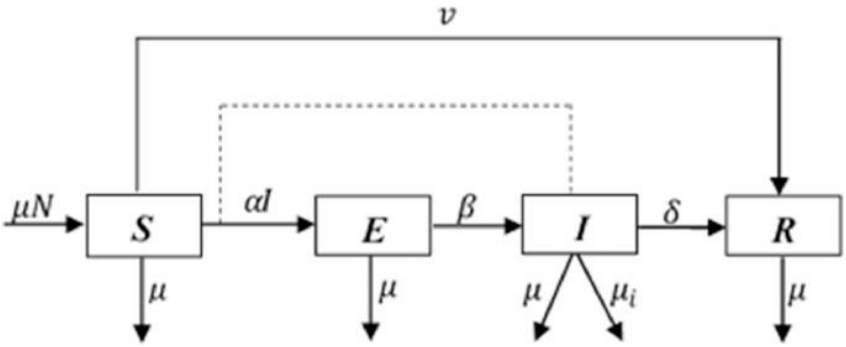

Figure 1: Schematic diagram of the SEIR model transmission for COVID-19.

Based on the schematic diagram in Figure 1, the rate of change in the number of people Suspected, Exposed, Infected, and Recovered over time in the SEIR mathematical model of the spread of COVID-19 can be interpreted as follows:

$$\frac{dS}{dt} = \mu - (\alpha I + \mu + v)S, \tag{1}$$

$$\frac{dE}{dt} = \alpha IS - (\beta + \mu)E, \tag{2}$$

$$\frac{dI}{dt} = \beta E - \left(\mu_i + \delta + \mu\right) I, \tag{3}$$

$$\frac{dR}{dt} = \delta I + vS - \mu R. \tag{4}$$

Definition of parameters of SEIR model for COVID-19 is presented in Table 1.

Table 1: Definition of parameters

Parameters	Definitions
μ	The birth/death rate
α	The transfer rate between $S(t)$ and $E(t)$
β	The transfer rate between $E(t)$ and $I(t)$
μ_i	The disease-induced death rate
δ	The recovery rate
v	Vaccine of suspected population

3 Stability Analysis of SEIR Model

3.1 Equilibrium Points

The equilibrium points that will be considered in this study are the disease-free equilibrium point (DFEP) to produce R_0 that will be used to determine the spread of pandemic COVID-19. Therefore, the endemic equilibrium point (EEP) is omitted in this work. To determine the equilibrium points, each equation in Equation (1)-(4) must be equal to zero.

3.1.1 Disease-free equilibrium point (DFEP)

The disease-free equilibrium point is where there is no spread of COVID-19 in which $E = I = 0$. Hence, the DFEP are as follow:

$$(S_0, E_0, I_0, R_0) = \left(\frac{\mu}{(\mu+v)}, 0, 0, \frac{v}{(\mu+v)}\right).$$

3.2 Stability Analysis of the model at DFEP

To determine the stability analysis of the equilibrium point at DFEP, the SEIR model needs to be linearized by using the Jacobian matrix. Based on Equation (1)-(4), the Jacobian matrix is given as:

$$J = \begin{bmatrix} -\left(\alpha I + \mu + v\right) & 0 & -\alpha S & 0 \\ \alpha I & -(\mu+\beta) & \alpha S & 0 \\ 0 & \beta & -\left(\mu_i + \delta + \mu\right) & 0 \\ v & 0 & \delta & -\mu \end{bmatrix} \tag{5}$$

The eigenvalues are determined, and the characteristic equation is as follows:

$$\begin{aligned}&\lambda^4+(A+B+C+D)\lambda^3+(AB+(A+B)(C+D)+CD-E)\lambda^2\\&+((A+B)(CD-E)+AB(C+D))\lambda+ABCD-ABE=0\end{aligned} \tag{6}$$

Where, $A=\mu, B=(\mu+v), C=(\mu+\beta), D=\left(\mu_i+\delta+\mu\right)$ and $E=\dfrac{\alpha\beta\mu}{(\mu+v)}$.

The number of possible negative real roots of Equation (6) depends on the signs of coefficients. To analyse this, we use the Descartes' rule of signs [7] on the characteristic polynomial below:

$$P(\lambda)=L_1\lambda^4+L_2\lambda^3+L_3\lambda^2+L_4\lambda+L_5, \tag{7}$$

where,

$$\begin{aligned}L_1&=1,\\L_2&=A+B+C+D,\\L_3&=AB+(A+B)(C+D)+CD-E,\\L_4&=(A+B)(CD-E)+AB(C+D),\\L_5&=ABCD-ABE.\end{aligned}$$

From the Descartes' rule of signs, the number of negative real zeros of P(λ) is either equal to the number of changes in sign of P(-λ) or less than this by an even number. Therefore, the characteristic polynomial (7) is multiplied by -1:

$$P(-\lambda)=L_1\lambda^4-L_2\lambda^3+L_3\lambda^2-L_4\lambda+L_5$$

The number of variations in P(-λ) is four. Hence, the characteristic polynomial has four negative roots. The disease-free equilibrium point of the model is locally asymptotically stable whenever $R_0 < 1$.

3.3 Basic Reproduction Number, R_0

The R_0 of the SEIR model is determined using the Next-Generation Matrix method [6]. The DFEP for the model is utilized to complete the calculation of R_0. Matrix **F** represents the rate of appearance of new infections in different compartments, while matrix **V** represents the rate of transfer of individuals from one compartment to another.

First, we need to regroup the system of ODEs into disease classes and non-disease classes. However, only the disease class were used to find matrix **F** and **V**. Therefore, matrix **F** and **V** are computed as follow:

$$\mathbf{F} = \begin{pmatrix} 0 & \dfrac{\alpha\mu}{\mu+v} \\ 0 & 0 \end{pmatrix}$$

$$\mathbf{V} = \begin{pmatrix} -\beta-\mu & 0 \\ \beta & -\mu_i-\delta-\mu \end{pmatrix}$$

Next, finding the inverse of **V.**

$$\mathbf{V}^{-1} = \begin{pmatrix} \dfrac{-\mu_i-\delta-\mu}{(\beta+\mu)(\mu_i+\delta+\mu)} & 0 \\ \dfrac{-\beta}{(\beta+\mu)(\mu_i+\delta+\mu)} & \dfrac{-1}{(\mu_i+\delta+\mu)} \end{pmatrix}$$

Lastly, matrix $\mathbf{FV}^{-1}$ is computed.

$$\mathbf{FV}^{-1} = \begin{pmatrix} \dfrac{-\alpha\beta\mu}{(\mu+v)(\beta+\mu)(\mu_i+\delta+\mu)} & \dfrac{-\alpha\mu}{(\mu+v)(\mu_i+\delta+\mu)} \\ 0 & 0 \end{pmatrix}$$

The basic reproduction number, $R_{0,}$ is the dominant eigenvalue of matrix $\mathbf{FV}^{-1}$ [6]. Therefore,

$$R_0 = \frac{\alpha\beta\mu}{(\mu+v)(\beta+\mu)(\mu_i+\delta+\mu)}.$$

The R_0 of the system (1)-(4) is locally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$.

4 Numerical Simulation of SEIR Model

The simulation of the SEIR model will be obtained using MATLAB. Several simulations are carried out by adjusting the parameters to understand the transmission dynamics of the COVID-19 outbreak. The initial condition are assumed to be *S(0) = 1000000, E(0) = 20000, I(0)= 10000, R(0) =15000* and initial parameter values of the model used in this simulation are presented in Table 2. These values are chosen randomly for the sake of example.

Table 2: Parameter values of SEIR model

Parameter	Definition	Estimated Value
μ	The birth/death rate	0.00625
α	The infection rate	0.75
β	The transfer rate between E and I	0.333
μ_i	The disease-induced death rate	0.006
δ	The recovery rate	0.125

In this simulation, the vaccination program for all individuals will also be considered, which will be administered in phases. As a result, we would consider *30%*, *50%*, and *90%* of the population in Malaysia to monitor the vaccine's effectiveness. However, the initial value of v is regarded as zero because we assume there is no vaccination plan yet.

4.1 Changes in α

The infection rate α will be changed to observe the spread of COVID-19 in a population. The infection rate varies from 0.75 to 0.55 and then rises to 0.85. Figures 2-5 display the curves for each class separately in each figure. The following results are analysed by comparing the curves to the base model.

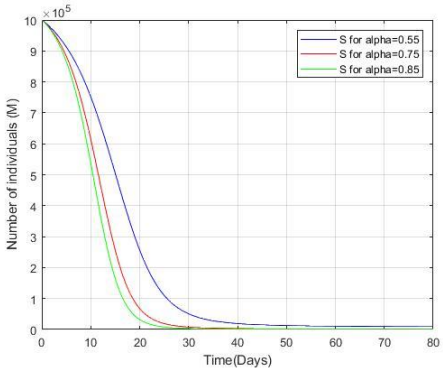

Figure 2: Variation in the number of *S* population

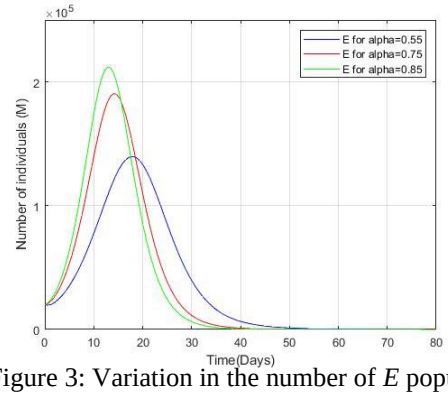

Figure 3: Variation in the number of *E* population

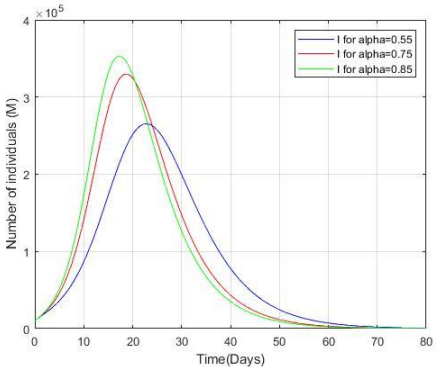

Figure 4: Variation in the number of *I* population

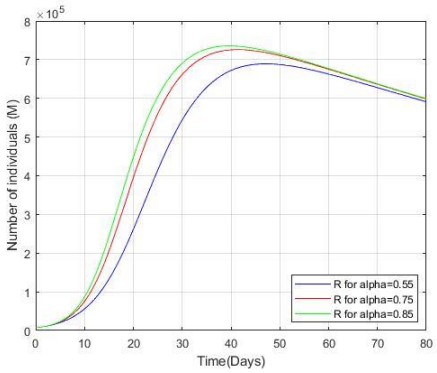

Figure 5: Variation in the number of *R* population

In particular, we can see that as the infection rate increases, the graph flattens out earlier (refer to Figure 2) compared to the initial value of α=0.75. Thus, if the α value increases, the population of susceptible individuals will decrease over time. Based on Equation (2), we can see that the relation between the rate of change of exposed population and α is directly proportional. The curve in Figure 3 peaked at α=0.55 on day 18, while at α=0.85, the curve peaked earlier, which is at day 12. Next, from Figure 4, when the α value rises, so does the rate of change among those infected with the disease. For all α values, we can see a difference at the peak of the curves. Then *I* curve with a higher α value flattens earlier than the curve with a lower α value. Figure 5 showed when α increased, and then the Recovered population

curve increased faster. When the value of α is reduced, the population of recovered individuals curve grows a little slower.

4.2 Changes in β

The rate at which individuals transition from the exposed to the infected classes, β increases from 0.333 to 0.6 and decreases to 0.1. The result obtained is as in the following figures. Figures 6 - Figure 9 represent the population curve for each class.

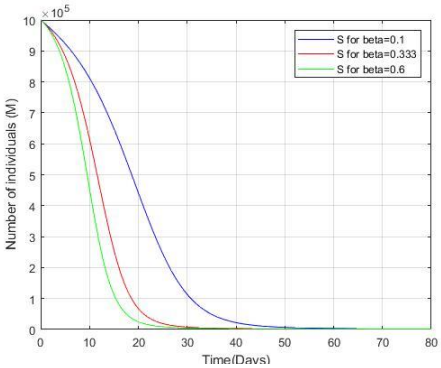

Figure 6: Variation in the number of *S* population

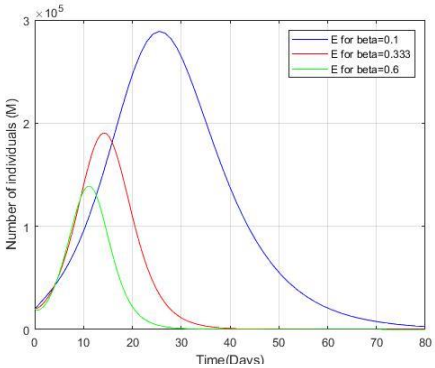

Figure 7: Variation in the number of *E* population

In Figures 6, the *S* curves for β=0.6 flattens out earlier than the curve for β=0.333. Hence, the susceptible population is decreasing when β increases. All *E* curves in Figure 7 shows a different pattern that describes the changes. If the value of β rises (β=0.6), the curve peaks sooner,

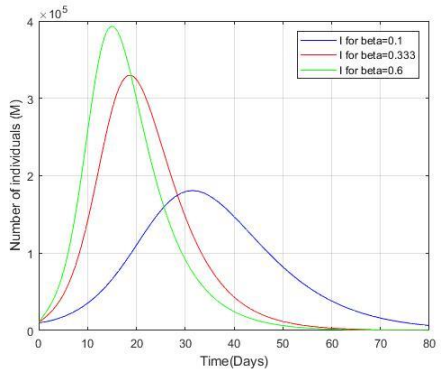

Figure 8: Variation in the number of *I* population

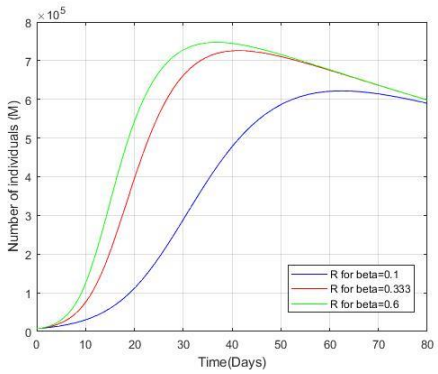

Figure 9: Variation in the number of *R* population

in 12 days, and fewer people are exposed to the disease. A higher β value helps to flatten the curve in as little as 25 days, while a lower β value takes 80 days to flatten the curve. All *I* curves showed significant variations when β was increased or decreased (refer to Figure 8). Increasing β would result in more people being infected in a shorter period. However, compared to the curve with a lower value of β, the graph flattens sooner. Next, when we look at all the curves in Figure 9, increasing the value of β causes major population changes. The population of recovered individuals grows steadily until it reaches a limit of more than 700000 individuals recovered at β=0.333.

4.3 Changes in δ

The recovery rate, δ, will be varied to 0.0625, 0.125, and 0.18 to study the changes in the population for each class. Figures 10-13 display the curves for each class separately in each figure. The following results are analysed by comparing the curves to the base model.

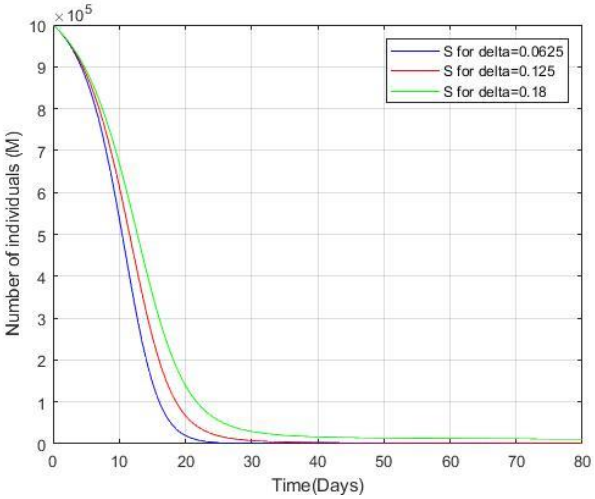

Figure 10: Variation in the number of *S* population

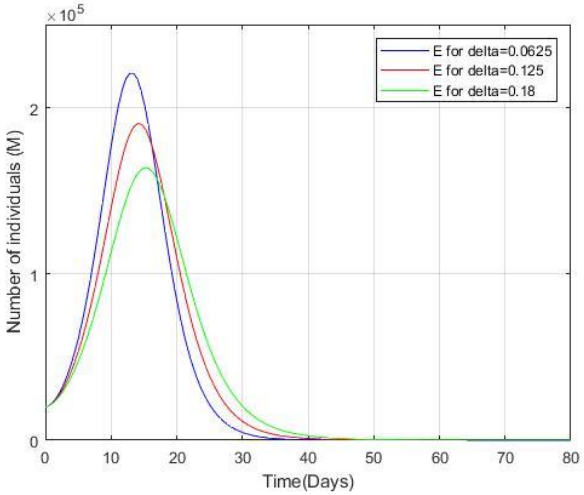

Figure 11: Variation in the number of *E* population

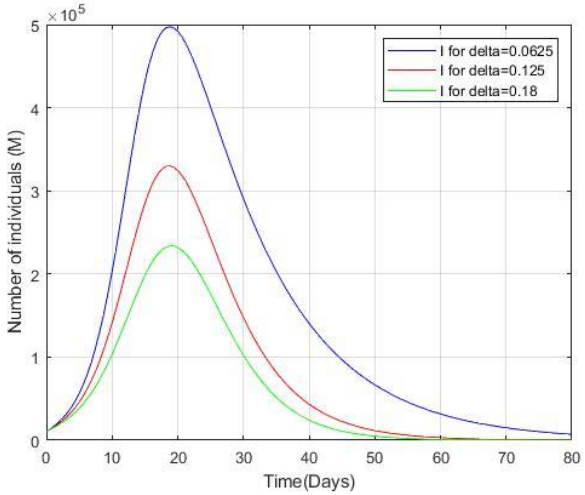

Figure 12: Variation in the number of *I* population

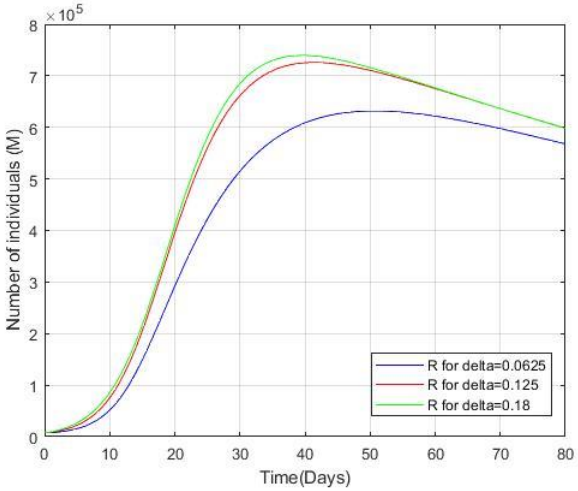

Figure 13: Variation in the number of *R* population

Figure 10 shows that as the recovery rate decreased (δ=0.0625), the *S* curve declined faster from a total population of 1000000. The number of susceptible populations continues to decline until there are no more individuals susceptible to infection. Meanwhile, from Figure 11, the *E* curve with δ=0.18 peaked later than the curve with δ=0.125 as an initial value. Therefore, the higher the value of δ, the lower the number of the exposed population. Next, Figure 12 shows that the maximum infected population reached when δ= 0.18 is just about 200000. Meanwhile, when δ= 0.0625, the maximum infected population is nearly 500000, significantly higher than the other δ values. Compared to a lower recovery rate, the curve for a higher recovery rate takes longer to flatten. In Figure 13, the pattern of the curves is almost similar. However, the *R* population curve at δ=0.18 increases faster than the *R* curve with a lower δ.

4.4 Vaccination Effectiveness

The vaccination program will be included in this section. The vaccine will be implemented to *30%*, *50%*, and *90%* of the population to observe the impact of the vaccine for the Suspected and Recovered population. Figures 14 and Figure 15 display the curves for the Suspected and Recovered population, respectively.

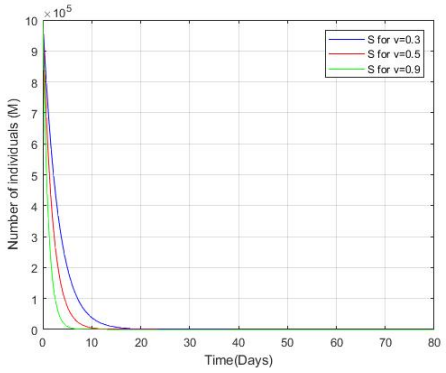

Figure 14: Variation in the number of *S* population for different *v* values.

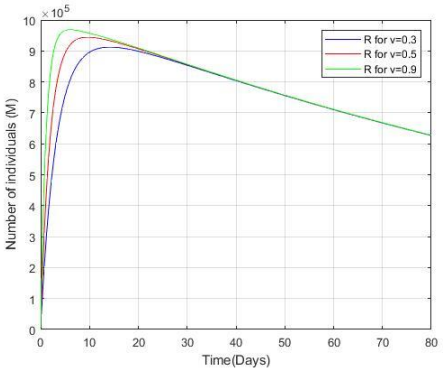

Figure 15: Variation in the number of *R* population for different *v* values.

According to Figure 14, the *30%* population that has been vaccinated takes a long time to reduce the number of Suspected populations, and the number of people recovered from COVID-19 is relatively small. The period is quite long, as shown in Figure 15. Then, if the vaccine is *50%* effective, the number of suspected populations will be reduced in a short period of time, with the number of people recovered of COVID-19 being high, around 900000 people in a short period of time, as seen in Figure 15. Furthermore, suppose a *90%* vaccine is administered. In that case, the number of suspected populations rapidly decreases, and the number of people recovering from COVID-19 exceeds nearly 1000000 in a very short period of time, as seen in Figure 15. It demonstrates that administering vaccines to the suspected community significantly impacts the overall population of recovered individuals. As a result, it is critical to provide vaccines administered to suspended COVID-19 individuals in Malaysia.

The basic reproduction number, R_0 for the endemic cases of COVID-19 with 0% vaccination is $R_0 = 5.59$. This mean that, if no vaccination given to the population, then the occurence of the disease will increase. Meanwhile, the value of R_0 become less than 1 when the vaccine is administered in the population as shown in Table 3.

Table 3: The value of R_0.

Vaccination in a population	Value of R_0
30%	0.11
50%	0.07
90%	0.04

From Table 3, we can see that the value of R_0 became less than 1 when the vaccine is given to the population. Hence, we can conclude that the numerical simulation above (Figure 14&15) shows the population converge to DFEP when $R_0 < 1$. Therefore, the pandemic of COVID-19 will eventually die over time.

5 Conclusion and Recommendations

The study's findings concluded that the SEIR model can be used as a reference model for COVID-19 spread. Analysis of the model provides an overview of global stability in the spread of COVID-19 and also provides information if Malaysia is in COVID-19 endemic status. The simulation results showed that vaccinations would speed up COVID-19 healing and give a predictive image of the number of COVID-19 cases in Malaysia. The findings can be used as a guide for early COVID-19 pandemic prevention in Malaysia.

In the future, further study of this model should be made to predict the cases according to different time and location and whether other decisions should be made for different states in Malaysia. However, reliable data is needed to enable all these possibilities to be incorporated in future models and dashboard. Other parameters such as the isolation period should be added into the model to achieve a more reliable approach to avoid the spread of COVID-19 that can be used in real-world situations. Therefore, more preventive measures can be suggested to prevent the transmission of COVID-19 outbreak, hence eliminating the infection from the population.

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