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A DYNAMIC SIR MODEL FOR THE SPREAD OF NOVEL CORONAVIRUS DISEASE 2019 (COVID-19) IN MALAYSIA

Nur Aziean Mohd Idris[1], Siti Khadijah Mohtar[2],
Zaileha Md Ali[3*], and Khadijah Abdul Hamid[4]

Faculty of Computer and Mathematical Sciences,
Universiti Teknologi MARA (UiTM), 40450 Shah Alam, Selangor, Malaysia
[1]nurazieans@tmsk.uitm.edu.my, [2]khadijahmohtar@gmail.com, [3*]zaileha@tmsk.uitm.edu.my,
[4]khadijah435@uitm.edu.my

ABSTRACT

The emergence of the first coronavirus disease 2019 (COVID-19) case in Malaysia has increased the number of infected cases. Hence, this study proposes a Susceptible-Infected-Recovery (SIR) epidemiological model of the COVID-19 epidemic to portray the outbreak's situation. The SIR model is numerically solved using the Fourth-order Runge-Kutta (RK4) method in Matlab®. The Euler method verifies that the graphical results of the SIR model are reliable and valid. In addition, this study analyses the stability of disease-free and endemic equilibriums of the SIR model by the Jacobian matrix. The results show the outbreak for phase 1 occurs in the first 100 days of the phase due to the increased infected cases in early March 2020. As for phase 2, the increases of infected cases in wave 2 make the outbreak occur throughout phase 2, with R_0 *being higher than phase 1. The infected population for phase 3 shows asymptotic behavior even though the infection rate increases, but the recovery rate is much higher than in phase 2. The local stability of the endemic equilibrium of all phases exists since the value of* R_0 *is more than one. The system is locally asymptotic stable for all three phases since the obtained eigenvalues are real and negative.*

Keywords: *COVID-19, SIR Model, Compartment Model, Epidemic Model, Infectious diseases, Stability*

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1. Introduction

A coronavirus is a large group of viruses that consist of genetic material surrounded by an envelope of protein spikes. Based on research by Kahn and McIntosh (2005), the first coronavirus was discovered and characterized by Tyrrell and Bynoe in 1965 when they found the coronavirus in human embryonic tracheal organ cultures obtained from the respiratory tract of an adult who had a common cold. In December 2019, one of the largest cities in the central part of China had brought the world's attention to the outbreak of atypical pneumonia caused by the zoonotic 2019 novel coronavirus (2019-nCoV).

Since the breaking news of the outbreak of 2019 novel coronavirus (2019-nCoV) in Wuhan happened, many researchers from different fields such as the National Health Commission, World Health Organization, mathematicians and medical experts have explored and studied the coronavirus issues in order to figure out the effectiveness and efficiency of interventions and recovery ways in decreasing the spread of the outbreak. On 31 January, 2020, Wu *et al.* (2020) published their research on inferring the number of infections in Wuhan by using the data from 31 December, 2019, to 28 January, 2020. They also forecasted the national and global growth of 2019-nCoV and predicted the effect of Wuhan's metropolitan-wide quarantine and surrounding cities. The outbreak of the disease had spread in China and to other countries, including Malaysia.

According to WHO Country Office in Malaysia, the first case of COVID-19 in Malaysia was detected on 24 January 2020. Within 3 few weeks, Malaysia had recorded the largest confirmed cases of COVID-19 infections in Southeast Asia. By 16 March, every state in the country had reported cases. The partial lockdown was imposed on 18 March. During the 2020 Movement Control Order (MCO) implementation, all movements and mass assembly across the country are prohibited immediately.

Even after the local government introduced strict restrictions and appropriate prevention policies to control the spread of the virus within a community, COVID-19 has been growing fast in Malaysia and has become a public health threat. Thus, it is crucial to understand the severity of this outbreak. Various methods and techniques have been highlighted to describe the severity of the problem and resort to the solution for this pandemic (Ariffin *et al.*, 2020; Ming *et al.*, 2020; Shao and Shan, 2020; Wu *et al.*, 2020). One of them is the Susceptible-Infectious-Recovered (SIR) model. The SIR model has divided the human population into three compartment classes: susceptible individuals, infected individuals, and recovered individuals from the disease. In the early twentieth century, the SIR model was developed by Ronal Ross and William Hamer in the early 20th century, which consists of a system of three coupled non-linear ordinary differential equations. Kermack and McKendrick were the SIR model pioneer who established their article on the “Applications of mathematics to medical problems” (Bacaer, 2011).

Many researchers have used the SIR model to study the spreading of various diseases. Several recent studies on SIR model for COVID-19 in Malaysia can be found in Wong *et al.* (2021), Salman *et al.* (2021), Ariffin *et al.* (2020), Law *et al.* (2020), Mahmud & Lim (2020), and Arifin *et al.* (2020), focusing on simulation of infectious trend in order to understand the dynamical behaviour of the SIR model in Malaysia. However, this study analyzes the infectious trend using actual data from 1 Mac 2020 until 31 December 2020. The actual data of the infected and recovery cases are curve fitted and the value of R^2 is determined. Both are calculated using the R software environment.

Differential equations of the SIR Model can be solved numerically, mainly using the Runge-Kutta method. The Runge-Kutta method is one of the most widely numerical methods used by researchers such as Ashgi *et al.* (2021), Kovalnogov (2020), Lede & Mungkasi (2019), Hossain *et al.* (2017) and Side *et al.* (2018). The method invented by German mathematicians Carl Runge and Wilhelm Kutta is a basic explicit method for numerical integration of differential equations. The fourth order Runge-Kutta (RK4) is preferably used since RK4 is more stable than the other order Runge-Kutta methods. Therefore, this method is ideal for solving a differential equation of the SIR model.

Local stability analysis also plays an essential role in the SIR model to control the endemic disease spread. Analysing the stability of the disease-free equilibrium could also help identify whether the outbreak will demise or increase in the future. The stability of the disease-free equilibrium points could be obtained using the Jacobian matrices and the basic reproduction number, R_0. Egbetade *et al.* (2018) and Tahir *et al.* (2019) introduced their research on the local stability of disease-free equilibrium and endemic equilibrium of the dynamic of infectious disease in a population. Egbetade *et al.* (2018) used eigenvalues of the Jacobian matrix and basic reproduction number, R_0 to determine the local stability of the equilibrium point of the SIR model for tuberculosis, hepatitis B, malaria, typhoid, cholera, measles and smallpox. Tahir *et al.* (2019) implemented the next-generation matrix approach to calculate a basic reproduction number, which determines the stability of the Ebola SIR model.

Modelling the SIR model for the COVID-19 outbreak is an essential way to provide a most straightforward framework to analyze the spread of the disease within a community in Malaysia. This paper aims to investigate the SIR model of COVID-19 based on daily cases in Malaysia to illustrate this outbreak within the stipulated time. Hence, the stability conditions of the disease-free equilibrium and the endemic equilibrium are also analyzed.

2. Formulation of SIR model for COVID-19

The human population can be divided into three components: the susceptible, the infected, and the fully recovered (Kermack & Kendrick, 1927). The system of the human population is presented in the compartment model, as shown in Figure 1. The model indicates some populations have been infected by the coronavirus disease 2019 (COVID-19) while others have not been infected yet. The increasing of susceptible groups will happen through the natural birth and fully recovered individuals who have lost their immunity. At the same time, the susceptible group also will decrease through the natural death and infectious group. The susceptible individual will acquire the COVID-19 infection through the connection with the symptomatic patients with show the symptoms of coronaviruses.

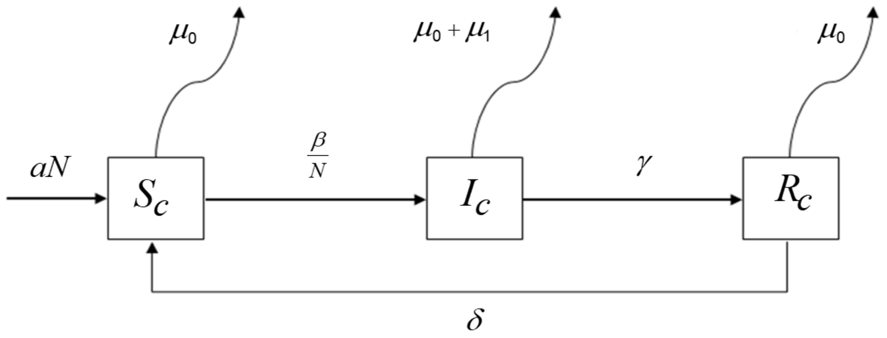


Figure 1. Flowchart of the compartments of SIR model

The dynamic of the human population for the SIR model of the COVID-19 in Figure 1 is represented by the differential equations below

$$\begin{aligned}\frac{dS_c}{dt}&=\alpha N-\frac{\beta I_c}{N}S_c-\mu_0 S_c+\delta R_c\\ \frac{dI_c}{dt}&=\frac{\beta I_c}{N}S_c-\left(\mu_0-\mu_1\right)I_c-\gamma I_c\\ \frac{dR_c}{dt}&=\gamma I_c-\mu_0 R_c-\delta R_c\end{aligned}\tag{1}$$

where, N, S_c, I_c, R_c represent the human population, the number of susceptible, the number of infected and the number of recovered individuals, respectively. All the variables are functions of time, *t.* The parameter α is the natural birth rate population, β is the infectious rate, μ_0 is the rate of natural death, μ_1 is he rate of death caused by the disease, γ is the recovery rate, and δ is the rate at which recovered people become susceptible due to low immunity or health related issues.

Assume that the number of human populations, N is constant. Thus, the total population of human at t, can be described as

$$N = S_c + I_c + R_c \tag{2}$$

Introducing dimensionless variables to normalize the system (1) as follows

$$S = \frac{S_c}{N}, I = \frac{I_c}{N}, R = \frac{R_c}{N} \tag{3}$$

Therefore, the simplified model of the COVID-19 for the human population as

$$\begin{aligned} \frac{dS}{dt} &= \alpha - \beta IS - \mu_0 S + \delta R \\ \frac{dI}{dt} &= \beta IS - (\mu_0 - \mu_1) I - \gamma I \\ \frac{dR}{dt} &= \gamma I - \mu_0 R - \delta R \end{aligned} \tag{4}$$

where S, I and R are dimensionless variables for the number of susceptible, the number of infected and the number of recovered individuals, respectively.

2.1 SIR Parameters

Secondary data is retrieved from the Crisis Preparedness and Response Centre (CPRC) by the Ministry of Health Malaysia (KKM). The data retrieval period of the COVID-19 cases is dated from 1 March until 31 December 2020.

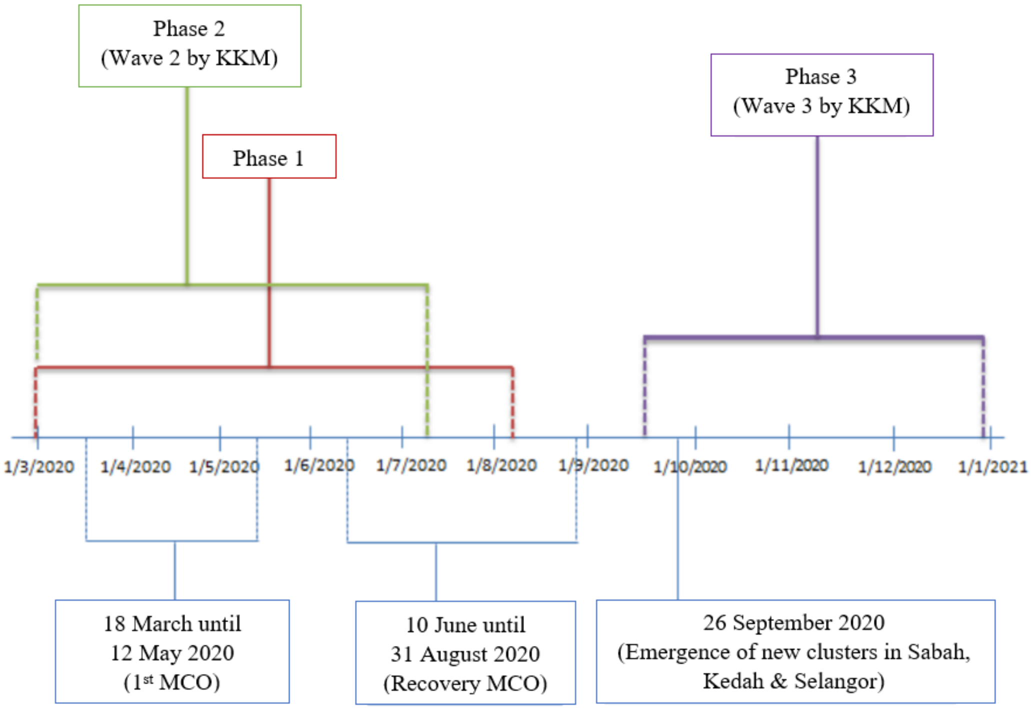


Figure 2. The timeline of COVID-19 in Malaysia

As shown in Figure 2, the analysis is divided into three phases: Phase 1 consists of data before the implementation of MCO until the end of the recovery MCO period (1 March

2020 to 7 August 2020). Phase 2 is for the second wave (1 March to 2 July 2020), and Phase 3 is for the third wave (20 September 2020 to 31 December 2020). Taking the data of the second and third waves of COVID-19 allows us to analyze the stability of the outbreak during the period given by the KKM by estimating the eigenvalues.

The values of the parameter estimated for each phase for infection rate (β) and recovery rate (γ) are obtained through the curve fitting process of the daily cases in R software environment. Meanwhile, the rate of death caused by the disease (μ_1), is estimated using the formula of the number of total deaths over the number of infected cases. The natural birth rate (α), natural death rate (μ_0) and the rate at which recovery people become susceptible due to low immunity or health-related issues (δ) are assumed as zero to simplify the SIR model.

3. Numerical Method/Runge-Kutta Method

The governing Equations (4) are solved numerically using the RK4 and assisted by Matlab® software.

The RK4 method commonly used is written as below (Burden,2010)

$$y_{n+1} = y_n + \frac{h}{6}\left(k_1 + 2k_2 + 2k_3 + k_4\right) \tag{5}$$

with

$$\begin{aligned} k_1 &= f\left(x_n + y_n\right) \\ k_2 &= f\left(x_n + \frac{1}{2}h, y_n + \frac{1}{2}hk_1\right) \\ k_3 &= f\left(x_n + \frac{1}{2}h, y_n + \frac{1}{2}hk_2\right) \\ k_4 &= f\left(x_n + \frac{1}{2}h, y_n + \frac{1}{2}hk_3\right) \end{aligned} \tag{6}$$

Where h is a step size and each of the k 's represents a slope.

4. Stability of The Model

This section focuses on how to obtain the disease-free equilibrium and the endemic equilibrium of system in (4).

4.1 Basic Reproduction Number

The basic reproduction number, R_0 could be described as the expected number of secondary disorders produced by a single infection in a completely susceptible population without immunity and preventive measures. When the infected individual infects more than one or $R_0 > 1$, the viruses can further spread in a population and become an outbreak. On the other hand, if $R_0 < 1$ or infected individual less than one, then the disease can be diminished. When

$R_0 = 1$, the outbreak becomes endemic since every infected person will only infect one person before recovering. According to Chuo at el. (2008), The basic reproduction number, R_0 for the SIR model will be defined as Equation (7).

$$R_0 = \frac{\beta S}{\mu_0 + \mu_1 + \gamma} \tag{7}$$

4.2 Local Stability of The Disease-Free Equilibrium Point

Diekmann et. al. (1990) stated the disease-free equilibrium point will be asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$. Let $\frac{dS}{dt} = \frac{dI}{dt} = \frac{dR}{dt} = 0$ and the disease-free equilibrium point is $J(P_0) = (1,0,0)$. The model has a disease-free equilibrium given by this Jacobian matrix $J(P_0)$:

$$J(P_0) = \begin{bmatrix} -\beta I - \mu_0 & \beta S & \delta \\ \beta I & -(\mu_0 + \mu_1) - \gamma & 0 \\ 0 & \gamma & -\mu_0 - \delta \end{bmatrix} \tag{8}$$

The eigenvalues are obtained by solving the matrix Equation (8).

If the eigenvalues, λ have negative real parts, thus the disease-free equilibrium point will become asymptotically stable. In other words, each infectious individual infects less than one other individual, and the pathogen will demise the population. Otherwise, if the eigenvalues λ have positive real parts, then the disease-free equilibrium point will become unstable, which means that there will be an exponential rise in the number of cases over time and epidemic results (Woolf, 2020).

4.3 Existence of The Endemic Equilibrium Point

Diekmann *et al.* (1990) stated the endemic equilibrium point $J(P_1) = (S_0, I_0, R_0)$ of the epidemic model will exists if $R_0 > 1$. Thus, the Jacobian matrix $J(P_1)$ for the system in (4)

$$J(P_1) = \begin{bmatrix} -\beta I - \mu_0 & -\beta S & \delta \\ \beta I & \beta S - (\mu_0 + \mu_1) - \gamma & 0 \\ 0 & \gamma & -\mu_0 - \delta \end{bmatrix} \tag{9}$$

5. Result and Discussion

The graphical results of the numerical solution to SIR model in (4) are presented in this section. Moreover, the stability of disease-free and endemic equilibriums of the SIR model is analyzed by the Jacobian matrix.

The SIR model for phase 1 is conducted for 160 days, from 1 March 2020 to 7 August 2020 with $R_0 = 1.733683152$. Phase 1 is initialized by setting 1 Mac 2020 as time, $t = 0$ with the initial conditions $S(0) = 1$, $I(0) = 0.2$ and $R(0) = 0$. Phase 2 is conducted for 124 days from

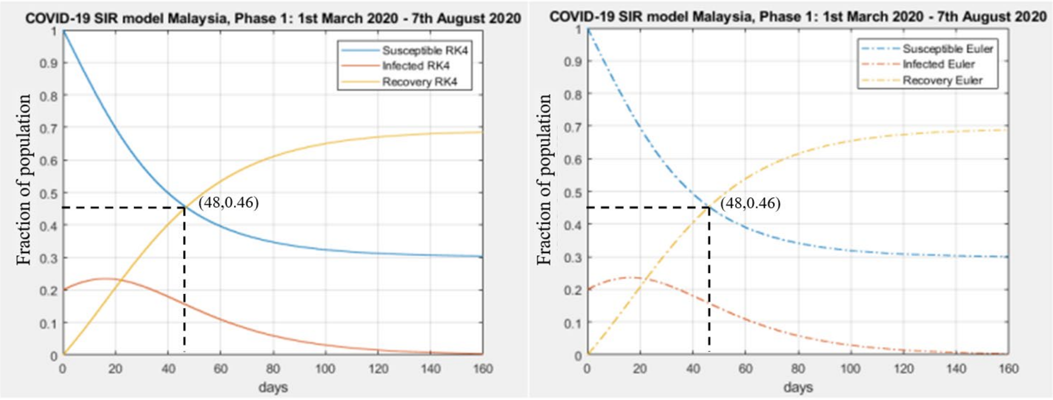
1 March 2020 to 2 July 2020 with $R_0 = 1.904371247$ and the same initial conditions in phase 1. Lastly, phase 3 is conducted for 103 days from 20 September 2020 to 31 December 2020 with $R_0 = 2.543103448$ and initial conditions $S(0) = 1$, $I(0) = 0.09$ and $R(0) = 0.01$.

5.1 Validation of The Methods

A Comparative study for the SIR model with the numerical results of the Euler method is performed to prove and validate the numerical results obtained from RK4 method by comparing the pattern of susceptible, infected and recovered individuals against time *t* (days). The values of the estimated parameter being considered in this study are listed in Table 1.

Table 1: The parameter values for phase 1, phase 2 and phase 3.

Parameters	**Phase 1**	**Phase 2**	**Phase 3**
Infection rate, β	0.079946685	0.05158641	0.26236209
Recovery rate, γ	0.046113781	0.027088421	0.10316611
Disease-induced death, μ_1	0.013907432	0.014122316	0.00331573



(a) (b)

Figure 3. The graphical comparison of SIR graph using (a) RK4 method and (b) Euler method for phase 1 with the initial conditions $S(0) = 1$, $I(0) = 0.2$ and $R(0) = 0$.

Figure 3 shows the graphical comparison of the SIR graph with the RK4 and Euler methods. The behavior of SIR in Figure 3(a) is the spitting image of Figure 3(b). The value at 44 days portrays 0.46 for both methods. These identical results verify that both methods are in agreement with one another. Hence, the numerical results obtained are considered reliable and valid.

5.2 Analysis of The Results

The dynamic behavior of the SIR model is investigated based on the simulation curves obtained from (2). This study focuses on three phases of daily COVID-19 data.

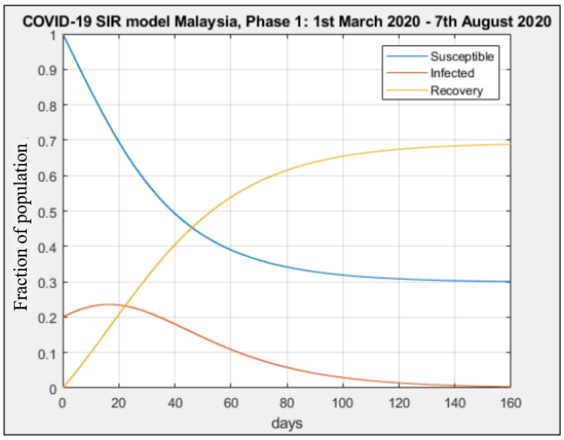


Figure 4. The SIR model for phase 1 (160 day) with $\beta = 0.079946685$, $\gamma = 0.046113781$ and $\mu_1 = 0.013907432$ and initial conditions $S(0)=1, I(0)=0.2, R(0)=0$.

Figure 4 shows the initial stage of day zero, $t = 0$ the infectious count has an upward trend until day 20 due to some peak cases between 15 March 2020 (day 15) to 26 March 2020 (day 26). However, the infected population started to decline steadily by exhibiting a downward trend from day 21 (21 March 2020) until day 160 (7 August 2020) since the implementation of MCO from 18 March 2020 (day 18) until 12 May 2020 (day 73). Meanwhile, the susceptible population decreases rapidly from day zero to day 120 (28th June 2020). On day 121, the susceptible graph remains asymptotically until day 160. For the recovered population, the graph started to significantly increase from day zero to day 160. The outbreak for phase 1 occurs in the first 100 days of the phase. After day 101, the outbreak is controllable until the end of the phase.

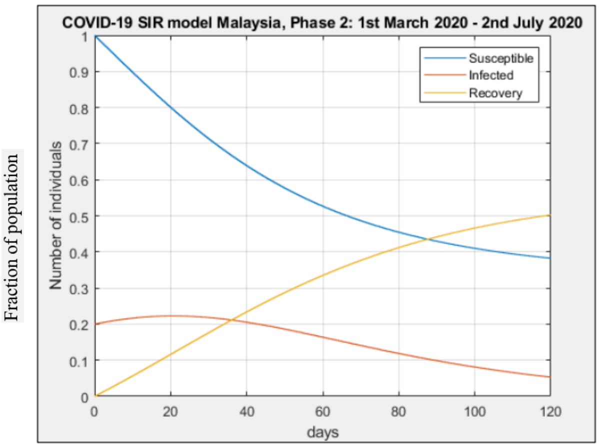


Figure 5. The SIR model for phase 2 (124 day) with $\beta = 0.05158641$, $\gamma = 0.027088421$ and $\mu_1 = 0.014122316$ and initial conditions $S(0)=1, I(0)=0.2, R(0)=0$.

Figure 5 portrays the results for phase 2 (second wave) from 1 March 2020 until 2 July 2020. The graph of infection on day zero noticeably increases until day 20. From the reported daily cases, there are few peak cases between day 20 (20 March 2020) and day 26 (26 March 2020), exceeding 200 cases per day. Since the implementation of MCO on day 18 (18th March 2020) until day 73 (12th May 2020), the infected graph gradually decreases from day 40 until day 120. Meanwhile, the susceptible population moderately decreases from day zero to day 120 (28th June 2020) after the recovery of MCO (RMCO) on 10 June 2020 (day 102) until 28 June 2020 (day 120). While the recovered population steadily increases from day 27 to day 120. The outbreak for phase 2 occurs due to the increase of infected cases with the value of R_0 higher than phase 1.

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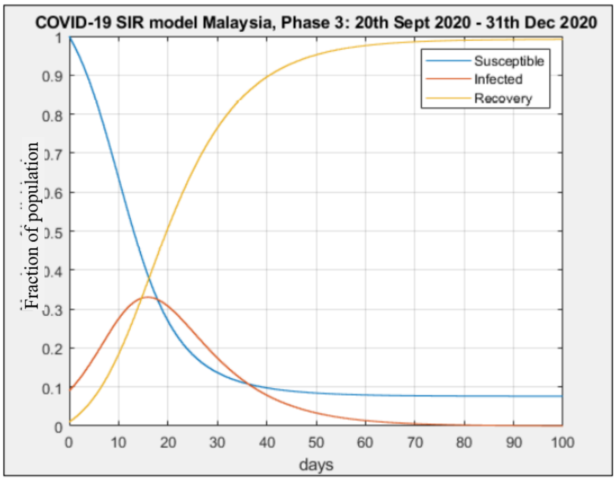

Figure 6. The SIR model for phase 3 (103 day) with $\beta = 0.262362091$, $\gamma = 0.10316611$ and $\mu_1 = 0.003315734$ and initial conditions $S(0) = 1, I(0) = 0.09, R(0) = 0.01$.

Figure 6 depicts phase 3 (wave 3), which is 20 September 2020 until 31 December 2020. The infected cases rose dramatically from day zero (20 September 2020) until day 16 (6 October 2020), which was caused by the appearance of new clusters in Sabah, Kedah and Selangor in the middle of September. These formed clusters exist when most people travel regionally within Sabah and the peninsula following the parliamentary Sabah on 26 September 2020. Meanwhile, the Sivagangga cluster in Kedah started when the restaurant owner visited a town exposed to the outbreak. After day 20, the infected population starts to decrease rapidly until day 70 and remains asymptotically from day 71 until day 100. The susceptible population decreases rapidly from day zero to day 40 (30 October 2020). After day 41, the susceptible population remains asymptotically until day 100. The recovery graph steeply increases until the end of phase 3. Over 88000 people were recovered after 28 December 2020. The graph of infected gradually shows asymptotic behavior even though the infection rate increases, but the recovery rate is much higher.

5.3 The analyzing of the stability of disease-free equilibrium points of SIR model by the Jacobian matrix

The disease-free equilibrium point will be asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$. In this section, the stability conditions for the disease-free equilibrium are analyzed with R_0 for phase 1, phase 2 and phase 3 are 1.733683152, 1.904371247 and 2.543103448, respectively. The eigenvalues obtained are used to determine the stability of the system are shown in Table 2.

Table 2: The eigenvalues for the stability of the disease-free equilibrium

	Eigenvalues
Phase 1	$\lambda_1 = 0, \lambda_2 = 0, \lambda_3 = -0.06$
Phase 2	$\lambda_1 = 0, \lambda_2 = 0, \lambda_3 = -0.0412$
Phase 3	$\lambda_1 = 0, \lambda_2 = 0, \lambda_3 = -0.1065$

Since eigenvalues are all real and negative, the system is locally asymptotic stable for all three phases which approaches asymptotically to COVID-19 free equilibrium points.

6. Conclusion

The SIR model for the COVID-19 disease in this study is a fundamental model to describe the situation of the outbreak. Moreover, the results of the SIR model depict an overall picture of the infectious of COVID-19 in Malaysia. The results indicate that the implementation of MCO, CMCO and RMCO has significantly affected the number of infected cases and recovered cases simultaneously. The first conclusion in this study is the outbreak for phase 1 occurs in the first 100 days of the phase between day 20 and day 26. Secondly, the increases of infected cases in wave 2 makes the outbreak occurs throughout phase 2 with the value of R_0 higher than phase 1. Moreover, the infected cases in phase 3 gradually shows asymptotic behavior even though the infection rate increases but the recovery rate is much higher. Lastly, the local stability of the endemic equilibrium of all phases exists since the value of R_0 is more than one. The system is locally asymptotic stable for all three phases, since the eigenvalues obtained are all real and negative. Further research can be done by adding new parameters such as incubation, vaccination and treatment to the current SIR model in order to reflect the real COVID-19 epidemic situation.

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