

A Performance of SIR Model in Predicting the Number of COVID-19 Cases in Malaysia based on Different Phase of COVID-19 Outbreaks

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HIGHLIGHTS

- Modelling on the first, second, third waves and endemic phases by using SIR model show that the number of infections reached maximum level in a very short time.
- The R_0 value in this model for all simulation is 5.1. This led to the outbreak of highly contagious disease and the severity can be considerate.
- The number of infected populations increase with the rate of disease transmission rate of infected (β) increases and vice versa.

ABSTRACT

Since December 2019, COVID-19 has quickly taken on a massive global form led to the World Health Organization (WHO) classified COVID-19 as a pandemic outbreak as a result. Due to a lack of information about the virus and the absence of medical services in the community during the early stages of this outbreak, the coronavirus spread quickly. Consequently, it becomes extremely difficult to control the influence of the disease outbreak. Thus, this study was aim to predict the peak numbers of the infected population on the first, the second, the third waves and endemic phase by utilizing a Susceptible-Infected-Recovered (SIR) predictive model between 25th January and 16th February 2020, corresponding to the entire first wave, the second, between 27th February 2020 and 30th June 2020, corresponding to part of the second wave, the current third wave began on 7th September 2020 and 1st April 2022, corresponding to the endemic phase, still present at the time of writing this article. The model retrieved the data from a reliable source on the Internet and its design is based on certain assumptions. The estimated reproductive value (R_0) in this model for all simulations is 5.1, which are interconnected factors that have contributed to the rapid increase in the number of COVID-19 cases. This led to the outbreak of a highly contagious disease. The number of infected populations increase with the rate of disease transmission rate of infected (β) increases and vice versa and the spread of COVID-19 from first, second, third waves and endemic reached maximum level in a very short time. The COVID-19 endemic in Malaysia is predicted to peak by the early of March 2020 for the first wave, mid of April 2020 for the second wave, early of October 2020 for the third wave and around April 22, 2022, for the endemic phase. The peak infected was predicted at 16,280,000 persons out of a total of susceptible individuals (S) 33,573,874. Therefore, in addition to



maintaining control measures at least until the anticipated peak time has passed, proper crisis management and efficient resource use are essential for successfully combating the endemic.

Keywords: SIR model, COVID-19, epidemiological model

INTRODUCTION

The COVID-19 pandemic is Malaysia's deadliest communicable disease outbreak since the 1918 Spanish Flu, which killed 34,644 people, or 1% of the then-British Malayan population. The Nipah virus outbreak in 1999 claimed the lives of 105 Malaysians, whereas the SARS outbreak in 2003 claimed the lives of only two people (Hashim et al., 2021). On January 25, 2020, COVID-19 was discovered for the first time in Malaysia. Multiple clusters have been discovered in Petaling District, with the first locally transmitted case reported on February 8th. Descriptive analyses of the epidemiology of the COVID-19 outbreak in Petaling are presented from the first case to the end of the first wave (Supramanian et al., 2021). Meanwhile, the second wave lasted from February 27 to June 30, 2020. Lastly, the third wave began on September 7, 2020. The Benteng Lahad Datu cluster in Sabah and the Tembok cluster in Kedah were the two largest contributors to the sudden increase in cases in the third wave. As announced by Malaysia's Prime Minister Ismail Sabri Yaakob on 8 March 2022 (Tuesday), Malaysia will begin its transition to the endemic phase from Friday, 1 April 2022.

This disease swiftly spreads throughout China, followed by a worldwide increase in the number of patients. The purpose of mathematical modeling is to represent different types of a real-world situation in mathematical language (Hui, 2020; Goel et al., 1971; Li et al., 2020; World Health Organization, 2020). Preventative measures to reduce the spread's impact have become more dependent on the use of mathematics. It has been proved and accepted that mathematical modelling is a valuable tool to understand the dynamics of infectious diseases. Further, the mathematical modelling tools will support in developing the control strategies of infectious diseases. Further, the mathematical modeling and tools will support in developing the control strategies of infectious diseases (Kucharski et al., 2021; Tuite et al., 2020; Panovska-Griffiths, 2020; Prem et al., 2020).

The transmission dynamics of diseases such as dengue fever, tuberculosis, diabetes, HIV-AIDS has been explicated by Egonmwan and Okuangahe (2019), Waziri et al., (2012), Takahashi et al., (2010), Tang et al., (2020), Side et al., (2017) and Ahmad and Budin (2012). Despite there are various methods, the principle remains the same for SIR model that is to find some parameters which enable the model to represent the actual recorded data. Therefore, SIR model can estimate future fatalities and offer time periods for infection drop in communities. Furthermore, when fresh data is fed into the model, it is simple to tweak the model's parameters to obtain the best-fit curves for predictive purposes. As a result, the predictive mathematical model may assist the government in containing and preventing the spread of C-19 in the country. In Malaysia, a couple of assessments have been made by investigators; for example, Salman et al., (2021) used to perform situation examination for COVID-19 by using a straightforward comprehensiveness class of SIR structure.

The main objective of this study was to generate COVID-19 projections in Malaysia using epidemiological models. Specifically, we implemented the SIR model in evaluating the peak rates of infected population of COVID-19 on the first, the second, the third waves and endemic phase within a specific period in Malaysia.

The rest of the paper is structured as follows. The details of the methodology are presented in the following section by formulating cases of COVID-19 using the SIR model. After that, the stability of the model equilibria is analyzed using the base reproduction number to understand the severity. Theoretical results



are then obtained by comparing the number of infected populations and finally a numerical illustration is produced to ensure that the theoretical results are relevant to the endemic in Malaysia.

METHODOLOGY

The simplest epidemic model assumes a constant population size, N . That is, there are no deaths or population movements that affect population size. Because most epidemics are over in a relatively short period of time compared to the average person's life span-the assumption of constant population size is reasonable for individuals in the population. To put it another way, because an epidemic occurs relatively quickly, the model does not need to include the natural deaths and births (vital public health statistics) rates. Epidemics of diseases such as influenza are common for example like measles, rubella, and chickenpox (Levin et al., 1989). Numerical simulation of model uses secondary data on the number of COVID-19 cases in Malaysia (Github) by using Maple software to predict the number of COVID-19 active cases in Malaysia specifically.

SIR Model Formulation for COVID-19

The SIR model on the spread of COVID-19 is divided into three compartments namely Suspected (S), Infected (I), and Recovered (R). A class of affected individuals can spread the infection to other people. The mathematical equations that formulated the rate of change in the number of people Suspected, Infected and Recovered over time in the SIR model are briefly as follow:

$$\frac{dS}{dt} = -\beta SI \quad (1)$$

$$\frac{dI}{dt} = (\beta S - r)I \quad (2)$$

$$\frac{dR}{dt} = rI \quad (3)$$

Definition of variables and parameters of SIR model for COVID-19 presented in Table 1.

Table 1: Definition of Variable/Parameter

Variable/Parameter	Description
N	Total population people in Malaysia (constant)
S	Susceptible are members of the population who do not have the disease at one point in time but may develop it later.
I	Infectives are members of the population who have already been infected by the disease at a given time and have the potential to spread it to others.
R	Individuals in the population who have recovered from the disease and are no longer infectious at the time t are referred to as the recovered.
β	Proportionality constant known as the infection rate.
r	Removal rate.

The SIR model is completed by giving each differential equation and initial condition. For this COVID-19 virus, it is assumed that anyone was immune at the beginning of the epidemic. Thus, almost everyone was susceptible where $S(0) = N$. $I(0)$ is assumed to be the infectious people (active cases) on the first date for



each phase. Meanwhile, the parameters β and r are both positive constants. This estimated value of parameters used in SIR model is fitted on data for each phase. The initial conditions for this model are initial number of susceptible $S(0) > 0$, the initial number of infectives $I(0) > 0$, and the initial number of recovered $R(0) = 0$.

Equilibrium and Stability Analysis

Based on equations (1) – (3), stability analysis is carried out to determine the disease-free equilibrium point and endemic equilibrium point. To determine the two equilibrium points, each equation in equations (1) - (3), must be equal to zero, or $\frac{dS}{dt} = 0$, $\frac{dI}{dt} = 0$ and $\frac{dR}{dt} = 0$, thus obtained:

$$-\beta SI = 0 \tag{4}$$

$$(\beta S - r)I = 0 \tag{5}$$

$$rI = 0 \tag{6}$$

To find the stability of COVID-19, the Jacobian matrix must be evaluated as well as its equilibrium points. From the maple output, the Jacobian matrix of the equation is:

$$J = \begin{bmatrix} -\beta I & -\beta S \\ \beta I & \beta S - r \end{bmatrix} \tag{7}$$

The equilibrium states in this model are at the points where $I = 0$, where $S = N$ is any positive constant (hence the equilibrium points are non-isolated). From the Maple output, there are two eigenvalues, 0 and $\beta S - r$.

Clark (2002) stated that if the circumstance for an endemic is satisfied, this second eigenvalue is positive, which means the equilibrium is unstable. Meanwhile, if the second eigenvalue is negative, there is no conclusion to the stableness of the linearization due to the zero eigenvalue. However, it is far apparent that the equation is not strictly stable even in that case, due to the fact any perturbation with non-zero I which decreases and consequently does not return to S (Clark, 2002). Since $S = N$, the second eigenvalue is positive precisely when $R_0 = \beta N / r > 1$ where R_0 is the basic reproduction number. Thus, an epidemic occurs when, and only when, each of the initially infective individuals infects more than one other individual.

Then, by the matrix's generation method (Diekmann et al., 2010), in the SIR model, the basic reproductive number, $R_0 = \beta N / r$.

- i) If $R_0 < 1$ indicate the disease-free equilibrium.
- ii) If $R_0 > 1$ indicate there is an endemic equilibrium.
- iii) If $R_0 = 1$ indicate no changes occur.



FINDINGS AND DISCUSSIONS

Model simulations are performed using Maple software. The initial values $S(0)$, $I(0)$ $R(0)$ and parameter values of the models used in this simulation for the first, the second, the third waves and endemic phase are presented in Table 2 and Table 3, with the basic reproduction number values R_0 is $R_0 = \beta N/r$.

Table 2: Initial Value of SIR Model for COVID-19 in Malaysia on First, Second, Third Waves and Endemic

Variable	Description				References
	First Wave	Second Wave	Third Wave	Endemic Phase	
$S(0)$	33,573,874	33,573,874	33,573,874	33,573,874	Github
$I(0)$	4	1	62	17476	Github
$R(0)$	0	0	0	0	-

Table 3: Parameter Value of SIR Model for COVID-19 in Malaysia

Parameter	Description	References
β	0.0000000156	Assumed
r	0.102	Assumed

During the fitting and simulation process, the optimized value of parameters β and r are adjusted manually to fit the recorded data as best as possible, based on a trial-and-error approach and visual inspections (Cooper et al., 2020). A preliminary analysis using non-linear fittings to fit the model to the published data (Github) provided at best inferior results to those obtained in this paper. Then to justify the model trial-and-error approach had been used with visual inspections, since the model solutions did not follow as close the published data (Cooper et al., 2020).

The eigenvalues based on equation (7) with the parameter values in Table 2 and Table 3 for the COVID-19 transmission SIR model for first, second, third waves and endemic phase simulations are written in Table 4.

Table 4: The Values of eigenvalue of SIR Model for COVID-19 in Malaysia

Phase	$S = N$ $S(t) + I(t) + R(t)$	$\lambda = \beta S - r$
First Wave	33,573,878	0.4217524968
Second Wave	33,573,875	0.42175245
Third Wave	33,573,936	0.4217534016
Endemic	33,591,350	0.42202506

Based on Table 4, the eigenvalues obtained for all phases are real and positive, based on (Clark, 2002) which indicates that the type of stability at this equilibrium point is asymptotic unstable. However, it is far apparent that the equation is not strictly stable even in that case, due to the fact any perturbation with non-zero I which decreases and consequently does not return to S. The basic reproduction numbers R_0 for all phases of COVID-19 in Malaysia is $R_0 = 5.134827788$ which means that if a person is infected with



COVID-19 it will infect 5 other people. Then, since $R_0 > 1$, there will be an epidemic. This calculation is used to determine the potential for epidemic spread in a susceptible population. The effective reproduction number determines the potential for epidemic spread at a specific time t under the control measures.

From Figure 1, the predicted peak of infected population on the endemic phase is at day 21 compared to the day 41 of infected population peak on first wave, day 45 for second wave and day 35 on third wave of COVID-19 in Malaysia. Therefore, the spread of COVID-19 in Malaysia on endemic phase reached the number of infections peaked in a very short time. Meanwhile, the peak of infected population for all phases was predicted at 16,280,000 individuals out of a total of susceptible individuals S is 33,573,874.

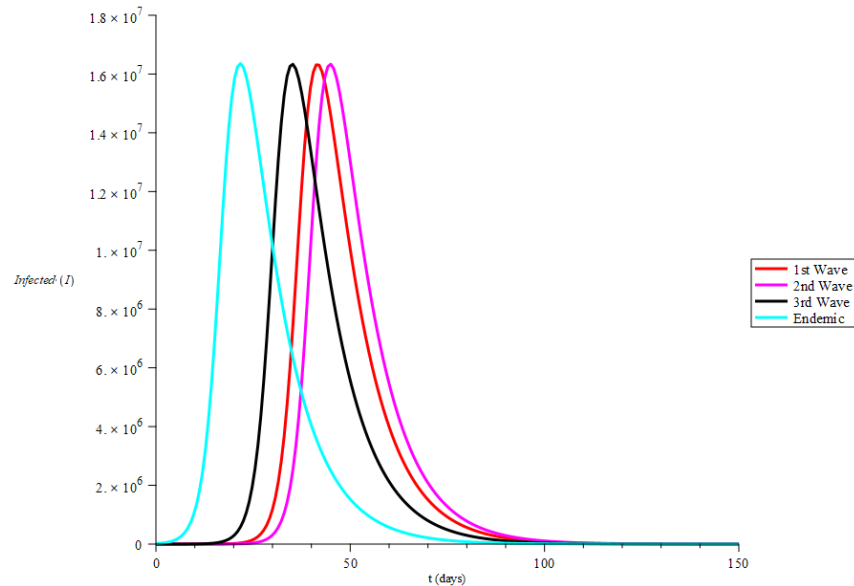
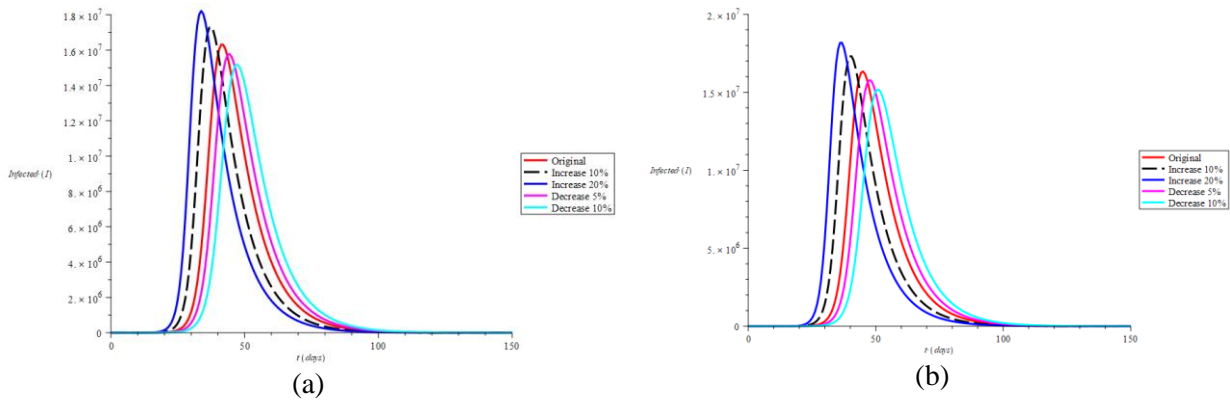


Figure 1: The model prediction graph of infected population for 150 days on first, second, third waves and endemic phase



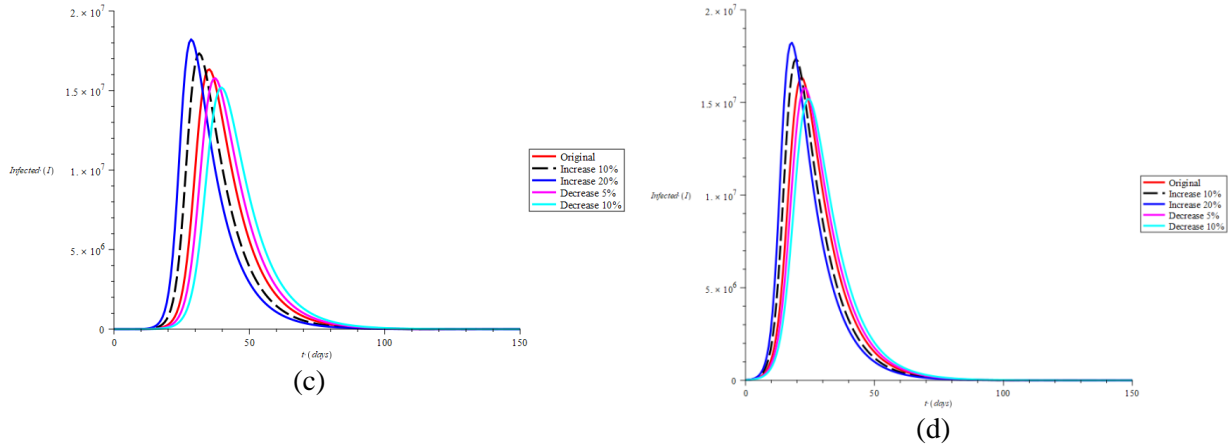


Figure 2: Relationship between of transmission rate of infection (β) and days for first wave (a), second wave (b), third wave (c) and endemic phase (d)

The relationship between of transmission rate of infected population (β) on the infected population and days for all phases is shown in Figure 2. From Figure 2, the number of infected populations $I(t)$ increases with the rate of infected population (β) increases and vice-versa for the first, second, third waves and endemic phase. Meanwhile, the peak of infected population reached maximum level in shorter time when the rate of infected population (β) increases and vice-versa. At the beginning stage, the disease spreads quickly among the infected population but after attending peak position, it starts to decrease. The decrease only occurs when the susceptible population numbers decrease and this decrease in susceptible numbers only occurred through the drastic actions taken by the Malaysia government.

CONCLUSION AND RECOMMENDATIONS

In this paper, an SIR epidemic model for pandemic COVID-19 in Malaysia where S , I and R represent susceptible population, infected and recovered populations, respectively. This study considers 4 periods of COVID-19 cases in Malaysia which is first wave, second wave, third wave and endemic period. Then we compute the basic reproduction number R_0 of the considered model. The first period, between 25th January and 16th February 2020, corresponding to the entire first wave, the second, between 27th February 2020 and 30th June 2020, corresponding to part of the second wave, the current third wave began on 7th September 2020 and 1st April 2022, corresponding to the endemic phase, still present at the time of writing this article. The SIR model provides a theoretical framework for investigation the COVID-19 viruses unfold at intervals communities. It is often applied to communities during this context if reliable data is available. Its power is additionally derived from the fact that, as new data are other to the model, it's straightforward to regulate its parameters and supply best-fit curves between the information and the model's predictions. In this context, it can provide estimates of the number of future deaths as well as time scales for the decline in the number of infections in communities. Our findings show that the SIR model is suited to predicting the epidemic trend caused by disease spread because it can accommodate surges and be adjusted to the recorded data. It is possible to predict the success of government interventions by comparing published data with predictions.



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CONFLICT OF INTEREST DISCLOSURE

The authors declare no conflict of interest in the subject matter or materials discussed in this manuscript.

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