



## Covid-19 Simulation in Malaysia Based on Susceptible-Infected-Recovered (SIR) Mathematical Model

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### ABSTRACT

The outbreak of Covid-19 in Wuhan in December 2019 shocked the world. After almost two years, Malaysia's Prime Minister announced in March 2022 that Malaysia was transitioning into the endemic phase of the disease on 1 April 2022. This study aims to investigate the spread of Covid-19 in Malaysia during the endemic phase by developing a susceptible-infected-recovered (SIR) model. The model was used to analyze the reproductive number based on the current number of infected individuals in Malaysia. The results indicate that the maximum number of infected individuals was reached within 50 days after the announcement of the endemic phase. The SIR model confirmed the endemic phase with a reproductive number of 5.1, which is greater than 0. The study also explored the impact of an increase or decrease in the transmission rate on the number of infected individuals during the endemic phase. The simulation results showed that the peak number of infected individuals was initially projected to be 16,540,000 persons on day-21, and this number was directly proportional to changes in the infected population. By formulating a mathematical model and analyzing the stability of its equilibria, the study provides a framework for understanding the dynamics of Covid-19 transmission in Malaysia. This can help policymakers and healthcare professionals to develop more effective interventions and strategies to manage the disease

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### 1. Introduction

COVID-19 is a highly infectious respiratory illness caused by the SARS-CoV-2 virus, first identified in Wuhan, China in late 2019 [1],[2]. The virus quickly spread to become a global pandemic, affecting millions of people worldwide. The symptoms of COVID-19 can range from mild to severe and include fever, cough, fatigue, loss of taste or smell, and difficulty breathing. By September 2021,



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very nearly two years later, Covid-19 was first recognised, more than 200 million affirmed cases and over 4.6 million lives were lost to the sickness [3]. Most infected people will experience mild to severe respiratory infection and will recover without any special therapy. According to studies, the Covid-19 virus spreads mostly between people within a two-metre radius of one another. The virus spreads by respiratory droplets produced by coughing, sneezing, or talking.

Understanding the Covid-19 pandemic is crucial for preparing for future actions and interventions should another pandemic arise. The lessons learned from the current pandemic can inform future preparedness and response efforts, including the development of effective public health policies and strategies. Therefore, it is essential to conduct research and analyses that provide insights into the dynamics of the pandemic, including its transmission and spread.

One such research approach is the use of mathematical models, such as the susceptible-infected-recovered (SIR) model, which can provide a theoretical framework for understanding the spread of infectious diseases like Covid-19. By analysing the reproductive number, which indicates the average number of people an infected individual will transmit the virus to, the SIR model can estimate the potential size and duration of an epidemic or pandemic. Historical data can be used to fit the model and calculate the reproductive number, providing insights into the dynamics of the pandemic and informing future interventions. Thus, the use of the SIR model is an important tool for understanding the spread of Covid-19 and preparing for potential future pandemics.

This study presents several main findings that shed light on the spread of Covid-19 in Malaysia. Firstly, the researchers formulated a mathematical model that incorporates a constant birth rate and death rate for the susceptible population (S). The model provides a framework for understanding the dynamics of Covid-19 transmission in Malaysia. Secondly, the study analyses the stability of the model's equilibria by using the basic reproduction number. This measure helps to determine the severity of Covid-19 transmission dynamics, indicating whether the disease is spreading rapidly or slowly. Thirdly, the researchers establish theoretical results by comparing the actual number of infected populations with the predicted number of infections. These results help to provide insights into the accuracy of the model and its usefulness for predicting the spread of Covid-19 in Malaysia. Finally, the study presents a numerical illustration that demonstrates the theoretical findings are consistent with the notion that Covid-19 is currently endemic in Malaysia. This highlights the importance of ongoing surveillance and monitoring to manage the disease and mitigate its impact on public health.

## 2. Literature Review

Covid-19 swiftly spreads throughout China, followed by a worldwide increase in the number of patients. Preventative measures to reduce the spread's impact have become more dependent on the use of mathematics. Hence, the future occurrence of a pandemic or endemic needs to be predicted so that the public health professionals can be alerted to the need for intervention by using these mathematical modelling approaches. 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 [4]–[7]. The purpose of mathematical modelling is thus to represent different types of real-world epidemiological in mathematical language [8]–[11].

The transmission dynamics of diseases such as dengue fever, tuberculosis, diabetes, HIV-AIDS has been explicated by [12]–[17]. According to [18], the SIR model is more appropriate for forecasting the Covid-19 pandemic and endemic since it can estimate future fatalities and offer time periods for rate of infections to 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 Covid-19 in the country. In Malaysia, a couple of prior research have been conducted by investigators to mathematically assess the nationwide spread of Covid-19. For example, [19] evaluated the transmission dynamics of Covid-19 by using a generalized type of SIR models that can be straightforwardly implemented. Last but not least, this technique will offer a decent prognostication result for evaluating public health and social measures in response to the COVID-19 epidemic and conjointly to form timely plans [20].

### 3. Methodology

The most basic epidemic model assumes that the population size,  $N$ , remains constant, implying that there are no factors such as population movements or deaths that would alter the size of the population. 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 [21]. Numerical simulation of model uses secondary data on the number of Covid-19 cases in Malaysia which provided worldwide dataset [22] as in Figure 1 by using Maple 2021.0 software to predict the number of Covid-19 cases in Malaysia as a measure to prevent the number of Covid-19 cases in Malaysia. The time taken to complete the simulation is 1.10 second and it was implemented by using MSI laptop, Intel (R) Core (TM) i7-10750H CPU @ 2.60GHz processor and 6GB RAM.

1	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	
	iso_code	continent	location	date	total_cases	new_cases	cases_smo	total_death	new_death	deaths_smo	cases_per	cases_per	smoothed	deaths_per	deaths_per	smoothed	production	icu_patient	patients_per	bsp_patient	patients_per	icu_adr	
112123	OWID_LMC		Lower mid	2020-05-17	396491	13461	11784.43	16125	381	323.571	117.891	4.002	3.504	4.795	0.113	0.096							
114820	MAC	Asia	Macao	2022-08-25	793	0	0	6	0	0	1154.955	0	0	8.739	0	0							
114821	MAC	Asia	Macao	2022-08-26	793	0	0	6	0	0	1154.955	0	0	8.739	0	0							
115713	MDG	Africa	Madagasci	2022-08-26	66615	0	2.286	1410	0	0	2303.77	0	0.079	48.763	0	0							
115714	MDG	Africa	Madagasci	2022-08-27	66615	0	2.286	1410	0	0	2303.77	0	0.079	48.763	0	0							
115715	MDG	Africa	Madagasci	2022-08-28	66626	11	1.571	1410	0	0	2304.15	0.38	0.054	48.763	0	0							
115716	MWI	Africa	Malawi	2020-03-29																			
115717	MWI	Africa	Malawi	2020-03-30																			
115718	MWI	Africa	Malawi	2020-03-31																			
115719	MWI	Africa	Malawi	2020-04-01																			
115720	MWI	Africa	Malawi	2020-04-02	3	3					0.151	0.151											
115721	MWI	Africa	Malawi	2020-04-03	3	0					0.151	0											
116598	MWI	Africa	Malawi	2022-08-28	87839	5	8	2676	0	0	4416.297	0.251	0.402	134.542	0	0							
116599	MYS	Asia	Malaysia	2020-01-24																			
116600	MYS	Asia	Malaysia	2020-01-25	4	4					0.119	0.119											
117397	MYS	Asia	Malaysia	2022-04-01	4219395	17476	16902	35013	30	42.286	125675	520.524	503.427	1042.864	0.894	1.259	0.78	259	7.714	3387	100.882		
117398	MYS	Asia	Malaysia	2022-04-02	4234087	14692	16011.86	35069	56	45.429	126112.6	437.602	476.914	1044.532	1.668	1.353	0.78	261	7.774	3207	95.521		
117399	MYS	Asia	Malaysia	2022-04-03	4246467	12380	15533	35099	30	48.714	126481.3	368.739	462.651	1045.426	0.894	1.451	0.77	256	7.625	2964	88.283		
117548	MDV	Asia	Maldives	2020-03-08	4	4					7.671	7.671											
117549	MDV	Asia	Maldives	2020-03-09	4	0					7.671	0											
117550	MDV	Asia	Maldives	2020-03-10	6	2					11.506	3.835											
117551	MDV	Asia	Maldives	2020-03-11	8	2					15.342	3.835											
117552	MDV	Asia	Maldives	2020-03-12	8	0					15.342	0											

Figure 1. Worldwide Covid-19 dataset

#### 3.1 SIR Model Formulation for Covid-19

The SIR model on the spread of Covid19 is represented by three compartments. Namely Susceptible (S), Infected (I), and Recovered (R) compartment. A class of affected individuals can spread the infection to other people. The mathematical equations that represented the rates of change in the number of people who are Susceptible, Infected and Recovered over time in the SIR model are given by equation (1), equation (2) and equation (3) respectively. Definition of variables and parameters of model SIR for Covid-19 are presented in Table 1.

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

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

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

Table 1. Definition of Variable/Parameter

Variable/Parameter	Description
N	Total number of individuals in the population of interests, $N = S + I + R$ .
S	Susceptible are members of the population who do not have the disease at one point in time but at risk to contract 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.
$\beta$	Proportionality constant known as the infection rate.
r	Removal rate.

For this model,  $\beta$  and  $r$  are both positive constants. The initial conditions for this model are the initial number of susceptible  $S(0) > 0$ , the initial number of infectives  $I(0) > 0$ , and the initial number of recovered  $R(0) = 0$ . By using maple coding as depicted in Figure 2, the graphs of endemic are plotted.

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[> restart : with(plots) : with(plottools) : with(DEtools) :
[> N := S(t) + In(t) + R(t) :

[> eqn1 := diff(S(t), t) = -beta*S(t)*In(t), S(0) = ic1 :

[> eqn2 := diff(In(t), t) = ((beta*S(t) - r)*In(t), In(0) = ic2 :

[> eqn3 := diff(R(t), t) = r*In(t), R(0) = ic3 :

[> r := .102 :

[> beta := 0.0000000156 :
[> ic1 := 33573874 : ic2 := 17476 : ic3 := 0 :

[> dsol := dsolve([eqn1, eqn2, eqn3], numeric) :

[> odeplot(dsol, [[t, S(t), color = blue], [t, In(t), color = red], [t, R(t), color = green]], t = 0 ..150,
view = [0 ..150, 0 ..34000000]) :
[> odeplot(dsol, [t, In(t), color = cyan], t = 0 ..150, view = [0 ..150, 0 ..16700000]) :

[> N := ic1 :
[>  $R_0 = \frac{\beta \cdot N}{r}$  :

```

Figure 2. Maple coding of endemic

### 3.2 Equilibrium and Stability Analysis

Based on equations (1) – (3), stability analysis was 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 the following equation (4), equation (5) and equation (6).

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

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

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

Then, the equilibrium found algebraically then stability shown by perturbing about equilibrium points (equations (4) – (6)). 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  $I = 0$ , and  $S = S^*$ , where  $S^* = N$  and  $N$  is any positive constant (hence the equilibrium points are non-isolated). From the Maple output, there are two eigenvalues, 0 and  $\beta S^* - r$ .

If the condition for an epidemic is satisfied, this second eigenvalue is positive, and the equilibrium is unstable. If the second eigenvalue is negative, there is no conclusion about the stability for the linearization because of the zero eigenvalue. However, it is obvious that the equation is not strictly stable even in that case, because any perturbation with non-zero  $I$  will lead to a situation in which  $S$  decreases and therefore does not return to  $S^*$  [23]. 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 generation method [24], the basic reproductive number is given by,  $R_0 = \beta N/r$ , where:

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

Figure 3 is the procedural steps taken for constructing the SIR model:

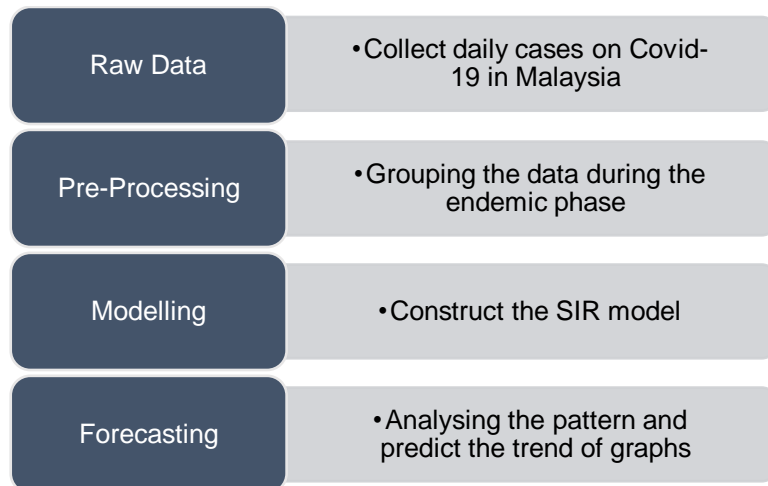


Figure 3. Flowchart of the procedure of the SIR Model

#### 4. Results and Discussion

In this section a comprehensive overview of the study's data collection is provided. The data for endemic phase was analysed by using Maple software to obtain the desired results. Data included in this analysis are those from endemic phase starting form 1 April 2022. The initial values of  $S(0)$ ,

$I(0)$ ,  $R(0)$  and others parameter values of the model used in this simulation are presented in Table 2 with the basic reproductive number values,  $R_0$  is obtained from the previous section  $R_0 = \beta N/r$ .

Table 2. Initial/Parameter values of SIR Model for Covid-19 in Malaysia

Variable/Parameter	Values
$S(0)$	33573874
$I(0)$	17476
$R_0$	5.137500588
$r$	0.102
$\beta$	0.0000000156

Integrating the following hypothetical endemic model with Maple from the Table 2, yields the result as depicted in Figure 4.

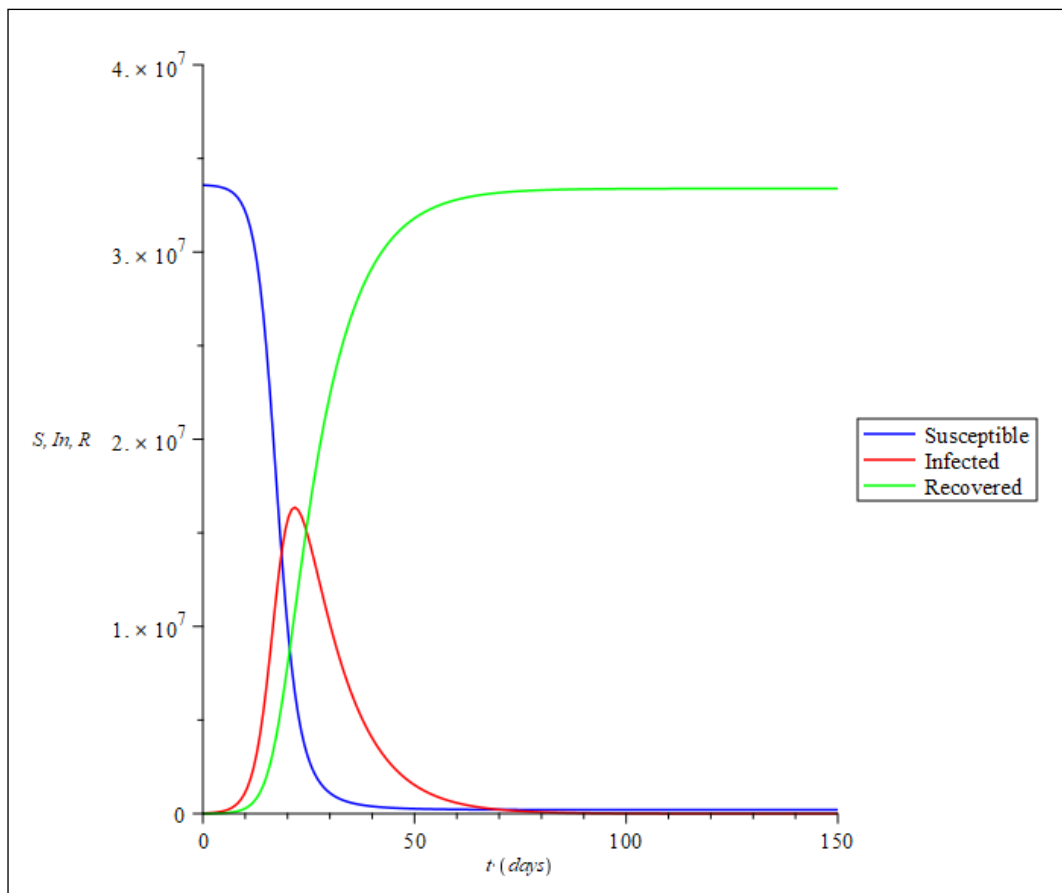


Figure 4. SIR Model for 150 days ahead after endemic

Based on Figure 4, the model is depicted in the graph above where the is from day 0 to day 150 after the endemic phase was proclaimed on 1 April 2022. Meanwhile the  $S$ ,  $I$ ,  $R$  is between 0 and 33573874 individuals. This model,  $S(t)$  reduces monotonically from 33573874 to about 1053000 whereas  $R(t)$  grows monotonically from 0 to around 31990000. When  $I(t)$  compared to the other two, it has a drastically distinct form.  $I(t)$  climb monotonically from 0 and reaches its maximum value of about at 16100000 approximately at day-21 then decreases monotonically to zero. The graph for  $I(t)$  is the most important. An epidemic develops in this model during the period when  $I(t)$  grow and then diminishes.

Next, for realizing the sensitive effect of the different model parameters on the proposed model numerically, we presented the time series plot of infected population  $I(t)$  at any time  $t$  for different values of the model parameter as depicted in Figure 5 by increasing the value of the infection rate,  $\beta$  by 10% and 20%. We also tested the downward effect of  $\beta$  by decreasing the value by 5% and 10%.

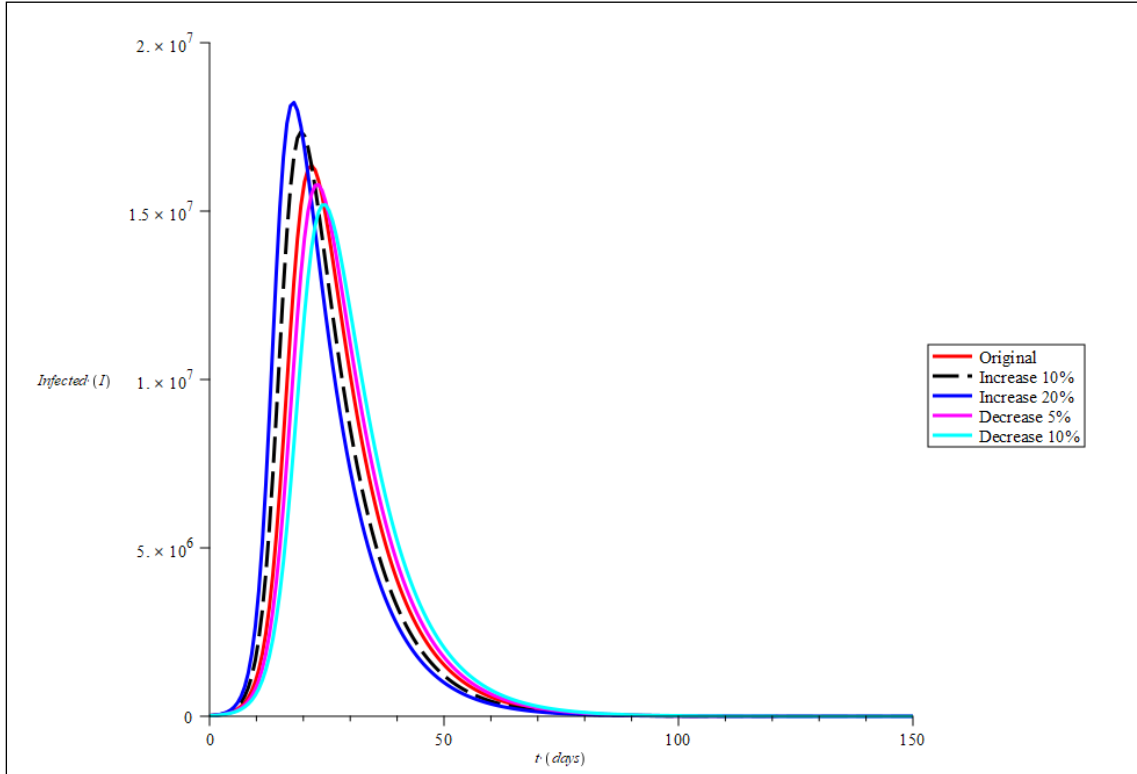


Figure 5. The effect of the rate of disease transmission rate

It is evident from Figure 5 that the number of infected populations  $I(t)$  increases with the rate of disease transmission rate of infection ( $\beta$ ) increases. On the other hand, Figure 5 also illustrates clearly that the number of infected populations  $I(t)$  decreases when rate of disease transmission rate of infection ( $\beta$ ) decreases. Therefore, it is observed that the increase in disease transmission rate of infection ( $\beta$ ) leads to a corresponding rise in the number of infected populations, which implies that the number of infected populations is significantly impacted by the increase in disease transmission rate of infection ( $\beta$ ).

## 5. Conclusion

The application of mathematical modelling theories has proven to be effective in understanding the temporal evolution and pattern of disease endemics, enabling reliable predictions of the impact of interventions on infected-susceptible incidence rates. This paper presents an epidemic model for endemic COVID-19 in Malaysia, incorporating susceptible, infected, and recovered populations. The study outlines the model's basic formulation and computes the basic reproduction number to evaluate its suitability for forecasting the endemic trend caused by disease propagation. Results indicate that the SIR model is adaptable to Covid-19 data and can handle surges in the number of cases, thereby providing a theoretical framework to capture the dynamics of the virus spread in Malaysia and its transition to the endemic phase. The model can also forecast virus evolution accurately, given precise statistics. Thus, this analysis can aid in implementing necessary measures to halt the spread of Covid-19 in Malaysia.

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Future studies could improve on the SIR model's accuracy by incorporating additional variables such as age, vaccination status, and mortality rate to produce more satisfactory results. Additionally, a different population value that follows a logistic growth model can be considered to enhance the model's forecasting capabilities.

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### Conflict of Interest

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

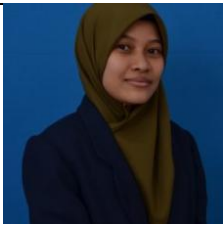


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