Solving SEIR Model Using Symmetrized Runge Kutta Methods

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Abstract. During these pandemic, SEIR model has become a popular topic among researchers. Such epidemiological model is said to be a great decision tool to forecast the behaviour of Covid19 outbreak for future actions. Following trend, this paper attempts to use symmetrized Runge Kutta methods; Implicit Midpoint Rule (IMR) and Implicit Trapezoidal Rule (ITR), to solve this model. The base method; IMR and ITR are tested with one-step symmetrization (1ASIMR, 1ASITR, 1PSIMR, and 1PSITR) and two-step symmetrization (2ASIMR, 2ASITR, 2PSIMR and 2PSITR) in both active and passive modes. Symmetrized Runge-Kutta method is best when using along stiff equations. Thus, we used high rate of disease transmission, β to study the efficiency of each method and predict the proportion of individuals in each category according to the SEIR model. All the parameters and values are obtained through official websites of Malaysia and calculated based on previous studies starting from 2nd December 2021 to 1st January 2022. The equilibrium points: disease free equilibrium (DFE) and the disease endemic equilibrium (DEE) are presented and calculated. Next, the basic reproduction number, R_0 is computed using the next generation method. The result depicted $R_0 > 1$, which indicates the disease has spread over. Finally, 2PSIMR is found to be the best method out of all. The efficiency of the methods is discussed and compared.

Keywords: Symmetrized RK methods · Covid19 · SEIR model · stiff system of ODEs · prediction of SEIR model

1 Introduction

1.1 Covid-19 Pandemic

A novel coronavirus disease (COVID-19) began to spread in Wuhan, the capital of Hubei Province, China, in early December 2019. The World Health Organization (WHO) classified it as a serious health threat by the end of 2019 [9] (He, Peng & Sun, 2020). Dong, Du and Gardner (2020) [6] stated that the SARS-CoV-2 virus has caused over 81 million confirmed cases worldwide since its appearance in late December 2020,

with approximately 2 million individuals dying as of early September 2020. There are currently no known preventive pharmaceutical interventions, and numerous behavioural intervention policies, such as lockdown, mandatory self-isolation, and facial covering orders, have been implemented to limit the spread of such a highly infectious disease to a level that current health and financial systems can sustain [3] (Bhouri, Costabal, Wang, Linka, Peirlinck, Kuhl & Perdikaris, 2021). While a lockdown is an effective first response to a pandemic, it is clear that this disease has significant social and economic implications. Aside from the immediate economic costs, there are significant social costs associated with unemployment, a widening of the educational gap, mental health issues, and shorter life expectancies as a result of poor physical and mental health [8] (Grimm, Mengel, & Schmidt, M, 2021). To summarise, accurately and objectively assessing the cost and value of restricted opening is becoming increasingly crucial, especially in light of recent increases in the number of people tested positive as a result of controversial policies in the United States. This is when the government begins to consider additional options as a foundation for their emergency decision [3] (Bhouri et al., 2021).

1.2   SEIR Model

In the last decades, mathematical models in epidemiology have been important tools in analysing the propagation and control of infectious disease [2]. As cited in Bouquet and Stigler [4], W. Kermack and A. McKendrick proposed the first model in 1927 to "explain the rapid rise and fall in the number of infected patients observed in epidemics such as the plague (London 1665–1666, Bombay 1906) and cholera (London 1865)". M. Anderson and M. May revived the Kermack– McKendrick model, sometimes known as the SIR model, for infectious disease propagation in 1979. Although this model has been successful in describing disease behaviour, it is unrealistic to ignore other compartments and control techniques such as immunisation, treatment, quarantine, isolation, and the impact of age and sex. As a result, several researchers have concentrated on developing more realistic simulations [18]. Egger, Johnson, Althaus, Schöni, Salanti, Low and Norris [7] described that mathematical modelling studies can be used to generate emergency guidelines or assess the pandemic potential of emerging outbreaks. A system of ordinary differential equations is generated based on the assumptions of the most basic model to a variety of modified models that are primarily focused on the assumptions of a disease may carry. Most of these models are nonlinear differential equations, whose dynamics may be deduced by looking at the eigenvalues of the linearized problem's Jacobian [5]. Nonlinear optimization techniques are commonly used to change these model parameters. It is important to find these parameters for calculating the basic reproduction number, which represents the expected number of new cases of infectious disease caused by an infected person. R_0 is crucial in determining how quickly the disease will spread and how control efforts will affect it. If $R_0 > 1$, disease spreads in epidemics, but if $R_0 < 1$, disease is eradicated [18]. Considering Covid19 cases, SEIR model is one of the most common models used to predict this disease outbreak. However, this model is expressed as a set of nonlinear ordinary differential equations for which no accurate analytic solution has yet been discovered (Piovella, 2020) [14]. According to Al-Smadi and Gumah [1], the population is divided into four compartments in the SEIR model: a susceptible compartment labelled S, in which all individuals are prone

to disease; an exposed compartment labelled *E*, in which all individuals are exposed to the virus but not yet infectious; an infected compartment labelled *I*, in which all individuals are infected and have risk of transmission; and a removed compartment labelled *R*, in which all individuals have been cleared from the infected cohort. The SEIR model employs four categories of data, the first of which is demographic data, which considers the population size of affected areas. Following that are the counts of cases, hospitalizations, and fatalities. The third one is the disease features from previous studies and finally, the intervention impact estimates are used to forecast how the disease would progress.

This paper is organized as follows: Sect. 2 will describe about the mathematical formulation used in this approach; Sect. 3 is for the method followed by model formulation, equilibrium point and basic reproduction number in Sect. 4. The next section illustrates the result and discussion in numerical analysis and some concluding remarks in Sect. 5.

2 Methodology

2.1 Data

The data for this study was gathered from Malaysia's official websites, which are cited in the reference source. The data were from December 2, 2021 and until January 1, 2022 [13]. The date was picked because it is the first Omicron variant instance in Malaysia on December 2nd. As a result, it piqued people's interest in learning more about what will happen when Omicron arrives in the country. It's worth noting that we're not only looking at Omicron variant cases in this model; we're looking at all Covid19 cases. The value of parameters is calculated by referring article by Mahmud and Lim [12]. These data are then being compared to each other using different methods to obtain the most accurate ones for a 100 days-prediction. The report data includes the number of total cases, active cases, recovered cases, and the death cases.

2.2 Method

Two symmetric Runge Kutta methods; IMR and ITR are compared with one-step and two-step symmetrization in both active and passive modes [15–17]. Below is the defining equation and Butcher tableau for IMR (Table 1) and ITR (Table 2).

Implementation in a Constant Step Size Setting
Active Symmetrization
A symmetrized value is computed and then used to propagate the numerical solution each time. Every step, every two steps, or every three steps can all be symmetrized.

Passive Symmetrization
In the passive mode, the implementation entails computing multiple steps with the symmetric technique, storing the update as well as the internal stage values at each step, and then applying symmetrization where necessary using the stored values.

Table 1. Defining equation and Butcher tableau for IMR

Defining Equation	Butcher Tableau

One-Step Symmetrization

$$y_n = \frac{y_{n-1}+2y_n+y_{n+1}}{4}$$

$$y_{n+1} = y_n + \tfrac{1}{4}(3k_1 + k_2)$$

$$k_1 = hf\left(x_n + \tfrac{1}{2}h,\, y_n + \tfrac{1}{2}k_1\right)$$

$$k_2 = hf\left(x_i + \tfrac{3}{2}h,\, y_n + k_1 + \tfrac{1}{2}k_2\right)$$

$\frac{1}{2}$	1	
$\frac{3}{2}$	1	$\frac{1}{2}$
	$\frac{3}{4}$	$\frac{1}{4}$

Two-Step Symmetrizatio

$$y_n = \frac{-y_{n-2}+4y_{n-1}+10y_n+2y_{n+1}-y_{n+2}}{16}$$

$$y_{n+1} = y_n + \tfrac{1}{16}(17k_1 + 13k_2 + 3k_3 - k_4)$$

$$k_1 = hf\left(x_n + \tfrac{1}{2}h,\, y_n + \tfrac{1}{2}k_1\right)$$

$$k_2 = hf\left(x_i + \tfrac{3}{2}h,\, y_n + k_1 + \tfrac{1}{2}k_2\right)$$

$$k_3 = hf\left(x_i + \tfrac{5}{2}h,\, y_n + k_1 + k_2 + \tfrac{1}{2}k_3\right)$$

$$k_4 = hf\left(x_i + \tfrac{7}{2}h,\, y_n + k_1 + k_2 + k_3 + \tfrac{1}{2}k_4\right)$$

$\frac{1}{2}$	$\frac{1}{2}$			
$\frac{3}{2}$	1	$\frac{1}{2}$		
$\frac{5}{2}$	1	1	$\frac{1}{2}$	
$\frac{7}{2}$	1	1	1	$\frac{1}{2}$
	$\frac{17}{16}$	$\frac{13}{16}$	$\frac{3}{16}$	$-\frac{1}{16}$

Table 2. Defining equation and Butcher tableau for ITR

Defining Equation	Butcher Tableau

One-Step Symmetrization

$$y_n = \frac{y_{n-1}+2y_n+y_{n+1}}{4}$$

$$y_{n+1} = y_n + \tfrac{1}{8}(3k_1 + 4k_2 + k_3)$$

$$k_1 = hf(x_n, y_n)$$

$$k_2 = hf\left(x_n + h,\, y_n + \tfrac{1}{2}k_1 + \tfrac{1}{2}k_2\right)$$

$$k_3 = hf\left(x_i + 2h,\, y_n + \tfrac{1}{2}k_1 + k_2 + \tfrac{1}{2}k_3\right)$$

0			
1	$\frac{1}{2}$	$\frac{1}{2}$	
2	$\frac{1}{2}$	1	$\frac{1}{2}$
	$\frac{3}{8}$	$\frac{1}{2}$	$\frac{1}{8}$

(continued)

Table 2. (*continued*)

Defining Equation	Butcher Tableau

Two-Step Symmetrization

$y_n = \frac{-y_{n-2}+4y_{n-1}+10y_n+4y_{n+1}-y_{n+2}}{16}$

$y_{n+1} = y_n + \frac{1}{32}(17k_1 + 2k_2 + 2k_3 - k_4)$

$k_1 = hf(x_n, y_n)$

$k_2 = hf(x_i + h, y_n + \frac{1}{2}k_1 + \frac{1}{2}k_2)$

$k_3 = hf(x_i + 2h, y_n + \frac{1}{2}k_1 + k_2 + \frac{1}{2}k_3)$

$k_4 = hf(x_i + 3h, y_n + \frac{1}{2}k_1 + k_2 + k_3 + \frac{1}{2}k_4)$

$k_5 = hf(x_i + 4h, y_n + \frac{1}{2}k_1 + k_2 + k_3 + k_4 + \frac{1}{2}k_5)$

0					
1	$\frac{1}{2}$	$\frac{1}{2}$			
2	$\frac{1}{2}$	1	$\frac{1}{2}$		
3	$\frac{1}{2}$	1	1	$\frac{1}{2}$	
4	$\frac{1}{2}$	1	1	1	$\frac{1}{2}$
	$\frac{17}{32}$	$\frac{15}{16}$	$\frac{1}{2}$	$\frac{1}{16}$	$-\frac{1}{32}$

3 Mathematical Formulation

We begin by considering the SEIR model that enables vital dynamics (births and deaths) to sustain an epidemic or allow new introductions to spread. The total population of Malaysia is approximately 32,655,000 by 2021. Susceptible phase will cover population in Malaysia aged 15–64 (working age) for 69.6% from the whole population as this age group affected the most than other age groups based on the Covid data analysis. Exposed population on the other hand, is the number of people screened during 30 days from 2nd December 2021 to 1st January 2022. The number of confirmed cases is presented as the infected population while recovered individuals depict the recovered population [12].

The highlighted component in this model is the parameters (transmission rate) which stands for stiffness parameter in this model. Value of β applied such as $\beta_1 = 6.47$. It is deemed high, i.e. stiff, according to Mahmud and Lim [12], but it is said to be consistent because WHO states that the virus has gone through at least three or four generations of transmission over the period. Other parameter used is parameter which describes about the rate of the exposed population become infectious, so $\frac{1}{m}$ is the mean latent period while and represent the birth and death rates, respectively. Parameter g that stands for the rate of recovery is obtained by $g = \frac{1}{\text{number of days to recover}}$ while parameter α is the rate of people died because of pandemic.

There is no transfer from the R class to the S class for the recovered persons; they are presumed to have immune protection. The incidence rate is IS/N, and the force of infection is I/N [11]. Below is the illustration of the SEIR model system (Fig. 1).

The dynamics of the Covid-19 transmission can be explained using the nonlinear ordinary differential equations (ODEs) listed below, which are based on Fig. 1.
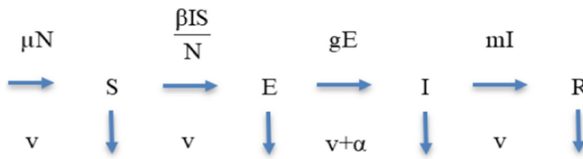
$$S' = \mu N - vS(t) - \frac{\beta I(t)S(t)}{N}, \tag{1}$$

Fig. 1. SEIR model

Table 3. Definition of variable/parameter

Variable/Parameter	Definition	Parameter Value
N(t)	Human population	26634116
S(t)	Suspected population	22727880
E(t)	Exposed population	3638067
I(t)	Infected population	123251
R(t)	Recovered population	144918
μ	Rate of natural birth	0.144
v	Rate of natural death	0.051
α	Rate of disease-related death	0.010
g	Rate of recovery	0.974
m	Probability of changing from E to I	1.428
β	Transmission rate	β = 6.47

$$E' = \frac{\beta I(t) S(t)}{N} - (m + v)E(t),$$

$$I' = mE(t) - (g + \alpha + v)I(t),$$

$$R' = gI(t) - vR(t)$$

subject to $S(0) \geq 0, E(0) \geq 0, I(0) \geq 0, R(0) \geq 0$, where $N(t) = S(t) + E(t) + I(t) + R(t)$ is the total population or we can add the equations in (1) such that,

$$N' = (b - d)N - aI \qquad (2)$$

The definition of each parameter and value is described in Table 3 [19, 20].

3.1 Equilibrium Points

By setting all the derivatives equal to zero,

$$S' = E' = I' = R' = 0 \qquad (3)$$

Two equilibrium points is obtained from system (1).

Disease Free Equilibrium (DFE)
E_0, or a common name for equilibrium point of free disease happens when there is no rate of infection occur [18]. Equilibrium point can be written as S_0, E_0, I_0, R_0. As this model follows the mathematical modelling in Li, et al. [11] the disease-free equilibrium is given by

$$E_0 = (S_0, E_0, I_0, R_0) = (1, 0, 0, 0). \tag{4}$$

Disease Endemic Equilibrium (DEE)
E^*, is defined as the equilibrium with all positive components such as,

$$S^* = \frac{N(m+v)(\alpha+g+v)}{\beta m} = \frac{N}{R_0} = 0.6451 \tag{5}$$

$$E^* = -\frac{N\left(v^2(v+\alpha+g+m)+m(\alpha v-\beta u+gv)\right)}{\beta m(m+v)}E_1\left(S^*, E^*, I^*, R^*\right)$$

$$= -\frac{N(Z_1)}{\beta m(m+v)} = 3.4208$$

$$I^* = -\frac{N\left(v^2(v+\alpha+g+m)+m(\alpha v-\beta u+gv)\right)}{\beta(m+v)(\alpha+g+v)}$$

$$= -\frac{N(Z_1)}{Z_2} = 2.2377$$

$$R^* = -\frac{Ng\left(v^2(v+\alpha+g+m)+m(av-\beta u+gv)\right)}{\beta v(m+v)(\alpha+g+v)}$$

$$= -\frac{Ng(Z_1)}{vZ_2} = 6.2654$$

where

$$R_0 = \frac{\beta m}{(m+v)(\alpha+g+v)}$$

$$Z_1 = v^2(v+\alpha+g+m)+m(\alpha v-\beta u+gv)$$

$$Z_2 = \beta(m+v)(\alpha+g+v)$$

The Jacobian matrix can be written as,

$$J = \begin{pmatrix} -(v+\frac{\beta I}{N}) & 0 & \frac{-\beta S}{N} & 0 \\ \frac{\beta I}{N} & -(m+v) & \frac{\beta S}{N} & 0 \\ 0 & m & -(g+\alpha+v) & 0 \\ 0 & 0 & g & -v \end{pmatrix}$$

3.2 Basic Reproduction Number, R_0

The estimated number of secondary cases developed by a single infected case introduced into a completely susceptible population is well-defined as the basic reproduction number. Only if the fundamental reproduction number is bigger than one can the disease spread in a population [10]. The method used to calculate R_0 is called the next generation matrix method. Thus, when $\beta = 6.47$, $R_0 = \frac{\beta m}{(m+v)(\alpha+g+v)} = 4.13$.

Theorem 1. *If* $R_0 \leq 1$, *then the disease-free equilibrium* $E_0 = (S_0, E_0, I_0, R_0)$ *of system* (1) *is globally asymptotically stable. If* $R_0 > 1$, *then the disease endemic equilibrium* $E_1 = (S^*, E^*, I^*, R^*)$ *of system (1) is globally asymptotically stable.*

4   Result and Discussion

We performed the numerical integration using MATLAB software with step size, $h = 0.1$ at time, $t = 30$ days. Table 4 stated each notation that will be used for numerical experiments.

4.1 Analysis of the Symmerized RK Method on SEIR Model

We first tested the efficiency according to the passive and active symmetrization. As a result, we find that the base method, IMR are more efficient than other methods followed by 2ASIMR and then ITR. This proves that, basically, both base method (IMR and ITR) are more efficient than active symmetrization (see Fig. 2(a)). In passive symmetrization, we note that all the IMR method and its symmerization are more efficient than ITR, 1PSITR and 2PSITR (see Fig. 2(b)).

Meanwhile, Fig. 3(a) depicts the efficiency diagram for all method listed in Table 1, while (b) is the efficiency diagram only for IMR, 1PSIMR and 2PSIMR as they are

Table 4. Notation for numerical experiments

| Abbreviation	Definition	Implementation
IMR	Base method IMR	–
ITR	Base method ITR	–
1ASIMR	One-step symmetrization of IMR	Active
2ASIMR	Two-step symmetrization of IMR	Active
1ASITR	One-step symmetrization of ITR	Active
2ASITR	Two-step symmetrization of ITR	Active
1PSIMR	One-step symmetrization of IMR	Passive
2PSIMR	Two-step symmetrization of IMR	Passive
1PSITR	One-step symmetrization of ITR	Passive
2PSITR	Two-step symmetrization of ITR	Passive

(a). Active Symmetrization
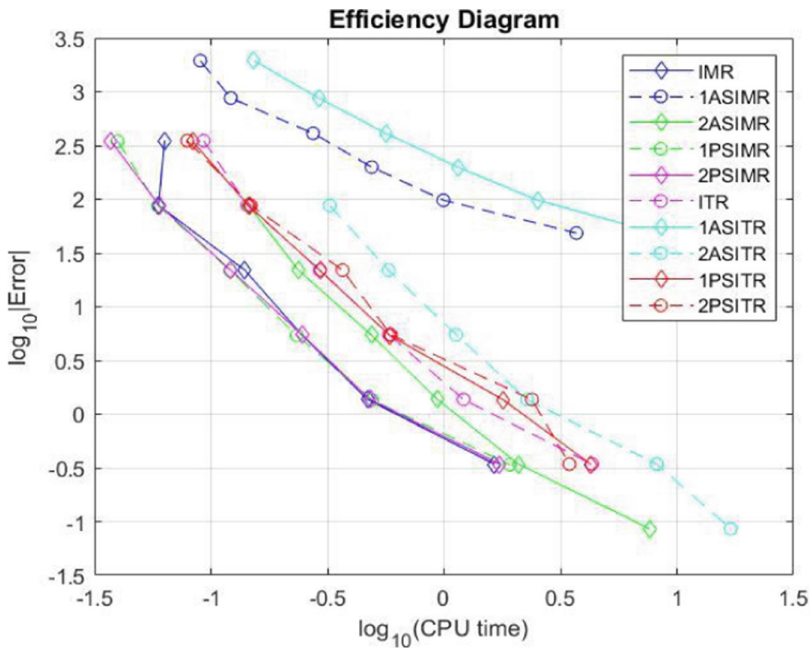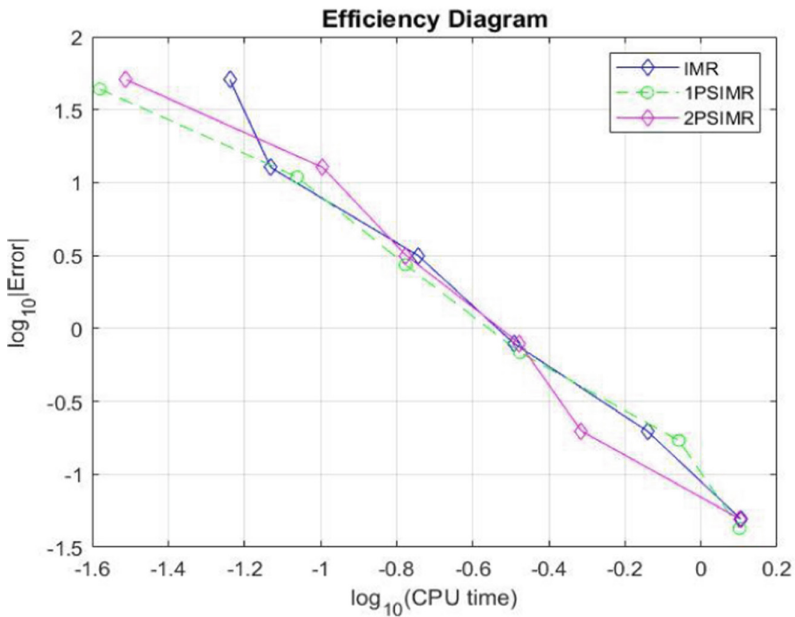

(b). Passive Symmetrization
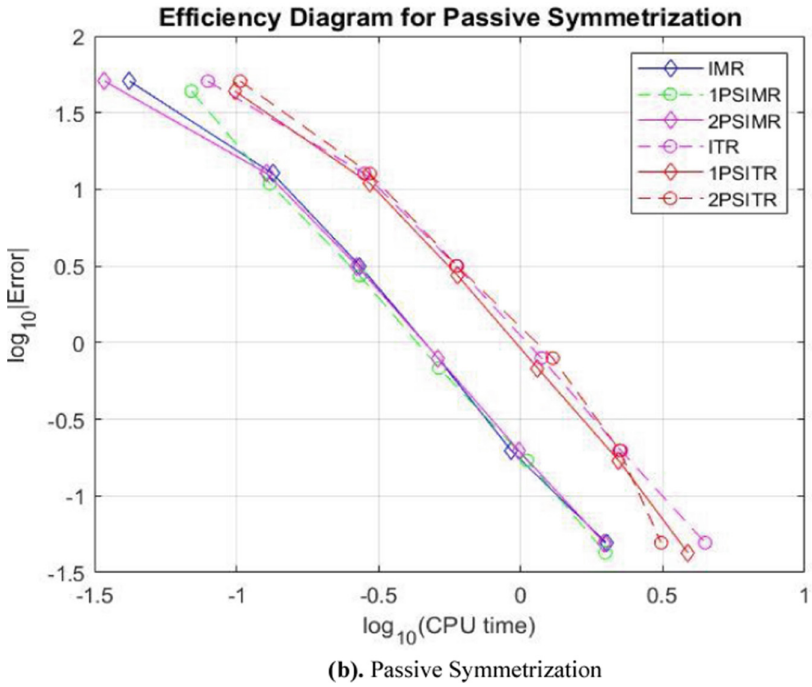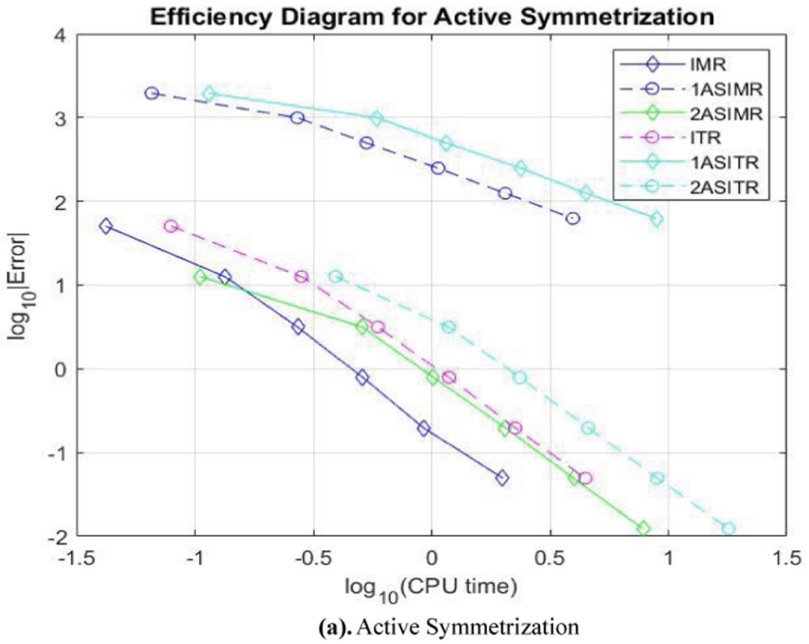
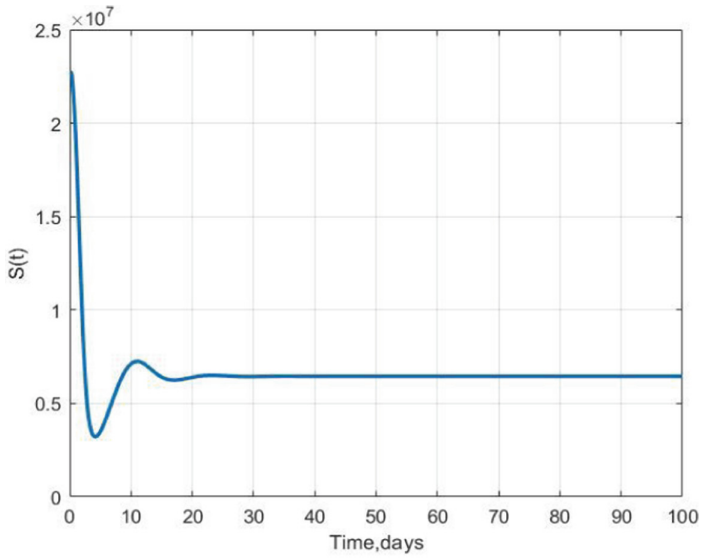**Fig. 2.** (a) Active Symmetrization (b) Passive Symmetrization

(a). Efficiency Diagram IMR, 1ASIMR, 2ASIMR, PSIMR, 2PSIMR, ITR, 1ASITR, 2ASITR, 1PSITR, and 2PSITR
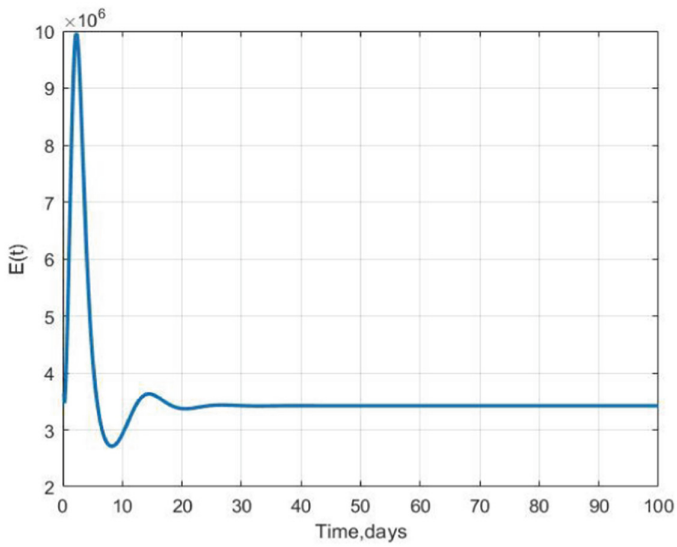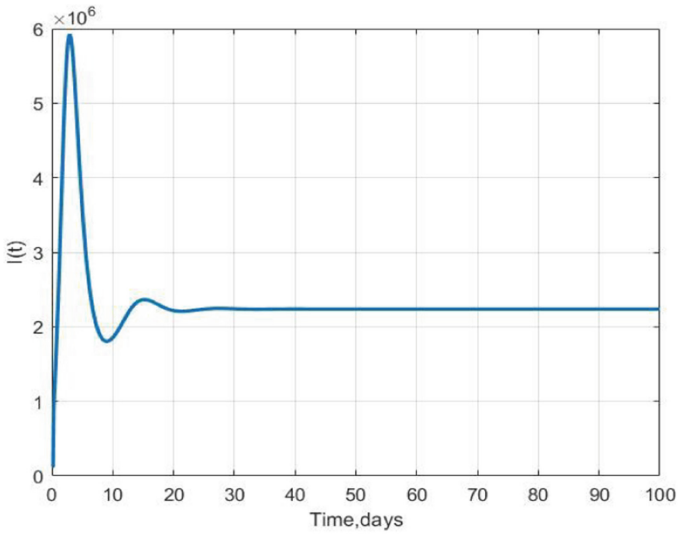

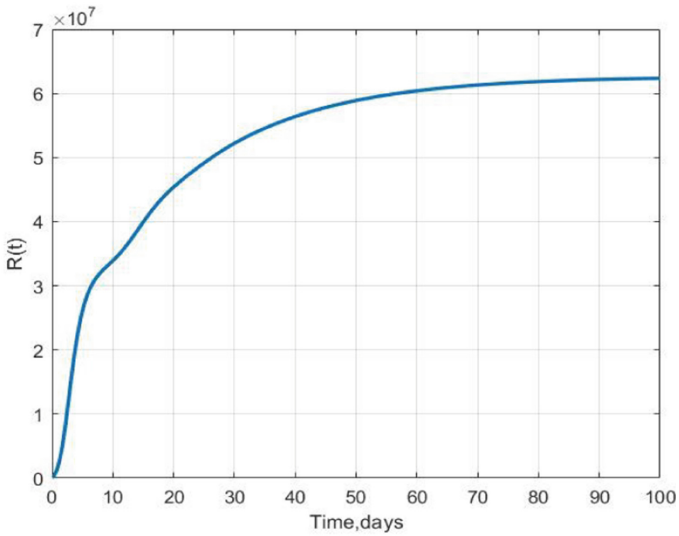**(b).** Efficiency Diagram IMR, 1PSIMR and 2PSIMR.

Fig. 3. (a) Efficiency Diagram IMR, 1ASIMR, 2ASIMR, PSIMR, 2PSIMR, ITR, 1ASITR, 2ASITR, 1PSITR, and 2PSITR (b) Efficiency Diagram IMR, 1PSIMR and 2PSIMR.

(a)

(b)

Fig. 4. Model prediction at $t = 100$ days, $h = 0.1$ (a) Susceptible Proportion (b) Exposed Proportion (c) Infected Proportion (d) Recovered Proportion

(c)

(d)

Fig. 4. (*continued*)

slightly accurate than other methods and it is difficult to differentiate which method is more efficient in (a). Therefore, it is observed that 2PSIMR is the most efficient method out of all.

4.2 Model Simulation

Based on the results we get; we extend the discussion to simulate the cases in Malaysia using 2PSIMR. The step sizes are subject to 0.1 at $t = 100$ days. As the data of this model is taken in the middle of the pandemic, the susceptible phase began with a high volume of people that are prone to disease. After 10 days, the number of susceptible individuals converge to the disease endemic equilibrium, at which is 6,451,000 people. In (b), the exposed individuals reached its peak at the maximum. This is due to the rate of transmission, β from the susceptible phase that enters the exposed phase is high. The population then started to decrease gradually and converges at $E^* = 3.4208 \times 10^7$, equivalent to 34,208,000 people. Infected population, on the other hand, behaves almost the same as exposed population, which indicates that most of the exposed population are infected by the disease. The graph then showed a declining behaviour and begins to converge at point $R^* = 2.2377 \times 10^7 = 22,377,000$ individuals (see Fig. 4(c)). The last phase, Fig. 4(d) indicates the recovered population of the model. As the rate of recovery is greater than the rate of death, it is observed that the number of recovered individuals has increased over time. The trajectory soon to converge at some point, $R^* = 6.2654 \times 10^7 = 62,654,000$ individuals. The overall simulation of the model is combined in Fig. 5.
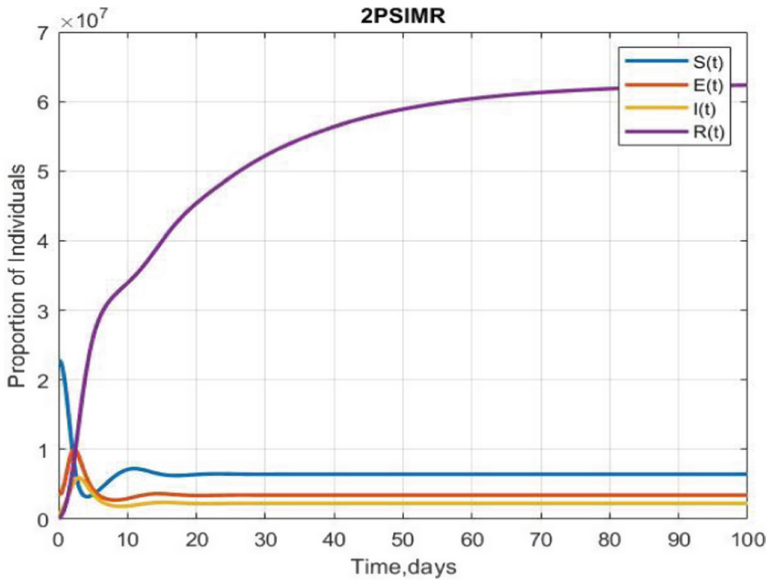

Fig. 5. Model simulation using 2PSIMR

5   Conclusion

In this research, SEIR model of Malaysia is analysed using different methods as discussed. At first, the model is presented according to $S(t)$, $E(t)$, $I(t)$, *and* $R(t)$ respectively and compared to each method. It is then revealed that IMR method and its symmetrized method are more efficient. Then the most efficient method is used to simulate the model for the next 100-days. Besides, the basic reproduction number is discussed and as the calculated $R_0 > 1$, it is concluded that the epidemic is spread. Thus, it is important to take precautions and follow the government rules as now we are in the state of living with the virus. Note that, as this model does not take any precautions into account, the analysis might change if one considered other parameters that brings the model more realistic.

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