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Numerical Analysis of An Improved Sir Model For COVID-19 Outbreak in Malaysia Using Variational Iteration Method

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Abstract: COVID-19 is a respiratory disease caused by a novel coronavirus. Its characteristics are distinct from those of the current disease. Since it is a new disease, there has been a lack of research that fits its characteristics. This study proposes to improve the Susceptible-Infection-Recovered (SIR) model to describe the outbreak of COVID-19 with the effects of vaccination and isolation strategies as a time delay factor. The model will be numerically solved by using the variational iteration method (VIM). The solutions consist of both numerical and graphical approaches using Maple21 software. The time delay factor is included in the improved model, and then its correctional function is obtained before starting the iteration. The value of the parameters is substituted into the product of the iteration, and the result obtained will be compared with the result from previous studies, graphically. The result concluded that the time delay factor played a vital role in flattening the curve of the outbreak in Malaysia.

Keywords: COVID-19, SEIR Model, Variational Iteration Method, Vaccination

1. Introduction

Coronavirus disease 2019 (COVID-19) is a new coronavirus strain that infects humans and causes a variety of illnesses and deaths, similar to severe acute respiratory syndrome (SARS) and Middle East respiratory syndrome (MERS). However, these diseases differ from COVID-19 in terms of their geographical spread [1].

The first wave of COVID-19 in Malaysia was caused by the first case on January 25, 2020. On February 4, 2020, a 41-year-old Malaysian who recently travelled back from Singapore was tested

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positive for COVID-19, which then infected his sister, making it the first case of the virus contracted via local transmission [2]. The second wave of the outbreak triggered the implementation of the first Movement Control Order (MCO). The increasing pattern of new cases per day continued with an average of 150 cases per day since the first rise of positive cases on March 15th, 2020. Additionally, the number of deaths caused by COVID-19 has escalated, with more than 60% of fatalities being patients over the age of 60 with underlying comorbidities.

On September 8th, 2020, the third wave of the COVID-19 outbreak began, with most reported cases coming from the Benteng LD cluster in Sabah and the Tembok cluster in Kedah. According to Malaysian Health Director-General Tan Sri Dr Noor Hisham Abdullah [3], the third wave is much more difficult than the first two because the Institute of Medical Research (IMR) detected the D614G-type mutation in virus samples. The new mutation is highly infectious and easily transmitted. The rise in the number of COVID-19 cases and overwhelming number of hospitalized patients is taking a toll on the front-liners, especially the healthcare workers.

Most of the previous analyses conducted used the traditional SIR model. Existing SIR models only focus on the rate of infection and the rate of recovery as parameters and consist of three basic compartments. This approach is lacking in terms of contact rates, the compartment before the infection, and the delay factor. Ariffin et al. proposed incorporating vaccination into the model for disease transmission dynamics analysis [4]. Vaccination could be the time delay factor as it will reduce the infection rate.

This research studies the incorporation of a new compartment, exposed (E), and vaccination rate into the SIR model. The numerical solution of the improved model is obtained by using the variational iteration method (VIM). A comparison of the result with the previous study is made to analyse the effect of the models on the trajectory of the COVID-19 outbreak in Malaysia.

2. Methodology

This section describes all terms related to the involved parameters and variables, the modification of the original equation, and the numerical method used to obtain the numerical solution. The method suggested is the variational iteration method. This method was used in terms of accuracy, computational simplification, and dependencies to get the results.

2.1 SIR Model

The Susceptible (*S*), Infected (*I*), and Recovered (*R*) model is utilized in epidemiological studies to demonstrate the relationship between the number of susceptible, infected, and recovered people. This traditional model assumed that the sum of S(*t*), I(*t*), and R(*t*) is equal to 1, representing the total population density, *N*, and no vaccination involved during the period [5], [6], [7]. The mathematical modelling is written as below:

$$\frac{dS}{dt}(t) = -\frac{\beta S(t) I(t)}{N}$$

$$\frac{dI}{dt}(t) = \frac{\beta S(t) I(t)}{N} - \gamma I(t)$$

$$\frac{dR}{dt}(t) = \gamma I(t) \qquad \text{Eq. 1}$$

where β is infection rate, and γ is recovery rate.

2.2 The Improved SIR Model

In this study, a new compartment is introduced, Exposed (E), into *Eq.*1, as suggested by Ariffin et al. [4]. The idea was adopted from the work of Harir et.al and then reconstructed based on the situation of COVID-19 in Malaysia [6]. Hence, the SEIR model for the COVID-19 in Malaysia without time delay factor is described as below:

$$\frac{dS}{dt}(t) = -\frac{\beta S(t)I(t)}{N} + \nu N(t) - \mu S(t)$$
$$\frac{dE}{dt}(t) = \frac{\beta S(t)I(t)}{N} - \alpha E(t) - \mu E(t) - \sigma E(t)$$
$$\frac{dI}{dt}(t) = \alpha E(t) - \gamma I(t) - \mu I(t)$$
$$\frac{dR}{dt}(t) = \gamma I(t) - \mu R(t) + \sigma E(t) \qquad \text{Eq. 2}$$

Where ν is the natural reproduction rate, μ is the deceased rate, α is the number of exposed people during quarantine, and σ is the test and treatment rates.

A new parameter, vaccination rate, ω, is introduced to the SEIR model above. This idea was adopted from the work of Wong et.al and Mungkasi [8], [9]. An assumption of ω equivalent to an artificial efficiency in vaccination is made because the vaccination strategy will be continuous, with a set rate applied to the remaining vulnerable class. Then, the vaccine efficacy factor is applied into the S(t) and R(t).

A multiplier factor, ε, is incorporated, which is defined as the ratio of the number of positive cases in the vaccine samples to the number of positive instances in the placebo sample during the clinical trials. Thus, the vaccine efficacy is given by $(1-\varepsilon)$. Furthermore, the self-isolation or self-quarantined is also being considered. Hence, I(t) and R(t) are also remodified.

Finally, the improved SIR model which incorporates vaccination, and isolation strategies as time delay factors, and E compartments is shown below:

$$\frac{dS}{dt}(t) = -\omega\varepsilon - \frac{\beta S(t)I(t)}{N} + \nu N(t) - \mu S(t)$$
$$\frac{dE}{dt}(t) = \frac{\beta S(t)I(t)}{N} - \alpha E(t) - \mu E(t) - \sigma E(t)$$
$$\frac{dI}{dt}(t) = \alpha E(t) - \hat{\gamma} I(t) - \mu I(t)$$
$$\frac{dR}{dt}(t) = \omega(1-\varepsilon) + \hat{\gamma} I(t) - \mu R(t) + \sigma E(t) \qquad \text{Eq. 3}$$

Where $\hat{\gamma} = \gamma - \hat{\rho}$ and $\hat{\rho}$ is the isolation rate of positive infected person in the population. Hence, the reproduction number, $\mathbf{R_0} = \frac{\beta}{\hat{\gamma}}$.

2.3 The Variational Iteration Method

The variational iteration method (VIM) was introduced by He [10]. The basic idea of this method is to find an approximate root of nonlinear equations. The main property of this method is to construct the correctional function which contains general Lagrange multiplier, λ, continuous approximate solution, u_{n+1}, and restricted variation, $\acute{u}_n$. The correctional function for *Eq*. 3 is constructed as below:

$$S_{n+1}(t) = S_n(t) + \int_0^t \lambda_1(\tau)\left\{\frac{dS_n(\tau)}{d\tau} + \omega\varepsilon + \frac{\beta \acute{S}_n(\tau)\acute{I}_n(\tau)}{N} - \nu\acute{N}_n(\tau) + \mu\acute{S}_n(\tau)\right\}d\tau$$

$$E_{n+1}(t) = E_n(t) + \int_0^t \lambda_2(\tau)\left\{\frac{dE_n(\tau)}{d\tau} - \frac{\beta \acute{S}_n(\tau)\acute{I}_n(\tau)}{N} + (\alpha+\mu+\sigma)\acute{E}_n(\tau)\right\}d\tau$$

$$I_{n+1}(t) = I_n(t) + \int_0^t \lambda_3(\tau)\left\{\frac{dI_n(\tau)}{d\tau} - \alpha\acute{E}_n(\tau) + (\hat{\gamma}+\mu)\acute{I}_n(\tau)\right\}d\tau$$

$$R_{n+1}(t) = R_n(t) + \int_0^t \lambda_4(\tau)\left\{\frac{dR_n(\tau)}{d\tau} - \omega(1-\varepsilon) - \hat{\gamma}\acute{I}_n(\tau) + \mu\acute{R}_n(\tau) - \sigma\acute{E}_n(\tau)\right\}d\tau \qquad \text{Eq. 4}$$

$\lambda_1, \lambda_2, \lambda_3, and\ \lambda_4$ are general Lagrange multipliers. Here $\acute{S_n}$, $\acute{E_n}$, $\acute{I_n}$, and $\acute{R_n}$ are the restricted variations, which means that they behave like constants. Making the correctional functional stationary with respect to $S_n(t), E_n(t), I_n(t),$ and $R_n(t)$, noticing that $\varrho\, \acute{S_n}(\tau) = \varrho\, \acute{E_n}(\tau) = \varrho\, \acute{I_n}(\tau) = \varrho\, \acute{R_n}(\tau) = 0$, yields

$$\varrho S_{n+1}(t) = \varrho S_n(t) + \varrho \int_0^t \lambda_1(\tau)\left\{\frac{dS_n(\tau)}{d\tau} + \omega\varepsilon + \frac{\beta \acute{S_n}(\tau)\acute{I_n}(\tau)}{N} - \nu \acute{N_n}(\tau) + \mu \acute{S_n}(\tau)\right\} d\tau = 0$$

$$\varrho E_{n+1}(t) = \varrho E_n(t) + \varrho \int_0^t \lambda_2(\tau)\left\{\frac{dE_n(\tau)}{d\tau} - \frac{\beta \acute{S_n}(\tau)\acute{I_n}(\tau)}{N} + (\alpha + \mu + \sigma)\acute{E_n}(\tau)\right\} d\tau = 0$$

$$\varrho I_{n+1}(t) = \varrho I_n(t) + \varrho \int_0^t \lambda_3(\tau)\left\{\frac{dI_n(\tau)}{d\tau} - \alpha \acute{E_n}(\tau) + (\hat{\gamma} + \mu)\acute{I_n}(\tau)\right\} d\tau = 0$$

$$\varrho R_{n+1}(t) = \varrho R_n(t) + \varrho \int_0^t \lambda_4(\tau)\left\{\frac{dR_n(\tau)}{d\tau} - \omega(1-\varepsilon) - \hat{\gamma}\acute{I_n}(\tau) + \mu \acute{R_n}(\tau) - \sigma \acute{E_n}(\tau)\right\} d\tau = 0 \qquad \text{Eq. 5}$$

Therefore, the Lagrange multiplier can be readily identified as $\lambda_1(\tau) = -1,\ \lambda_2(\tau) = -1, \lambda_3(\tau) = -1, and\ \lambda_4(\tau) = -1$. Consequently, the iteration formula can be obtained as:

$$S_{n+1}(t) = S_n(t) - \int_0^t \left\{\frac{dS_n(\tau)}{d\tau} + \omega\varepsilon + \frac{\beta \acute{S_n}(\tau)\acute{I_n}(\tau)}{N} - \nu \acute{N_n}(\tau) + \mu \acute{S_n}(\tau)\right\} d\tau$$

$$E_{n+1}(t) = E_n(t) - \int_0^t \left\{\frac{dE_n(\tau)}{d\tau} - \frac{\beta \acute{S_n}(\tau)\acute{I_n}(\tau)}{N} + (\alpha + \mu + \sigma)\acute{E_n}(\tau)\right\} d\tau$$

$$I_{n+1}(t) = I_n(t) - \int_0^t \left\{\frac{dI_n(\tau)}{d\tau} - \alpha \acute{E_n}(\tau) + (\hat{\gamma} + \mu)\acute{I_n}(\tau)\right\} d\tau$$

$$R_{n+1}(t) = R_n(t) - \int_0^t \left\{\frac{dR_n(\tau)}{d\tau} - \omega(1-\varepsilon) - \hat{\gamma}\acute{I_n}(\tau) + \mu \acute{R_n}(\tau) - \sigma \acute{E_n}(\tau)\right\} d\tau \qquad \text{Eq. 6}$$

From *Eq*. 6, note that:

$$\int_0^t \left\{\frac{dS_n(\tau)}{d\tau}\right\} d\tau = S_n(t) - S_n(0)$$

$$\int_0^t \left\{\frac{dE_n(\tau)}{d\tau}\right\} d\tau = E_n(t) - E_n(0)$$

$$\int_0^t \left\{\frac{dI_n(\tau)}{d\tau}\right\} d\tau = I_n(t) - I_n(0)$$

$$\int_0^t \left\{\frac{dR_n(\tau)}{d\tau}\right\} d\tau = R_n(t) - R_n(0) \qquad \text{Eq. 7}$$

In addition, for all n, *Eq*. 7 guarantee that:

$$S_n(0) = S_0, E_n(0) = E_0, I_n(0) = I_0, R_n(0) = R_0 \qquad \text{Eq. 8}$$

Lastly, by taking *Eq*. 7 into account, the equations *Eq*. 6 can be simplified as below:

$$S_{n+1}(t) = S_n(t) - \int_0^t \left\{\omega\varepsilon + \frac{\beta \acute{S_n}(\tau)\acute{I_n}(\tau)}{N} - \nu \acute{N_n}(\tau) + \mu \acute{S_n}(\tau)\right\} d\tau$$

$$E_{n+1}(t) = E_n(t) - \int_0^t \left\{-\frac{\beta \acute{S_n}(\tau)\acute{I_n}(\tau)}{N} + (\alpha + \mu + \sigma)\acute{E_n}(\tau)\right\} d\tau$$

$$I_{n+1}(t) = I_n(t) - \int_0^t \{-\alpha \acute{E_n}(\tau) + (\hat{\gamma} + \mu)\acute{I_n}(\tau)\} d\tau$$

$$R_{n+1}(t) = R_n(t) - \int_0^t \{-\omega(1-\varepsilon) - \hat{\gamma}\acute{I_n}(\tau) + \mu \acute{R_n}(\tau) - \sigma \acute{E_n}(\tau)\} d\tau \qquad \text{Eq. 9}$$

3. Results and Discussion

The spread of the COVID-19 is simulated in this section. Firstly, the value of parameters and initial approximation are determined, some are adopted from the previous study by Harir et al. and open data of COVID-19 in Malaysia dated from 25th January 2020 until 1st July 2022 [6],[11]. Assume that the value for $\mathbf{R_0} = 0.91$ and is constant [12]. Maple21 is used to compute the iteration of the improved SEIR model using the VIM algorithm as shown in Appendix A. A comparison with the SEIR model from Harir et al. is made, which will be denoted as reference model [6]. Further analysis and the effect of the time delay factor and E compartment towards the model is discussed.

3.1 Numerical Solution of The Improved SEIR Model

All the parameter values in Table 3.1 are substituted into Eq. 9 to obtain the following system on the first iteration:

$$\begin{aligned} S_1(t) &= 3585 - 22.557929t \\ E_1(t) &= 10 - 5.103270833t \\ I_1(t) &= 5 + 3.155t \\ R_1(t) &= 6.7878t \end{aligned} \quad \text{Eq. 10}$$

$$\begin{aligned} S_2(t) &= 3585 - 45.11585834t - 1.307569824t^2 + 0.005779289236\,t^3 \\ E_2(t) &= 10 - 10.20654167t + 3.780363386t^2 - 0.00577928936t^3 \\ I_2(t) &= 5 + 6.31t - 3.569905833t^2 \\ R_2(t) &= 13.5756t + 1.141408271t^2 \end{aligned} \quad \text{Eq. 11}$$

$$\begin{aligned} S_3(t) &= 3585 - 67.67378751t + 1.070860755t^3 - 3.922709471t^2 + 8.376778\text{5} \\ &\quad \times 10^{-7}t^6 - 2.292072854 \times 10^{-4}t^5 - 49.315452209 \times 10^{-3}t^4 \\ E_3(t) &= 10 - 15.3098125t + 11.34109016t^2 - 2.262016181t^3 \\ &\quad + 0.01067647482t^4 - 2.292072854 \times 10^{-4}t^5 - 8.376778517 \\ &\quad \times 10^{-7}t^6 \\ I_3(t) &= 5 + 9.4650t - 10.70971750t^2 + 2.161176487t^3 - 1.155857847 \\ &\quad \times 10^{-3}t^4 \\ R_3(t) &= 20.3634t + 3.424224813t^2 - 0.9700948877t^3 - 2.051647679 \times 10^{-4}t^4 \end{aligned} \quad \text{Eq. 12}$$

Table 1: Parameter values for SEIR model simulation

Notation	Value	Description
$N(0)$	3600	Total number of populations, N(t)=S(t)+E(t)+I(t)+R(t)
$S(0)$	3585	Number of susceptible people at time, $t = 0$
$E(0)$	10	Number of exposed people at time, $t = 0$
$I(0)$	5	Number of infected people at time, $t = 0$
$R(0)$	0	Number of recovered people at time, $t = 0$
ω	0.830	The vaccination rate
ε	0.340	The multiplier factor
β	0.877	The infectivity rate
ν	0.016/N	The natural reproduction rate
μ	0.005	The deceased rate
σ	0.142	Test and treatment rate
α	0.800	The number of people exposed during incubation period
$\hat{\gamma}$	0.964	The recovery rate

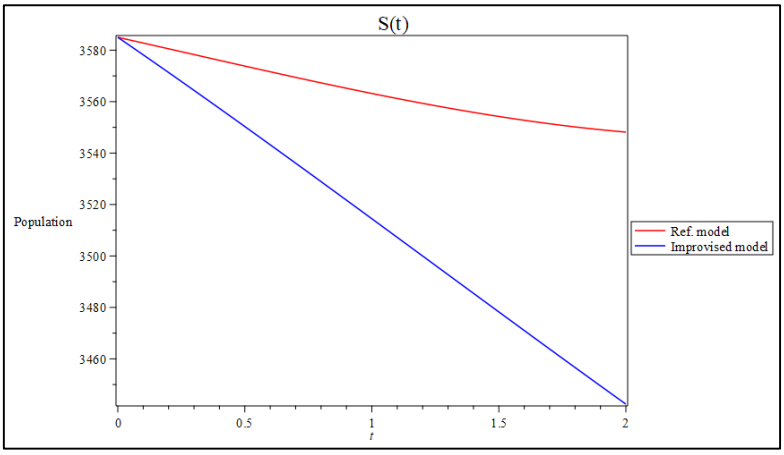

Figure 1: Comparison of reference and improved model for compartment S at t (in day) =0…2

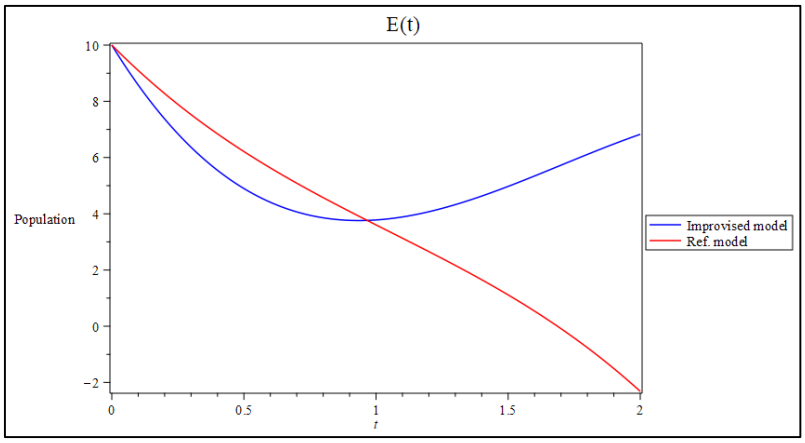

Figure 2: Comparison of reference and improved model for compartment E at t (in day) = 0…2

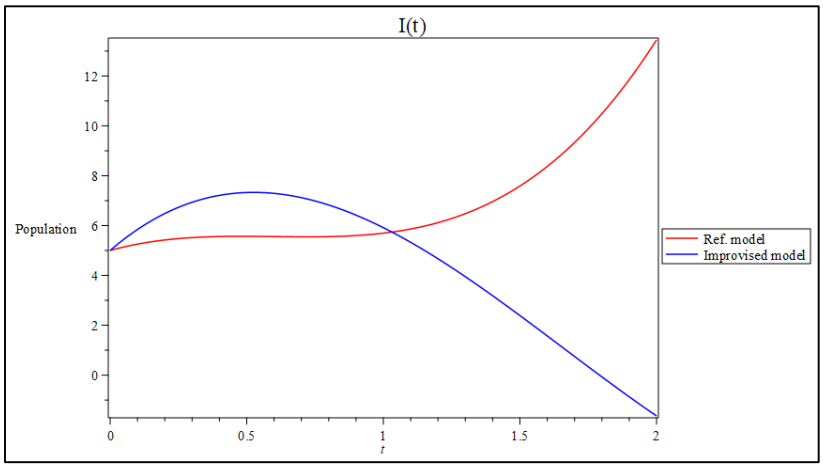

Figure 3: Comparison of reference and improved model for compartment I at t (in day) = 0…2

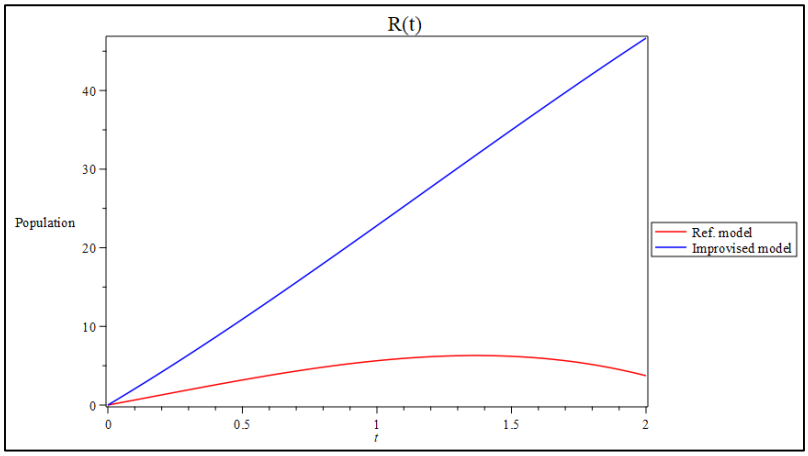

Figure 4: Comparison of reference and improved model for compartment R at t (in day) = 0…2

3.2 Discussions

The value of all parameters and initial approximation are constant for both models except for β and γ. For the model from previous study, the value of $\beta = 0.897$ and $\gamma = 0.986$. Differ from the improved model, the model from previous study excludes the time delay factors such as vaccination, and isolation strategies. The time series plot is then produced to compare the trajectory of both models for all compartments, as shown in Figure 1, Figure 2, Figure 3, and Figure 4.

From Figure 1, the line for the improved model started to diverge from the reference model, and both decreased. Figure 2 shows that the trajectory of both models for compartment E decreased notably and started to diverge from each other approximately at $t = 1$. Compared to Figure 3, it shows that the curves made by the improvised model started substantially decreasing, approximately at $t = 1$. The line made by the improvised model in Figure 4 accelerates dramatically around $t = 2$.

The curve produced by the reference model in Figure 1 has a higher population number than the curve produced by the improved model at t = 2. This is because Harir et al. considered the number of travellers entering the population in the SEIR model. In the improved model, those numbers were not considered due to the uncertainty in the rate at which people travelled in and out of the population. This indicates that the growth of susceptible people will be slow when using the improved model. This would fit the situation of the outbreak in Malaysia, as the government had implemented the restriction order at an early stage.

A different observation is found in Figure 2. The improvised model shows a higher exposed population compared to the reference model at $t = 2$. Figure 3 has the opposite observation as Figure 2. The number of infected populations shown by the reference model is higher than the improved model. This is because no isolation strategy is implemented in the reference model for compartment I.

On the contrary, the curve made by the improved model in Figure 4 has a higher population number than the curve produced by the reference model at $t = 2$. This indicates that more infected people will be recovered within a short period of time. In the improved model, the vaccination rate and isolation rate are implemented.

However, a different result will be shown for $t > 2$ because VIM is accurate only for small time domain, based on the study by Mungkasi [9]. For $t > 2$, the number of populations for exposed and recovered will decline and turns negative which indicates that the death in the population will be increase.

4. Conclusion

The main findings in this study are to solve the improved SIR model by using VIM, and to analyse the effect of new parameters towards the model. For the improved model, new parameters such as $\hat{\gamma}$, ω, and ε are introduced. These parameters act as the time delay factor. A new compartment, E, is also included in the improved model.

To solve the improved model numerically, the variational iteration method is applied. The correctional function of the model is obtained before proceeding to find the iteration. In this study, the researcher decided to find the solution after three terms. The process of obtaining the numerical solution is conducted in Maple21. By using this method, it does not require any complex calculation. Time series plot is plotted to visualize the trajectory of all compartments in the model and compared with the reference model [6]. The value of parameters used for both models are constant except for parameters β and γ. The value of β and γ used in the reference model is slightly higher than the one that the researcher used in the improved model. In the improved model, isolation strategy is applied thus the new recovery rate will be affected by the isolation rate, $\hat{\rho}$. A slight difference can make a notable change.

In the comparison of the simulation, the reference model that neglected the time delay factors showed a higher number of susceptible, and infected people. The higher the infection rate, the greater the number of people in these three compartments. Without vaccination, the number of infected people will increase rapidly.

To summarize, vaccination and isolation strategies are critical components of the effort to contain the COVID-19 outbreak, particularly in Malaysia. The introduction of vaccination at the early stage of the epidemic could prevent it from spreading. However, this effort is understandably difficult, as the process to create a suitable vaccine consumes more time. Hence, an isolation strategy is dependable to slow down the infection rate. Moreover, the SEIR model that was numerically solved using VIM is only limited for a small-time domain which could lead to inaccurate forecasts of COVID-19 outbreak in Malaysia. For further research, the researcher proposes to study the numerical solution of the improved model with vaccination rate and isolation strategy by using Runge-Kutta's 4^{th} order with a bigger time domain.

Acknowledgement

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Appendix A

Variational iteration method scheme on Maple21:

$$restart:$$

$$s0 := a;\ ex0 := b;\ c0 := c;\ r0 := d;\ N := s0 + ex0 + c0 + r0;$$

$$\omega := f; \varepsilon := g;\ \beta := h; \nu := j/N; \mu := k; \sigma := l; \alpha := x; \gamma := y;$$

$$s1 := s0 - int\{(\omega * \varepsilon + \beta * s0 * c0/N - \nu * N + \mu * s0), t = 0..\tau\};$$

$$ex1 := ex0 - int\{(-\beta * s0 * c0/N + (\alpha + \mu + \sigma) * ex0), t = 0..\tau\};$$

$$c1 := c0 - int\{(-\alpha * ex0 + (\lambda + \mu) * c0), t = 0..\tau\};$$

$$r1 := r0 - int\{(-\omega(1 - \varepsilon) - \lambda * c0 + \mu * r0 - \sigma * ex0), t = 0..\tau\};$$

$$s2 := s1 - int\{(\omega * \varepsilon + \beta * s1 * c1/N - \nu * N + \mu * s1), t = 0..\tau\};$$

$$ex2 := ex1 - int\{(-\beta * s1 * c1/N + (\alpha + \mu + \sigma) * ex1), t = 0..\tau\};$$

$$c2 := c1 - int\{(-\alpha * ex1 + (\lambda + \mu) * c1), t = 0..\tau\};$$

$$r2 := r1 - int\{(-\omega(1 - \varepsilon) - \lambda c1 + \mu * r1 - \sigma * ex1), t = 0..\tau\};$$

...

$$sm := s_{m-1} - int\{(\omega\varepsilon + \beta s_{m-1} c_{m-1}/N - \nu * N + \mu s_{m-1}), t = 0..\tau\};$$

$$exm := ex_{m-1} - int\{(-\beta s1 c_{m-1}/N + (\alpha + \mu + \sigma) ex_{m-1}), t = 0..\tau\};$$

$$cm := c_{m-1} - int\{(-\alpha ex_{m-1} + (\lambda + \mu) c_{m-1}), t = 0..\tau\};$$

$$rm := r_{m-1} - int\{(-\omega(1 - \varepsilon) - \lambda c_{m-1} + \mu r_{m-1} - \sigma ex_{m-1}), t = 0..\tau\};$$

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