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Modelling the Early Outbreak of COVID-19 Disease in Malaysia Using SIRS Model with 4-Step Adams-Bashforth-Moulton Predictor-Corrector Method

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ABSTRACT

Compartmental models have gained tremendous usage in various fields, including epidemiology, pharmacokinetics, and ecology, to describe the dynamics of a system consisting of interacting compartments one need to understand that the challenges in using compartmental models is solving the system of ordinary differential equations (ODEs) that govern the dynamics of the compartments. In this study, we propose the use of the Adam-Bashforth predictor method to solve compartmental models formed from COVID-19 data in Malaysia between Match 24 to April 23, 2020 and we showcased its promising results. The Adam-Bashforth predictor method is a widely used numerical method for solving ODEs. It uses previous solution values to calculate the next solution value, and the solutions is refined by using another fashion of the formula known as ABM correction formula. We improved the performance of the Adam-Bashforth predictor method by using the first four solutions of the fourth-order Runge-Kutta method RK4, which is another popular numerical method for solving ODEs, using the compartmental models. Our results showed that the Adam-Bashforth predictor method enhanced with the fourth-order Runge-Kutta method for accuracy and computational efficiency was able to capture the trend in the COVID-19 dataset used. Generally, the Adam-Bashforth method was about 2.5 times faster than the fourth-order Runge-Kutta method while maintaining similar accuracy. So merging two of them will in no doubt provide a better accuracy in solving the epidemiological model, the Adam-Bashforth method showed significantly accuracy, particularly in the early stages of the outbreak. The Adam-Bashforth predictor method is a promising numerical method for solving compartmental models. It offers better accuracy and computational efficiency, can be particularly useful in scenarios where accurate and fast predictions of compartmental dynamics are crucial. The model will be of great importance to the Malaysian Government, the Ministry of Health, and other stakeholders in disease management for an immediate and timely response to disease outbreaks.

Keywords: Adam-Bashforth Predictor, COVID-19, Runge-Kutta method

1 INTRODUCTION

Infectious disease mathematical modelling can be thought of as an intellectual representation of a physical phenomenon constructed using logic, relations, and equations to envision the perspectives of an epidemic's general behaviour, opening up avenues for research into visualization of impact of specific factors on disease transmission and providing an epidemic's general behaviour as addressed by epidemic curves [1]. Additionally, it enables projections of the epidemic's longevity, infection rate, population size, and disease evaluation. A good technique for predicting the incidence of infectious diseases is modelling in the context of mathematics. Accomplished plant health and public health care delivery is facilitated by predicting the anticipated outcome of an epidemic in animals, plants, and other living things [2]. After collecting accurate data about an epidemic, models employ reasonable assumptions, hypotheses, and special mathematical skills to identify the compartments that make up different infectious diseases. These parameters are then used to assess the effects of various treatments, such as mass vaccination, isolation, and quarantine, among others, to retard the spread of diseases and project future growth patterns based on the data accumulated. Infectious disease transmission dynamics are better understood and more apparent when represented using mathematical models. The saying that things become clearer when seen in the light of mathematics has promoted the acceptability of mathematical models [3]. These models are crucial in quantifying potential infectious disease control, management and prevention techniques [4;5]. Numerous compartmental models have been proposed by different scholars to model infectious diseases, ranging from the very traditional SIR model to more complicated types [6].

According to [7], modelling techniques can be broadly categorised into three major groups: mathematical models sometimes referred to as "state-space models," statistical based methods that monitor outbreaks while discovering spatial patterns of actual epidemics [7; 8]. Lastly, most celebrated recent approach that is reigning in the modelling community is machine learning or empirical methods for forecasting the evolution of an epidemic [9]. All these methods are based on dynamic systems for predicting the evolution of "theoretical" or ongoing epidemic spread. The three methods mentioned above span the majority of the literature in the area of modelling infectious diseases, and each has produced wonderful results. They have used in identifying and addressing numerous outbreaks in the past [10].

The COVID-19 pandemic, caused by the SARS-CoV-2 virus, emerged in December 2019 when the mysterious cases of pneumonia was noticed in the city of Wuhan, a city in China and it rapidly spread worldwide, turning into one of the most significant global health crises. By January 30, 2023, it had resulted in more than 700 million confirmed cases and over 6 million deaths [11]. This unprecedented threat highlighted the importance of understanding the transmission patterns and dynamics of infectious diseases, which could aid in epidemiological trend analysis and the evaluation of outbreak prevention measures [12; 13]. The pandemic posed various challenges, including delays in symptom onset and testing due to the virus's incubation period. Mathematical models, such as compartmental models, have played a crucial role in addressing these challenges and have garnered attention from researchers across diverse fields [14;15].

Malaysia, like many other countries, faced the impact of the pandemic. The country's first confirmed case was reported on January 25, 2020 [16]. The initial wave, lasting until February 15, 2020, saw 22 recorded cases, primarily imported from the disease's epicentre [17;18]. However, communal transmission sparked the second wave, with a sudden surge in cases attributed to a major religious gathering that occurred at the Sri Petaling Mosque from February 27 to March 2, 2020, involving both local and overseas attendees. This rapid transmission was facilitated by the virus's mode of transmission through infected droplets, leading to the unpreparedness of Malaysia [19]. Malaysia is one of the countries in Asia that is massively hit by the pandemic that claimed the lives of more than

35,000 people and left over 5 million people with a tale to tell the unborn generation [20]. The pandemic has had a devastating impact on the country, with significant loss of life and numerous economic setbacks.

The COVID-19 pandemic prompted extensive research and proposals, particularly in epidemiology. Mathematical modelling, including compartmental models, played a significant role in understanding disease transmission dynamics and informing preventive measures. These models, which compartmentalise the population for the study of disease transmission, have been instrumental in studying various infectious diseases. The pandemic highlighted the need for interdisciplinary efforts and mathematical modelling to address public health exigencies and better prepare for future disease outbreaks [21;22].

SIRS model is one of the most prominent model that has been deployed to capture the dynamic of infectious diseases within a population, "SIRS" means Susceptible-Infectious-Recovered-Susceptible. It is a modification of SIR, which stands for Susceptible, Infected, and Recovered, its construction and analysis have been an inspiration, which subsequently led to the development of many more variants. Compartmental models gained widespread acceptance among mathematicians, with many of these advancements credited to [23]. In SIRS model, individuals are originally regarded as susceptible (S), on infected, they can move to the Infected (I) compartment, there they are infectious and can transfer the disease to other individuals, after recovering from the disease, they move to the Recovered (R) compartment, where they are still susceptible to the disease when there is no immunity or lost their immunity. However, the movement of individuals between these compartments is governed by a set of differential equations that dictate the transmission rate, recovery rate, and even death. Using the model, it is possible to simulate the progression of the disease through time and assess the effects of various interventions, including vaccination or social distancing, on its spread. Modelling society has also witnessed proposal of other compartmental models like SEIR (Susceptible, Exposed, Infected, and Recovered) and SIRD (Susceptible, Infected, Recovered, Deceased), which include features for further compartmentalising for exposed individuals as well as deceased individuals respectively. In this research the models can be employed to investigate various aspects of the disease's dynamics, such as the influence of mortality on its spread or the function of pre-symptomatic transmission. The SIRS model will be utilised to monitor the spreading of the disease among the susceptible, which is the main target group to safeguard from getting infected, while making efforts to secure more from the infectious population and transfer them to the susceptible population. Our proposed SIRS model will be solved using the Adams-Bashforth-Moulton Predictor-Corrector (ABPC) numerical method. Parameters' estimations are obtained from the information made available by [24] for COVID-19 from March 24 to April 23, 2020. The results generated from the hybrid simulation were plotted and visualised to comprehend the disease dynamics and the effects of each parameter and intervention.

2 MODEL FORMULATION

The total population, which is denoted by N, is divided into three groups: those who are vulnerable to the disease, generally called susceptible, which is denoted by S, the second group, is called infected population, which is denoted by I, and the third group are those that have recovered from the disease and it is denoted by R. The relationship between the total population and other compartments is given as $N = S + I + R$. One apparent phenomenon about the compartmental model is that one can reasonably guess correctly the number of different compartments that constitute the model from its name. Figure 1 depicts the mechanism involved in the dynamical movement of the disease among the population under consideration, since no single individual can be in more than one compartment at the same time.

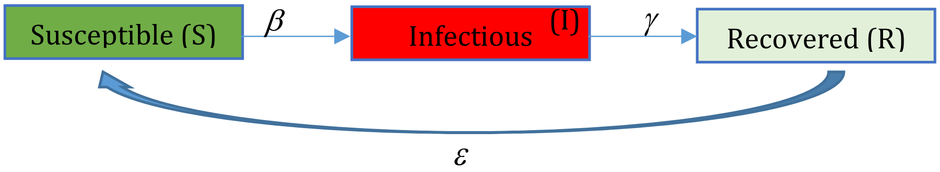

Figure 1: Representation of dynamic movement of diseases in SIRS model

Susceptible-infected-removed-susceptible (SIRS) model is used in this studies to demonstrate the transmission of COVID-19 disease in Malaysia. Equations (1-3) are deployed to capture the spread of disease within the population. These equations describe the movement across different stages of infection and transmission within a known population. The model is particularly useful for studying infectious diseases and understanding the dynamics of how diseases spread. The three compartmental equations represent the mechanism of transmission of different states of individuals within the population. Equations (1-3) are formed by considering factors that can lead to an increase or decrease in each of the compartments. The susceptible compartment will increase based on the birth rate (μ) and recovery rate (ε) while it will decrease based on the death rate (ν) and infection rate (β). Combining these parameters will lead to equation (1). Events leading to an increment of the compartment takes positive sign while those that lead to a decrease in the size of the compartment takes a negative sign. Thus, this information is used to form equations (1-3), an illustration of the movement of the individual within the compartment is shown in Figure 1. We can then formulate comparative governing equations of the SIRS model as follows:

$$\frac{dS}{dt} = \mu N - \frac{\beta SI}{N} + \varepsilon R - \nu S. \tag{1}$$

$$\frac{dI}{dt} = \frac{\beta SI}{N} - \left(\gamma + \nu\right) I. \tag{2}$$

$$\frac{dR}{dt} = \gamma I - \left(\varepsilon + \nu\right) R. \tag{3}$$

where

μ : Birth rate of the population

ν : Death rate of the population

β : Transmission rate of the disease

ε : Transfer rate of the individuals from recovery compartment to re-entering susceptible class

γ : Recovery rate

S : Susceptible population that might contract the disease

I : Number of infectious individuals or active cases

R : Removal class where the individuals have recovered or deceased

N : Total population where $N = S + I + R$

From the fact that $N = S + I + R$ we have $s + i + r = 1$ by dividing through by N

$$\frac{ds}{dt} = \mu - \beta is + \varepsilon r - \nu s. \tag{4}$$

$$\frac{di}{dt} = \beta is - (\gamma + \nu) i. \tag{5}$$

$$\frac{dr}{dt} = \gamma i - (\varepsilon + \nu) r. \tag{6}$$

By translation, $r(t) = 1 - s(t) - i(t)$, the above system can be further simplified into a smaller number of systems of two ordinary differential equations (ODE) in equation (7)

$$\begin{aligned} \frac{ds}{dt} &= \mu - \beta is + \varepsilon(1 - s - i) - \nu s, \\ \frac{di}{dt} &= \beta is - (\gamma + \nu) i. \end{aligned} \tag{7}$$

Using the same data utilised by (24). we arrived at the following set of parameters as the initial values for each of the compartments as, $s(0) = 0.783$, $i(0) = 0.192$ and $r(0) = 0.025$, also the following parameters were also computed from actual data of the infected population from March 24, 2020 until April 23, 2020, $\mu = \nu = 0.00005$, $\beta = 0.19$, $\gamma = 0.065$ and $\varepsilon = 0.0009$. Models of this nature are characterised by two steady state, namely, the pandemic equilibrium (PE), which is denoted by (S^*, I^*, R^*) and disease-free steady state (DFSS) denoted by $\left(\frac{\mu N}{\upsilon}, 0, 0\right)$. The determination of stability can be done using local stability analysis, which is an important tool that facilitates the understanding of system behaviour around equilibrium and detecting whether a small utterance will make the system return to the point or diverge from the point. Local stability involves first identifying equilibrium points, performing linearization, calculating the Jacobian matrix, and subsequently finding the eigenvalues of the matrix. By examining the characteristics of these eigenvalues, one can determine the local stability of the equilibrium point based on the sign of the real part of each eigenvalue.

Another variable to look for in any epidemic is basic reproductive number sometimes called the basic reproduction number which is often denoted by R_0. In a community where everyone is vulnerable to infection with no external source of infection or immune against an infection by any means, either naturally or through vaccination, R_0 of an infection is the anticipated number of cases that can be directly credited to one case of infection. To understand the dynamics of infectious diseases and predict their transmission, basic reproduction number R_0 offers good leverage by providing sensible information regarding the progression of an infectious disease. In epidemiological language R_0 is defined as

$$R_0 = \frac{\beta}{\gamma} \tag{8}$$

Regardless of the disease's initial state, the value of the number R_0 decides which limiting value will be approached. In epidemiology, if $R_0 < 1$ the infection will frail and consequently fade out, forcing the number of infected people to get closer to zero or eventually have a numerical value of ($I = 0$), and $S = N$. When the value $R_0 = 1$ each existing infection will produce one more new infection, this instance will compel the infection into stagnation, which will not lead to either an outbreak or an epidemic, thus, leading to the disease-free steady state. However, with $R_0 > 1$, the infection status will persist and keep growing uncontrollably, in fact, the bigger the value of R_0, the bigger the threat of an infectious disease. Such R_0 forms the endemic equilibrium, which $I = N - \alpha / \beta$ thus, corresponds to $S = \alpha/\beta$ [25]. However, achieving pandemic equilibrium (PE) or disease-free steady state (DFSS) revolves around controlling the spread of an infectious disease within the population, either through prevention, quarantine, isolation, medication, vaccination, heath education and many other means that can balance the infection rate and recovery rate. It's crucial to note that reaching and preserving a pandemic equilibrium or steady state devoid of disease can be difficult and may call for continuous efforts. The particular approach will change based on the illness and its symptoms. Experts in public health and epidemiologists can benefit from using mathematical models, including compartmental models, to better understand and forecast the dynamics of disease and the effects of different measures.

4 DATA INFORMATION, COMPUTER REQUIREMENTS AND FLOWCHART

In our study of COVID-19 transmission in Malaysia, we analysed the transmission dynamics based on daily active cases. We sourced our data from the open-source repository on Github (accessible at: https://github.com/MoH-Malaysia/covid19-public) for the period spanning March 24 to April 23, 2023. This dataset aligns with the data used in [26]. The essential parameters required for model development were obtained from the same source and within same time frame. To streamline the computational process, we conducted the simulations using MATLAB R2022a on a laptop equipped with an Intel(R)Core(TM) i5-8250U processor and 8GB of RAM. The laptop was running the Microsoft Windows 11 Home Version 10.0 operating system. The flowchart that demonstrates the procedures in the formulation of our hybrid model.

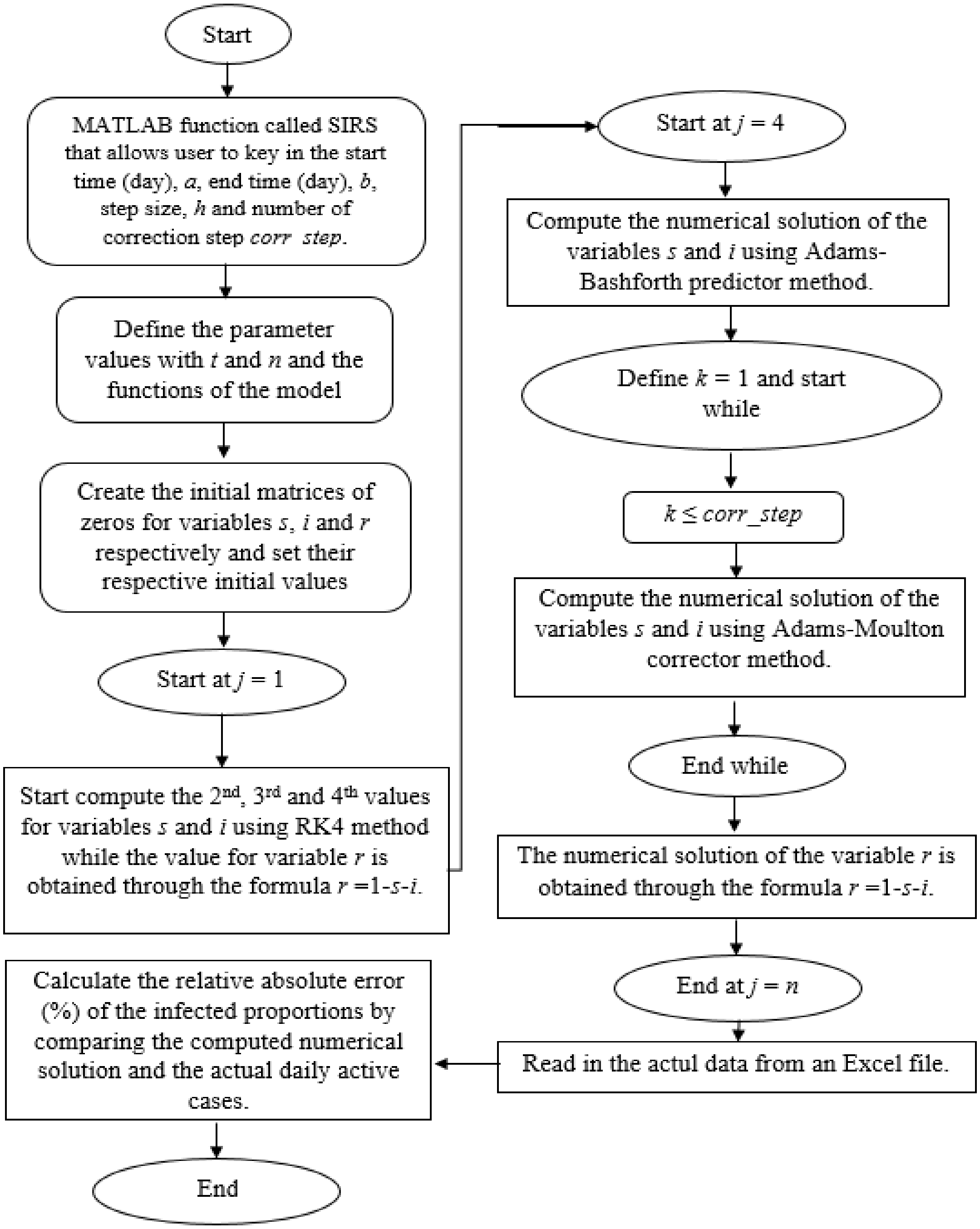

Figure 2: The Flowchart Describing the Methodology

5 MATHEMATICAL FORMULATION

Our compartmental equations are solved using a hybrid of Runge-Kutta of order 4 (RK4) and the Adam-Bashforth Predictor-Corrector method (ABPC). The first four solutions of the compartmental model are obtained using the RK4. The Adam-Bashforth Predictor Corrector Method (ABPC) is a multistep method that uses the Adam Bashforth method as the predictor and the Adam Moulton method as the corrector. It is sometimes called the Adam Bashforth-Moulton (ABM) method. The predictor part computes roughly an approximation of the desired solution, while the corrector part corrects the approximation solution obtained from the predictor part. The corrector part can be applied more than once for possible improvement. The hybrid enjoys the stability and accuracy of RK4 by performing the initial integration of the compartmental model, which helps in ensuring that the solution remains stable over short time steps, and the combined advantages of the explicit and implicit techniques of Adams-Bashforth and Adams-Moulton, respectively.

The formula for Runge-Kutta 4^{th} order is given as

$$s_{i+1} = s_i + \frac{h}{6}(k_1 + 2(k_2 + k_3) + k_4). \tag{9}$$

where

$$k_1 = hf(t_i, s_i),$$

$$k_2 = f(t_i + \frac{1}{2}h, s_i + \frac{1}{2}hk_1),$$

$$k_3 = f(t_i + \frac{1}{2}h, s_i + \frac{1}{2}hk_2),$$

$$k_4 = f(t_i + h, s_i + hk_3).$$

The general representation of multistep methods called Adams method involve the integration of the function of the form

$$y(t_{n+1}) = y(t_n) + \int_{t_n}^{t_{n+1}} \left(f(t, y(t)) \right) dt. \tag{10}$$

where $f(t, y(t) = p_4(x)$ as described in equation (11).

The derivation of Adams- Bashforth method formula is obtained by interpolating the polynomial for $f(t, y(t))$ which passes through the four distinct points $(t_{n-3}, f_{n-3}), (t_{n-2}, f_{n-2}), (t_{n-1}, f_{n-1})$ and (t_n, f_n). interpolating polynomial can be wrtten as:

$$p_4(x) = f_{n-3}L_{n-3}(t) + f_{n-2}L_{n-2}(t) + f_{n-1}L_{n-1}(t) + f_nL_n(t). \tag{11}$$

where , $L_{n-3}(t)$, $L_{n-2}(t), L_{n-1}(t)$ and $L_n(t)$ are Lagrange polynomial basis, substitute equation (11) into equation (10) and simplify leads to:

$$y_{n+1} = y_n + f_{n-3}\int_{t_n}^{t_{n+1}} L_{n-3}(t)dt + f_{n-2}\int_{t_n}^{t_{n+1}} L_{n-2}(t)dt + f_{n-1}\int_{t_n}^{t_{n+1}} L_{n-1}(t)dt + f_n\int_{t_n}^{t_{n+1}} L_n(t)dt. \tag{12}$$

Integrating equation (12) yield equation (13) which is Adams-Bashforth of order 4

Predictor:

$$S_{i+1} = S_i + \frac{h}{24}(55f_i - 59f_{i-1} + 37f_{i-2} - 9f_{i-3}). \tag{13}$$

However, due the implicit nature of an Adams-Moulton technique, this often requires finding the root of a nonlinear equation to update the solution at the next time step, it may not be practicable. As an alternative, we can create an Adams-Moulton predictor-corrector method by combining an Adams-Moulton method with an Adams-Bashforth method. Such a process works as follows: we compute a first approximation to y_{n+1} using the Adams-Bashforth method, and designate it $\hat{y}_{n+1}$. We then evaluate $f(t_{n+1}, \hat{y}_{n+1})$, after which we utilised the Adams-Moulton method as if it were an explicit method, we then compute y_{n+1}, but instead of solving the equation, we use $f(t_{n+1}, \hat{y}_{n+1})$ in place of $f(t_{n+1}, y_{n+1})$, the corrector Adams-Moulton is shown in equation (14).

Corrector:

$$S_{i+1} = S_i + \frac{h}{24}(9f_{i+1} + 19f_i + 5f_{i-1} - f_{i-2}). \tag{14}$$

6 MODIFICATION OF 4TH ORDER RUNGE-KUTTA METHOD TO COMPARTMENTAL EQUATION

In order to apply ABM in solving the compartmental equations, we need to have two version of the differential equations, one for susceptible population and the other for infected population, the modification is shown below,

We define $f(t,s,i) = \mu - \beta is + \varepsilon(1 - s - i) - \nu s$ and $g(t,s,i) = \beta is - (\gamma + \nu)i$. Starting from $n = 0$ until $n = 3$, we form the RK4 relation as

$$s_{n+1} = s_n + \frac{h}{6}\left(k_1 + 2k_2 + 2k_3 + k_4\right),$$
$$i_{n+1} = i_n + \frac{h}{6}\left(l_1 + 2l_2 + 2l_3 + l_4\right),$$
$$r_{n+1} = 1 - s_{n+1} - i_{n+1}. \tag{15}$$

where

$$k_1 = f\left(t_n, s_n, i_n\right),$$
$$l_1 = g\left(t_n, s_n, i_n\right),$$
$$k_2 = f\left(t_n + 0.5h, s_n + 0.5hk_1, i_n + 0.5hl_1\right),$$
$$l_2 = g\left(t_n + 0.5h, s_n + 0.5hk_1, i_n + 0.5hl_1\right),$$
$$k_3 = f\left(t_n + 0.5h, s_n + 0.5hk_2, i_n + 0.5hl_2\right),$$
$$l_3 = g\left(t_n + 0.5h, s_n + 0.5hk_2, i_n + 0.5hl_2\right),$$
$$k_4 = f\left(t_n + h, s_n + hk_3, i_n + hl_3\right),$$
$$l_4 = g\left(t_n + h, s_n + hk_3, i_n + hl_3\right).$$

The results of s_0, s_1, s_2, s_3 and i_0, i_1, i_2, i_3 were obtained from equation (15), we need to continue the process until the desired day say n, for each time step t, the solutions s_0, s_1, s_2, s_3 and i_0, i_1, i_2, i_3 are fed into the Adams-Bashforth predictor method. The obtained predicted solution are subsequently fed into the Adams-Moulton corrector method for improvement, whereas the value for variable r is obtained with the formula $r_{n+1} = 1 - s_{n+1} - i_{n+1}$.

7 MODIFICATION OF ADAMS-MOULTON PREDICTOR AND CORRECTOR METHOD TO COMPARTMENTAL EQUATIONS

The predictor formulas used for the variables s and i are as follows.

$$s_{n+1}^{0} = s_n + \frac{h}{24}\left[55f\left(t_n, s_n, i_n\right) - 59f\left(t_{n-1}, s_{n-1}, i_{n-1}\right) + 37f\left(t_{n-2}, s_{n-2}, i_{n-2}\right) - 9f\left(t_{n-3}, s_{n-3}, i_{n-3}\right)\right],$$
$$i_{n+1}^{0} = i_n + \frac{h}{24}\left[55g\left(t_n, s_n, i_n\right) - 59g\left(t_{n-1}, s_{n-1}, i_{n-1}\right) + 37g\left(t_{n-2}, s_{n-2}, i_{n-2}\right) - 9g\left(t_{n-3}, s_{n-3}, i_{n-3}\right)\right]. \tag{16}$$

$$s_{n+1}^{k} = s_n + \frac{h}{24}\left[9f\left(t_{n+1}, s_{n+1}^{k-1}, i_{n+1}^{k-1}\right) + 19f\left(t_n, s_n, i_n\right) - 5f\left(t_{n-1}, s_{n-1}, i_{n-1}\right) + f\left(t_{n-2}, s_{n-2}, i_{n-2}\right)\right],$$
$$i_{n+1}^{k} = i_n + \frac{h}{24}\left[9g\left(t_{n+1}, s_{n+1}^{k-1}, i_{n+1}^{k-1}\right) + 19g\left(t_n, s_n, i_n\right) - 5g\left(t_{n-1}, s_{n-1}, i_{n-1}\right) + g\left(t_{n-2}, s_{n-2}, i_{n-2}\right)\right]. \tag{17}$$

8 RESULT AND DISCUSSION

The compartmental model that describes the rates of change for each compartment (S, I, R) is presented in equations (4-6). The compartment is transformed into a system of linear equations using the Runge-Kutta of order 4 (RK4) technique. This was necessitated so that equation (4) and (5) can be reformed as schemes that can be solved iteratively, both equations have sets of unknowns, which were denoted by k_i and l_i $(i = 1, 2, 3, 4)$, k_i are computed for the susceptible population while that of infectious were computed as I_i, both k_i and I_i are very important constants in obtaining subsequent values of s_n and i_n in equation (15). The values of S_0 and I_0 were the initial values of susceptible and infectious populations from where s_0 and i_o were obtained respectively, first three solutions of s_n and i_n were obtained from RK4. The obtained solutions for (s_0, s_1, s_2, s_3) and $(\mathrm{i}_0, \mathrm{i}_1, \mathrm{i}_2, \mathrm{i}_3)$ were used in the Adam-Bashforth predictor to predict the subsequent values of the susceptible and infected population. Adam-Mouton corrector method was used to correct the earlier result, which produced a trend in COVID-19 dynamics in Malaysia within the specific interval. A series of solutions obtained from the simulation for both susceptible, infected, and recovered populations were plotted to visualise the outcome.

Figure 3(a) depicts the time series graph for the SIRS model computed numerically as result obtained from the Adam-Bashforth Predictor-Corrector (ABPC) method. The black curve represents the susceptible proportion, red curve represents the infected proportion, and the green curve indicates the removed proportion, while blue dot crosses represent the actual infected population obtained from the dataset from March 24 to April 23, 2020. It can be observed that results obtained from our models show a great deal of similarity with the actual COVID-19 incidence in Malaysia within the stipulated period; they also share a great resemblance to the graph and results obtained by [24], who use an entirely different approach.

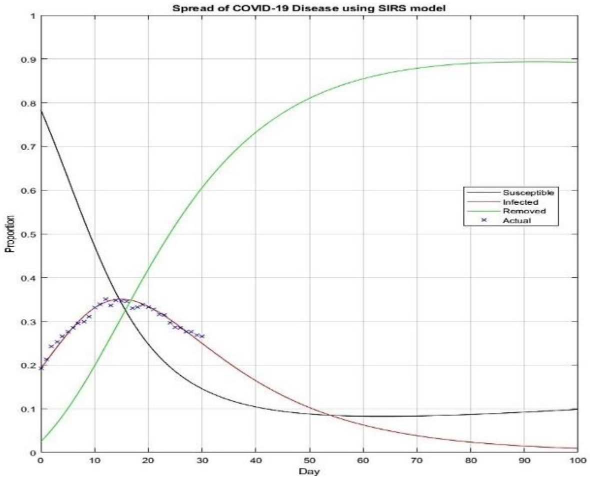

Figure 3(a): Time Series Plot for Susceptible, Infected and Recovered Portions for 100 days

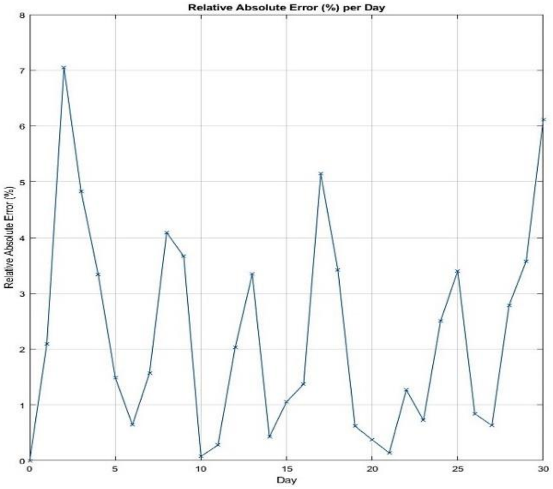

Figure 3(b): The Relative Absolute Error of the Infected Portion for 30 days

However, the situation at the beginning is an indicator of serious concern as the reproductive number corresponds to the dynamics of basic SIRS model is roughly, 2.9231. This period can be assumed as the period at which Malaysian Government and other stakeholders in the Ministry of Health were trying to get full detail and accurate information on the dynamic of the transmission of COVID-19, as such, infected agents spread the diseases to the susceptible unknowingly. We proclaimed that our model is consistent with the number of reported active COVID-19 cases in Malaysia, which increases and reaches its peak between the first two weeks of April, 2020, with the highest number of infections hitting 2596 active cases recorded in a single day. Infection cases increase unchecked on a daily basis until it reaches an acme; the infection curve represented in Figure 3 by the red curve reached its acme around the second week of April 2020. However, as the number of active cases starts declining, it can be observed that our SIRS model predicts that active cases will eventually decline and infection will consequently die out.

As time goes on $R_0 \leq 1$, which signaled the presence of medical resources and preventive methods to combat the free spread of COVID-19 among the population. An obvious reason was that the Federal Government of Malaysia on March 18, 2020 implemented a number of national quarantine and cordon sanitaire measures known as the Malaysia Government Movement Control Order (Perintah Kawalan Pergerakan Kerajaan Malaysia), or simply MCO or PKP [27], whose effects were not immediately felt until the middle of April, 2020. MCO measures place limitations on mobility, gathering, and international travel, as well as the closure of businesses, industries, governments, and educational institutions, thus, the MCO breaks down the infection pattern. Additionally, Figure 3(b) showed small relative absolute errors on each day, which justified that the proposed model is indeed accurate and suitable for capturing accurate information pertaining the spread of COVID-19 disease in Malaysia in the period under review. The numerical results using Adams-Bashforth-Moulton predictor-corrector method and actual data are compared using different step size, $h = 0.50, 0.25, 0.20, 0.10$ and 0.01, and number of correction steps, $k = 1, 2, 3, 4$ and 5. The mean and standard deviation for the relative absolute error for each pair of step size and correction steps are depicted in Figure 4.

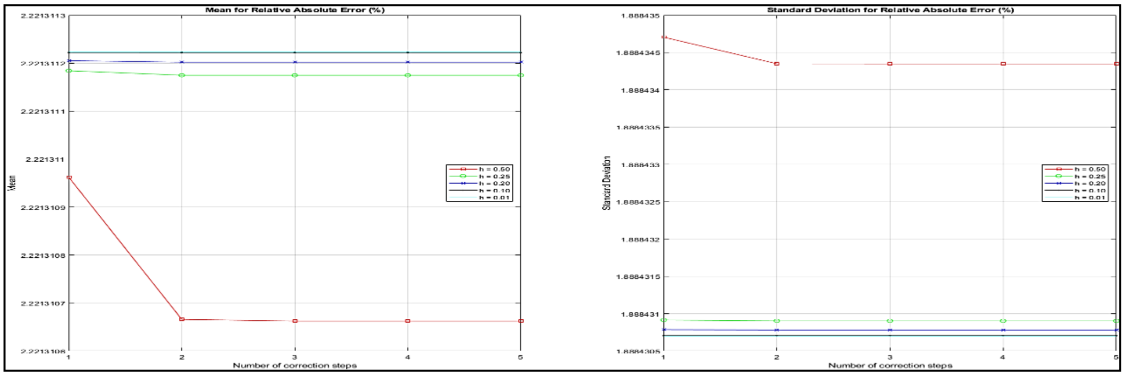

Figure 4: Graphs of Mean and Standard Deviation for Relative Absolute Error against Number of Correction steps, $k = 1, 2, 3, 4$ and 5 for step size, $h = 0.50, 0.25, 0.20, 0.10$ and 0.01

For each fixed step size h, it is discovered that as the number of correction steps, k increases from 1 to 3, the mean and standard deviation for relative absolute error greatly decreases, but approaches a constant as k further increases. On the other hand, for each fixed number of correction steps, k, we can observe that as the step size, h decreases from 0.50 to 0.01, the standard deviation for relative absolute error decreases and approaches a constant value, but its mean for relative absolute error increases and approaches a constant value. Thus, for this proposed model, it is recommended to use step size $h = 0.10$ and number of correction step, $k = 3$ as the numerical results obtained are more consistent with just a little sacrification in the precision, and also save the computational cost and time without having to use a smaller step size or to iterate more loops of correction in each time step, the mean and standard deviation for the relative absolute error for each pair of step size and correction steps are presented in Table 1 and Table 2 respectively.

Table 1: Mean for relative absolute error (%) for step size, $h = 0.50, 0.25, 0.20, 0.10$ and 0.01, and number of correction steps, $k = 1, 2, 3, 4$ and 5

Step size	Number of correction steps				
	1	2	3	4	5
0.50	2.22131096221356	2.22131066574317	2.22131066228168	2.22131066228364	2.22131066228483
0.25	2.22131118424822	2.22131117483234	2.22131117477350	2.22131117477345	2.22131117477345
0.20	2.22131120513294	2.22131120201004	2.22131120199436	2.22131120199434	2.22131120199434
0.10	2.22131122206507	2.22131122196488	2.22131122196461	2.22131122196461	2.22131122196461
0.01	2.22131122350033	2.22131122350033	2.22131122350033	2.22131122350033	2.22131122350033

Table 2: Standard deviation for relative absolute error (%) for step size, $h = 0.50, 0.25, 0.20, 0.10$ and 0.01, and number of correction steps, $k = 1, 2, 3, 4$ and 5

Step size	Number of correction steps				
	1	2	3	4	5
0.50	1.88843470542901	1.88843434942738	1.88843434784179	1.88843434785582	1.88843434785582
0.25	1.88843091445384	1.88843090303029	1.88843090301369	1.88843090301381	1.88843090301380
0.20	1.88843078474446	1.88843078097997	1.88843078097603	1.88843078097606	1.88843078097606
0.10	1.88843070459000	1.88843070447092	1.88843070447088	1.88843070447088	1.88843070447088
0.01	1.88843069963029	1.88843069963029	1.88843069963029	1.88843069963029	1.88843069963029

9 CONCLUSION

In this research, we have demonstrated that the Adam-Bashforth predictor method is an effective technique for solving compartmental model solutions. This method allows for the efficient computation of future time steps by using previous solutions and present data to approximate the future solution. By utilising this method, researchers can gain a better understanding of how different compartments interact with one another over time, which can inform decision-making in various fields such as epidemiology, pharmacology, and ecology. However, it is important to note that the accuracy of the Adam Bashforth predictor method can be affected by factors such as the step size, the order of the method, and the stability of the model. Therefore, careful consideration and validation of the results are necessary to ensure the reliability of the solution. In the absence of adequate medical facilities, decisions such as Strict Standard Operating Procedure (SOP) such as wearing masks, restricting outdoor activities, prohibiting large gatherings, and closing borders can effectively reduce the infection rate in Malaysia. As demonstrated in this research, the number of infected cases of infectious diseases can be reduced effectively. However, this may have an adverse effect in the long run due to its negative impact on the country's economy.

As mentioned earlier, in solving a system of ordinary differential equations (ODEs) numerically, it is more accurate to set the step size to be as small as possible for better accuracy of the numerical simulation results. In addition, a pair of predictor-corrector numerical models is recommended to be used, as we can "correct" the solution as many times as we wish to reduce its relative and absolute error. However, smaller step sizes and a higher number of correction steps may increase the computational burden and consume a lot of time.

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