



Semi-analytic solutions of an SIR-type epidemic model using the Taylor matrix method

Revina Dian Agustine, Jonathan Hoseana*, and Benny Yong

Center for Mathematics and Society, Faculty of Science, Parahyangan Catholic University, Bandung 40141, Indonesia.

Abstract

We apply the Taylor matrix method to generate semi-analytic solutions of a recently introduced SIR-type epidemic model for the spread of COVID-19, focusing on the case where the actual solution spirals towards a limit cycle. We assess the accuracy of these semi-analytic solutions in estimating the peaks of the epidemic waves, comparing them with semi-analytic solutions generated using the differential transform method. Since the model's analytic solution is not easily obtainable, we calculate the errors relative to the numerical solution generated by the fourth-order Runge-Kutta method with a sufficiently small step size. The results show that the errors produced by the Taylor matrix method decay faster than those produced by the differential transform method, indicating the superiority of the former method over the latter. However, this superiority comes with the trade-off of a significantly longer computation duration.

Keywords. Taylor matrix, SIR, Epidemic model, Differential transform, Runge-Kutta.

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1. INTRODUCTION

The recent COVID-19 pandemic has intensified research efforts in mathematical epidemiology. Indeed, over the last few years, the literature has experienced a significant rise in the development of novel epidemic models aimed at understanding, predicting, and controlling the spread of infectious diseases. Many of such models, designed to capture not only the complex dynamics of the disease itself but also the effectiveness of various interventions, take the form of non-linear systems of differential equations that are difficult, if not impossible, to solve analytically. Accordingly, in studies employing such models, methods that can generate approximate solutions become of interest. Typically, to generate such solutions, mathematicians resort to numerical methods [20, Chap. 22].

Numerical methods are not without limitations. In particular, such methods rely fundamentally on discretization, a concept known to potentially alter the behaviour of solutions of differential equations. The latter is observed even in one of the simplest population models, the logistic differential equation [25, sec. 1.1], all of whose solutions approach a finite limit known as the carrying capacity, while its well-known discretized counterpart, the logistic difference equation [25, sec. 2.3], exhibits the so-called period-doubling cascade, which leads to the presence of not only oscillatory but also chaotic solutions for certain parameter values. Recently, the same phenomenon has been observed to occur in some discretized epidemic models [14, 22, 28].

Such numerical methods' limitations have motivated the search for alternatives. A class of methods that could serve as powerful, discretization-free alternatives is semi-analytic methods. Such methods, when applied to a system of differential equations, aim to generate a sequence of functions that estimate the system's analytic solution within a neighbourhood of interest. Examples of such methods include the differential transform method [3, 9, 23, 33], the variational iteration method [15–17, 30, 31], the homotopy analysis method [5, 18, 21], the Adomian decomposition method [1, 2], as well as the Taylor matrix method and its variants [7, 11, 12, 26, 27]. Many of these methods have been applied to epidemic models [6, 8, 10, 13, 24, 29]. In particular, Ucar and Celik, in 2022, applied the Taylor

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* Corresponding author. Email: j.hoseana@unpar.ac.id.

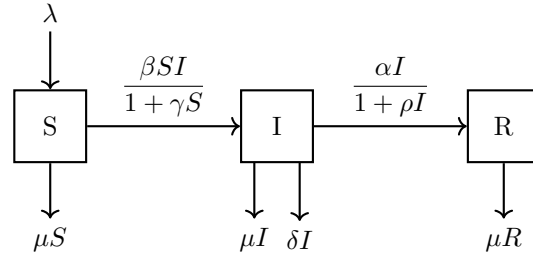


FIGURE 1. The compartment diagram of the SIR-type model (1.1).

matrix method to generate semi-analytic solutions of the Kermack-McKendrick SIR-type epidemic model, analyzing the results in the context of COVID-19 [29].

The Kermack-McKendrick SIR-type model [19], one of the simplest epidemic models, combines a bilinear incidence rate with a linear recovery rate while disregarding demographic factors and eradication interventions. Numerous more realistic SIR-type models have been constructed through modifications of this model. In particular, Yong et al. [32], in 2022, constructed the SIR-type model

$$\begin{cases} \frac{dS}{dt} = \lambda - \mu S - \frac{\beta SI}{1 + \gamma S}, \\ \frac{dI}{dt} = -\mu I - \delta I + \frac{\beta SI}{1 + \gamma S} - \frac{\alpha I}{1 + \rho I}, \\ \frac{dR}{dt} = -\mu R + \frac{\alpha I}{1 + \rho I}, \end{cases} \quad (1.1)$$

to assess the effect of the susceptible individuals' cautiousness level $\gamma \in [0, 1]$ and hospitals' bed-occupancy rate $\rho \in [0, 1]$ on the spread of COVID-19. Here, as customary, $S = S(t)$, $I = I(t)$, and $R = R(t)$ denote, respectively, the number of susceptible, infected, recovered individuals at time $t \geq 0$. The positive parameters λ , μ , δ , β , α represent, respectively, the recruitment rate, the death coefficient, the death coefficient increment due to COVID-19, the incidence coefficient, and the recovery coefficient. The rational-form incidence rate $\beta SI / (1 + \gamma S)$ captures the effect of the susceptible individuals' cautiousness on decelerating transmission, while the rational-form recovery rate $\alpha I / (1 + \rho I)$ captures the effect of the hospitals' bed occupancy in decelerating recovery. The model's compartment diagram is displayed in Figure 1. For details on the model's construction, we refer the reader to [32, sec. 1].

Inspired by the work of Ucar and Celik [29], the objective of the present paper is to apply the Taylor matrix method to the model (1.1). More specifically, we shall apply the Taylor matrix method to generate semi-analytic solutions of the model (1.1) using a set of parameter values that gives rise to a dynamical behaviour that is not present in the Kermack-McKendrick model: convergence towards a limit cycle [32, Case VI in Tbl. 3]. In such a case, the number of infected individuals oscillates over time, and we aim to assess the accuracy of the semi-analytic solutions in estimating the local maxima of the oscillations, i.e., the so-called peaks of the epidemic waves. For comparison, we shall carry out the same estimation using the semi-analytic solutions generated by the differential transform method. Since the model's analytic solution is not easily obtainable, we shall calculate the errors with respect to the numerical solution generated by the fourth-order Runge-Kutta method with a sufficiently small step size.

The rest of the paper is organized as follows. In the upcoming section 2, we describe the three methods involved in this paper: the Taylor matrix method, the differential transform method, and the fourth-order Runge-Kutta method. Subsequently, in section 3, considering a specific numerical scenario, i.e., that in which the solution of the model (1.1) converges to a stable limit cycle, we compare the performance of the Taylor matrix and differential transform methods in estimating the first two appearing epidemic peaks, computing the errors relative to the numerical solution provided by the fourth-order Runge-Kutta method. In the final section 4, we state our conclusions and describe avenues for future research.



2. THE METHODS

In this section, we discuss the application of three non-analytic methods to generate the solution of our model (1.1), namely, the semi-analytic Taylor matrix method (subsection 2.1) and differential transform method (subsection 2.2), as well as the numerical fourth-order Runge-Kutta method (subsection 2.3). The semi-analytic methods rely on the notion of Taylor polynomials of a function, a definition of which shall now be provided [4, Def. 9.7.3].

Definition 2.1. Let F be a function that is differentiable N times, and let t_0 be a real number. The N -th *Taylor polynomial* of F about $t = t_0$ is given by

$$\hat{F}_N(t) = \sum_{n=0}^N \frac{F^{(n)}(t_0)}{n!} (t - t_0)^n,$$

where $F^{(n)}$ denotes the n -th derivative of F . The N -th Taylor polynomial of F about $t = 0$ is also known as the N -th *Maclaurin polynomial* of F .

2.1. The Taylor matrix method. Let us first describe how we generate semi-analytic solutions of the model (1.1) using the Taylor matrix method, which is largely based on the work of Ucar and Celik [29]. Given a non-negative integer N , we shall generate an approximate solution $(\hat{S}, \hat{I}, \hat{R}) = (\hat{S}(t), \hat{I}(t), \hat{R}(t))$ given by the Maclaurin-polynomial forms

$$\hat{S}_N(t) = \sum_{n=0}^N S_n t^n, \quad \hat{I}_N(t) = \sum_{n=0}^N I_n t^n, \quad \text{and} \quad \hat{R}_N(t) = \sum_{n=0}^N R_n t^n, \quad (2.1)$$

where, for every $n \in \{0, 1, 2, \dots, N\}$,

$$S_n = \frac{S^{(n)}(0)}{n!}, \quad I_n = \frac{I^{(n)}(0)}{n!}, \quad \text{and} \quad R_n = \frac{R^{(n)}(0)}{n!}.$$

In particular, $(S_0, I_0, R_0) = (S(0), I(0), R(0))$ is the accompanying initial condition.

We begin by writing

$$\begin{bmatrix} \hat{S}(t) \end{bmatrix} = \begin{bmatrix} S_0 t^0 + S_1 t^1 + S_2 t^2 + \dots + S_N t^N \end{bmatrix} = \begin{bmatrix} 1 & t & t^2 & \dots & t^N \end{bmatrix} \begin{bmatrix} S_0 \\ S_1 \\ S_2 \\ \vdots \\ S_N \end{bmatrix} = \mathbf{T}(t)\mathbf{S},$$

and, similarly,

$$\begin{bmatrix} \hat{I}(t) \end{bmatrix} = \mathbf{T}(t)\mathbf{I} \quad \text{and} \quad \begin{bmatrix} \hat{R}(t) \end{bmatrix} = \mathbf{T}(t)\mathbf{R},$$

where

$$\mathbf{T}(t) = \begin{bmatrix} 1 & t & t^2 & \dots & t^N \end{bmatrix}, \quad \mathbf{S} = \begin{bmatrix} S_0 \\ S_1 \\ S_2 \\ \vdots \\ S_N \end{bmatrix}, \quad \mathbf{I} = \begin{bmatrix} I_0 \\ I_1 \\ I_2 \\ \vdots \\ I_N \end{bmatrix}, \quad \text{and} \quad \mathbf{R} = \begin{bmatrix} R_0 \\ R_1 \\ R_2 \\ \vdots \\ R_N \end{bmatrix}.$$

Next, computing the derivatives of the expressions in (2.1), we obtain

$$\begin{bmatrix} \hat{S}'(t) \end{bmatrix} = \begin{bmatrix} 1S_1 t^0 + 2S_2 t^1 + \dots + NS_N t^{N-1} \end{bmatrix}$$

$$= \begin{bmatrix} 1 & t & t^2 & \cdots & t^N \end{bmatrix} \begin{bmatrix} 0 & 1 & 0 & \cdots & 0 \\ 0 & 0 & 2 & \cdots & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & 0 & \cdots & N \\ 0 & 0 & 0 & \cdots & 0 \end{bmatrix} \begin{bmatrix} S_0 \\ S_1 \\ S_2 \\ \vdots \\ S_N \end{bmatrix}$$

$$= \mathbf{T}(t)\mathbf{BS},$$

and, similarly,

$$\begin{bmatrix} \hat{I}'(t) \end{bmatrix} = \mathbf{T}(t)\mathbf{BI} \quad \text{and} \quad \begin{bmatrix} \hat{R}'(t) \end{bmatrix} = \mathbf{T}(t)\mathbf{BR},$$

where

$$\mathbf{B} = \begin{bmatrix} 0 & 1 & 0 & \cdots & 0 \\ 0 & 0 & 2 & \cdots & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & 0 & \cdots & N \\ 0 & 0 & 0 & \cdots & 0 \end{bmatrix}.$$

Finally, to form an approximant $\hat{S}(t)\hat{I}(t)$ for the expression $S(t)I(t)$ present in the model (1.1), we notice that

$$\begin{aligned} \begin{bmatrix} \hat{S}(t)\hat{I}(t) \end{bmatrix} &= \begin{bmatrix} (S_0t^0 + S_1t^1 + \cdots + S_Nt^N) (I_0t^0 + I_1t^1 + \cdots + I_Nt^N) \end{bmatrix} \\ &= \begin{bmatrix} 1 & t & \cdots & t^N \end{bmatrix} \begin{bmatrix} 1 & t & \cdots & t^N & 0 & 0 & \cdots & 0 & 0 & 0 & \cdots & 0 \\ 0 & 0 & \cdots & 0 & 1 & t & \cdots & t^N & 0 & 0 & \cdots & 0 \\ 0 & 0 & \cdots & 0 & 0 & 0 & \cdots & 0 & 1 & t & \cdots & t^N \end{bmatrix} \begin{bmatrix} S_0I_0 \\ \vdots \\ S_0I_N \\ S_1I_0 \\ \vdots \\ S_1I_N \\ S_2I_0 \\ \vdots \\ S_2I_N \\ \vdots \\ S_NI_N \end{bmatrix} \\ &= \begin{bmatrix} 1 & t & \cdots & t^N \end{bmatrix} \begin{bmatrix} 1 & t & \cdots & t^N & 0 & 0 & \cdots & 0 & 0 & 0 & \cdots & 0 \\ 0 & 0 & \cdots & 0 & 1 & t & \cdots & t^N & 0 & 0 & \cdots & 0 \\ 0 & 0 & \cdots & 0 & 0 & 0 & \cdots & 0 & 1 & t & \cdots & t^N \end{bmatrix} \begin{bmatrix} S_0\mathbf{I} \\ S_1\mathbf{I} \\ S_2\mathbf{I} \\ \vdots \\ S_N\mathbf{I} \end{bmatrix} \\ &= \mathbf{T}(t)\mathbf{T}^*(t)\tilde{\mathbf{S}}, \end{aligned}$$

where

$$\mathbf{T}^*(t) = \begin{bmatrix} \mathbf{T}(t) & \mathbf{O} & \cdots & \mathbf{O} \\ \mathbf{O} & \mathbf{T}(t) & \cdots & \mathbf{O} \\ \vdots & \vdots & \ddots & \vdots \\ \mathbf{O} & \mathbf{O} & \cdots & \mathbf{T}(t) \end{bmatrix}, \quad \text{and} \quad \tilde{\mathbf{S}} = \begin{bmatrix} S_0\mathbf{I} \\ S_1\mathbf{I} \\ \vdots \\ S_N\mathbf{I} \end{bmatrix}.$$



We thus assume that the approximate solution $(\hat{S}, \hat{I}, \hat{R}) = (\hat{S}(t), \hat{I}(t), \hat{R}(t))$ of our model (1.1) has its coefficients satisfying the system of equations

$$\begin{cases} \mathbf{T}(t)\mathbf{B}\mathbf{S} - \lambda + \mu\mathbf{T}(t)\mathbf{S} + \frac{\beta\mathbf{T}(t)\mathbf{T}^*(t)\bar{\mathbf{S}}}{1 + \gamma\mathbf{T}(t)\mathbf{S}} = 0, \\ \mathbf{T}(t)\mathbf{B}\mathbf{I} + \mu\mathbf{T}(t)\mathbf{I} + \mu'\mathbf{T}(t)\mathbf{I} - \frac{\beta\mathbf{T}(t)\mathbf{T}^*(t)\bar{\mathbf{S}}}{1 + \gamma\mathbf{T}(t)\mathbf{S}} + \frac{\alpha\mathbf{T}(t)\mathbf{I}}{1 + \rho\mathbf{T}(t)\mathbf{I}} = 0, \\ \mathbf{T}(t)\mathbf{B}\mathbf{R} + \mu\mathbf{T}(t)\mathbf{R} - \frac{\alpha\mathbf{T}(t)\mathbf{I}}{1 + \rho\mathbf{T}(t)\mathbf{I}} = 0. \end{cases} \quad (2.2)$$

Letting

$$\begin{aligned} \mathbf{D}_1(t) &= \mathbf{T}(t)\mathbf{B} + \mu\mathbf{T}(t), & \mathbf{H}_1(t) &= \frac{\beta\mathbf{T}(t)\mathbf{T}^*(t)}{1 + \gamma\mathbf{T}(t)\mathbf{S}}, \\ \mathbf{D}_2(t) &= \mathbf{T}(t)\mathbf{B} + \mu\mathbf{T}(t) + \mu'\mathbf{T}(t) + \frac{\alpha\mathbf{T}(t)}{1 + \rho\mathbf{T}(t)\mathbf{I}}, & \mathbf{H}_2(t) &= -\frac{\beta\mathbf{T}(t)\mathbf{T}^*(t)}{1 + \gamma\mathbf{T}(t)\mathbf{S}}, \end{aligned}$$

we rewrite the system's first two equations as the system

$$\begin{cases} \mathbf{D}_1(t)\mathbf{S} + \mathbf{H}_1(t)\bar{\mathbf{S}} = \lambda, \\ \mathbf{D}_2(t)\mathbf{I} + \mathbf{H}_2(t)\bar{\mathbf{S}} = 0, \end{cases}$$

which can further be rewritten in the matricial form

$$\mathbf{D}(t)\bar{\mathbf{S}}\mathbf{I} + \mathbf{H}(t)\bar{\mathbf{S}} = \mathbf{G}(t), \quad (2.3)$$

where

$$\begin{aligned} \mathbf{D}(t) &= \begin{bmatrix} \mathbf{D}_1(t) & \mathbf{O} \\ \mathbf{O} & \mathbf{D}_2(t) \end{bmatrix}, & \bar{\mathbf{S}}\mathbf{I} &= \begin{bmatrix} \mathbf{S} \\ \mathbf{I} \end{bmatrix}, & \mathbf{G}(t) &= \begin{bmatrix} \lambda \\ 0 \end{bmatrix}, \\ \mathbf{H}(t) &= \begin{bmatrix} \mathbf{H}_1(t) & \mathbf{O} \\ \mathbf{O} & \mathbf{H}_2(t) \end{bmatrix}, & \bar{\mathbf{S}} &= \begin{bmatrix} \bar{\mathbf{S}} \\ \bar{\mathbf{S}} \end{bmatrix}. \end{aligned}$$

Next, we define the so-called collocation points

$$t_s = \frac{b}{N}s, \quad s \in \{0, 1, \dots, N\}.$$

Substituting these into (2.3) gives the $N + 1$ matricial equations

$$\mathbf{D}(t_s)\bar{\mathbf{S}}\mathbf{I} + \mathbf{H}(t_s)\bar{\mathbf{S}} = \mathbf{G}(t_s), \quad s \in \{0, 1, \dots, N\},$$

which can be written as a single matricial equation

$$\tilde{\mathbf{D}}\bar{\mathbf{S}}\mathbf{I} + \tilde{\mathbf{H}}\bar{\mathbf{S}} = \tilde{\mathbf{G}}, \quad (2.4)$$

where

$$\begin{aligned} \tilde{\mathbf{D}} &= \begin{bmatrix} \mathbf{D}(t_0) & \mathbf{O} & \cdots & \mathbf{O} \\ \mathbf{O} & \mathbf{D}(t_1) & \cdots & \mathbf{O} \\ \vdots & \vdots & \ddots & \vdots \\ \mathbf{O} & \mathbf{O} & \cdots & \mathbf{D}(t_N) \end{bmatrix}, & \bar{\mathbf{S}}\mathbf{I} &= \begin{bmatrix} \bar{\mathbf{S}}\mathbf{I} \\ \bar{\mathbf{S}}\mathbf{I} \\ \vdots \\ \bar{\mathbf{S}}\mathbf{I} \end{bmatrix}, & \tilde{\mathbf{G}} &= \begin{bmatrix} \mathbf{G}(t_1) \\ \mathbf{G}(t_2) \\ \vdots \\ \mathbf{G}(t_N) \end{bmatrix}, \\ \tilde{\mathbf{H}} &= \begin{bmatrix} \mathbf{H}(t_0) & \mathbf{O} & \cdots & \mathbf{O} \\ \mathbf{O} & \mathbf{H}(t_1) & \cdots & \mathbf{O} \\ \vdots & \vdots & \ddots & \vdots \\ \mathbf{O} & \mathbf{O} & \cdots & \mathbf{H}(t_N) \end{bmatrix}, & \bar{\mathbf{S}} &= \begin{bmatrix} \bar{\mathbf{S}} \\ \bar{\mathbf{S}} \\ \vdots \\ \bar{\mathbf{S}} \end{bmatrix}. \end{aligned}$$

Finally, we write the accompanying initial condition $(S_0, I_0) = (S(0), I(0))$ as the matricial equations

$$\mathbf{T}(0)\mathbf{S} = \lambda_1 \quad \text{and} \quad \mathbf{T}(0)\mathbf{I} = \lambda_2,$$

which are to be used to replace the lowermost two rows in the matricial Equation (2.4). The resulting matricial equation is then solved using, e.g., matrix inversion, to obtain the coefficients $S_0, \dots, S_N$ and $I_0, \dots, I_N$ in our approximate solution (2.1), and consequently expressions for $\hat{S}(t)$ and $\hat{I}(t)$ as polynomials in t . Substituting these coefficients into (2.2) then gives an expression for $\hat{R}(t)$ as a polynomial in t .

2.2. The differential transform method. Let us now discuss the differential transform method [3, 9, 23, 33]. First, to solve semi-analytically a differential equation in an unknown function $y = y(x)$ using the differential transform method, we consider the Taylor series of the function y at a point $x = x_0$, namely,

$$y(x) = \sum_{k=0}^{\infty} \frac{(x - x_0)^k}{k!} \left[\frac{d^k y(x)}{dx^k} \right]_{x=x_0}. \quad (2.5)$$

The differential transform of $y(x)$ is defined to be

$$Y(k) = \frac{1}{k!} \left[\frac{d^k y(x)}{dx^k} \right]_{x=x_0}.$$

In other words, $Y(k)$ is defined as the coefficient of $(x - x_0)^k$ in the Taylor series (2.5). We thus seek an approximate solution of the form

$$\hat{y}_N(x) = \sum_{k=0}^N Y(k)(x - x_0)^k,$$

for some non-negative integer N . The differential transforms of some commonly encountered functions can be found in, e.g., [23, Tbl. 1].

Direct application of the differential transform to both sides of the three equations in our model (1.1) requires the computation of the differential transform of rational expressions, which is neither straightforward nor readily found in most differential transform tables. In this paper, let us assume that the rational expressions $[\beta \sum_{l=0}^k S(k-l)I(l)]/[1 + \gamma S(k)]$ and $\alpha I(k)/[1 + \rho I(k)]$ can be used as substitutes for the differential transforms of the rational expressions $\beta SI/(1 + \gamma S)$ and $\alpha I/(1 + \rho I)$, respectively, thereby letting our semi-analytic solution of the model (1.1) be generated by the system

$$\begin{cases} (k+1)S(k+1) = \lambda - \mu S(k) - \frac{\beta \sum_{l=0}^k S(k-l)I(l)}{1 + \gamma S(k)}, \\ (k+1)I(k+1) = -\mu I(k) - \mu' I(k) + \frac{\beta \sum_{l=0}^k S(k-l)I(l)}{1 + \gamma S(k)} - \frac{\alpha I(k)}{1 + \rho I(k)}, \\ (k+1)R(k+1) = +\mu R(k) + \frac{\alpha I(k)}{1 + \rho I(k)}, \end{cases}$$

where $S(k)$, $I(k)$, and $R(k)$ denote the differential transforms of $S(t)$, $I(t)$, and $R(t)$, respectively.

The system's first equation is equivalent to

$$S(k+1) + \gamma \sum_{l=0}^k S(k-l)S(l+1) = \frac{\lambda - \mu S(k) + \lambda \gamma S(k) - \mu \gamma \sum_{l=0}^k S(k-l)S(l) - \beta \sum_{l=0}^k S(k-l)I(l)}{k+1},$$

while its second and third equations are equivalent to

$$\begin{aligned} I(k+1) + \rho \sum_{l=0}^k I(k-l)I(l+1) + \gamma \sum_{l=0}^k S(k-l)I(l+1) + \rho \gamma \sum_{l_2=0}^k \sum_{l_1=0}^{l_2} I(k-l_2)S(l_2-l_1)I(l_1+1) \\ = \frac{-I(k)(\mu + \delta + \alpha) - \sum_{l=0}^k I(k-l)I(l)(\mu \rho + \delta \rho) - \sum_{l=0}^k S(k-l)I(l)(\mu \gamma + \delta \gamma - \beta + \gamma \alpha)}{k+1} \\ - \frac{\sum_{l_2=0}^k \sum_{l_1=0}^{l_2} I(k-l_2)S(l_2-l_1)I(l_1)(\mu \rho \gamma + \delta \rho \gamma - \rho \beta)}{k+1}, \end{aligned}$$



and to

$$R(k+1) + \rho \sum_{l=0}^k I(k-l)R(l+1) = \frac{-\mu R(k) - \mu\rho \sum_{l=0}^k I(k-l)R(l) + \alpha I(k)}{k+1},$$

respectively. Given an initial condition $(S(0), I(0), R(0))$, the last three equations serve as recursions which enable an iterative computation of the coefficients of our approximate solution $(\hat{S}, \hat{I}, \hat{R}) = (\hat{S}(t), \hat{I}(t), \hat{R}(t))$ given by

$$\hat{S}_N(t) = \sum_{k=0}^N S_N(k) (t - t_0)^k, \quad \hat{I}_N(t) = \sum_{k=0}^N I(k) (t - t_0)^k, \quad \hat{R}_N(t) = \sum_{k=0}^N R(k) (t - t_0)^k,$$

of the model (1.1), for some initially chosen N and t_0 .

2.3. The fourth-order Runge-Kutta method. Finally, let us discuss the application of the fourth-order Runge-Kutta method [20, sec. 22.5] to our model (1.1). Given an initial condition $(S_0, I_0, R_0) = (S(0), I(0), R(0))$, fixing a step size $h > 0$ and defining the time-step

$$t_i = ih,$$

for every non-negative integer i , the method generates the numerical solution $((S_i, I_i, R_i))_{i=0}^\infty$ of the model (1.1), where, for every non-negative integer i ,

$$S_i \approx S(t_i), \quad I_i \approx I(t_i), \quad \text{and} \quad R_i \approx R(t_i),$$

via the recursion

$$\begin{cases} S_{i+1} = S_i + \frac{h}{6} (k_1 + 2k_2 + 2k_3 + k_4), \\ I_{i+1} = I_i + \frac{h}{6} (l_1 + 2l_2 + 2l_3 + l_4), \\ R_{i+1} = R_i + \frac{h}{6} (m_1 + 2m_2 + 2m_3 + m_4), \end{cases}$$

where

$$\begin{aligned} k_1 &= \lambda - \mu S_i - \frac{\beta S_i I_i}{1 + \gamma S_i}, & l_1 &= -\mu I_i - \mu' I_i + \frac{\beta S_i I_i}{1 + \gamma S_i} - \frac{\alpha I_i}{1 + \rho I_i}, \\ m_1 &= -\mu R + \frac{\alpha I_i}{1 + \rho I_i}, & k_2 &= \lambda - \mu \left(S_i + \frac{k_1}{2} \right) - \frac{\beta (S_i + k_1/2) (I_i + l_1/2)}{1 + \gamma (S_i + k_1/2)}, \\ l_2 &= -\mu \left(I_i + \frac{l_1}{2} \right) - \mu' \left(I_i + \frac{l_1}{2} \right) + \frac{\beta (S_i + k_1/2) (I_i + l_1/2)}{1 + \gamma (S_i + k_1/2)} - \frac{\alpha (I_i + l_1/2)}{1 + \rho (I_i + l_1/2)}, \\ m_2 &= -\mu \left(R_i + \frac{m_1}{2} \right) + \frac{\alpha (I_i + l_1/2)}{1 + \rho (I_i + l_1/2)}, & k_3 &= \lambda - \mu \left(S_i + \frac{k_2}{2} \right) - \frac{\beta (S_i + k_2/2) (I_i + l_2/2)}{1 + \gamma (S_i + k_2/2)}, \\ l_3 &= -\mu \left(I_i + \frac{l_2}{2} \right) - \mu' \left(I_i + \frac{l_2}{2} \right) + \frac{\beta (S_i + k_2/2) (I_i + l_2/2)}{1 + \gamma (S_i + k_2/2)} - \frac{\alpha (I_i + l_2/2)}{1 + \rho (I_i + l_2/2)}, \\ m_3 &= -\mu \left(R_i + \frac{m_2}{2} \right) + \frac{\alpha (I_i + l_2/2)}{1 + \rho (I_i + l_2/2)}, & k_4 &= \lambda - \mu (S_i + k_3) - \frac{\beta (S_i + k_3) (I_i + l_3)}{1 + \gamma (S_i + k_3)}, \\ l_4 &= -\mu (I_i + l_3) - \mu' (I_i + l_3) + \frac{\beta (S_i + k_3) (I_i + l_3)}{1 + \gamma (S_i + k_3)} - \frac{\alpha (I_i + l_3)}{1 + \rho (I_i + l_3)}, \\ m_4 &= -\mu (R_i + m_3) + \frac{\alpha (I_i + l_3)}{1 + \rho (I_i + l_3)}. \end{aligned}$$

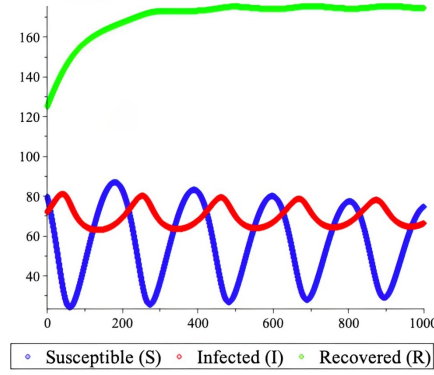


FIGURE 2. The solution $(S(t), I(t), R(t))$ associated with the initial condition $(S_0^{(1)}, I_0^{(1)}, R_0^{(1)}) = (80, 72, 125)$ of the model (1.1) with parameter values given by (3.1).

3. COMPUTATION AND DISCUSSION

In this section, we compare the performance of the Taylor matrix method with that of the differential transform method in estimating the so-called epidemic peaks, i.e., the local maxima of the number of infected individuals in the solutions of the model (1.1), using the errors calculated with respect to the numerical fourth-order Runge-Kutta method. Our computation uses the following set of parameters for which the solutions of the model (1.1) exhibit a dynamical behaviour that is not found in the Kermack-McKendrick SIR-type model, namely, convergence to a stable limit cycle [32, eqn. (8) and Case VI]:

$$\beta = 0.05, \quad \lambda = 10, \quad \mu = 0.01, \quad \mu' = 0.1, \quad \alpha = 0.2, \quad \rho = 0.1, \quad \text{and} \quad \gamma = 0.35. \quad (3.1)$$

Furthermore, defining

$$S_0^{(1)} = 80, \quad I_0^{(1)} = 72, \quad R_0^{(1)} = 125, \quad \text{and} \quad S_0^{(2)} = 70, \quad I_0^{(2)} = 75, \quad R_0^{(2)} = 167,$$

we shall apply the two semi-analytic methods to estimate only the first two epidemic peaks occurring in the solution of the model (1.1) associated to the initial condition $(S_0^{(1)}, I_0^{(1)}, R_0^{(1)})$. Figure 2 displays a plot of this solution, generated using the fourth-order Runge-Kutta method with step size $h = 0.1$. The numbers of infected individuals at the first and second peaks are $I_{\max}^{(1)} \approx 81.22280291$ and $I_{\max}^{(2)} \approx 81.14784694$, respectively, which are achieved at $t = t_{\max}^{(1)} = 41$ and at $t = t_{\max}^{(2)} = 259.8$, respectively. To estimate the first epidemic peak, we shall use the initial condition $(S_0^{(1)}, I_0^{(1)}, R_0^{(1)})$ itself, while to estimate the second epidemic peak, we shall use the approximate initial condition $(S_0^{(2)}, I_0^{(2)}, R_0^{(2)})$. The results are visualised in Figures 3 and 4. In the Taylor matrix method, the parameter N determines the sizes of the matrices involved in the matrices in the matricial equation to be solved, whereas in the differential transform method, the same parameter determines the number of iterations.

As expected, the semi-analytic solutions depart from the numerical solution as $t \rightarrow \infty$. However, as $N \rightarrow \infty$, the semi-analytic solutions provide increasingly accurate approximations for the numerical solution. Figures 3 and 4 also show that for the largest utilized value of N , i.e., $N = 8$, the approximant $\hat{I}(t)$ obtained using the Taylor matrix method appears to be closer to the numerical solution compared to that obtained using the differential transform method.

In Tables 1 and 2, we compare the errors of the estimates of the first and second epidemic peaks provided by the semi-analytic solutions of our model (1.1) generated by the Taylor matrix and differential transform methods, calculated with respect to those provided by the numerical solution generated by the fourth-order Runge-Kutta method. The errors are calculated using the formulae

$$\mathcal{E}_N^{(1)} = \sum_i |I_i - \hat{I}_N(ih)|, \quad \text{and} \quad \mathcal{E}_N^{(2)} = |I_{t_{\max}} - \hat{I}_N(t_{\max}h)|,$$



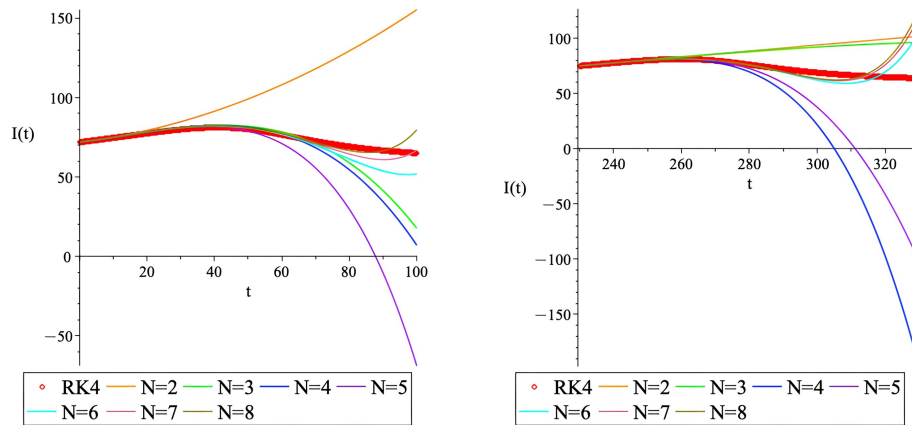


FIGURE 3. The time-evolution of the size of the infected subpopulation near the first (left) and second (right) epidemic peaks obtained using the Taylor matrix method with various values of N , and using the fourth-order Runge-Kutta method.

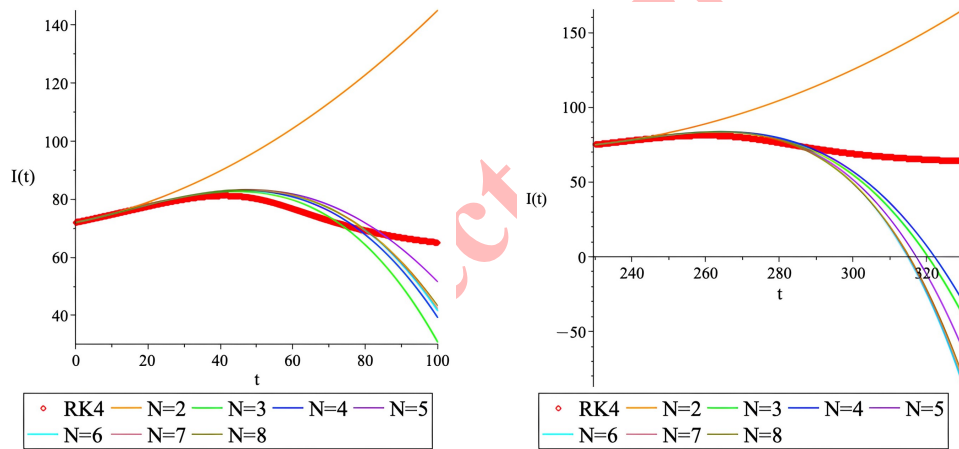


FIGURE 4. The time-evolution of the size of the infected subpopulation near the first (left) and second (right) epidemic peaks obtained using the differential transform method with various values of N , and using the fourth-order Runge-Kutta method.

where $\mathcal{E}_N^{(1)}$ represents a cumulative error, while $\mathcal{E}_N^{(2)}$ represents the error at the respective peak. The summation in the formula for $\mathcal{E}_N^{(1)}$ is carried out over all values of i for which $t_i = ih$ ranges from 0 to 100 in the case of the first peak, and from 230 to 330 in the case of the second peak. In the expression for $\mathcal{E}_N^{(2)}$, we replace $t_{\max}$ with $t_{\max}^{(1)} = 41$ in the case of the first peak, and with $t_{\max}^{(2)} = 259.7$ in the case of the second peak.

Figures 5 and 6 show that the errors associated to the two semi-analytic methods exhibit decreasing trends as $N \rightarrow \infty$, albeit with fluctuations rather than monotonic. It is apparent that the errors produced by the Taylor matrix method decreases to zero faster than those produced by the differential transform method, as $N \rightarrow \infty$. In particular, for $N = 8$, the Taylor matrix method provides the most accurate estimate of the second epidemic peak, with the smallest error $\mathcal{E}_8^{(2)}$ of approximately 0.004. However, such a high accuracy comes at a cost: a longer computation

TABLE 1. The errors of the estimations of the first epidemic peak by the two semi-analytic methods with respect to the numerical solution generated by the fourth-order Runge-Kutta method, along with the respective semi-analytic methods' computation durations in seconds.

N	Taylor matrix			Differential transform		
	$\mathcal{E}_N^{(1)}$	$\mathcal{E}_N^{(2)}$	Duration	$\mathcal{E}_N^{(1)}$	$\mathcal{E}_N^{(2)}$	Duration
2	29240.256	10.965	4.747	25828.257	9.242	0.311
3	6544.322	1.481	13.627	4606.333	1.355	0.470
4	8202.949	1.181	33.992	3741.377	1.596	0.544
5	20303.300	0.300	58.658	2873.646	1.738	0.636
6	3419.027	0.874	69.944	3565.476	1.691	0.789
7	1666.082	0.903	141.484	3501.628	1.692	1.009
8	1402.185	0.712	203.321	5384.348	1.693	1.330

TABLE 2. The errors of the estimations of the second epidemic peak by the two semi-analytic methods with respect to the numerical solution generated by the fourth-order Runge-Kutta method, along with the respective semi-analytic methods' computation durations in seconds.

N	Taylor matrix			Differential transform		
	$\mathcal{E}_N^{(1)}$	$\mathcal{E}_N^{(2)}$	Duration	$\mathcal{E}_N^{(1)}$	$\mathcal{E}_N^{(2)}$	Duration
2	14854.870	2.084	3.671	36074.520	7.746	0.467
3	13486.191	1.939	8.480	17222.802	2.304	0.501
4	45098.325	0.376	19.578	15610.786	2.377	0.590
5	29324.767	0.153	34.920	20665.705	2.301	0.693
6	3843.227	0.007	77.214	23939.511	2.284	0.950
7	4529.173	0.004	135.224	23653.042	2.285	1.106
8	4967.815	0.004	201.033	23546.477	2.285	1.238

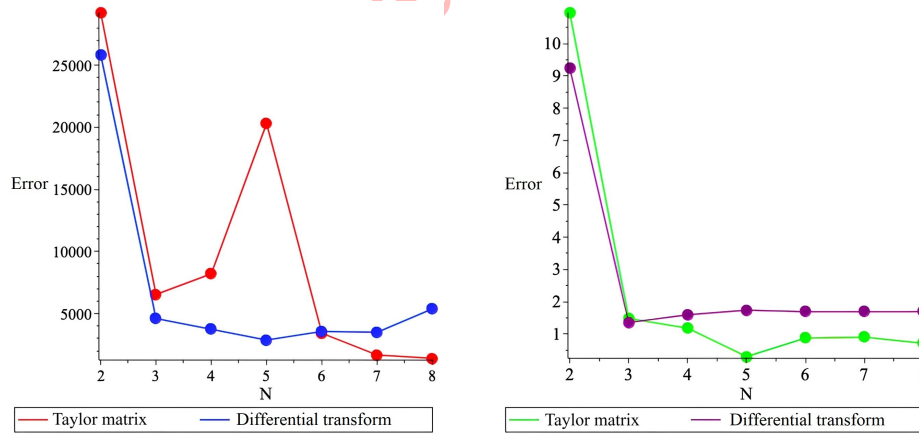


FIGURE 5. The errors $\mathcal{E}_N^{(1)}$ (left) and $\mathcal{E}_N^{(2)}$ (right) produced by the Taylor matrix and differential transform methods in the estimation of the first epidemic peak, as functions of N .

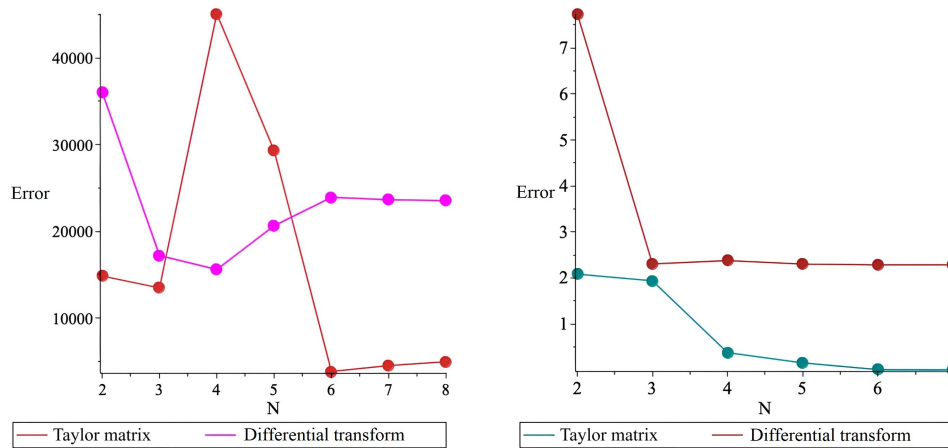


FIGURE 6. The errors $\mathcal{E}_N^{(1)}$ (left) and $\mathcal{E}_N^{(2)}$ (right) produced by the Taylor matrix and differential transform methods in the estimation of the second epidemic peak, as functions of N .

duration. Indeed, from Tables 1 and 2, we can see that the Taylor matrix method generally requires a remarkably longer computation duration compared to the differential transform method, especially for the larger values of N .

4. CONCLUSIONS AND FUTURE RESEARCH

We have applied the Taylor matrix method to generate semi-analytic solutions of a recently introduced SIR-type epidemic model, using these solutions to estimate the emerging epidemic peaks. We have compared the method's performance with that of the differential transform method. The results reveal that the errors produced by the Taylor matrix method decay faster than those produced by the differential transform method, where the errors are calculated with respect to the numerical solution generated by the fourth-order Runge-Kutta method. This shows the superiority of the Taylor matrix method over the differential transform method. However, the Taylor matrix method requires a notably longer computation duration than the differential transform method.

This research could be extended in a number of ways. First, one could apply the two semi-analytic methods used in this paper and other semi-analytic methods to generate approximate solutions for other epidemic models, particularly those involving rational-form incidence and recovery rates. The assumption we used in our application of the differential transform method to deal with such rates is hoped to motivate the proposal of alternative assumptions, which further open opportunities for accuracy comparisons. In addition, the computation of estimates of the second epidemic peak, which we performed using an approximate initial condition, could also be performed using the initial condition used to estimate the first epidemic peak. For this purpose, to avoid excessively large error values, one could select epidemic models that generate relatively short inter-peak time intervals.

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Uncorrected Proof

