

# An Accurate Analytical-Numerical Iterative Method for the Susceptible-Infected-Recovered Epidemic Models

Sudi Mungkasi

Department of Mathematics, Sanata Dharma University, Yogyakarta, Indonesia

[sudi@usd.ac.id](mailto:sudi@usd.ac.id)

## ABSTRACT

### Article History:

Received : 13-01-2021

Revised : 28-04-2021

Accepted : 01-05-2021

Online : 26-10-2021

### Keyword:

Epidemic Problem;  
Infectious Disease;  
Numerical Solution;  
SIR Model;  
Vital Dynamics.

We consider Susceptible-Infected-Recovered (SIR) models of infectious disease spread without and with vital dynamics. We recall some existing analytical approximate iterative methods for solving these models. We observe that all these methods solve the models accurately only for points close to the initialisation. These methods produce inaccurate, and even, unrealistic solutions to the SIR models if the time domain is sufficiently large. In this paper, our research objective is to propose an analytical-numerical iterative method, which is able to solve the SIR models accurately on the whole domain. The research method used is quantitative mathematical modelling with simulation. By implementing this analytical-numerical iterative method into a finite number of small consecutive subintervals of the domain, our research results show that the proposed method produces accurate solutions to the SIR models on the whole domain.



<https://doi.org/10.31764/jtam.v5i2.3876>



This is an open access article under the [CC-BY-SA](https://creativecommons.org/licenses/by-sa/4.0/) license

## A. INTRODUCTION

Susceptible-Infected-Recovered (SIR) models have been trusted for simulation of the spread of various infectious diseases (Harko et al., 2014). SIR models are very important in the prediction of the spread of various infectious diseases. Therefore, a simple but accurate method for solving these models is always desired.

A number of articles have reported some properties, applications, and extensions of SIR models. Properties of SIR models have been reported by Gatto & Schellhorn (2021), Turkeyilmazoglu (2021), Wu et al. (2021), as well as Kröger & Schlickeiser (2020). Interestingly, SIR models have been used to simulate the transmission of the new Coronavirus SARS-COV-2, which we know that this virus results in the global pandemic COVID-19 (Alenezi et al., 2021; Alqahtani, 2021; Din & Algehyne, 2021; Telles et al., 2021; Cadoni & Gaeta, 2020; Ifiguis et al., 2020). Due to their simplicity and flexibility, SIR models have been extended to more complex models, such as, SEIR, BSEIR, SEIAR, and SEIQR models (Rahimi et al., 2021; Ucan et al., 2021; De la Sen et al., 2020; Heng & Althaus 2020).

Some analytical approximate methods have been available in the literature for solving SIR models. These methods are of the type of iterative and non-iterative. Non-iterative methods that provide analytical approximate solutions are, for example, that proposed by Barlow & Weinstein, 2020. Iterative methods are also available, such as variational iteration methods.

Rafei et al., (2007) proposed a variational iteration method in order to solve the classical SIR model. The analytical approximate iterative method is simple to implement and accurate for points close to the initialisation, but inaccurate for points far from the initialisation (Mungkasi, 2021, 2020a, 2020b). In this paper, we limit our work to iterative methods. We aim to propose a new iterative method that is accurate on the whole domain.

Several modifications of the variational iteration method have been proposed. One of the modifications is by optimising the Lagrange multipliers involved in the iterative formulas (He, 2000; Biazar & Ghazvini, 2007; Darvishi et al., 2007). Another modification is by implementing the Gauss-Seidel technique in the variational iteration scheme (Alderremy et al., 2020; Rangkuti et al., 2016; Tatari & Dehghan, 2009; Salkuyeh, 2008; Youssef & El-Arabawy, 2007). Unfortunately, we show by computational experiments in this paper that these variational iteration modifications do not improve much the accuracy of the method in solving the SIR models, which are nonlinear.

Our main contribution in this paper is to propose a combination of analytical and numerical techniques in solving the SIR models both without and with vital dynamics. That is, we propose a piecewise variational iteration method into a finite number of subintervals of the domain. We use the variational iteration method as our basis in our proposed method. We obtain that implementation of the variational iteration method piecewisely on the given domain leads to accurate solutions to the SIR models on that whole given domain.

We recall the SIR epidemic models both without and with vital dynamics. As the name suggests, the whole population of the system consist of three compartments, namely, susceptible (S), infected (I), and recovered (R) subpopulations. Each of the subpopulations are disjoint. We denote  $t$  the time variable,  $x(t)$  the susceptible subpopulation,  $y(t)$  the infected subpopulation, and  $z(t)$  the recovered subpopulation. The vital dynamics include birth and death rates. We assume that, in the system, the total population

$$N = x(t) + y(t) + z(t) \tag{1}$$

is constant.

The SIR model without vital dynamics is (Harko et al., 2014; Jordan & Smith, 2007; Rafei et al., 2007; Biazar, 2006; Kermack & McKendrick, 1927):

$$\frac{dx}{dt} = -\beta x(t)y(t), \tag{2}$$

$$\frac{dy}{dt} = \beta x(t)y(t) - \gamma y(t), \tag{3}$$

$$\frac{dz}{dt} = \gamma y(t). \tag{4}$$

Here  $\beta$  is the infection rate and  $\gamma$  is the recovery rate. Adding equations (2)-(4), we obtain that  $dN/dt = 0$ , which agrees with our assumption that the total population  $N$  is constant.

The SIR model with vital dynamics is (Harko et al., 2014; Brauer & Castillo-Chavez, 2012; Brauer et al., 2008; Murray, 2002; Daley & Gani, 2001):

$$\frac{dx}{dt} = -\beta x(t)y(t) + \mu(N - x(t)), \tag{5}$$

$$\frac{dy}{dt} = \beta x(t)y(t) - (\gamma + \mu)y(t), \tag{6}$$

$$\frac{dz}{dt} = \gamma y(t) - \mu z(t). \tag{7}$$

Here the birth and the death rates are equal and denoted by  $\mu$ . Addition of equations (5)-(7) confirms our assumption that the total population  $N = x(t) + y(t) + z(t)$  is constant.

The initial conditions are the values of  $x(t)$ ,  $y(t)$ , and  $z(t)$  at time  $t = 0$ , and in general, denoted by

$$x(0) = x_0 \text{ and } y(0) = y_0 \text{ and } z(0) = z_0 \quad (8)$$

where  $x_0$ ,  $y_0$ , and  $z_0$  are known constants. For computational experiments in this paper, we take the following initial conditions (Rafei et al., 2007; Biazar, 2006):

$$x_0 = 20, \quad y_0 = 15, \quad z_0 = 10, \quad (9)$$

for all cases. For the case of the SIR model without vital dynamics, we take the following parameters (Rafei et al., 2007; Biazar, 2006):

$$\beta = 0.01 \quad \text{and} \quad \gamma = 0.02. \quad (10)$$

For the case of the SIR model with vital dynamics, we take the additional parameter

$$\mu = 0.04. \quad (11)$$

All variational iteration solutions are to be compared with reference solutions. The reference solutions are generated using the ode45 code of the MATLAB software with the relative tolerance is  $2.22045 \times 10^{-14}$  and the absolute tolerance is  $10^{-15}$ . Please note that the value of the relative tolerance  $2.22045 \times 10^{-14}$  is the machine epsilon of the MATLAB software up to four significant figures of decimal places, and the value of the absolute tolerance  $10^{-15}$  is below the machine epsilon. Therefore, any evaluation of computational error is maintained to be as accurate as possible.

The rest of this paper is structured as follows. First, existing variational iteration methods and their behaviour for solving the SIR models are presented; then, we propose a new piecewise variational iteration method for solving the SIR models accurately. Afterwards, computational results are presented and discussed. Finally, the paper is concluded with some remarks that our research objective has been achieved. Please note that the research objective of this paper is to propose a new analytical-numerical iterative method, which is able to solve the SIR models accurately on a large domain.

## B. METHODS

The type of research of this paper is modelling with simulation. To achieve our research objective, the present section consists of six subsections. We recall four variational iteration methods existing in the literature and provide the proposed method for solving the SIR epidemic models. The first is the scheme according to Rafei et al., (2007). The second is the Gauss-Seidel implementation to the first scheme. The third is a modified variational iteration method according to Biazar & Ghazvini (2007), Darvishi et al. (2007), as well as He (2000). The fourth is the Gauss-Seidel implementation to the third scheme. We also investigate the behaviour of the solutions produced using these four variational iteration methods existing in the literature, and obtain that the produced solutions are not accurate, and even not realistic, for large time values. After that, we present our proposed method in order to solve the SIR epidemic models accurately.

### 1. Rafei-Daniali-Ganji (RDG) scheme

We note that the SIR model (2)-(4) is a special case of the SIR model (5)-(7) by setting  $\mu = 0$ . Rafei et al. (2007) proposed a variational iteration scheme for solving the SIR model (2)-(4) without vital dynamics. In this subsection, we extend the derivation of Rafei et al. (2007) in order to solve the more general SIR model (5)-(7) involving vital dynamics. We shall call the resulting scheme as the RDG scheme due to Rafei et al. (2007), that is, Rafei-Daniali-Ganji (RDG).

The correction functionals for equations (5)-(7) due to Rafei et al. (2007) are taken as

$$x_{i+1}(t) = x_i(t) + \int_0^t \lambda_1(\tau) \left[ \frac{dx_i(\tau)}{d\tau} + \beta \bar{x}_i(\tau) \bar{y}_i(\tau) - \mu(N - \bar{x}(\tau)) \right] d\tau, \quad (12)$$

$$y_{i+1}(t) = y_i(t) + \int_0^t \lambda_2(\tau) \left[ \frac{dy_i(\tau)}{d\tau} - \beta \bar{x}_i(\tau) \bar{y}_i(\tau) + (\gamma + \mu) \bar{y}_i(\tau) \right] d\tau, \quad (13)$$

$$z_{i+1}(t) = z_i(t) + \int_0^t \lambda_3(\tau) \left[ \frac{dz_i(\tau)}{d\tau} - \gamma \bar{y}_i(\tau) + \mu \bar{z}_i(\tau) \right] d\tau, \quad (14)$$

where  $\lambda_1(\tau)$ ,  $\lambda_2(\tau)$ , and  $\lambda_3(\tau)$  are Lagrange multipliers; the restricted variations  $\bar{x}_i(\tau)$ ,  $\bar{y}_i(\tau)$ , and  $\bar{z}_i(\tau)$  mean  $\delta \bar{x}_i(\tau) = 0$ ,  $\delta \bar{y}_i(\tau) = 0$ , and  $\delta \bar{z}_i(\tau) = 0$ , respectively.

We operate variations in equations (12)-(14), and we have

$$\delta x_{i+1}(t) = \delta x_i(t) + \delta \int_0^t \lambda_1(\tau) dx_i(\tau), \quad (15)$$

$$\delta y_{i+1}(t) = \delta y_i(t) + \delta \int_0^t \lambda_2(\tau) dy_i(\tau), \quad (16)$$

$$\delta z_{i+1}(t) = \delta z_i(t) + \delta \int_0^t \lambda_3(\tau) dz_i(\tau). \quad (17)$$

Then, we implement integration in equations (15)-(17) by parts, and we have

$$\delta x_{i+1}(t) = \delta [x_i(t)(1 + \lambda_1(t))] - \delta \int_0^t \frac{d\lambda_1(\tau)}{d\tau} x_i(\tau) d\tau, \quad (18)$$

$$\delta y_{i+1}(t) = \delta [y_i(t)(1 + \lambda_2(t))] - \delta \int_0^t \frac{d\lambda_2(\tau)}{d\tau} y_i(\tau) d\tau, \quad (19)$$

$$\delta z_{i+1}(t) = \delta [z_i(t)(1 + \lambda_3(t))] - \delta \int_0^t \frac{d\lambda_3(\tau)}{d\tau} z_i(\tau) d\tau. \quad (20)$$

Based on equations (18)-(20), we obtain stationary conditions

$$\lambda_1'(\tau) = 0, \quad 1 + \lambda_1(\tau)|_{\tau=t} = 0, \quad (21)$$

$$\lambda_2'(\tau) = 0, \quad 1 + \lambda_2(\tau)|_{\tau=t} = 0, \quad (22)$$

$$\lambda_3'(\tau) = 0, \quad 1 + \lambda_3(\tau)|_{\tau=t} = 0. \quad (23)$$

Therefore, the Lagrange multipliers are

$$\lambda_1(\tau) = \lambda_2(\tau) = \lambda_3(\tau) = -1. \tag{24}$$

The variational iteration method of Rafei et al., (2007) for solving equations (5)-(7) is

$$x_{i+1}(t) = x_i(t) - \int_0^t \left[ \frac{dx_i(\tau)}{d\tau} + \beta x_i(\tau)y_i(\tau) - \mu(N - x_i(\tau)) \right] d\tau, \tag{25}$$

$$y_{i+1}(t) = y_i(t) - \int_0^t \left[ \frac{dy_i(\tau)}{d\tau} - \beta x_i(\tau)y_i(\tau) + (\gamma + \mu)y_i(\tau) \right] d\tau, \tag{26}$$

$$z_{i+1}(t) = z_i(t) - \int_0^t \left[ \frac{dz_i(\tau)}{d\tau} - \gamma y_i(\tau) + \mu z_i(\tau) \right] d\tau. \tag{27}$$

In this paper, iterative formulas (25)-(27) are called the RDG scheme due to Rafei et al. (2007), that is, Rafei-Daniali-Ganji (RDG).

**2. Gauss-Seidel-Rafei-Daniali-Ganji (GS-RDG) scheme**

An idea to improve the convergence speed of the iterations of the RDG scheme to the exact solution is by using the newest values in each of next iterations. This idea follows from the Gauss-Seidel technique for solving systems of linear algebraic equations. It has been implemented by a number of authors, such as Alderremy et al. (2020), Rangkuti et al. (2016), Tatari & Dehghan (2009), Salkuyeh (2008), as well as Youssef & El-Arabawy (2007). In this paper, the resulting scheme of the implementation of the Gauss-Seidel technique to the scheme of Rafei et al., (2007) is called the Gauss-Seidel-Rafei-Daniali-Ganji (GS-RDG) scheme.

Observing the models (2)-(4) and (5)-(7), we identify that the equation for  $y(t)$  involves more parameters than those for  $x(t)$  and  $z(t)$ . For this reason, in the GS-RDG scheme we rearrange the order of equations (2)-(4) and that of (5)-(7) to be for  $y(t)$ ,  $x(t)$ , and  $z(t)$ , respectively. The GS-RDG scheme is

$$y_{i+1}(t) = y_i(t) - \int_0^t \lambda_1(\tau) \left[ \frac{dy_i(\tau)}{d\tau} + \beta x_i(\tau)y_i(\tau) + (\gamma + \mu)y_i(\tau) \right] d\tau, \tag{28}$$

$$x_{i+1}(t) = x_i(t) - \int_0^t \left[ \frac{dx_i(\tau)}{d\tau} + \beta x_i(\tau)y_{i+1}(\tau) - \mu(N - x_i(\tau)) \right] d\tau, \tag{29}$$

$$z_{i+1}(t) = z_i(t) - \int_0^t \left[ \frac{dz_i(\tau)}{d\tau} - \gamma y_{i+1}(\tau) + \mu z_i(\tau) \right] d\tau. \tag{30}$$

**3. Modified-Rafei-Daniali-Ganji (MRDG) scheme**

The original variational iteration method was proposed by He (1999). For systems of equations Biazar & Ghazvini (2007), Darvishi et al. (2007), as well as He (2000) presented a rather different scheme. In this paper, that different scheme for solving equations (5)-(7) is called the modified-Rafei-Daniali-Ganji (MRDG) scheme.

The correction functionals for equations (5)-(7) due to He (2000) are taken as

$$x_{i+1}(t) = x_i(t) + \int_0^t \left[ \frac{dx_i(\tau)}{d\tau} + \beta \bar{x}_i(\tau)\bar{y}_i(\tau) - \mu(N - x(\tau)) \right] d\tau, \tag{31}$$

$$y_{i+1}(t) = y_i(t) + \int_0^t \lambda_2(\tau) \left[ \frac{dy_i(\tau)}{d\tau} - \beta \bar{x}_i(\tau) \bar{y}_i(\tau) + (\gamma + \mu)y(\tau) \right] d\tau, \quad (32)$$

$$z_{i+1}(t) = z_i(t) + \int_0^t \lambda_3(\tau) \left[ \frac{dz_i(\tau)}{d\tau} - \gamma \bar{y}_i(\tau) + \mu z(\tau) \right] d\tau, \quad (33)$$

where  $\lambda_1(\tau)$ ,  $\lambda_2(\tau)$ , and  $\lambda_3(\tau)$  are Lagrange multipliers; the restricted variations  $\bar{x}_i(\tau)$ ,  $\bar{y}_i(\tau)$ , and  $\bar{z}_i(\tau)$  mean  $\delta \bar{x}_i(\tau) = 0$ ,  $\delta \bar{y}_i(\tau) = 0$ , and  $\delta \bar{z}_i(\tau) = 0$ , respectively.

We operate variations to equations (31)-(33), and we have

$$\delta x_{i+1}(t) = \delta x_i(t) + \delta \int_0^t \lambda_1(\tau) \left[ \frac{dx_i(\tau)}{d\tau} + \mu x_i(\tau) \right] d\tau, \quad (34)$$

$$\delta y_{i+1}(t) = \delta y_i(t) + \delta \int_0^t \lambda_2(\tau) \left[ \frac{dy_i(\tau)}{d\tau} + (\gamma + \mu)y_i(\tau) \right] d\tau, \quad (35)$$

$$\delta z_{i+1}(t) = \delta z_i(t) + \delta \int_0^t \lambda_3(\tau) \left[ \frac{dz_i(\tau)}{d\tau} + \mu z_i(\tau) \right] d\tau. \quad (36)$$

Then, we implement integration in equations (34)-(36) by parts, and we have

$$\delta x_{i+1}(t) = \delta [x_i(t)(1 + \lambda_1(t))] - \delta \int_0^t \left( \frac{d\lambda_1(\tau)}{d\tau} - \mu \lambda_1(\tau) \right) x_i(\tau) d\tau, \quad (37)$$

$$\delta y_{i+1}(t) = \delta [y_i(t)(1 + \lambda_2(t))] - \delta \int_0^t \left( \frac{d\lambda_2(\tau)}{d\tau} - (\gamma + \mu)\lambda_2(\tau) \right) y_i(\tau) d\tau, \quad (38)$$

$$\delta z_{i+1}(t) = \delta [z_i(t)(1 + \lambda_3(t))] - \delta \int_0^t \left( \frac{d\lambda_3(\tau)}{d\tau} - \mu \lambda_3(\tau) \right) z_i(\tau) d\tau. \quad (39)$$

Based on equations (37)-(39), we obtain stationary conditions

$$\lambda_1'(\tau) - \mu \lambda_1(\tau) = 0, \quad 1 + \lambda_1(\tau)|_{\tau=t} = 0, \quad (40)$$

$$\lambda_2'(\tau) - (\gamma + \mu)\lambda_2(\tau) = 0, \quad 1 + \lambda_2(\tau)|_{\tau=t} = 0, \quad (41)$$

$$\lambda_3'(\tau) - \mu \lambda_3(\tau) = 0, \quad 1 + \lambda_3(\tau)|_{\tau=t} = 0. \quad (42)$$

Therefore, the Lagrange multipliers are

$$\lambda_1(\tau) = -e^{\mu(\tau-t)}, \quad \lambda_2(\tau) = -e^{(\gamma+\mu)(\tau-t)}, \quad \lambda_3(\tau) = -e^{\mu(\tau-t)}. \quad (43)$$

The MRDG scheme for solving equations (5)-(7) is

$$x_{i+1}(t) = x_i(t) - \int_0^t e^{\mu(\tau-t)} \left[ \frac{dx_i(\tau)}{d\tau} + \beta x_i(\tau)y_i(\tau) - \mu(N - x_i(\tau)) \right] d\tau, \tag{44}$$

$$y_{i+1}(t) = y_i(t) - \int_0^t e^{(\gamma+\mu)(\tau-t)} \left[ \frac{dy_i(\tau)}{d\tau} - \beta x_i(\tau)y_i(\tau) + (\gamma + \mu)y_i(\tau) \right] d\tau, \tag{45}$$

$$z_{i+1}(t) = z_i(t) - \int_0^t e^{\mu(\tau-t)} \left[ \frac{dz_i(\tau)}{d\tau} - \gamma y_i(\tau) + \mu z_i(\tau) \right] d\tau. \tag{46}$$

**4. Gauss-Seidel-modified-Rafei-Daniali-Ganji (GS-MRDG) scheme**

For the implementation of the Gauss-Seidel technique into the MRDG scheme, once again we implement the idea of Alderremy et al. (2020), Rangkuti et al. (2016), Tatari & Dehghan (2009), Salkuyeh (2008), as well as Youssef & El-Arabawy (2007). Again, we rearrange the order of the equations to be for  $y(t)$ ,  $x(t)$ , and  $z(t)$ , respectively. The resulting scheme is called the GS-MRDG scheme.

The GS-MRDG scheme is given by

$$y_{i+1}(t) = y_i(t) - \int_0^t e^{(\gamma+\mu)(\tau-t)} \left[ \frac{dy_i(\tau)}{d\tau} - \beta x_i(\tau)y_i(\tau) + (\gamma + \mu)y_i(\tau) \right] d\tau, \tag{47}$$

$$x_{i+1}(t) = x_i(t) - \int_0^t e^{\mu(\tau-t)} \left[ \frac{dx_i(\tau)}{d\tau} + \beta x_i(\tau)y_{i+1}(\tau) - \mu(N - x_i(\tau)) \right] d\tau, \tag{48}$$

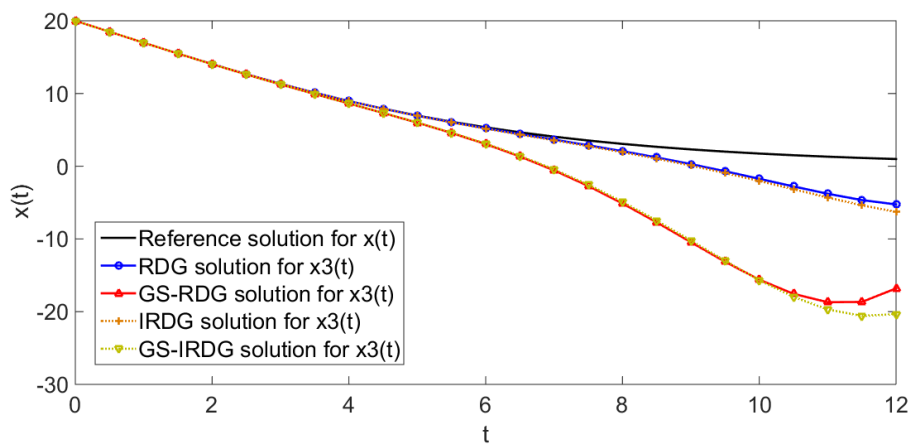
$$z_{i+1}(t) = z_i(t) - \int_0^t e^{\mu(\tau-t)} \left[ \frac{dz_i(\tau)}{d\tau} - \gamma y_{i+1}(\tau) + \mu z_i(\tau) \right] d\tau. \tag{49}$$

**5. Behaviour of the existing variational iteration solutions**

In this subsection, we investigate the behaviour of the existing variational iteration solutions to the SIR epidemic models without and with vital dynamics.

The behaviour of the RDG, GS-RDG, MRDG, and GS-MRDG solutions to the SIR model without vital dynamics are as follows. All RDG, GS-RDG, MRDG, and GS-MRDG solutions give accurate approximations to the exact solutions around the initial conditions. However, they are not accurate for the values of  $t$  far from the initial points. The RDG, GS-RDG, MRDG, and GS-MRDG solutions at their third iterations together with the reference solutions are shown in Figure 1 for  $x(t)$ . These solutions are inaccurate and unrealistic for large values of  $t$ . In Figure 1, all RDG, GS-RDG, MRDG, and GS-MRDG solutions give negative numbers of population  $x(t)$  at  $t = 12$ .

An attempt to overcome this inaccuracy is by increasing the number of iterations of the variational iteration method. However, the RDG, GS-RDG, MRDG, and GS-MRDG solutions are still inaccurate and unrealistic for sufficiently large values of  $t$ . We can also double check these results in Figure 1 of Rafei et al. (2007) confirming that for large values of  $t$ , the RDG solutions are inaccurate and unrealistic. They approaches either  $\infty$  or  $-\infty$  as  $t$  tends to  $\infty$ . Note that similar behaviour occurs for the RDG, GS-RDG,MRDG, and GS-MRDG solutions  $y(t)$  and  $z(t)$ , but we do not show the plots in this paper as their behaviour is clearly the same.



**Figure 1.** Reference solution  $x(t)$  together with RDG, GS-RDG, MRDG, and GS-MRDG solutions of the SIR model without vital dynamics for  $x_3(t)$  at their third iteration.

Now we report here the behaviour of the RDG, GS-RDG, MRDG, and GS-MRDG solutions to the SIR model with vital dynamics. Similar to the results for the SIR model without vital dynamics, all RDG, GSRDG, MRDG, and GS-MRDG solutions give accurate approximations to the exact solutions around the initial conditions. They are inaccurate for the values of  $t$  far from the initial point of time. These solutions are inaccurate for large values of  $t$ . We may increase the number of iterations of the variational iteration method in the hope to get more accurate solutions. However, all RDG, GS-RDG, MRDG, and GS-MRDG solutions are still inaccurate and unrealistic for sufficiently large values of  $t$ . The larger the value of  $t$  leads to the more inaccurate the RDG, GS-RDG, MRDG, and GS-MRDG solutions.

### 6. Proposed piecewise variational iteration method for SIR epidemic models

In this subsection, we propose an analytical-numerical iterative method, which is a piecewise variational iteration method for solving SIR epidemic models. We observe that the RDG scheme is the simplest existing scheme amongst the available existing scheme presented in the previous subsections, yet it behaves similarly to other existing schemes. That is, it is accurate around the initial conditions and becomes less and less accurate at points far from the initialisations. The piecewise variational iteration method that we propose takes the strength of the RDG scheme and avoid the weakness of this scheme.

The piecewise variational iteration method combines analytical and numerical techniques. The analytical technique is the RDG scheme. The numerical technique is the implementation of the RDG scheme in a finite number of subintervals of the domain. Therefore, we obtain a very accurate method for solving SIR epidemic models. In this paper, we call the piecewise variational iteration method for solving the SIR models (2)-(4) and (5)-(7) the piecewise Rafei-Daniali-Ganji (PW-RDG) scheme, which is the analytical-numerical iterative method that we propose. As equations (2)-(4) are special cases of equations (5)-(7), we shall focus our work in this subsection on equations (5)-(7).

The RDG scheme for solving equations (5)-(7) can be simplified to

$$x_{i+1}(t) = x(0) + \int_0^t [-\beta x_i(\tau)y_i(\tau) + \mu(N - x_i(\tau))] d\tau, \tag{50}$$

$$y_{i+1}(t) = y(0) + \int_0^t [\beta x_i(\tau)y_i(\tau) - (\gamma + \mu)y_i(\tau)] d\tau, \tag{51}$$



$$z_{i+1}(t) = z(0) + \int_0^t [\gamma y_i(\tau) - \mu z_i(\tau)] d\tau. \tag{52}$$

Suppose that we want to find the solutions to the SIR epidemic models on the time domain  $[0, T]$  for a given positive constant  $T$ . Suppose also that we want to use  $K$  number of iterations of the RDG scheme into our PW-RDG scheme. Here  $K$  is a specified positive integer. The PW-RDG scheme works as follows:

- The interval  $I = [0, T]$  is discretised into a finite number of discrete time  $t_0, t_1, t_2, \dots, t_j$ , so we have uniform subintervals  $I_j$ , where  $j = 1, 2, 3, \dots, J$  for a specified positive integer  $J$ . Here  $I_j = [t_{j-1}, t_j]$ , where the time step  $\Delta t = t_j - t_{j-1}$  is constant,  $t_0 = 0$  and  $t_j = T$ .
- The simplified RDG scheme (50)-(52) is iterated  $K$  times in each of subintervals  $I_1, I_2, I_3, \dots, I_j$  consecutively. Here  $x_{i,j}(t)$  means the PW-RDG solution for  $x(t)$  at the  $i$ th iteration of the RDG scheme on the  $j$ th subinterval.
- The PW-RDG scheme is for  $j = 1, 2, \dots, J$  and for  $i = 0, 1, 2, \dots, K - 1$  given by

$$x_{i+1,j}(t) = x_{K,j-1}(t_{j-1}) + \int_{t_{j-1}}^t [-\beta x_{i,j}(\tau)y_{i,j}(\tau) + \mu(N - x_{i,j}(\tau))] d\tau, \tag{53}$$

$$y_{i+1,j}(t) = y_{K,j-1}(t_{j-1}) + \int_{t_{j-1}}^t [\beta x_{i,j}(\tau)y_{i,j}(\tau) - (\gamma + \mu)y_{i,j}(\tau)] d\tau, \tag{54}$$

$$z_{i+1,j}(t) = z_{K,j-1}(t_{j-1}) + \int_{t_{j-1}}^t [\gamma y_{i,j}(\tau) - \mu z_{i,j}(\tau)] d\tau, \tag{55}$$

where we set that

$$x_{i,0}(t_0) = x(0), \quad y_{i,0}(t_0) = y(0), \quad z_{i,0}(t_0) = z(0) \tag{56}$$

for all  $i$ . We also set that

$$x_{0,j}(t) = x_{K,j-1}(t_{j-1}), \tag{57}$$

$$y_{0,j}(t) = y_{K,j-1}(t_{j-1}), \tag{58}$$

$$z_{0,j}(t) = z_{K,j-1}(t_{j-1}), \tag{59}$$

for all  $j$ .

- As a special case, if we take  $K = 1$ , then the iteration of the PW-RDG scheme is done once for each subinterval and the resulting scheme is:

$$x_{1,j}(t) = x_{1,j-1}(t_{j-1}) + (t - t_{j-1}) [-\beta x_{1,j-1}(t_{j-1})y_{1,j-1}(t_{j-1}) + \mu(N - x_{1,j-1}(t_{j-1}))], \tag{60}$$

$$y_{1,j}(t) = y_{1,j-1}(t_{j-1}) + (t - t_{j-1}) [\beta x_{1,j-1}(t_{j-1})y_{1,j-1}(t_{j-1}) - (\gamma + \mu)y_{1,j-1}(t_{j-1})], \tag{61}$$

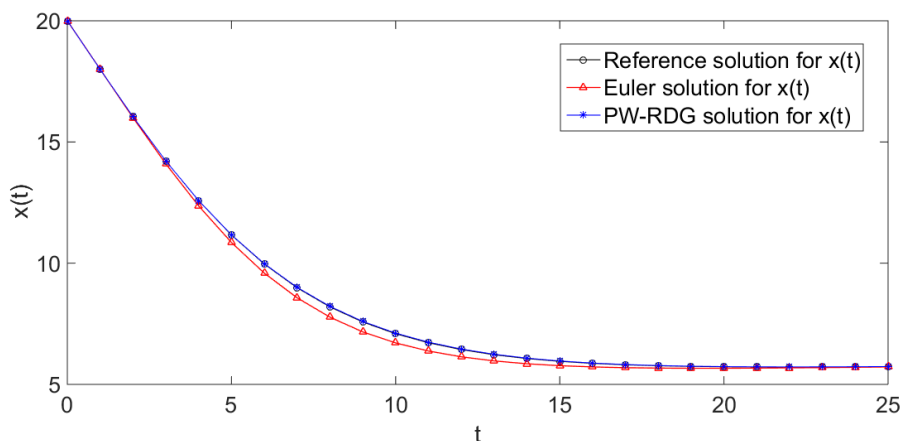
$$z_{1,j}(t) = z_{1,j-1}(t_{j-1}) + (t - t_{j-1})[\gamma y_{1,j-1}(t_{j-1}) - \mu z_{1,j-1}(t_{j-1})]. \quad (62)$$

### C. RESULTS AND DISCUSSION

We recall that the type of research of this paper is modelling with simulation. The mathematical models, equations (2)-(4) and (5)-(7), have been presented in the Introduction section. The solving methods (including the one that we propose) have been given in the Methods section. In line with our research objective and the solving methods, now, in this section we shall present the results of our computational experiments on our proposed PW-RDG method and give discussion about them. We provide the results in a figure representative for the solution curves and in tables for the convergence rates of the PW-RDG solutions.

#### 1. Results and discussion for the SIR model without vital dynamics

Simulation results of the PW-RDG scheme for the SIR model without vital dynamics are as follows. The PWRDG solutions using two iterations in the RDG scheme (using  $K = 2$ ) together with the Euler and the reference solutions are shown in Figure 2 for  $x(t)$ . In this figure, we use  $t = 1$ . We obtain accurate PW-RDG solutions in the whole domain. In addition, Figure 2 show that the RDG solutions (using  $K = 2$ ) are more accurate than the standard Euler solutions. (Note that the same behaviour occurs for solutions  $y(t)$  and  $z(t)$ .)



**Figure 2.** Reference, Euler, and PW-RDG solutions (PW-RDG using  $K = 2$ ) of the SIR model without vital dynamics for  $x(t)$ .

To investigate the convergence rates of the PW-RDG solutions, we record the average of the absolute errors in Table 1 when we use  $K = 1$ , which means that only one RDG iteration is applied in the PW-RDG scheme; in Table 2 when we use  $K = 2$ , which means that two RDG iterations are evolved in the PW-RDG scheme; and in Table 3 when we use  $K = 3$ , which means that three RDG iterations are implemented in the PW-RDG scheme. The convergence rate (error order) is computed using the formula

$$\text{Error order} = \frac{\log\left(\frac{E_1}{E_2}\right)}{\log\left(\frac{\Delta t_1}{\Delta t_2}\right)} \quad (63)$$

in which we assume that if we use time step  $\Delta t_1$ , the average of absolute errors is  $E_1$ ; if we use time step  $\Delta t_2$ , the average of absolute errors is  $E_2$ . We infer from Tables 1-3 that as  $\Delta t$  tends to zero, the error orders approach  $K$ . This suggests that to obtain a PW-RDG method having  $K$ th order of accuracy, we need to implement  $K$  number of RDG iterations in the PW-RDG scheme.

**Table 1.** Order of accuracy of the PW-RDG method with one iteration ( $K = 1$ ) for the SIR model without vital dynamics. Here  $E_x, E_y,$  and  $E_z$  are the average of absolute errors for  $x(t), y(t),$  and  $z(t),$  respectively, computed in the corresponding discrete time. The error order approaches 1.

$\Delta t$	$E_x$	$E_x$ order	$E_y$	$E_y$ order	$E_z$	$E_z$ order
2.5	0.5492554	–	0.6310201	–	0.1165101	–
1.0	0.2430276	0.89	0.2654760	0.94	0.0451447	1.03
0.5	0.1250796	0.96	0.1350267	0.98	0.0223067	1.02
0.2	0.0508945	0.98	0.0545387	0.99	0.0088479	1.01
0.1	0.0255915	0.99	0.0273573	1.00	0.0044115	1.00

**Table 2.** Order of accuracy of the PW-RDG method with two iterations ( $K = 2$ ) for the SIR model without vital dynamics. Here  $E_x, E_y,$  and  $E_z$  are the average of absolute errors for  $x(t), y(t),$  and  $z(t),$  respectively, computed in the corresponding discrete time. The error order approaches 2.

$\Delta t$	$E_x$	$E_x$ order	$E_y$	$E_y$ order	$E_z$	$E_z$ order
2.5	0.1377848	–	0.1556682	–	0.0185411	–
1.0	0.0170910	2.28	0.0200790	2.24	0.0030384	1.97
0.5	0.0039697	2.11	0.0047312	2.09	0.0007768	1.97
0.2	0.0006093	2.05	0.0007326	2.04	0.0001263	1.98
0.1	0.0001503	2.02	0.0001812	2.02	0.0000318	1.99

**Table 3.** Order of accuracy of the PW-RDG method with three iterations ( $K = 3$ ) for the SIR model without vital dynamics. Here  $E_x, E_y,$  and  $E_z$  are the average of absolute errors for  $x(t), y(t),$  and  $z(t),$  respectively, computed in the corresponding discrete time. The error order approaches 3.

$\Delta t$	$E_x$	$E_x$ order	$E_y$	$E_y$ order	$E_z$	$E_z$ order
2.5	0.5492554	–	0.0201791	–	0.0020808	–
1.0	0.2430276	3.25	0.0010459	3.23	0.0001249	3.07
0.5	0.1250796	3.12	0.0001214	3.11	0.0000153	3.03
0.2	0.0508945	3.05	0.0000074	3.05	0.0000010	3.01
0.1	0.0255915	3.02	0.0000009	3.02	0.0000001	3.00

## 2. Results and discussion for the SIR model with vital dynamics

The behaviour of simulation results for the SIR model with vital dynamics is similar to those in the case of the SIR model without vital dynamics. That is, we obtain accurate PW-RDG solutions in the whole domain, even for large values of  $t$ .

Results about orders of accuracy of the PW-RDG scheme for solving the SIR model with vital dynamics are recorded in Tables 4-6. Tables 4 contains the errors and the error orders when we use only one RDG iteration in the PW-RDG scheme, and we obtain that the resulting scheme is of the first order of accuracy. That is, as  $\Delta t$  approaches zero, the error order tends to one. Table 5 contains the errors and the error orders when we use two RDG iterations in the PW-RDG scheme, and the resulting scheme is of the second order of accuracy. Furthermore, if we apply three RDG iterations in the PW-RDG scheme, we obtain that the scheme is of third order of accuracy, as indicated in Table 6. To obtain solutions with small errors, we should take small time step  $\Delta t$ . Further, to get higher order accurate PW-RDG method, we need to use more RDG iterations in our proposed PW-RDG scheme.

**Table 4.** Order of accuracy of the PW-RDG method with one iteration ( $K = 1$ ) for the SIR model with vital dynamics. Here  $E_x, E_y,$  and  $E_z$  are the average of absolute errors for  $x(t), y(t),$  and  $z(t),$  respectively, computed in the corresponding discrete time. The error order approaches 1.

$\Delta t$	$E_x$	$E_x$ order	$E_y$	$E_y$ order	$E_z$	$E_z$ order
2.5	0.4108263	–	0.4681403	–	0.0869522	–
1.0	0.1771760	0.92	0.1939965	0.96	0.0324878	1.07
0.5	0.0905963	0.97	0.0982654	0.98	0.0157995	1.04
0.2	0.0367262	0.99	0.0396248	0.99	0.0062168	1.02
0.1	0.0184425	0.99	0.0198666	1.00	0.0030909	1.01

**Table 5.** Order of accuracy of the PW-RDG method with two iterations ( $K = 2$ ) for the SIR model with vital dynamics. Here  $E_x, E_y,$  and  $E_z$  are the average of absolute errors for  $x(t), y(t),$  and  $z(t),$  respectively, computed in the corresponding discrete time. The error order approaches 2.

$\Delta t$	$E_x$	$E_x$ order	$E_y$	$E_y$ order	$E_z$	$E_z$ order
2.5	0.0875634	–	0.1010713	–	0.0149249	–
1.0	0.0113417	2.23	0.0134358	2.20	0.0022068	2.09
0.5	0.0026780	2.08	0.0031870	2.08	0.0005423	2.02
0.2	0.0004145	2.04	0.0004951	2.03	0.0000860	2.01
0.1	0.0001025	2.02	0.0001226	2.01	0.0000215	2.00

**Table 6.** Order of accuracy of the PW-RDG method with three iterations ( $K = 3$ ) for the SIR model with vital dynamics. Here  $E_x, E_y,$  and  $E_z$  are the average of absolute errors for  $x(t), y(t),$  and  $z(t),$  respectively, computed in the corresponding discrete time. The error order approaches 3.

$\Delta t$	$E_x$	$E_x$ order	$E_y$	$E_y$ order	$E_z$	$E_z$ order
2.5	0.0105877	–	0.0122606	–	0.0016811	–
1.0	0.0005556	3.22	0.0006537	3.20	0.0001006	3.07
0.5	0.0000648	3.10	0.0000767	3.09	0.0000123	3.03
0.2	0.0000040	3.05	0.0000047	3.04	0.0000008	3.01
0.1	0.0000005	3.02	0.0000006	3.02	0.0000001	3.01

#### D. CONCLUSION AND SUGGESTIONS

An analytical-numerical iterative method has been proposed to solve the SIR epidemic models without and with vital dynamics. We obtain that analytical approximate methods cannot provide accurate solutions for large time domains in solving these models. In contrast, our proposed analytical-numerical iterative method solves the models accurately in the whole domain. The order of accuracy of our proposed method can be increased simply by taking more number of iterations of the variational iteration method being implemented piecewisely. In addition, taking smaller size of subintervals in the analytical-numerical iterative method leads to smaller error.

With the promising results in this paper, at least two future research directions are suggested as follows. First, research on extending the method for solving partial differential equations could be conducted. Second, parallel and/or distributed algorithm of the proposed method is also possible to do. Each topic can be carried out independently.

#### ACKNOWLEDGEMENTS

This work was sponsored by Sanata Dharma University and Ministry of Education, Culture, Research and Technology of the Republic of Indonesia. Sudi Mungkasi thanks the LPPM USD research grant with contract number 035/Penel./LPPM-USD/V/2020 and the DRPM World Class Research grant with announcement number B/112/E3/RA.00/2021.

## REFERENCES

- Alderremy, A. A., Chamekh, M., & Jeday, F. (2020). Semi-analytical solution for a system of competition with production a toxin in a chemostat. *Journal of Mathematics and Computer Science*, 20(2), 155–160. <http://dx.doi.org/10.22436/jmcs.020.02.07>
- Alenezi, M. N., Al-Anzi, F. S., & Alabdulrazzaq, H. (2021). Building a sensible SIR estimation model for COVID-19 outspread in Kuwait. *Alexandria Engineering Journal*, 60(3), 3161–3175. <https://doi.org/10.1016/j.aej.2021.01.025>
- Alqahtani, R. T. (2021). Mathematical model of SIR epidemic system (COVID-19) with fractional derivative: stability and numerical analysis. *Advances in Difference Equations*, 2021, 2. <https://doi.org/10.1186/s13662-020-03192-w>
- Barlow, N. S., & Weinstein, S. J. (2020). Accurate closed-form solution of the SIR epidemic model. *Physica D*, 408, 132540. <https://doi.org/10.1016/j.physd.2020.132540>
- Biazar, J. (2006). Solution of the epidemic model by Adomian decomposition method. *Applied Mathematics and Computation*, 173(2), 1101–1106. <https://doi.org/10.1016/j.amc.2005.04.036>
- Biazar, J., & Ghazvini, H. (2007). He's variational iteration method for solving linear and non-linear systems of ordinary differential equations. *Applied Mathematics and Computation*, 191(1), 287–297. <https://doi.org/10.1016/j.amc.2007.02.153>
- Brauer, F., & Castillo-Chavez, C. (2012). *Mathematical Models in Population Biology and Epidemiology* (Second Edi.) Springer. <https://doi.org/10.1007/978-1-4614-1686-9>
- Brauer, F., van den Driessche, P., & Wu, J. (2008). *Mathematical Epidemiology*. Springer. <https://doi.org/10.1007/978-3-540-78911-6>
- Cadoni, M., & Gaeta, G. (2020). Size and timescale of epidemics in the SIR framework. *Physica D*, 411, 132626. <https://doi.org/10.1016/j.physd.2020.132626>
- Daley, D. J., & Gani, J. (2001). *Epidemic Modelling: An Introduction*. Cambridge University Press. <https://www.cambridge.org/id/academic/subjects/statistics-probability/applied-probability-and-stochastic-networks/epidemic-modelling-introduction?format=PB> (Accessed on 28 April 2021)
- Darvishi, M. T., Khani, F., & Soliman, A. A. (2007). The numerical simulation for stiff systems of ordinary differential equations. *Computers and Mathematics with Applications*, 54(7–8), 1055–1063. <https://doi.org/10.1016/j.camwa.2006.12.072>
- De la Sen, M., Ibeas, A., & Agarwal, R. P. (2020). On confinement and quarantine concerns on an SEIAR epidemic model with simulated parameterizations for the COVID-19 pandemic. *Symmetry*, 12(10), 1646. <https://doi.org/10.3390/sym12101646>
- Din, R. U., & Algehyne, E. A. (2021). Mathematical analysis of COVID-19 by using SIR model with convex incidence rate. *Results in Physics*, 23, 103970. <https://doi.org/10.1016/j.rinp.2021.103970>
- Gatto, N. M., & Schellhorn, H. (2021). Optimal control of the SIR model in the presence of transmission and treatment uncertainty. *Mathematical Biosciences*, 333, 108539. <https://doi.org/10.1016/j.mbs.2021.108539>
- Harko, T., Lobo, F. S. N., & Mak, M. K. (2014). Exact analytical solutions of the Susceptible-Infected-Recovered (SIR) epidemic model and of the SIR model with equal death and birth rates. *Applied Mathematics and Computation*, 236, 184–194. <https://doi.org/10.1016/j.amc.2014.03.030>
- He, J. H. (2000). Variational iteration method for autonomous ordinary differential systems. *Applied Mathematics and Computation*, 114(2–3), 115–123. [https://doi.org/10.1016/S0096-3003\(99\)00104-6](https://doi.org/10.1016/S0096-3003(99)00104-6)
- He, J. H. (1999). Variational iteration method – a kind of non-linear analytical technique: some examples. *International Journal of Non-Linear Mechanics*, 34(4), 699–708. [https://doi.org/10.1016/S0020-7462\(98\)00048-1](https://doi.org/10.1016/S0020-7462(98)00048-1)
- Heng, K., & Althaus, C. L. (2020). The approximately universal shapes of epidemic curves in the Susceptible-Exposed-Infectious-Recovered (SEIR) model. *Scientific Reports*, 10, 19365. <https://doi.org/10.1038/s41598-020-76563-8>
- Ifguis, O., El Ghozlani, M., Ammou, F., Moutcine, A., & Abdellah, Z. (2020). Simulation of the final size of the evolution curve of Coronavirus epidemic in Morocco using the SIR model. *Journal of Environmental and Public Health*, 2020, 9769267. <https://doi.org/10.1155/2020/9769267>
- Jordan, D. W., & Smith, P. (2007). *Nonlinear Ordinary Differential Equations* (Fourth Edi.) Oxford

- University Press. <https://global.oup.com/academic/product/nonlinear-ordinary-differential-equations-9780199208258?cc=us&lang=en> (Accessed on 28 April 2021)
- Kermack, W. O., & McKendrick, A. G. (1927). A contribution to the mathematical theory of epidemics. *Proceedings of the Royal Society A*, 115(772), 700–721. <https://doi.org/10.1098/rspa.1927.0118>
- Kröger, M., & Schlickeiser, R. (2020). Analytical solution of the SIR-model for the temporal evolution of epidemics. Part A: time-independent reproduction factor. *Journal of Physics A: Mathematical and Theoretical*, 53(50), 505601. <https://doi.org/10.1088/1751-8121/abc65d>
- Mungkasi, S. (2021). Variational Iteration and successive approximation methods for a SIR epidemic model with constant vaccination strategy. *Applied Mathematical Modelling*, 90, 1–10. <https://doi.org/10.1016/j.apm.2020.08.058>
- Mungkasi, S. (2020a). Improved variational iteration solutions to the SIR model of dengue fever disease for the case of South Sulawesi. *Journal of Mathematical and Fundamental Sciences*, 52(3), 297–311. <https://doi.org/10.5614/j.math.fund.sci.2020.52.3.4>
- Mungkasi, S. (2020b). Successive approximation, variational iteration, and multistage-analytical methods for a SEIR model of infectious disease involving vaccination strategy. *Communication in Biomathematical Sciences*, 3(2), 114–126. <https://doi.org/10.5614/cbms.2020.3.2.3>
- Murray, J. D. (2002). *Mathematical Biology: I. An Introduction* (Third Edi.) Springer. <https://doi.org/10.1007/b98868>
- Rafei, M., Daniali, H., & Ganji, D. D. (2007). Variational iteration method for solving the epidemic model and the prey and predator problem. *Applied Mathematics and Computation*, 186(2), 1701–1709. <https://doi.org/10.1016/j.amc.2006.08.077>
- Rahimi, I., Gandomi, A. H., Asteris, P. G., & Chen, F. (2021). Analysis and prediction of COVID-19 using SIR, SEIQR, and machine learning models: Australia, Italy, and UK cases. *Information*, 12(3), 109. <https://doi.org/10.3390/info12030109>
- Rangkuti, Y. M., Novalia, E., Marhaini, S., & Humairah, S. (2016). Variational iteration method with Gauss-Seidel technique for solving avian human influenza epidemic model. *Bulletin of Mathematics*, 8(1), 29–41. <https://talenta.usu.ac.id/bullmath/article/view/12> (Accessed on 28 April 2021)
- Salkuyeh, D. K. (2008). Convergence of the variational iteration method for solving linear systems of ODEs with constant coefficients. *Computers and Mathematics with Applications*, 56(8), 2027–2033. <https://doi.org/10.1016/j.camwa.2008.03.030>
- Tatari, M., & Dehghan, M. (2009). Improvement of He's variational iteration method for solving systems of differential equations. *Computers and Mathematics with Applications*, 58(11–12), 2160–2166. <https://doi.org/10.1016/j.camwa.2009.03.081>
- Telles, C. R., Lopes, H., & Franco, D. (2021). SARS-COV-2: SIR model limitations and predictive constraints. *Symmetry*, 13(4), 676. <https://doi.org/10.3390/sym13040676>
- Turkyilmazoglu, M. (2021). Explicit formulae for the peak time of an epidemic from the SIR model. *Physica D: Nonlinear Phenomena*, 422, 132902. <https://doi.org/10.1016/j.physd.2021.132902>
- Ucakan, Y., Gulen, S., & Koklu, K. (2021). Analysing of tuberculosis in Turkey through SIR, SEIR and BSEIR mathematical models. *Mathematical and Computer Modelling of Dynamical Systems*, 27(1), 179–202. <https://doi.org/10.1080/13873954.2021.1881560>
- Wu, S.-L., Chen, L., & Hsu, C.-H. (2021). Traveling wave solutions for a diffusive age-structured SIR epidemic model. *Communications in Nonlinear Science and Numerical Simulation*, 98, 105769. <https://doi.org/10.1016/j.cnsns.2021.105769>
- Youssef, I. K., & El-Arabawy, H. A. (2007). Picard iteration algorithm combined with Gauss-Seidel technique for initial value problems. *Applied Mathematics and Computation*, 190(1), 345–355. <https://doi.org/10.1016/j.amc.2007.01.058>