Mathematical Modelling of Epidemic Transmission Dynamics and Numerical Analysis

A. Bhuvaneswari[1] and S. Mathankumar[2]

Abstract

This research explores the dynamics of epidemic construction employing the traditional Susceptible-Infectious-Recovered (SIR) epidemiological framework within a population. Iterative methods can be performed to address the group of nonlinear ordinary differential equations. To analyze the given model, we employ the Variational Iteration Method (VIM). To prove the efficiency and exactness of the VIM, we perform a comparison assessment with the classical Runge-Kutta method, a broadly used numerical method. We formulate the iterative protocols for each method and implement them in MatLab R2025a to produce numerical observations over a specified period of time. This research offers important awareness of the transmission and oversight of infectious diseases. The numerical representation reinforces that the VIM provides an effective approach for identifying the epidemic patterns and for framing control tactics.

[1,2]Department of Mathematics, Dr. N.G.P. Arts and Science College, Coimbatore, Tamil Nadu, India
abhuvaneswariabw@gmail.com*
Corresponding author

Keywords: Correction functionals, Epidemic models, Lagrange multipliers, Runge-Kutta method, SIR model, System of equations, VIM

2010 MSC Subject Classification: 97M10; 34A34; 97M60; 97N40; 97N80

Introduction

The research on mathematical modelling of infectious disease is for analyzing and forecasting the epidemic outbreaks. Among the various mathematical methods, first-order non-linear ordinary differential equations are broadly adopted to represent the dynamic associations between various compartments within a population. The equations represent the connections between susceptible individuals, infected individuals, and the number of individuals who have recovered, which change over time as a result of the disease progression and the healing processes [1,2,3,4,5].

For studying epidemiology, the SIR model is the well-known compartmental framework. It was introduced by Kermack and McKendrick to explain the spread of infectious diseases within the population by classifying the population into three interconnected compartment groups, namely susceptible (S), infected (I), and recovered (R). The movement of population from one group to another is described by a system of nonlinear differential equations [7,13]. Due to its simple and flexible structure, the SIR model has been applied in various situations like information transmission, rumor propagation, and network dynamics. In epidemiology, it has been mainly applied to study the spread of several diseases where there is a public health issue.

Deriving exact analytical solutions for the nonlinear SIR model is often a challenging one. Hence, to study the behavior of the model, the researchers focus on approximate iterative methods [6,9]. Among various methods, the VIM, proposed by Ji-Huan He, is a repetitive, effective technique to address both linear and nonlinear differential equations. The numerical technique VIM constructs correction functionals using variational theory and gradually approaches the solution with low computational effort. Because of its flexibility and simple implementation, it is a highly effective approach for analyzing epidemic models [10,11].

In this article, the variational iteration method is employed to examine the SIR epidemic model. To demonstrate the accuracy of VIM, the comparison is done with the traditional Runge-Kutta method. MatLab is used to compute the numerical outcomes and generate the graphical representation. The comparative analysis highlights that the variational iteration method is an effective and reliable approach for epidemic analysis [8,12,14,15].

This research is structured in the following manner: Section 2 explores the core concepts associated with the differential equations and the general SIR framework. In Section 3, we describe the construction of the main mathematical structure, the iterative technique, and the algorithm formulated for addressing the defined set of differential equations. Section 4 provides the numerical simulations and graphical results obtained from the VIM and Runge-Kutta method, along with the analysis of the outcomes. Finally, this paper concludes with the summary of the main findings and discusses the possible directions for future work.

Essential ideas and Terminology

In this section, we consider multiple crucial concepts necessary for studying the dynamics of epidemic models and for identifying resolutions to epidemic crises.

Definition

A differential equation is a mathematical expression that involves a function y(x) with one or more of its derivatives. It represents the function that changes with respect to an independent variable. Since, the derivative is represented as a limit; the first derivative of a function y(x) is referred as follows:

$$\frac{dy}{dx} = lim_{\Delta x \to 0} \frac{y(x+\Delta x) - y(x)}{\Delta x}.$$

Definition

Let g: R $\rightarrow$ F be a mapping that assigns real numbers to real values. The function g is considered to be continuous at a point u0 $\in$R if, for each $\epsilon > 0$, there exists a $\delta > 0$ such that

$|u-u_0| < \delta$ implies that $|g(u)-g(u_0)| < \epsilon$.

This means that a small changes in u near u0 produce only small changes in the value of the function.

Definition

The SIR model is a compartmental mathematical framework used to describe the transmission of pathogens among a population Balderrama et al. [4]. The population is split into three segments: S(t): Susceptible, indicating individuals who haven't been infected yet but can catch the disease. I(t): Infectious, referring to persons who are infected and able to transmit the illness to others. R(t): Recovered or Eliminated refers to people who have acquired immunity post-recovery from the illness or those who have been removed.

The SIR framework is described by the system of ordinary differential equations:

$$\frac{dS}{dt} = -\beta SI,$$
$$\frac{dI}{dt} = \beta SI - \gamma I,$$
$$\frac{dR}{dt} = \gamma I.$$

where β represents the transmission rate of the disease through contact between individuals, and γ indicates the rate at which infected individuals recover from the disease Malik and Althobaiti [16]. During the simulation, the total population is assumed to remain unchanged, without births or deaths taken into account.

Figure 1: Flow chart diagram for SIR model

Figure 1 shows the compartmental diagram of the SIR model illustrating the movement of population from one compartment to another.

Epidemic model Formulation and Methodology

Here, the traditional Susceptible-Infected-Recovered (SIR) framework is utilized to study the dynamics of epidemic disease in a community. This model classifies the whole population into three distinct and non-overlapping compartments that describe the progression of an illness over time. Here, S(t) represents the number of individuals who are able to get disease easier at time (t). I(t) denote the number of people who can spread disease at the time (t). R(t) represents the number of people cured at time (t) Vijaya et al. [6].

The dynamics of the model are defined by the subsequent collection of nonlinear ordinary differential equations:

$$\frac{dS(t)}{dt} = -p_1 S(t)I(t) + p_3 I(t) \quad (1)$$
$$\frac{dI(t)}{dt} = p_1 S(t)I(t) - p_3 I(t) - p_2 I(t) \quad (2)$$
$$\frac{dR(t)}{dt} = p_2 I(t) \quad (3)$$

where p1 represents the infection rate, indicating the speed at which susceptible individuals

can contract the infection through exposure to infected individuals; p2 indicates the removal rate, where infected individuals either improve or are removed from the group; and p3 denotes the rehabilitation rate, indicating the infected individuals return to the susceptible group due to loss of immunity.

The initial requirements for the epidemic frameworks are S (0) = S0, I (0) = I0, and R (0) = R0.

The model helps to understand the behavior of the epidemic disease under the given conditions. The total population is N = S0+I0+R0, the time step is h, and the final time is at T.

Figure 2: Flow chart diagram for the epidemic model

In Figure 2, we examine the epidemic model and the movement of the population among three compartments.

The methods for determining the structure of equations are outlined below.

Variational Iteration Method (VIM)

The Variational Iteration Method (VIM) is an effective mathematical approach used for solving both linear and nonlinear differential equations. This method produces a sequence of successive approximate solutions that gradually converge to the exact solution using a correction functional that includes a Lagrange multiplier [17,18].

Consider the differential equation

$$L[u(t)] + N[u(t)] = g(t)$$

here L signifies a linear operator, N denotes a nonlinear operator, and g(t) refers a specific function. In the Variational Iteration Method (VIM), the approximate solution is constructed through a correction functional given by the correction functional in VIM is represented as:

$$u_{n+1}(t) = u_n(t) + \int_0^t \lambda(\tau)\big(L[\,u_n(\tau)] + N\,[u_n(\tau)] - g(\tau)\big)\,d\tau,$$

where un(t) indicates the nth approximation solution and λ(τ) signifies the Lagrange multiplier, which is determined optimally through variational theory.

The process begins with an initial value u0(t). Considering the above formula, the successive approximations u1(t), u2(t), …. are determined, and the iterative process is continued until the sequence approaches the required solution.

Now, consider the equation (1), (2), and (3) with respect to the time variable t:

$$\begin{aligned}\frac{dS(t)}{dt} &= -p_1 S(t)I(t) + p_3 I(t),\\ \frac{d\,I(t)}{dt} &= p_1 S(t)I(t) - p_2 I(t) - p_3 I(t),\\ \frac{dR(t)}{dt} &= p_2 I(t),\end{aligned}$$

Subject to the starting conditions S (0) = S0, I (0) = I0, and R (0) = R0.

The procedure for the Variational Iteration Method (VIM) is presented below:

Step 1: Assign S0(t) = S (0), I0(t) = I (0), and R0(t) = R (0).

Step 2: Consider the correction functional:

$$S_{n+1}(t) = S_0 + \int_0^t (-p_1 S_n(t) I_n(t) + p_3 I_n(t))\,d\tau,$$

$$I_{n+1}(t) = I_0 + \int_0^t (p_1 S_n(t) I_n(t) - p_2 I_n(t) - p_3 I_n(t))\,d\tau,\quad R_{n+1}(t) = R_0 + \int_0^t p_2 I_n(\tau)\,d\tau$$

Step 3: Compute (S_(n+1),I_(n+1),R_(n+1)), from S_n,I_n,R_n

Step 4: The iteration process is continued until the required level of accuracy is obtained. That is, the process is terminated when
$|S_{n+1} - S_n| < \epsilon$, $|I_{n+1} - I_n| < \epsilon$, $|R_{n+1} - R_n| < \epsilon$.

Step 5: Once convergence is achieved, the functions Sn(t), (In(t), and Rn(t) are considered as the approximate solutions for the SIR epidemic system.

Due to its flexibility, rapid convergence, and strong effectiveness in handling non-linear equations, the VIM is widely used in fields such as physics, engineering, and biology.

3.2 Runge-Kutta method

The Fourth-Order Runge-Kutta technique is a commonly used numerical approach for obtaining the approximate solutions of ordinary differential equations typically expressed as:

$$\frac{dy}{dx} = f(x, y), y(x_0) = y_0.$$

The RK4 method computes yn+1 from yn using the following expression:

$$k_1 = hf(x_n, y_n)$$
$$k_2 = hf(x_n + \frac{h}{2}, y_n + \frac{k_1}{2})$$
$$k_3 = hf(x_n + \frac{h}{2}, y_n + \frac{k_2}{2})$$
$$k_4 = hf(x_n + h, y_n + k_3)$$
$$y_{n+1} = y_n + \frac{1}{6}[k_1 + 2k_2 + 2k_3 + k_4]$$

where h represents the step size, and k1, k2, k3, and k4 are the intermediate slopes used in the calculation.

The RK4 method is an effective numerical technique, as it achieves a good trade-off between computational efficiency and precision.

MatLab is used to analyze the SIR framework using the variational iteration approach and the fourth-order Runge-Kutta technique. Its plotting functions clearly illustrate how the system changes over time under different conditions and parameter values. This approach helps in studying the behavior of the nonlinear differential equations and enables efficient simulation [19,20].

Illustration

To explore the dynamics of the epidemic disease transmission structure, we perform numerical simulations using the group of ordinary differential equations described in the mathematical framework. To generate numerical outcomes for the SIR structure, we initially tackle the framework using the variational iteration method and then implement the fourth-order Runge-Kutta technique and perform successive integrations with MatLab, consistently improving the approximations of the susceptible, infected, and recovered functions until convergence is achieved [21,22,23].

The epidemic model is solved numerically using a time step size of h = 0.1, over the simulation period t ∈ [0, 10].

We consider the following SIR epidemic model equation (1), (2), and (3) with respect to time variable t:

$$\frac{dS(t)}{dt} = -p_1 S(t) I(t) - p_3 I(t),$$
$$\frac{dI(t)}{dt} = p_1 S(t) I(t) - p_3 I(t) - p_2 I(t),$$
$$\frac{dR(t)}{dt} = p_2 I(t).$$

Consider the initial values S (0) = 620, I (0) = 10, and R (0) = 70 and the parameters p1 = 0.001, p2 = 0.072, and p3 = 0.005. The total population is given by N = S (0) + I (0) + R (0) = 700.

Here, S(t) denotes the count of susceptible individuals at time t, I(t) represent the number of infected individuals at time t, and R(t) indicates the count of people who have either recovered or been removed at time t. The parameter p1 signifies the rate of transmission, p2 denotes the rate of recovery or removal, and p3 describes the rate at which recovered individuals become susceptible again due to loss of immunity [24,25,26].

To address the SIR framework equations, we use the variational iteration approach. Here MatLab is used for solving the epidemic framework and correction functionals are computed. The numerical findings are presented in the table below.

Table 1: Numerical results of the SIR model from t=0 to t=1.0 using VIM

Time(days)	S(t)	I(t)	R(t)
0.0	620.0000	10.0000	70.0000
0.1	619.3505	10.5734	70.0761
0.2	618.6646	11.1788	70.1566
0.3	617.9403	11.8180	70.2417
0.4	617.1757	12.4927	70.3316
0.5	616.3685	13.2049	70.4267
0.6	615.5165	13.9563	70.5271
0.7	614.6175	14.7492	70.6333
0.8	613.6690	15.5855	70.7455
0.9	612.6685	16.4675	70.8641
1.0	611.6133	17.3974	70.9893

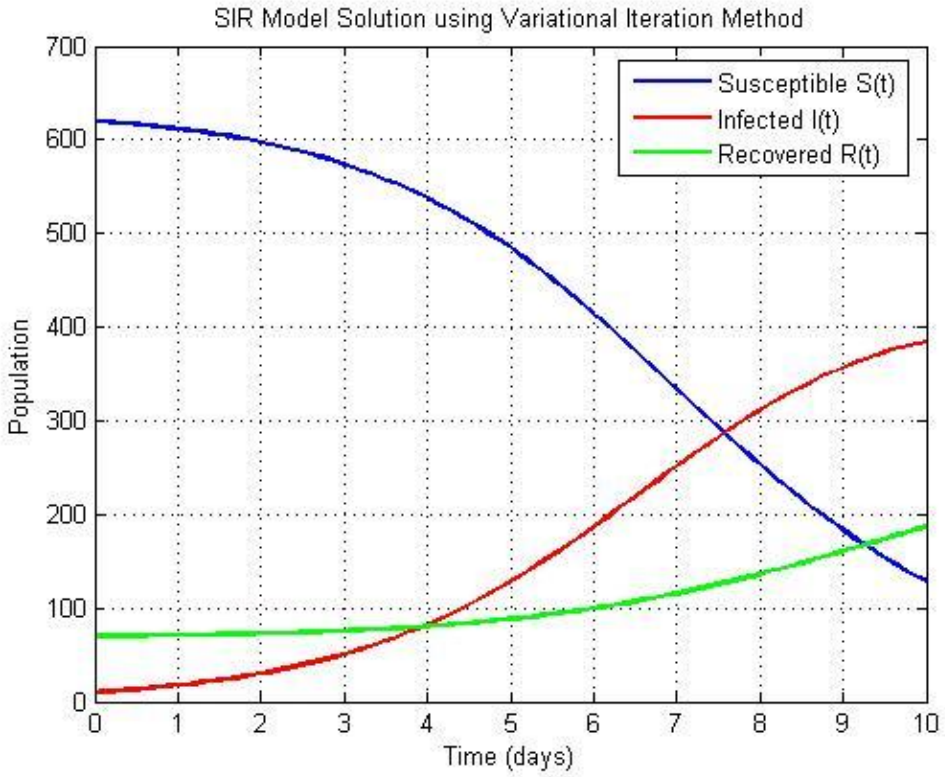

Figure 3: Time evolution of the SIR model compartments using VIM

We subsequently utilize the RK4 method to address the epidemic framework, and the numerical findings along with the graphs are presented below.

Table 2: Numerical results of the SIR model from t=0 to t=1.0 using RK4

Time(days)	S(t)	I(t)	R(t)
0.0	620.0000	10.0000	70.0000
0.1	619.3683	10.5577	70.0740
0.2	618.7022	11.1457	70.1521
0.3	617.9997	11.7658	70.2346
0.4	617.2590	12.4194	70.3216
0.5	616.4782	13.1083	70.4135
0.6	615.6552	13.8343	70.5105
0.7	614.7879	14.5993	70.6128
0.8	613.8740	15.4052	70.7208
0.9	612.9111	16.2541	70.8347
1.0	611.8970	17.1481	70.9550

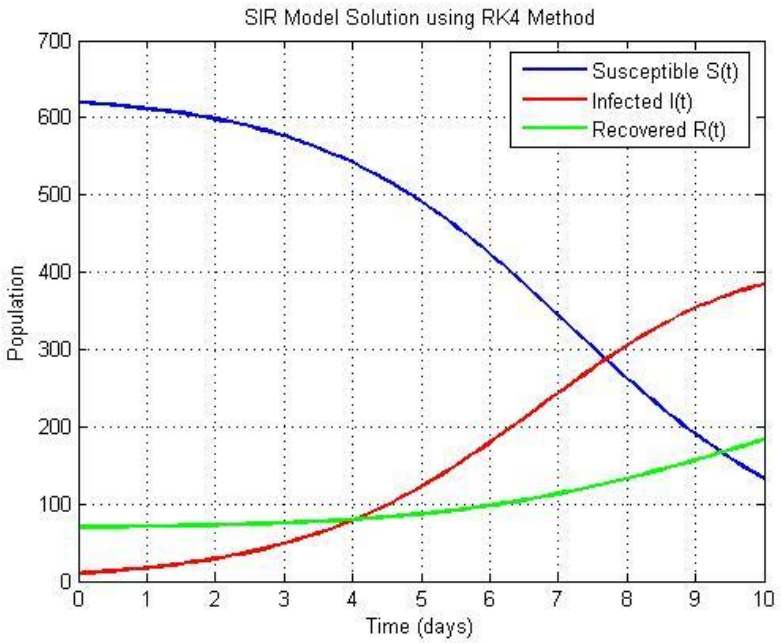

Figure 4: Time evolution of the SIR model compartments using RK4 method

Table 3: Comparison of S(t) using RK4 method and VIM

Time t	S(t) (RK4)	S(t) (VIM)
0.0	620.0000	620.0000
0.1	619.3683	619.3505
0.2	618.7022	618.6646
0.3	617.9997	617.9403
0.4	617.2590	617.1757
0.5	616.4782	616.3685
0.6	615.6552	615.5165
0.7	614.7879	614.6175
0.8	613.8740	613.6690
0.9	612.9111	612.6685
1.0	611.8970	611.6133

Table 4: Comparison of I(t) using RK4 method and VIM

Time t	I(t) (RK4)	I(t) (VIM)
0.0	10.0000	10.0000
0.1	10.5577	10.5734
0.2	11.1457	11.1788
0.3	11.7658	11.8180
0.4	12.4194	12.4927
0.5	13.1083	13.2049
0.6	13.8343	13.9563
0.7	14.5993	14.7492
0.8	15.4052	15.5855
0.9	16.2541	16.4675
1.0	17.1481	17.3974

Table 5: Comparison of R(t) using RK4 method and VIM

Time t	R(t) (RK4)	R(t) (VIM)
0.0	70.0000	70.0000
0.1	70.0740	70.0761
0.2	70.1521	70.1566
0.3	70.2346	70.2417
0.4	70.3216	70.3316
0.5	70.4135	70.4267
0.6	70.5105	70.5271
0.7	70.6128	70.6333
0.8	70.7208	70.7455
0.9	70.8347	70.8641
1.0	70.9550	70.9893

The error analysis equations that are relevant to every compartment S(t), I(t), and R(t) are given below:

$\text{Error}_S(t) = |S_{VIM}(t) - S_{RK4}(t)|$,
$\text{Error}_I(t) = |I_{VIM}(t) - I_{RK4}(t)|$,
$\text{Error}_R(t)\ |R_{VIM}(t) - R_{RK4}(t)|$.

Table 6: Error analysis of the compartments between VIM and RK4 method

Time t	$\lvert\text{Error}_S(t)\rvert$	$\lvert\text{Error}_I(t)\rvert$	$\lvert\text{Error}_R(t)\rvert$
0.0	0.0000	0.0000	0.0000
0.1	0.0178	0.0157	0.0021
0.2	0.0376	0.0331	0.0045
0.3	0.0594	0.0522	0.0071
0.4	0.0833	0.0733	0.0100
0.5	0.1097	0.0966	0.0132
0.6	0.1387	0.1220	0.0166
0.7	0.1704	0.1499	0.0205
0.8	0.2050	0.1803	0.0247
0.9	0.2426	0.2134	0.0294
1.0	0.2837	0.2493	0.0343

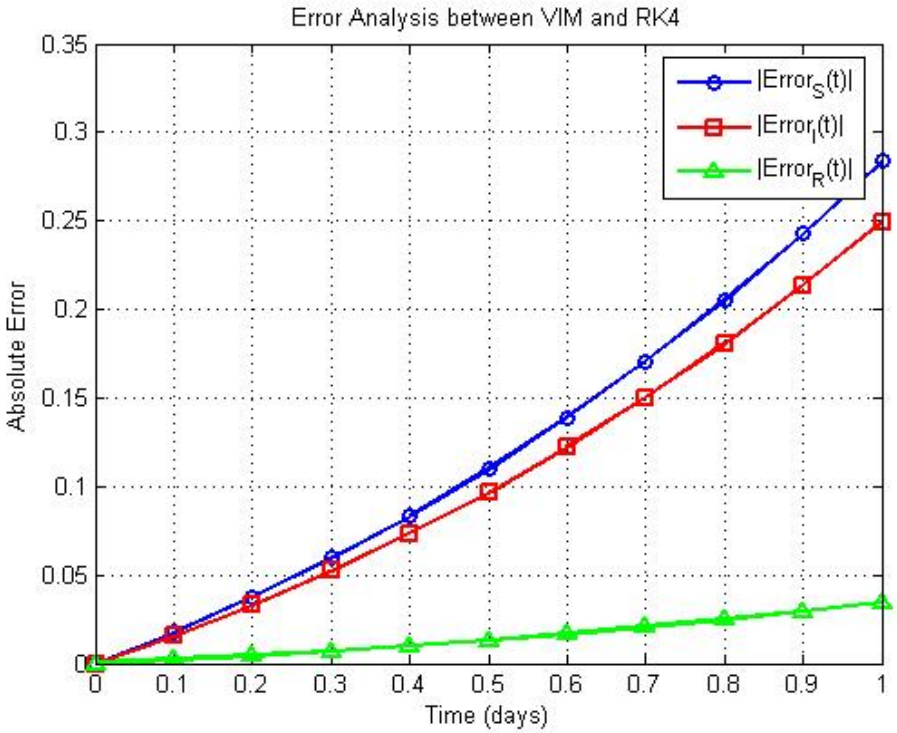

Figure 5: Error analysis of the compartments between VIM and RK4 method

Using MatLab, the numerical outcomes are generated, and the graphs are designed for a period of 10 days. In Table 1 and Table 2, the numerical observations obtained for the susceptible S population, infected I population, and recovered R populations are displayed. And it is observed that the total population N = S + I + R = 700 remains constant throughout the entire simulation period. In both methods, we observe that the susceptible population gradually decreases over time, whereas the recovered population increases accordingly. At the same time, the infected population shows a steady decrease, which is reliably associated with the effects of recovery and removal processes in the model.

As illustrated in Figure 3, the VIM provides highly accurate numerical outcomes of the epidemic framework. Similarly, Figure 4 shows that the RK4 approximation follows the same epidemic trends. The numerical findings reveal that the infection spread slowly within the population. This behavior of the model mainly occurs due to the low infection rate p1 = 0.001 and relatively high removal rate p2 = 0.072. The model suggests that with the given parameter settings, the epidemic will disappear without causing a major outbreak.

In Table 3, Table 4, and Table 5, it is observed that the number of susceptible, infected, and recovered individuals obtained using the VIM matches with the numerical results produced by the RK4 method. In both approaches, minor differences appear in the third or fourth decimal places throughout the entire simulation period. The susceptible population S decreases over time, indicating that VIM captures the same infection dynamics as RK4. The infected population rises initially and then declines, with peak infection occurring approximately on the same day. The recovered population R increases in both methods, showing identical growth of recovery rates. From the comparison table of numerical values, we observe that the susceptible population is lower and the recovered population is higher in the VIM when compared to the RK4 method. This approach shows that VIM is highly accurate and reliable for tackling the SIR epidemic models.

Table 6 presents the error analysis for perfect understanding of the epidemic dynamics. From Figure 5, we observed that the error in S(t) grows faster, as the susceptible population has a strong influence on the spread of infection dynamics and reacts highly responsively to changes in the contact rate. The error in I(t) also increases but remains slightly lower than that of S(t), showing

the balance between infections and recovery processes. The error in R(t) is minimal, indicating that both methods are consistent in predicting the number of recovered individuals. Here both RK4 and VIM have demonstrated strong potential for solving compartmental epidemic models, and their comparative performance provides valuable insights for epidemic analysis.

Hence, the graphical representation and numerical outcomes obtained from the VIM and RK4 methods show the minor differences, indicating a strong agreement between the two approaches. From the numerical findings we observe that as the susceptible population decreases over time, there is a rapid growth in the number of infected individuals. At the same time, the recovered population increases gradually as time progresses. However, in VIM there is a smaller number of susceptible populations, and it greatly improves the recovery rate. We observe that the variational iteration method quickly converges to the precise solution with fewer computational steps. Hence, comparisons with conventional techniques, particularly RK4, demonstrate that the proposed method VIM offers precise, effective, and rapid solutions for the SIR epidemic model. This paper allows researchers and public health authorities to model and comprehend the impact of various factors on disease spread and assist them with improved intervention plans

Conclusion

This research examined the epidemic framework using two specific numerical approaches, namely the variational iteration technique and the Runge-Kutta method. The VIM offers a flexible framework for obtaining the analytical solutions for the proposed model. The comparison analysis represents that VIM is an efficient and accurate numerical approach for solving the given epidemic models. The incorporation of time-varying factors describes the changes in infection, recovery, and vaccination rates over time. These improvements provide a further understanding of epidemic transmission dynamics and assist in effective prediction and control measures. Future research can extend this article by including additional compartments, such as vaccinated, asymptomatic, and quarantined individuals, for a further understanding of the real-world situations more accurately. The semi-analytical approaches, such as the Homotopy analysis technique and the Adomian decomposition method, may be applied for the research. These approaches can be applied to investigate other epidemic transmissions, like COVID-19, Ebola, or dengue, to control the outbreaks. For future research, we can use the optimal control theory to evaluate the efficient intervention strategies for controlling the disease outbreak.

Acknowledgements

The authors wish to convey their heartfelt gratitude to the anonymous reviewers for their valuable remarks and recommendations, which greatly enhanced the article's quality.

Funding

Not applicable.

Data availability

No data was used for the research described in the article.

Declaration of competing interest

The authors declare that they have no competing interests. All authors contributed extensively in the development and finalization of this research. The final manuscript was reviewed and approved by both authors.

References

1. Abdy, M., Side, S., Annas, S., Nur, W. & Sanusi, W.,” An SIR epidemic model for COVID-19 spread with fuzzy parameter: the case of Indonesia,” Advances in Difference Equations, vol. 2021, no.1, pp. 1-12, 2021.
2. [Aguiar, M., Steindorf, V., Srivastav, A.K., Stollenwerk, N. & Kooi, B.W.,” Bifurcation analysis

of a two infection SIR-SIR epidemic model with temporary immunity and disease enhancement," Nonlinear Dynamics, vol. 112, no.15, pp. 13621-13639, 2024.

3. Avram, F., Adenane, R. & Ketcheson, D.I.," A Review of Matrix SIR Arino Epidemic Models," Mathematics, vol. 9, no.1, pp. 1-25, 2021.
4. Balderrama, R., Peressutti, J., Pinasco, J.P., Vazquez, F. & de la Vega, C.S.," Optimal control for a SIR epidemic model with limited quarantine," vol. 12, no.1, pp. 1-10, 2022.
5. Chawla, S.R., Ahmad, S., Khan, A., Albalawi, W., Nisar, K.S. & Ali, H.M.," Stability analysis and optimal control of a generalized SIR epidemic model with harmonic mean type of incidence and nonlinear recovery rates," Alexandria Engineering Journal, vol. 97, no.1, pp. 44-60, 2024.
6. D.K.C. Vijaya, Gowda, P.D. & Hadimani, B.," A numerical study on the dynamics of SIR epidemic model through Genocchi wavelet collocation method," Scientific Reports, vol. 15, no.1, pp. 1-12, 2025.
7. Garibaldi, P., Moen, E.R. & Pissarides, C.A.," Modelling contacts and transitions in the SIR epidemics model," Covid Economics, vol. 5, no.1, pp. 1-21, 2020.
8. Ghaneai, H. & Hosseini, M.M.," Variational iteration method with auxiliary parameter for solving wave-like and heat-like equations in large domains," Computers & Mathematics with Applications, vol. 69, no.5, pp. 363-373, 2015.
9. Gunasekaran, N., Vadivel, R., Zhai, G. & Vinoth, S.," Finite-time stability analysis and control of stochastic SIR epidemic model," Biomedical Signal Processing and Control, vol. 86, pp. 1-12, 2023.
10. Ji-Huan He," Variational iteration method-a kind of non-linear analytical technique: Some examples," International Journal of Nonlinear Mechanics, vol. 34, no.4, pp. 699-708, 1999.
11. Ji-Huan He," Variational iteration method for autonomous ordinary differential systems," Applied Mathematics and Computation, vol. 114, no.2-3, pp. 115-123, 2000.
12. Ji-Huan He," Variational iteration method - Some recent results and new interpretations," Journal of Computational and Applied Mathematics, vol. 207, no.1, pp. 3-17, 2007.
13. Inokuti, M., Sekine, H. & Mura, T.," General use of the Lagrange multiplier in non-linear mathematical physics," Variational Method in the Mechanics of Solids, pp. 156-162, 1978.
14. Li, S.," SIR Epidemic Model with General Nonlinear Incidence Rate and Levy Jumps," Mathematics, vol. 12, no.2, pp. 1-18, 2024.
15. Li, B., Eskandari, Z. & Avazzadeh, Z.," Dynamical Behaviors of an SIR Epidemic Model with Discrete Time," Fractal and Fractional, vol. 6, no.11, pp. 1-20, 2022.
16. Malik, K. & Althobaiti, S.," Impact of the infected population and nonlinear incidence rate on the dynamics of the SIR model," Advances in Continuous and Discrete Models, vol. 2025, no.1, pp. 1-15, 2025.
17. Narayanamoorthy, S. & Mathankumar, S.," Variational iterative method: an approximate numerical scheme for solving system of linear Volterra fuzzy integro-differential equations," Advances in Difference Equations, vol. 2018, no.1, pp. 1-15, 2018.
18. Odibat, Z.M.," A study on the convergence of variational iteration method," Mathematical and Computer Modelling, vol. 51, no.9-10, pp. 1181-1192, 2010.
19. Prodanov, D.," Analytical solutions and parameter estimation of the SIR epidemic model," Mathematical Analysis of Infectious Diseases, Academic Press, pp. 163-189, 2022.
20. Prodanov, D.," Analytical Parameter Estimation of the SIR Epidemic Model: Applications to the COVID-19 Pandemic," Entropy, vol. 23, no.1, pp. 1-15, 2021.

21. Singh, P. & Gupta, A.,” Generalized SIR (GSIR) epidemic model: An improved framework for the predictive monitoring of COVID-19 pandemic,” ISA Transactions, vol. 124, pp. 31-40, 2022.
22. Tang, X. & Chen, Y.,” Analysis of the Diffusion SIR Epidemic Model with Networked Delay and Nonlinear Incidence Rate,” Journal of Mathematics, vol. 2024, no.1, pp. 1-12, 2024.
23. Tian, C., Zhang, Q. & Zhang, L.,” Global stability in a networked SIR epidemic model,” Applied Mathematics Letters, vol. 107, pp. 106-112, 2020.
24. Hajji, M., Sayari, S. & Zaghdani, A.,” Mathematical analysis of an SIR epidemic model in a continuous reactor-deterministic and probabilistic approaches,” Journal of the Korean Mathematical Society, vol. 58, no.1, pp. 45-67, 2021.
25. Qazza, A. & Saadeh, R.,” On the Analytical Solution of Fractional SIR Epidemic Model,” Applied Computational Intelligence and Soft Computing, vol. 2023, pp. 1-12, 2023.
26. Svoboda, D., Havelka, O., Holendova, J. & Kraft, J.,” An epidemiological model of SIR in a nano technological innovation environment,” Heliyon, vol. 11, no.3, pp. 1-12, 2025.