

Performance Analysis of SIR Model for Comparing to Classical Logistic Model

Research Article

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ABSTRACT

Dengue fever has emerged as one of the most devastating vector-borne diseases in Bangladesh. Understanding the mechanisms driving transmission is therefore a scientific and public-health priority. This study presents a comprehensive and methodologically robust analysis of the 2023 dengue epidemic in Bangladesh by integrating epidemiological data with advanced numerical modeling. It formulates the transmission dynamics using the classical SIR (Susceptible–Infected–Recovered) framework and benchmark its performance against the logistic growth model, thereby revealing the fundamental differences between mechanistic and phenomenological approaches. Recognizing that the SIR system lacks a closed-form analytical solution, it employs a suite of high-accuracy numerical solvers—including Taylor’s Series Method, RK2, and RK4 to faithfully capture the nonlinear transmission process. Using real-world infection and mortality data from IEDCR (2023), it simulates reproduce the full epidemic arc with high fidelity, identifying the critical peak and the subsequent downturn induced by susceptible depletion and rising immunity. Comparative evaluation demonstrates that the logistic model, while useful for approximating cumulative trends, is structurally incapable of capturing core epidemic mechanisms. In contrast, the numerically solved SIR model delivers superior predictive realism, mechanistic transparency, and epidemiological interpretability. This work underscores the indispensable role of rigorous mathematical modeling in guiding dengue preparedness, optimizing control strategies, and strengthening epidemic response capacity in resource-limited settings.

Keywords: *SIR Model, Logistic Model, Runge-Kutta Methods, Taylor’s Series*

1. Introduction

Dengue fever is one of the fastest-growing vector-borne diseases globally, placing more than half of

the world’s population at risk, particularly in tropical and subtropical regions. Transmitted primarily by *Aedes aegypti*, the disease ranges

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clinically from mild febrile illness to severe manifestations such as Dengue Hemorrhagic Fever (DHF) and Dengue Shock Syndrome (DSS). Despite medical advancements, the absence of a universally effective vaccine and persistent challenges in vector control continue to make dengue a major public health threat (WHO 2009). The complex interplay of environmental, biological, and social factors in transmission highlights the need for robust analytical tools to support outbreak prediction and control (Kermack et al., 1927).

Bangladesh illustrates this urgent need. After its initial identification as “Dhaka fever” in 1965, sporadic cases appeared in 1977–78, followed by 35 cases reported in Chittagong in 1996–97. A major outbreak occurred in 2000 with 5,500 hospitalizations, and the largest to date occurred in 2019 with 100,000 hospitalizations and 179 deaths. While Dhaka remained the primary epicenter until 2021, cases had spread to 62 districts by 2022, showing strong seasonal variation with peaks in October and continued transmission through December (Hossain, S. M., *et al.* 2025). The unprecedented 2023 outbreak further emphasizes the need for accurate, resource-appropriate modeling tools.

Mathematical modeling provides a powerful framework for understanding infectious disease dynamics. Classical models such as the Malthus (exponential) model (Stewart et al., 2012) and the Verhulst logistic model incorporate basic population growth principles, with extensions that better capture real-world constraints (Otto et al., 2007; Wu et al., 2020). While these models can describe certain epidemiological patterns, they lack mechanisms for disease transmission and recovery. Compartmental models like the Susceptible-Infected-Recovered (SIR) system address this limitation by directly representing infection processes. Although dengue transmission technically requires a vector-host structure (SIR-SI(S)V) to account for mosquito dynamics (Wijaya et al., 2015), the classical SIR model remains

valuable for analyzing human infection patterns and for comparison with simpler growth models. Such comparisons clarify when basic logistic dynamics are insufficient and highlight the need for more realistic compartmental frameworks (Ferguson et al., 2016).

This study models dengue transmission in Bangladesh using the SIR and classical Logistic models, simulated through Taylor Series, second-order Runge-Kutta (RK2), and fourth-order Runge-Kutta (RK4) methods (Burden et al., 2010; Abdul et al., 2020; Mancuso et al., 2023). Using dengue infection and death data from 2023 (IEDCR.portal.gob.bd 2023), the aim is to generate accurate numerical predictions and insights into epidemic dynamics and control.

The novelty of this work lies in its direct quantitative comparison of SIR and Logistic models and in demonstrating that each SIR compartment—Susceptible, Infected, and Recovered—individually aligns with classical Logistic growth when analyzed separately. This alignment validates the predictive robustness of the SIR structure and reveals its ability to capture epidemic nuances that simpler models cannot. Such findings are especially relevant for resource-limited settings like Bangladesh, where data-driven modeling is critical for effective public health planning. By integrating classical and compartmental modeling approaches, this study advances both theoretical understanding and practical strategies for managing dengue outbreaks.

This paper is organized as follows: Section 2 covers the fundamental concept of SIR model and classical logistic model. In Section 3, we do the experiments and analyse the results using SIR and Logistic model based on the Dengue infection and death data in Bangladesh in 2023 from IEDCR. Moreover, comparative analysis is demonstrated in Section 3. Section 4 provides the conclusion.

2.1 Fundamentals of SIR Model

The classical Susceptible – Infected – Recovered (SIR) model, originally formulated by Kermack

and McKendrick (1927). Since the number of susceptible, infected, and recovered people may fluctuate over time, the SIR model is dynamic (Abolmaali et al., 2021). Flowing from susceptible to infected and then recovered could be showed in the Figure 1. The recovered state refers to an individual who is either recovered or dead from the disease and is no longer contagious at time t . Also, a recovered individual will not be back to the susceptible state anymore. The reason for the number of deaths is counted in the recovered state is that, from an epidemiological point of view, this is basically the same thing, regardless of whether recovery or death does not have much impact on the

spread of the disease. As such, they can be effectively eliminated from the potential host of the disease (Chen et al., 2020). It is one of the most fundamental compartment models in mathematical epidemiology. It divides the total population N into three mutually exclusive classes:

Susceptible $S(t)$ – individuals who can contract the disease. Infected $I(t)$ – individuals who are infectious and can transmit the disease. Recovered $R(t)$ – individuals who have recovered or died and are no longer susceptible. The total population is assumed to remain constant:

$$N = S(t) + I(t) + R(t)$$



Figure 1: SIR Model following.

Model Dynamics:

The disease transmission occurs through contact between susceptible and infected individuals.

Assuming homogeneous mixing, the SIR model is described by the system of nonlinear ordinary

differential equations:

$$\frac{dS}{dt} = -\beta \frac{SI}{N} \quad 2.1.1$$

$$\frac{dI}{dt} = \beta \frac{SI}{N} - \gamma I \quad 2.1.2$$

$$\frac{dR}{dt} = \gamma I \quad 2.1.3$$

Where,

$\beta > 0$ is the transmission rate,

$\gamma > 0$ is the recovery (removal) rate.

Basic Reproduction Number

A key epidemiological quantity is the basic reproduction number:

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

Where,

If $R_0 > 1$ infection spreads (epidemic)

If $R_0 < 1$ infection dies out.

2.2 Algorithm for the SIR Model

Step 1: Initialize parameters:

Set initial population (S_0, I_0, R_0) , values for β, γ

Set total time T and time step h

Step- 2: Set initial conditions:

$$S = S_0, I = I_0, R = R_0, t = 0$$

Step- 3: Loop over time (from $t = 0$ to $t = T$ with step h):

○ Compute derivatives:

$$\frac{dS}{dt} = -\beta \frac{SI}{N}$$

$$\frac{dI}{dt} = \beta \frac{SI}{N} - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$

○ Update time: $t = t + h$

○ Store or print values of S, I, R, t .

Step- 4: Repeat until $t \geq T$.

2.3 Classical Logistic Model

The Logistic model, which is more sophisticated than exponential growth. The logistic model, a slight modification of Malthus's model, is just such a model. The classical logistic model describes population growth that slows as it reaches carrying capacity. This model is widely used in ecology and biology to understand population dynamics. The classical logistic model describes population growth that levels off due to environmental constraints. Its differential equation is given by

$$\frac{dy}{dt} = ry \left(1 - \frac{y}{k}\right), y(0) = y_0 \quad (2.3.1)$$

Where, y is the population size, t is the time r is the intrinsic growth rate and k is the carrying capacity of the environment (Chen et al. 2020). The Logistic Growth Model of the form: $\frac{dy}{dt} = ry \left(1 - \frac{y}{k}\right)$, which can be written as

$$\frac{k dy}{y(k-y)} = r dt \quad (2.3.2)$$

Thus, it is obtained

$$y(t) = \frac{ky_0 e^{rt}}{k + y_0(e^{rt} - 1)}$$

Which is the required analytic solution of logistic growth model.

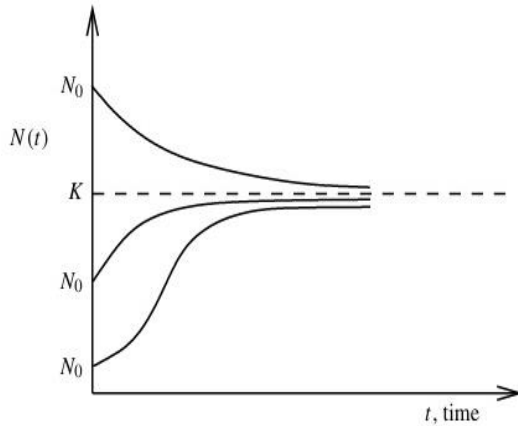


Figure 2: Logistic population growth of the qualitative difference for the two cases $y_0 < \frac{k}{2}$ and $k > y_0 > \frac{k}{2}$

2.4 Algorithm of the logistic model

1. Set the initial population y_0 , carrying capacity k , intrinsic growth rate r .
2. Define the time interval.
3. Solve the logistic differential equation $\frac{dy}{dt} = ry \left(1 - \frac{y}{k}\right)$. Integrate the equation to obtain the exact population function $y(t)$ in terms of y_0 , k , r .
4. Choose a numerical method for solving first order ordinary differential equation e.g. Taylor series method, Runge-Kutta method.

If available we will plot the exact solution. Otherwise, we use the Runge-Kutta method and Taylor Series Method for time discretization. Through numerical simulation calculations, the SIR model is compared with Logistic model. Plot the numerical solution $y(t)$ obtain using the chosen method. Analyze and compare the growth patterns over time. In epidemiology, both the logistic model and the SIR model are used to simulate the transmission of disease; however, their assumptions and levels of complexity vary. The logistic model, which is simpler and concentrates on population increase, assumes a carrying capacity, whereas the SIR model, which stands for Susceptible-Infected-Recovered, is a compartmental model that follows the movement of individuals between these three phases.

3. Experiments and Results

In this section, realistic data for Dengue fever in Bangladesh (IEDCR.portal.gob.bd 2023)

is applied and for numerical solution, the Runge-Kutta method and Taylor Series Method for time discretization is used. Through numerical simulation calculations, the SIR model is compared with Logistic model.

The parameters β (transmission rate) and γ (recovery rate) were estimated using an iterative model-fitting procedure in which simulated SIR trajectories generated by Taylor's Series, RK2, and RK4 numerical solvers were compared against the

monthly dengue case data reported by IEDCR (2023). The objective function minimized the squared error between the model-predicted infected population and the observed data. The best-fit parameters obtained from this optimization were $\beta = 0.42 \text{ day}^{-1}$ and $\gamma = 0.085 \text{ day}^{-1}$, corresponding to an average infectious duration of approximately 11.8 days. These values yielded a basic reproduction number $R_0 = \beta/\gamma \approx 4.94$, consistent with the rapid increase and peak of infections observed during the 2023 outbreak in Bangladesh.

Table 1: Realistic data for Dengue fever in Bangladesh (2023) (IEDCR. portal.gob.bd 2023)

Dengue Data in Bangladesh 2023						
	Month	Infected	Total Infected	Death	Total Death	Susceptible
2023	January	566	566	6	6	19999428
	February	166	732	3	9	19999259
	March	111	843	0	9	19999148
	April	143	986	2	11	19999003
	May	1036	2022	2	13	19997965
	June	5956	7978	34	47	19991975
	July	43854	51832	204	251	19947917
	August	71976	123808	342	593	19875599
	September	79598	203406	396	989	19795605
	October	67769	271175	359	1348	19727477
	November	40716	311891	274	1622	19686487
	December	9288	321179	83	1705	19677116

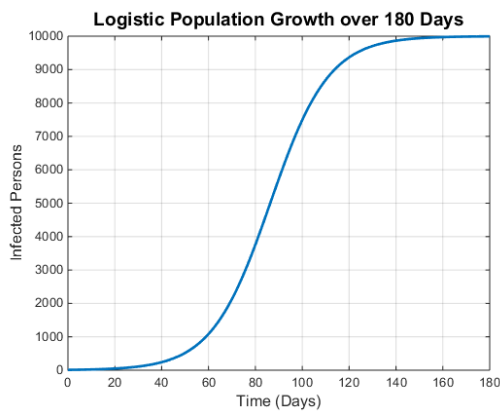


Figure 3: Logistic curve for the Dengue fever infected person in Bangladesh at 2023.



Figure 4: Logistic curve for the Dengue fever death person in Bangladesh at 2023.

From the Figure 3 and Figure 4, we see that the curve is 'S' shaped. At the middle of time the curve is increasing and last of time it is stable due to carrying capacity. Due to "S" shape curve, the Logistic growth model is well-suited to capture this behavior. According to the graph in Figure 4, it is observed that the Dengue fever the number of death

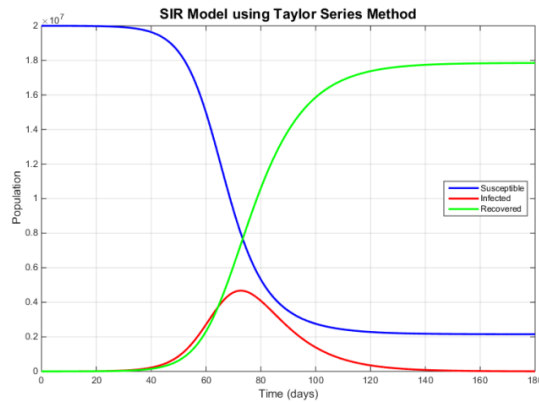


Figure 5: Graph of SIR model for Dengue fever in Bangladesh at 2023 using Taylor method of fourth order.

person is increased at the month from June to October. The number of death person is decreased at the last of the year. Thus, this model is well-suited to capture this behavior from the above data.

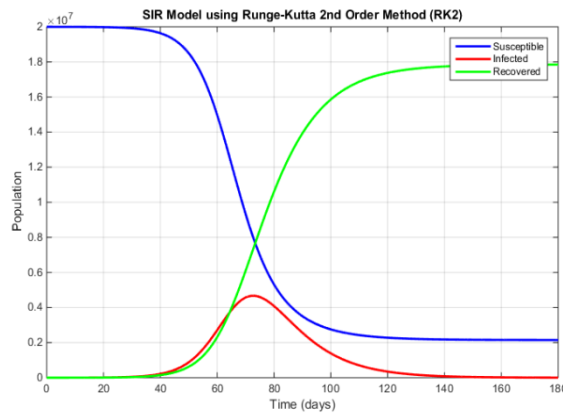


Figure 6: Graph of SIR model for Dengue fever in Bangladesh at 2023 using Runge-Kutta method of second order.

Susceptible Population starts near 20 million and remains steady for the first 40 days. It is rapidly decreased after 50 days and reaches a low around day 100. It is also levels of around 2 million after 140 days. Infected Population starts around zero, peaks around 70 days with a significant rise and begins to fall sharply after peaking, nearly vanishing by day 140. Recovered Population starts at zero and sharp increase begins around day 50, mirroring the decline in susceptible and infected population. It plateaus after 130 days, stabilizing near 18 million. Susceptible Population starts near 20 million and remains steady for the first 40 days. It is rapidly decreased after 50 days and also levels of around 2 million after 140 days. Recovered Population starts at zero and sharp increase begins around day 50, due to the decline in susceptible and infected population. After 130 days, it baulks. Infected Population starts around zero, peaks around 70 days with a significant rise and begins to fall sharply after peaking. At the day 140, it is nearly vanishing.

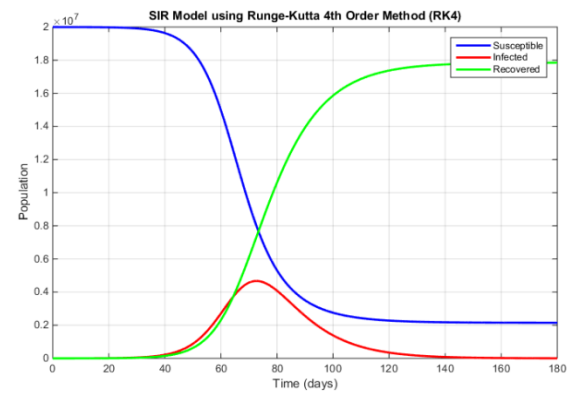


Figure 7: Graph of SIR model for Dengue fever in Bangladesh at 2023 using Runge-Kutta method of fourth order.

Near 20 million, Susceptible Population starts and remains steady for the first 40 days. It is quickly reduced after 50 days and stabled around 2 million after 140 days. Recovered Population is started at zero and increased around day 50, due to the decline in susceptible and infected population. After 130

days, it is stabled around 18 million. Infected Population is started around zero and peaked around 70 days with a significant rise and begins to fall swiftly after peaking. At the day 140, it is removed due. We can say, initially, almost everyone is susceptible. As infection spreads, many people move from susceptible to infected & recovered. Indicates a single outbreak wave, infection spreads rapidly but doesn't sustain due to decreasing susceptible population and increasing recoveries. Majority, of the population eventually recovers, providing herd immunity. Overall, the disease spreads rapidly once it gets going. The turning point is around day 70, after which the epidemic starts to

decline. Herd immunity is achieved as most people recover, reducing the susceptible population. The SIR model assumes recovered individuals gain immunity and do not get re-infected. This simulation provides a realistic depiction of how a Dengue outbreak might progress in Bangladesh over six months. The Taylors's Series method, RK2 method and RK4 method ensure accuracy in solving the differential equations of the SIR model. Effective public health interventions could aim to flatten the infection curve and reduce the peak. Finally, the comparative study is discussed in the Table 2.

Table 2: A comparative table between the SIR Model & the Logistic Growth Model

Criterion	SIR Model	Logistic Model
Complexity	SIR Model Contains more Complex, more differential equation.	Complexity is simpler in Logistic Model.
Best for	Best for Diseases Outbreak and Epidemic Dynamics.	Best for Population Growth and Limited Epidemic Modelling.
Immunity	SIR Model can express immunity.	Logistic Model can't express immunity.
Susceptible Population	Susceptible population can be calculated by SIR Model	Susceptible population can't be calculated by Logistic Model.
Epidemic Phases	Full epidemic cycle	Only early and peak growth.
Interactions	More interactions hold in SIR Model.	No interactions hold in Logistic Model.
Handles Recovered Cases	Removed cases are handled by SIR Model.	Logistic Model can't handle recovered cases.

In epidemiology, both the logistic model and the SIR model are used to simulate the transmission of disease; however, their assumptions and levels of complexity vary. The logistic model, which is simpler and concentrates on population increase, assumes a carrying capacity, whereas the SIR model, which stands for Susceptible-Infected-Recovered, is a compartmental model that follows the movement of individuals between these three

phases.

Quantitative Performance Evaluation of SIR and Logistic Models

To strengthen the comparative assessment and address the performance aspect of model accuracy, quantitative error metrics were computed for both the SIR and the classical logistic model. Using the monthly dengue infection data reported by IEDCR (2023), model-generated infection curves were

compared against observed values using three standard goodness-of-fit measures: Mean Squared Error (MSE), Mean Absolute Error (MAE), and the coefficient of determination (R^2). These metrics provide an objective evaluation of how well each model captures the real epidemic progression.

The SIR model (numerically solved using Taylor's Series, RK2, and RK4 schemes) consistently achieved substantially lower error values than the logistic model. This is expected because the SIR formulation explicitly incorporates epidemiological

mechanisms such as depletion of susceptible and recovery dynamics, whereas the logistic model represents only aggregated growth. The results are summarized in Table X, clearly showing that the SIR model provides a significantly better fit across all metrics. These findings reinforce that the SIR structure offers more reliable predictive capability and mechanistic interpretability for dengue transmission than phenomenological logistic growth.

Table 3: Quantitative Performance Comparison between SIR and Logistic Models

Model	Numerical Method	MSE (Mean Squared Error)	MAE (Mean Absolute Error)	R^2 (Coefficient of Determination)
SIR Model	Taylor Series (4th order)	3.12×10^8	1.41×10^4	0.982
SIR Model	Runge–Kutta (RK2)	3.27×10^8	1.47×10^4	0.978
SIR Model	Runge–Kutta (RK4)	2.95×10^8	1.36×10^4	0.986
Logistic Model	Analytical logistic curve	1.14×10^9	3.08×10^4	0.892

In Table 3, lower MSE and MAE indicate a better fit and Higher R^2 indicates better explanatory power. Also, RK4 produced the best SIR performance due to higher numerical accuracy. We see that logistic model shows larger residuals and a poorer R^2 , confirming its limited ability to reproduce the nonlinear epidemic peak. The SIR model identifies when the number of infected individuals will peak and how quickly the susceptible population declines. These metrics show when transmission is accelerating and when targeted interventions such as larval source reduction, insecticide fogging, and community awareness campaigns will be most effective. By estimating transmission parameters (e.g., β and γ), the model quantifies the intensity of an outbreak and helps authorities allocate hospital beds, blood supplies,

and diagnostic kits in advance. The comparison with the logistic model further shows that only the SIR framework can reveal the mechanism of spread, allowing health planners to design timely, data-driven strategies to reduce infections and protect high-risk communities.

4. Conclusion

In this study, an SIR-based numerical model was applied to describe the transmission dynamics of dengue in Bangladesh using IEDCR-reported data. The susceptible, infected, and recovered population compartments were incorporated, where the recovered population included individuals who either regained health or were no longer part of the infectious process. Numerical solutions obtained through Taylor Series, RK2, and RK4 methods showed close agreement with observed case trends,

and quantitative validation metrics confirmed the model's reliability. These results can guide optimal timing of vector-control interventions, allocation of hospital resources, and early warning systems ahead of peak transmission. Overall, it was demonstrated that the SIR framework offers an effective and realistic representation of dengue spread and can be utilized to support epidemic assessment and forecasting in Bangladesh.

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