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Mathematical Modeling of Dengue Virus Transmission Using a Host-Vector SEIR-SEI Model

Abdullah Ahmed Foisal[1*], Khadiza Begum[2], Md. Nowros Raihan Sayel[2], Abdullah Al Mamun[2]

[1]Assistant Professor, Department of Mathematics, University of Barishal, Barishal-8254, Bangladesh
[2]Department of Mathematics, University of Barishal, Barishal-8254, Bangladesh

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***Corresponding author:** Abdullah Ahmed Foisal
Assistant Professor, Department of Mathematics, University of Barishal, Barishal-8254, Bangladesh

Abstract **Review Article**

Dengue fever has emerged as a significant public health concern in Bangladesh, with a marked increase in fatalities in recent years. To analyze its transmission dynamics, this study introduces a compartmental mathematical model combining the SIER (Susceptible–Exposed–Infectious–Recovered) framework for the human population and the SEI (Susceptible–Exposed–Infectious) model for the mosquito vector population. The model identifies equilibrium points and calculates the basic reproduction number (R_0), a critical threshold parameter that determines whether the disease will spread or die out. Conditions leading to both disease-free and endemic equilibria are established, with the stability of these points shown to be dependent on the value of R_0 to estimate the infection rate, data on infected individuals were collected from various health institutions across Bangladesh. Using MATLAB, numerical simulations were conducted to explore the impact of key parameters on disease transmission and to validate the analytical findings. The study concludes by identifying the most sensitive parameter influencing R_0, providing insights for targeted intervention strategies.

Keyword: Dengue, host, vector, SEIR model, basic reproductive number, simulation.

INTRODUCTION

Dengue fever is a mosquito-borne viral disease transmitted to humans primarily through the bites of infected *Aedes aegypti* and *Aedes albopictus* mosquitoes [1]. It remains one of the most pressing public health challenges in tropical and subtropical regions worldwide [2]. Over the past two decades, reported dengue cases have surged dramatically, rising from 505,430 cases in 2000 to 2.4 million in 2010, and reaching 3.3 million by 2015 [3]. Concurrently, fatalities increased from 960 in 2000 to 4,032 in 2015, with deaths doubling from approximately 3,500 (2015) to over 7,500 (2024) [4], [5]. As of mid-2025, dengue continues to pose a severe global health threat, with over 3 million cases and 1,400 deaths reported annually, predominantly affecting tropical regions in the Americas, Southeast Asia, and the Pacific [6]. Notably, Southeast Asia and the Western Pacific account for 75% of global dengue cases [1]. With an estimated 100–400 million infections occurring each year [2], dengue remains a leading cause of epidemic outbreaks, particularly in developing nations such as Bangladesh.

This study develops a mathematical model based on ordinary differential equations (ODEs) to analyze the transmission dynamics of dengue virus (DV). Numerical simulations are performed to evaluate disease behavior under varying epidemiological conditions. The findings aim to support data-driven outbreak control strategies in Bangladesh and other dengue-endemic regions with comparable environmental and socioeconomic challenges.

BACKGROUND

Dengue virus (DENV), part of the Flaviviridae family, is spread by Aedes aegypti and Aedes albopictus mosquitoes. It can cause mild dengue fever or progress to severe diseases like dengue hemorrhagic fever (DHF) and dengue shock syndrome (DSS) [7]. First identified in the 1940s, DENV exists as four distinct serotypes (DENV-1 to DENV-4), with a fifth (DENV-5) reported in 2013, each capable of inducing severe disease

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upon secondary infection due to antibody-dependent enhancement (ADE) [8]. *Dengue remains endemic in over 100 tropical and subtropical regions, infecting nearly 390 million people annually. The disease's growing reach is fueled by urbanization, climate change, and the rise in global travel* [2] [9].

DATA SOURCES

This research uses data from 2023 and 2025 cases in Dhaka, Bangladesh. The data was obtained from (World Health organization) WHO and Directorate General of Health Services (DGHS), Ministry of Health and Family Welfare, Bangladesh.

DV outbreaks in Bangladesh

Dengue was first documented in Bangladesh as "Dacca fever" in 1964 [10]. The first major outbreak occurred in 2000, driven by DENV-3, which remained the dominant serotype in subsequent years [11]. Historically, DENV-1 and DENV-2 were predominant until 2016, but DENV-3 re-emerged as the leading serotype in 2019 [12]. By 2023, DENV-2 had replaced DENV-3 as the most prevalent strain [13].

Bangladesh faced its worst dengue outbreak in 2023, surpassing all previous records in its 24-year outbreak history [7]. As of December 31, 2023, the country reported 321,179 confirmed cases and 1,705 deaths, with cases surging rapidly from late June onward. The case fatality rate (CFR) of 0.53% was higher than in previous years [14]. By 2024, reported cases reached 71,056 with 350 deaths, indicating persistent transmission [15]. The surge in dengue cases has been linked to unusually high temperatures, extreme humidity, and erratic rainfall, creating ideal breeding conditions for Aedes mosquitoes [16].

Numbers of dengue cases in Bangladesh are given in the following table (According to Directorate General of Health Services (DGHS))

Table -1: Dengue Outbreaks in Bangladesh from 2000 to 2024

Year	**Cases**	**Deaths**	**CFR (%)**
2000	5,551	93	1.68%
2001	2,430	32	1.32%
2002	6,104	58	0.95%
2003–2015	Low cases (Yearly avg. <2,000)	Minimal deaths	**~0.5–1.0%** (estimated)
2016	6,060	14	0.23%
2017	2,769	8	0.29%
2018	10,148	26	0.26%
2019	**101,354**	**179**	**0.18%**
2020	1,405	3	0.21%
2021	28,429	105	0.37%
2022	62,382	281	0.45%
2023	**321,179**	**1,705**	**0.53%**
2024	110,000	575	0.52%

Epidemic Models

In epidemiology, compartmental modeling is widely used to analyze infectious viruses and has proven highly effective in successfully predicting epidemic outcomes. A compartmental model divides populations into distinct groups, with each group's disease-related characteristics described by differential equations. Some commonly used epidemic models include SIS, SID, SIR, and SEIR.

The Kermack-McKendrick model, the simplest compartmental model, is also known as the SIR model [17]. However, for many infectious diseases where infected individuals can carry the infection without immediate symptoms (e.g., chickenpox, dengue, malaria, tuberculosis), the SEIR model is more commonly applied. These epidemic models effectively analyze the dynamics of infectious diseases, and with additional compartments, they can more accurately simulate real-world scenarios. As a result, compartmental modeling serves as a powerful tool for predicting the behavior of even the most dangerous diseases today.

The Basic SEIR Model

The SEIR model is a mathematical framework used to simulate the spread of infectious diseases by categorizing the population into four compartments:

- **Susceptible (S):** Individuals who are vulnerable to contracting the disease.
- **Exposed (E):** Individuals who have been infected but are not yet infectious, representing the incubation or latent period.
- **Infectious (I):** Individuals who are currently capable of transmitting the disease to others.
- **Removed (R):** Individuals who have either recovered and gained immunity or have died, thus no longer participating in disease transmission.

Each compartment's population changes over time, denoted as functions S(t), E(t), I(t), and R(t), where 't' represents time. The total population at any given time is the sum of all compartments:

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

The dynamics are governed by:

$$\frac{dS}{dt} = -\beta\frac{SI}{N}$$
$$\frac{dE}{dt} = \beta\frac{SI}{N} - \sigma E$$
$$\frac{dI}{dt} = \sigma E - \gamma I$$
$$\frac{dR}{dt} = \gamma I$$

Where:

β = transmission rate (infectious contacts per unit time).
σ = incubation rate ($1/\sigma$ = average latent period).
γ = recovery rate ($1/\gamma$ = average infectious period).
Basic Reproduction Number, $R_0 = \frac{\beta}{\gamma}$

Mathematical Model for Transmissions of Dengue

The SIR model for dengue virus in Bangladesh can be used to understand and simulate the spread of dengue in a human population, considering both human and mosquito (vector) dynamics. Below is the SEIR (Susceptible-Exposed-Infected-Recovered) version of this model, incorporating an **Exposed (E)** compartment for both humans and vectors to account for latent periods.

The assumptions for this model are; total population must be constant, no vertical transmission, no immunity loss in humans, and vectors do not recover.

Variables:

Human Population (SEIR structure)
Susceptible (S_h) – Individuals not yet infected.
Exposed (E_h) – Infected but not yet infectious (dengue has an incubation period).
Infected (I_h) – Symptomatic/asymptomatic and capable of transmitting the virus to mosquitoes.
Recovered (R_h) – Gained immunity
With total population size $N_h = S_h + E_h + I_h + R_h$

Mosquito Population (SEI structure, since mosquito don't recover)
Susceptible (S_v) – Mosquitoes not carrying the virus.
Exposed (E_v) – Mosquitoes infected but not yet infectious.
Infected (I_v) – Infectious mosquitoes capable of transmitting dengue.
With total vector population size $N_v = S_v + E_v + I_v$
The ordinary differential equations are:
Human Dynamics (SEIR)

$$\left.\begin{aligned}\frac{dS_h}{dt} &= \wedge_h - \beta_h S_h\frac{I_v}{N_h} - \mu_h S_h\\ \frac{dE_h}{dt} &= \beta_h S_h\frac{I_v}{N_h} - \gamma_h E_h - \mu_h E_h\\ \frac{dI_h}{dt} &= \gamma_h E_h - \sigma_h I_h - \mu_h I_h\\ \frac{dR_h}{dt} &= \sigma_h I_h - \mu_h R_h\end{aligned}\right\} \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (1)$$

Mosquito Dynamics (SEI)

$$\left.\begin{aligned}\frac{dS_v}{dt} &= \wedge_v - \beta_v S_v\frac{I_h}{N_h} - \mu_v S_v\\ \frac{dE_v}{dt} &= \beta_v S_v\frac{I_h}{N_h} - \gamma_v E_v - \mu_v E_v\\ \frac{dI_v}{dt} &= \gamma_v E_v - \mu_v I_v\end{aligned}\right\} \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (2)$$

Where,

$\wedge_h$ = Recruitment rate of humans
$\wedge_v$ = Recruitment rate of mosquitoes
β_h = Human infection rate (mosquito bites)
β_v = Mosquito infection rate (from humans)
γ_h = Human incubation rate (1/incubation period)
γ_v = Mosquito incubation rate
σ_h = Human recovery rate
μ_h = Human natural mortality rate
μ_v = Mosquito mortality rate

And $S_h(0) > 0$, $I_h(0) > 0$, $R_h(0) = 0$ and $S_v(0) > 0$, $I_v(0) > 0$ and all parameters are positive.

Disease Free Equilibrium

At DFE, no infection exists:

$$E_h = I_h = R_h = 0, \quad E_v = I_v = 0.$$

Thus, the human and mosquito populations are entirely susceptible:

$$S_h = \frac{\Lambda_h}{\mu_h} = N_h, \quad S_v = \frac{\Lambda_v}{\mu_v} = N_v.$$

Thus, the DFE is: $(S_h^0, E_h^0, I_h^0, R_h^0, S_v^0, E_v^0, I_v^0) = (N_h, 0,0,0, N_v, 0,0)$

Endemic Equilibrium

All infected compartments (E_h, I_h, E_v, I_v) are non-zero.

Putting all equations in system (1) and (2) equal zero, we have

$$I_v^* = \frac{\gamma_v}{\mu_v} E_v^*.$$

$$E_v^* = \frac{\beta_v S_v^* I_h^*}{(\gamma_v + \mu_v) N_h}.$$

$$S_v^* = \frac{\mu_v N_v}{\mu_v + \beta_v \frac{I_h^*}{N_h}}.$$

$$I_h^* = \frac{\gamma_h}{\sigma_h + \mu_h} E_h^*.$$

$$E_h^* = \frac{\beta_h S_h^* I_v^*}{(\gamma_h + \mu_h) N_h}.$$

Stability of equilibrium points

The DFE is locally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$.

EE is locally asymptotically stable when $R_0 > 1$ (under certain parameter conditions).

Basic reproductive number:

we compute R_0 using the next-generation matrix (NGM) method.

We decompose the system into new infections (F) and transitions between compartments (V).

Jacobian matrix

$$J = \begin{bmatrix} \frac{\partial \dot{E}_h}{\partial E_h} & \frac{\partial \dot{E}_h}{\partial I_h} & \frac{\partial \dot{E}_h}{\partial E_v} & \frac{\partial \dot{E}_h}{\partial I_v} \\ \frac{\partial \dot{I}_h}{\partial E_h} & \frac{\partial \dot{I}_h}{\partial I_h} & \frac{\partial \dot{I}_h}{\partial E_v} & \frac{\partial \dot{I}_h}{\partial I_v} \\ \frac{\partial \dot{E}_v}{\partial E_h} & \frac{\partial \dot{E}_v}{\partial I_h} & \frac{\partial \dot{E}_v}{\partial E_v} & \frac{\partial \dot{E}_v}{\partial I_v} \\ \frac{\partial \dot{I}_v}{\partial E_h} & \frac{\partial \dot{I}_v}{\partial I_h} & \frac{\partial \dot{I}_v}{\partial E_v} & \frac{\partial \dot{I}_v}{\partial I_v} \end{bmatrix} = \begin{bmatrix} -(\gamma_h + \mu_h) & 0 & 0 & \beta_h \\ \gamma_h & -(\sigma_h + \mu_h) & 0 & 0 \\ 0 & \beta_v \frac{N_v}{N_h} & -(\gamma_v + \mu_v) & 0 \\ 0 & 0 & \gamma_v & -\mu_v \end{bmatrix}$$

$$F = \begin{bmatrix} 0 & 0 & 0 & \beta_h \\ 0 & 0 & 0 & 0 \\ 0 & \beta_v \frac{N_v}{N_h} & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}, \quad V = \begin{bmatrix} -(\gamma_h + \mu_h) & 0 & 0 & 0 \\ \gamma_h & -(\sigma_h + \mu_h) & 0 & 0 \\ 0 & 0 & -(\gamma_v + \mu_v) & 0 \\ 0 & 0 & \gamma_v & -\mu_v \end{bmatrix}$$

$$\mathrm{F}V^{-1} = \begin{bmatrix} 0 & 0 & \frac{\beta_h \gamma_v}{\mu_v(\gamma_v + \mu_v)} & \frac{\beta_h}{\mu_v} \\ 0 & 0 & 0 & 0 \\ \frac{\beta_v \gamma_h N_v}{(\gamma_h + \mu_h)(\sigma_h + \mu_h) N_h} & \frac{\beta_v N_v}{(\sigma_h + \mu_h) N_h} & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

The spectral radius (dominant eigenvalue) of FV^{-1} is:

$$\mathrm{R}_0 = \sqrt{\frac{\beta_h \beta_v \gamma_h \gamma_v N_v}{\mu_v N_h (\gamma_h + \mu_h)(\sigma_h + \mu_h)(\gamma_v + \mu_v)}}$$

When, $\mathrm{R}_0 > 1$: Dengue spreads (endemic equilibrium stable) and if, $\mathrm{R}_0 < 1$: Dengue dies out (DFE stable).

SEIR epidemic model

Human Dynamics (SEIR)

$$\left.\begin{aligned} \frac{dS_h}{dt} &= -\beta_h S_h \frac{I_v}{N_h} \\ \frac{dE_h}{dt} &= \beta_h S_h \frac{I_v}{N_h} - \gamma_h E_h \\ \frac{dI_h}{dt} &= \gamma_h E_h - \sigma_h I_h \\ \frac{dR_h}{dt} &= \sigma_h I_h \end{aligned}\right\} \dots\dots\dots\dots\dots\dots\dots\dots\dots\dots (3)$$

Mosquito Dynamics (SEI)

$$\left.\begin{aligned} \frac{dS_v}{dt} &= -\beta_v S_v \frac{I_h}{N_h} \\ \frac{dE_v}{dt} &= \beta_v S_v \frac{I_h}{N_h} - \gamma_v E_v \\ \frac{dI_v}{dt} &= \gamma_v E_v \end{aligned}\right\} \dots\dots\dots\dots\dots\dots\dots\dots\dots\dots (4)$$

The basic reproductive number for epidemic model is,

$$\mathrm{R}_0 = \sqrt{\frac{\beta_h \beta_v \gamma_h \gamma_v}{\sigma_h(\gamma_h + \mu_h)(\gamma_v + \mu_v)}}$$

Numerical simulations

For the epidemic model, (from 2023 outbreak)

The nonlinear system in (3) and (4) can be solved using the numerical methods and we can observe the dynamics of the model. The total population of Dhaka city was $\mathrm{N_h}$ =23.2 million [18]. Here, the parameters are taken as $\gamma_h = \frac{1}{5}, \gamma_v = \frac{1}{10}, \sigma_h = \frac{1}{7}, \mu_h = \frac{1}{74.67*365}$ (life expectancy for 2023 was **74.67**) , $\mu_v = \frac{1}{14}$ .The rest of the values are listed below (time 120 days):

Parameter	**Value**	**Reference**
β_h	0.9	estimated
β_v	0.7	estimated
γ_h	0.2	[7]
γ_v	0.1	[7]
σ_h	0.142857	[9]
μ_h	3.6691e-5	[18]
μ_v	0.0714286	[7]
$S_h(0)$	$N_h - 225$	estimated
$E_h(0)$	135	estimated
$I_h(0)$	90	[13]
$R_h(0)$	0	By model

Using these parameter values and initial conditions we can solve the system in (3) and (4) by ODE solver using MATLAB. We generated a graph to analyze the dynamics of susceptible, exposed, infected and recovered population.

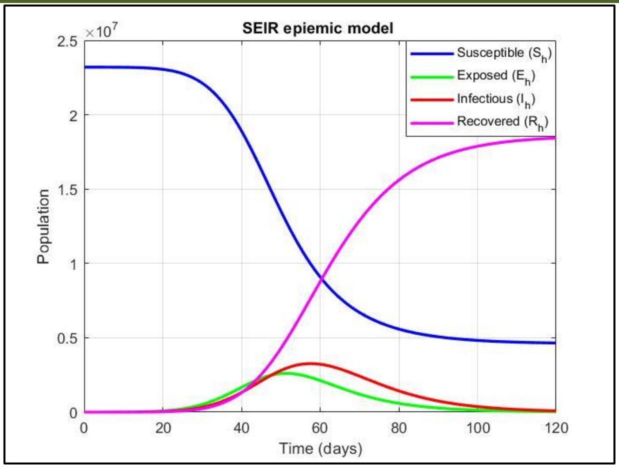

Figure-1: Population sizes for epidemic model with basic reproduction number R_0 = 1.6038

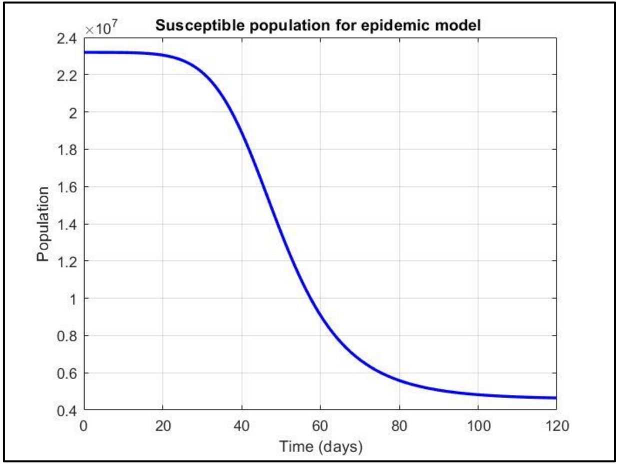

Figure-2: Susceptible individuals for epidemic model.

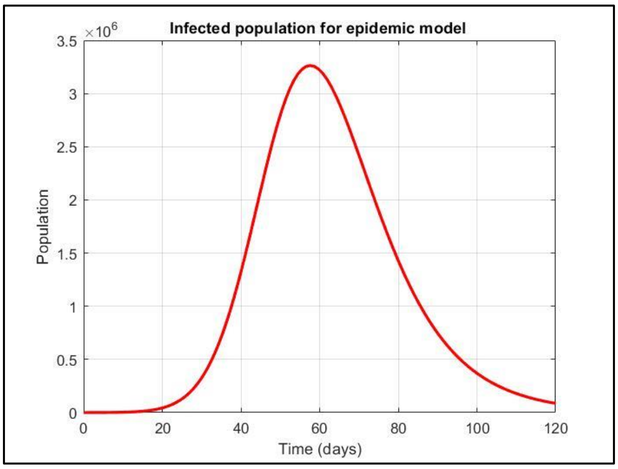

Figure-3: Infected individuals for epidemic model

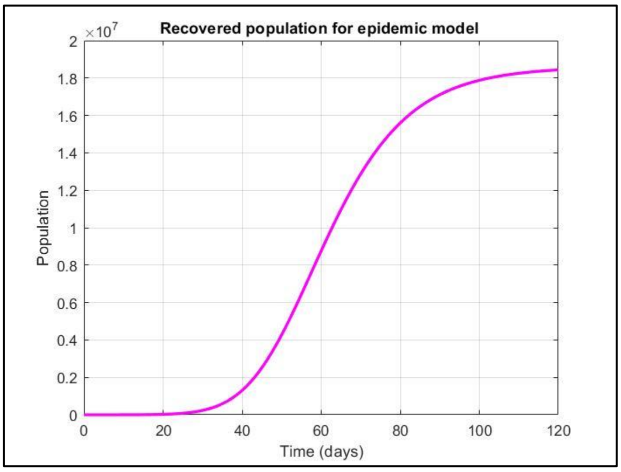

Figure-4: Recovered individuals for epidemic model

The result of the simulation for the individual population classes is represented in Figure-1. From Figure-2 & Figure-3, these show that the susceptible population is decreasing and the recovered population is increasing. The infectious class is shown in Figure- 3 and it shows that the infectious population increased at first but decreased after a certain time. The basic reproduction number **R_0 = 1.6038**. So, the people of Bangladesh witnessed an endemic situation at that time.

For the **endemic** model, (from 1st June, 2025)
The nonlinear system in (1) and (2) can be solved using the numerical methods and we can observe the dynamics of the model. The total population of Dhaka city is N_h =24.6 million [18]. Here, the parameters are taken as $\gamma_h = \frac{1}{5}$, $\gamma_v = \frac{1}{10}$, $\sigma_h = \frac{1}{7}$, $\mu_h = \frac{1}{74.7*365}$ (life expectancy for 2025 is **74.7**), $\mu_v = \frac{1}{14}$

Parameter	Value	Reference
β_h	0.5	estimated
β_v	0.3	estimated
γ_h	0.2	[7]
γ_v	0.1	[7]
σ_h	0.142857	[9]
μ_h	3.6676e-5	[18]
μ_v	0.0714286	[7]
$S_h(0)$	$N_h - 72$	estimated
$E_h(0)$	42	estimated
$I_h(0)$	30	[19]
$R_h(0)$	0	By model

Using these parameter values and initial conditions we can solve the system in (1) and (2) by ODE solver using MATLAB. We generated a graph to analyze the dynamics of susceptible, exposed, infected and recovered population.

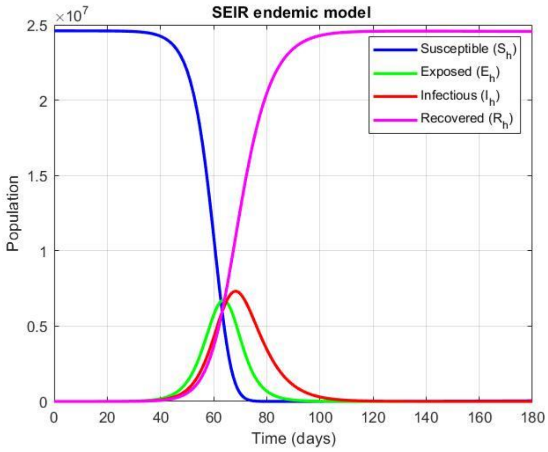

Figure-5: Population sizes for endemic model with basic reproduction number $R_0 = 1.3095$

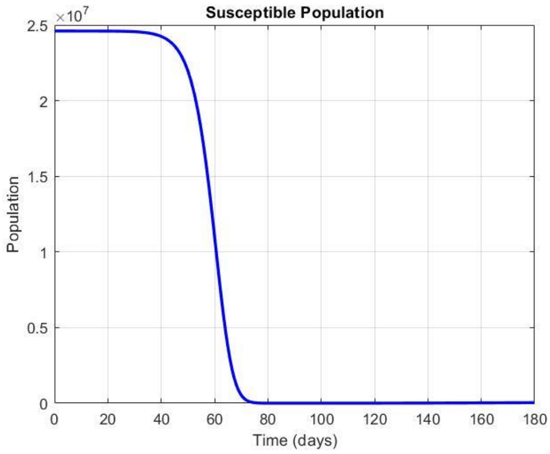

Figure-6: Susceptible individuals for endemic model

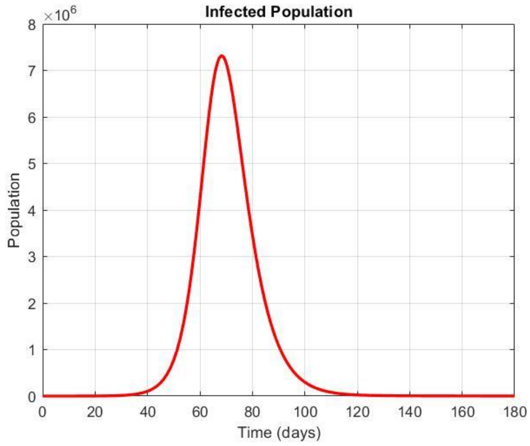

Figure-7: Infected individuals for endemic model

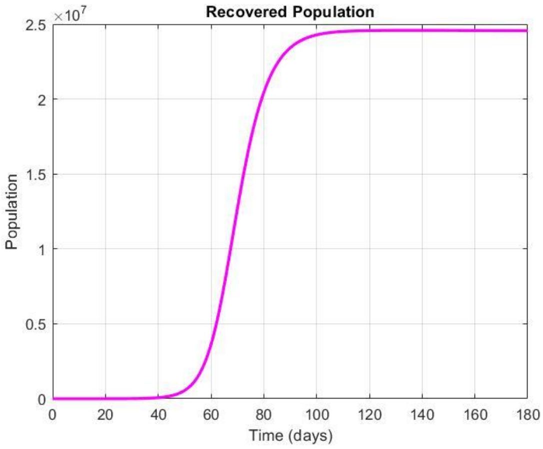

Figure-8: Recovered individuals for endemic model

The result of the simulation for the individual population classes is represented in Figure-5. From Figure-6 & Figure-8, these show that the susceptible population is decreasing and the recovered population is increasing. The infectious class is shown in Figure- 7 and it shows that the infectious population increased at first but decreased after a certain time. The basic reproduction number $\mathbf{R_0 = 1.3095}$. So, there is a high possibility of an endemic situation if proper steps are not taken.

Possible Scenario

Here is the possible number of dengue-infected individuals and the transmission phase in Dhaka city from June to November 2025, presented in tabular form based on historical data trends, 2023–2024 outbreak patterns, and climate-sensitive predictive models:

Table-3: Dengue Transmission Scenario: Dhaka City (June–November 2025)

Month	Estimated Infected Cases	Transmission Phase
June	5,000-6,000	Onset
July	8,000-12,000	Rapid Rise
August	20,000-25,000+	Peak
September	15,000-20,000	High plateau
October	10,000-15,000	Decline begins
November	5,000-10,000	Tail End

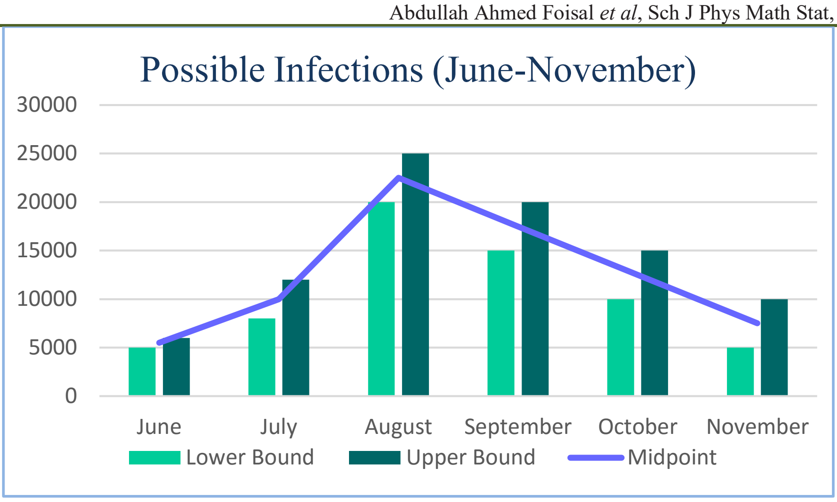

Figure-9: Graphical representation of possible scenario

CONCLUSION

Simple and relevant mathematical models have been developed and analyzed to describe dengue transmission with saturated incidence rates for both human and vector populations. Key quantities, including the disease-free equilibrium, endemic equilibrium, and basic reproduction number (R_0), have been derived. Possible scenario for June to November also showed. The analysis reveals that the endemic equilibrium exists when $R_0 > 1$. Parameter values for infection were estimated using real-world data from health institutions in Bangladesh. Numerical simulations, implemented via MATLAB, demonstrate that the disease diminishes when $R_0 < 1$ but persists when $R_0 > 1$. To achieve complete eradication, increasing mosquito mortality rates is essential. Given the urgency of the situation, policymakers in Bangladesh must take immediate action to enhance vector control measures and improve treatment facilities. Without decisive intervention, dengue outbreaks could escalate, leading to significant loss of life.

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