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Mathematical Modeling and Analysis of dengue dynamics through numerical simulation

Safiullah Mussa*

MS Mathematics University of Engineering and Technology, Peshawar.

**Corresponding author: Safiullah Mussa*

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ABSTRACT **Original research paper**

Dengue fever is among the most rapidly expanding mosquito-borne infections, requiring precise models to understand and mitigate its spread. Unlike classical malaria studies that employ coupled SI–SI frameworks for humans and vectors, this work introduces a human-centered SEIR model that explicitly incorporates the exposed and recovered classes. This structure captures both the incubation delay before infectiousness and the transition to temporary immunity after recovery, offering a more faithful representation of dengue dynamics. The basic reproduction number R_0 is derived using the next generation matrix method, serving as the threshold between eradication and persistence. Parametric sensitivity analysis through normalized forward indices identifies the parameters with the strongest impact onR_0, guiding effective intervention priorities. Numerical simulations further illustrate the influence of these parameters on outbreak progression, confirming that targeted reductions in transmission can markedly suppress epidemic peaks. By combining rigorous analysis with computational experiments, this study advances the theoretical understanding of dengue while providing practical insights for disease control strategies.

Keywords: Mathematical Modeling, Infectious Diseases, Dengue Dynamics, Basic Reproduction Number, Next Generation Matrix Method, Sensitivity Analysis, Numerical Simulation.

1. Introduction

Mosquito-borne diseases, particularly dengue fever, remain one of the most pressing public health concerns worldwide. The virus responsible for dengue is primarily transmitted to humans by ***Aedes*** mosquitoes, causing a wide spectrum of clinical manifestations ranging from mild febrile illness to severe and sometimes fatal hemorrhagic fever [1]. The global burden of dengue is particularly heavy in Asia, where the World Health Organization (WHO) estimates that nearly 34% of worldwide cases occur, posing serious challenges to healthcare systems and exerting a substantial economic impact [2].

In recent years, mathematical modeling has emerged as a powerful tool for understanding the transmission dynamics of dengue and for evaluating potential control strategies. These models provide valuable insights into how the disease spreads within human populations, how interventions may alter epidemic outcomes, and which parameters most strongly influence disease persistence. Several researchers [3, 5, and 6] have proposed mathematical frameworks to capture dengue dynamics under different biological and epidemiological assumptions. Buonomo and Vargas [6], in particular, investigated threshold conditions using the classical basic reproduction number, R_0. However, existing models often suffer from specific limitations, such as

oversimplified compartmental structures or neglect of latency and recovery effects.

To address these gaps, the present study extends the model of Buonomo and Vargas by incorporating both ***exposed*** and ***recovered*** compartments. This refined SEIR framework provides a more accurate representation of dengue transmission by accounting for the incubation period prior to infectiousness as well as the transition to temporary immunity following recovery. The basic reproduction number is derived to characterize disease persistence through both human-to-vector and vector-to-human transmission pathways. Furthermore, the proposed model is solved numerically to illustrate the temporal progression of the epidemic and to evaluate the influence of key epidemiological parameters. This study not only contributes to the theoretical understanding of dengue transmission but also offers practical insights for designing effective public health strategies to mitigate its impact.

2. Preliminaries

2.1. Mathematical Modeling

Mathematical modeling provides a powerful way to represent real-world systems through equations that capture their behavior and interactions. By translating complex processes into mathematical form, it enables deeper analysis and prediction. Such models have wide-ranging applications across biology, medicine, engineering, economics, environmental science, and beyond [10].

2.2. Infectious Diseases

Infectious diseases arise when pathogenic microorganisms such as bacteria, viruses, fungi, or parasites invade the body and disrupt normal functions. They spread through direct contact, contaminated food or water, insect vectors, or environmental exposure [11]. Examples include influenza, tuberculosis, malaria, and dengue, ranging in severity from mild to life-threatening. Advances in vaccines, antimicrobial drugs, and public health interventions have greatly reduced their global burden, yet challenges such as antibiotic resistance and emerging pathogens continue to pose serious threats.

2.3. Relation between Infectious Diseases and Mathematical Modeling

Mathematical modeling offers a structured way to study infectious disease dynamics by translating biological processes into equations. Frameworks like the SIR model and its extensions help simulate outbreaks, evaluate interventions, and predict outcomes. From guiding COVID-19 responses to shaping strategies against malaria and dengue, modeling has become an essential tool for both understanding disease ecology and informing public health decisions.

2.4. ODEs Based Mathematical Modeling

Ordinary differential equation (ODE) based mathematical modeling is a fundamental approach for studying dynamic processes in epidemiology. By dividing populations into compartments such as susceptible, exposed, infectious, and recovered ODEs describe how individuals transition between states over time. These models capture the continuous evolution of disease spread, allowing researchers to analyze thresholds like the basic reproduction number, predict outbreak patterns, and test the effectiveness of interventions such as vaccination or vector control.

2.5. Basic Reproduction Number

The basic reproduction number, R_0, is a key threshold parameter in infectious disease modeling. It represents the expected number of secondary infections generated by a single infectious individual in an entirely susceptible population. If$R_0 < 1$, each infection leads to less than one new case on average, and the disease eventually dies out. Conversely, if$R_0 > 1$, the infection can spread and potentially cause an epidemic.

2.6. Next Generation Matrix Method

The next generation matrix (NGM) method is used to study the local stability of the disease-free equilibrium. The system is separated into new infection terms and transition terms, and their Jacobians at the DFE form the matrices $F$and V. The next generation matrix is then

$$K = FV^{-1}$$

And the basic reproduction number is given by

$$R_0 = \rho(FV^{-1}),$$

Where ρ denotes the spectral radius. If$R_0 < 1$, the disease-free equilibrium is locally asymptotically stable, while $R_0 > 1$ implies instability and the possibility of an epidemic.

2.7. Sensitivity Analysis and Sensitivity Index

Sensitivity analysis is a quantitative technique used to determine how changes in input variables affect the output of a model or system. It is commonly used in fields like mathematics, epidemiology, finance, engineering, and environmental science to assess the robustness and predictability of models. By systematically varying one or more input parameters and examining the effect on the output, researchers and analysts can identify which inputs have the greatest impact and which are less significant.

The sensitivity index of a parameter y with respect to a variable x is calcu lated using the normalized forward sensitivity index formula:

$$r_x{}^y = \frac{\partial x}{\partial y} \times \frac{y}{x}$$

2.8. Numerical Simulation

Numerical simulation is employed to study the behavior of the proposed SEIR model under different parameter values. Since the system of nonlinear ODEs cannot be solved analytically, standard numerical methods such as the Runge–Kutta scheme are used to approximate solutions. Simulations illustrate the temporal evolution of susceptible, exposed, infectious, and recovered populations, and allow us to visualize how parameters like transmission rate, recovery rate, and disease-induced mortality influence the epidemic curve. These results complement the analytical findings by confirming threshold dynamics and highlighting the role of key parameters in shaping outbreak outcomes.

3. Main Work

3.1. Proposed Model

In this section our main mathematical model for dengue transmission is presented. Which is basically the extension of SI-SI model of malaria. The human population in SI-SI model just consists of two classes, one is susceptible and the other is infected. In this work we just focus on the human population and extend this class to a more biological realistic model. We included two more classes to the human population one is exposed class and the other is recovered class. So our new mathematical model is called SEIR model of dengue dynamics.

By adding to new classes to the human population of previously SI-SI model we have formulated the following mathematical model:

$$\frac{dS_h}{dt} = \mu N_h - \frac{\beta q S_h}{pI_h + qS_h} I_m - \mu S_h \quad (1)$$

$$\frac{dE_h}{dt} = \frac{\beta q S_h}{pI_h + qS_h} I_m - \delta E_h - \mu E_h \quad (2)$$

$$\frac{dI_h}{dt} = \delta E_h - YI_h - \mu I_h - QI_h \quad (3)$$

$$\frac{dR}{dt} = YI_h + \mu I_h + QI_h - \mu R \quad (4)$$

All the model's parameters are presented in the following table

Parameters	Description
S_h	Number of susceptible humans
S_m	Number of susceptible mosquitoes
E_h	Exposed class of humans
E_m	Exposed class of mosquitoes
μ	Death and birth rates of humans
N_h	Population of humans
N_m	Population of mosquitoes
β	Transmission rate in humans
q	Mosquitoes that bite humans at probability that human is susceptible
p	Mosquitoes that bite humans at probability that human is infected
I_h	Number of infected humans
I_m	Number of infected mosquitoes
δ	rate of exposed humans to be infected
Y	rate at which infectious people recover from illness
Q	rate of infectious people dying due to virus

The human population equations describe the progression of dengue infection across four classes. The susceptible class (S_h) increases through births (μN_h)and decreases by infection and natural mortality (μS_h).The infection term $\frac{\beta q S_h}{pI_h + qS_h} I_m$ represents the force of infection, where β is the transmission probability, q is the likelihood a mosquito bites a susceptible human, and p is the probability of biting an infected human; this fraction models the competition between susceptible and infected humans for mosquito bites. Newly infected individuals enter the exposed class (E_h,progress to the infectious class (I_h) at rate δ, or die naturally. Infectious humans then recover at rate Y, die naturally

(μ), or due to the disease (Q). Finally, the recovered/removed class (R)accumulates individuals leaving infection through recovery or death, with only natural mortality reducing its size. Together, these terms capture the essential mechanisms of dengue transmission, highlighting the role of infection pressure, incubation, recovery, and mortality in shaping disease dynamics.

3.2. The Basic Reproduction Number:

To obtain R_0 we use the next generation matrix method

$$R_0 = \text{Spectral radius of } G$$

Spectral radius is

$$\rho(G) = max\{|\lambda_1|, |\lambda_2|\}$$

The next generation matrix G is

$$G = FV^{-1}$$

We have the following new infection terms and transition termsInfection terms

$$F_1 = \frac{\beta q S_h}{pI_h + qS_h} I_m$$

$$F_2 = 0$$

Transition terms

$$V_1 = (\delta + \mu)E_h$$

$$V_2 = -\delta E_h + (Y + \mu + Q)I_h$$

Now we have to compute Jacobians for both the infection and transition terms as

$$\text{F} = \begin{bmatrix} 0 & \frac{-\beta p}{q} \\ 0 & 0 \end{bmatrix}$$

and

$$V = \begin{bmatrix} \delta + \mu & 0 \\ -\delta & Y + \mu + Q \end{bmatrix}$$

Further we need to find V^{-1}

$$V^{-1} = \begin{bmatrix} \frac{1}{\delta + \mu} & 0 \\ \frac{\delta}{(\delta + \mu)(Y + \mu + Q)} & \frac{1}{Y + \mu + Q} \end{bmatrix}$$

The next generation matrix G is

$$G = FV^{-1}$$

$$G = \begin{bmatrix} \frac{-\beta p \delta}{q(\delta + \mu)(Y + \mu + Q)} & \frac{-\beta p}{q(Y + \mu + Q)} \\ 0 & 0 \end{bmatrix}$$

Spectral radius is

$$\rho(G) = max\{|\lambda_1|, |\lambda_2|\}$$

$$\rho(G) = \frac{\beta p \delta}{q(\delta + \mu)(Y + \mu + Q)}$$

So

$$R_0 = \frac{\beta p \delta}{q(\delta + \mu)(Y + \mu + Q)}$$

The above equation represents the basic reproduction number of the dengue virus in the human population. It quantifies the average number of secondary human infections generated by a single infected human in a completely susceptible environment

3.3. Sensitivity analysis

Sensitivity analysis is a technique used to assess how changes in the input variables of a model or system affect its output. By altering one or more input variables and observing the resulting changes in the output, analysts can identify which inputs are most influential or critical to the outcome. To perform this we use the table 4.2 as base line values for the parameters.

The sensitivity index of a parameter y with respect to a variable x is calculated using the normalized forward sensitivity index formula:

$$r_x^y = \frac{\partial x}{\partial y} \times \frac{y}{x}$$

A positive sensitivity index means that increasing y will increase x, while a negative sensitivity index means an inverse effect.

To calculate the sensitivity index of R_{HV} with respect to a parameter such as β, one typically uses a formula:

$$r_{\beta}^{R_{HV}} = \frac{\partial R_{HV}}{\partial \beta} \times \frac{\beta}{R_{HV}}$$

Using the above procedure the sensitivity indices of concerned parameters are obtained manually and presented in the following table 3.2.

$$R_0 = \frac{\beta p \delta}{q(\delta + \mu)(Y + \mu + Q)}$$

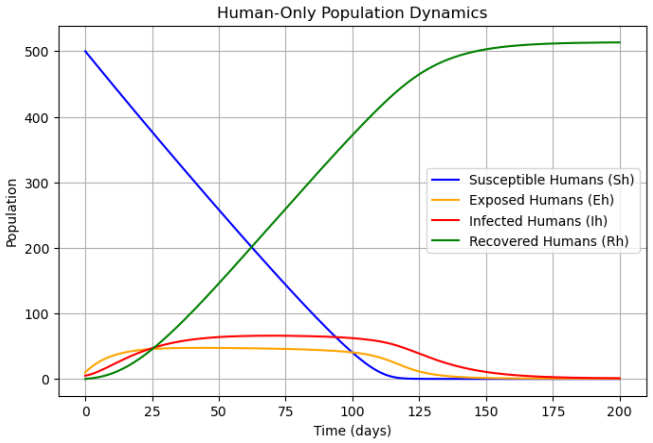
Parameters	Sensitivity Index
β	1
p	1
q	-1
δ	0.000092
μ	0.00000000183
Y	-0.9999
Q	-0.0000197

Table 3.2: Sensitivity Indices of the parameters

3.4.Numerical Simulation

The numerical simulation of the SEIR model describes the progression of dengue infection in a closed population. The results show that the susceptible class decreases continuously as individuals become exposed to the virus. The exposed class initially grows, attains a peak, and then declines as individual's transition into the infectious stage. The infectious class rises after a short delay, reaches its maximum, and subsequently decreases due to recovery and disease-induced mortality. Meanwhile, the recovered class grows monotonically throughout the simulation, eventually stabilizing as immunity accumulates within the population.

These dynamics highlight the typical epidemic wave generated by an SEIR framework. The interplay between susceptible depletion, transient growth in the exposed and infectious classes, and eventual stabilization through recovery reflects the theoretical behavior of compartmental epidemic models.



4. Conclusion

This study developed and analyzed an SEIR model for dengue transmission to capture the essential features of disease dynamics more realistically than traditional SI-based frameworks. By incorporating the exposed and recovered classes, the model reflects both the incubation period prior to infectiousness and the acquisition of temporary immunity after recovery. Analytical results, particularly the derivation of the basic reproduction number using the next generation matrix method, established the threshold conditions for disease eradication or persistence. Sensitivity analysis further identified the parameters with the strongest influence on transmission potential, offering guidance for prioritizing intervention strategies. Numerical simulations confirmed these theoretical findings, illustrating how variations in key parameters affect outbreak progression and long-term system stability. Overall, the integration of analytical techniques and computational experiments provides a comprehensive understanding of dengue dynamics. The findings not only advance the theoretical framework for epidemic modeling but also deliver practical insights for designing effective control measures, including targeted vector management and strategies to reduce human-to-mosquito transmission.

Appendix 4.2

Table 4.2: Parameter values used in the model

Parameter	Parameter value	Unit
μ	0.0000456	day^{-1}
β	0.25	days^{-1}
δ	0.5	days^{-1}
κ	0.375	days^{-1}
Q	0.001493	year^{-1}
K	0.5	days^{-1}
ϕ	0.245	days^{-1}
η	0.033	days^{-1}
Y	0.2081	days^{-1}

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