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Bifurcation analysis of dengue hemorrhagic fever model with logistic growth rate in aquatic stage

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Abstract This work analyzes the transmission dynamics of dengue hemorrhagic fever (DHF) by incorporating the aquatic phase and logistic growth rate for mosquitoes population. The model accounts for human-mosquito interactions and explores the role of disease-induced mortality. We investigate the existence and stability of equilibria, particularly focusing on the phenomenon of backward bifurcation. Our analysis demonstrates that the disease-free equilibrium is globally asymptotically stable when the basic reproduction number less than unity in the absence of disease-induced mortality. However, when disease-induced mortality is considered, backward bifurcation emerges, leading to the coexistence of multiple equilibria in the range basic reproduction number between critical reproduction number and one. A Lyapunov function approach confirms the global stability of the endemic equilibrium when basic reproduction number more than unity. Furthermore, we show that neglecting disease-induced mortality eliminates backward bifurcation, ensuring a unique endemic equilibrium. Numerical simulations support our theoretical findings, illustrating different stability behaviors under varying initial conditions.

Keywords Aquatic Stage, Backward Bifurcation, Dengue Hemorrhagic Fever, Logistic Growth Rate, Mathematical Modeling

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1. Introduction

Dengue hemorrhagic fever (DHF) remains a significant public health challenge in many tropical and subtropical regions worldwide. The disease, caused by the dengue virus and transmitted primarily through *Aedes* mosquitoes, continues to exhibit complex transmission dynamics that are influenced by environmental, biological, and sociological factors [1]. Mathematical modeling serves as a powerful tool for understanding these dynamics, providing a structured framework to analyze the intricate interactions between host (human) and vector (mosquito).

The mathematical framework developed in this paper builds upon the classical SI (Susceptible-Infected) epidemiological models for both host and vector. A novel feature of this model is the inclusion of an additional compartment L_n, representing the pre-adult mosquito population in the aquatic stage, which includes eggs, larvae, and pupae, combined with the logistic growth rate to describe their dynamics. The logistic growth rate is introduced to realistically model the density-dependent regulation of mosquito populations in the aquatic stage, as environmental factors such as limited resources and space significantly impact mosquito development [2]. This

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inclusion acknowledges the critical role of mosquito population dynamics in shaping the transmission patterns of DHF.

Bifurcation analysis is a mathematical technique used to investigate qualitative changes in the behavior of a system as parameters vary [3]. In this context, backward bifurcation is a phenomenon characterized by the coexistence of a locally asymptotically stable disease-free equilibrium and a locally asymptotically stable endemic equilibrium. This situation highlights a more complex and challenging scenario for disease control, as it indicates that reducing R_0 below one may not be sufficient to eliminate the disease. In this work, we focus on a model with a standard transmission rate and incorporate disease-induced mortality, both of which significantly influence the system dynamics and contribute to the occurrence of backward bifurcation.

This study extends previous research as a reference, including bifurcation analysis of two-infection SIR-SIR epidemic models with temporary immunity and disease enhancement [4], backward bifurcation arising from declining immunity against emerging infectious diseases [5], and stability analysis and backward bifurcation in SEIQR epidemic models with nonlinear innate immunity [6]. Additionally, authors in [7, 8, 9, 10, 11] have also explored the spread of DHF in the context of mathematical modeling. In summary, this study provides a comprehensive bifurcation analysis of a DHF transmission model incorporating mosquito breeding dynamics in the aquatic stage. The results highlight the potential for complex equilibrium structures, including backward bifurcation, which underscores the importance of carefully tailored intervention strategies to control DHF outbreaks.

2. Model formulation

In this section, we describe the host-vector model of DHF transmission framed within the SI (Susceptible-Infected) epidemiological structure for both host (human) and vector (mosquito). The human population is divided into two subpopulations: the susceptible human (S_m) and the infected human (I_m). The aquatic stage represents the mosquito development phase encompassing eggs, larvae, and pupae, highlighting the critical pre-adult population dynamics. This stage accounts for the early life stages of mosquitoes, and the compartment L_n is introduced to represent the total population in this aquatic phase. The adult mosquito population is also divided into two subpopulations: the susceptible mosquito (S_n) and the infected mosquito (I_n).

The total human population is expressed as $N_m = S_m + I_m$. Similarly, the total mosquito population is expressed as $N_n = S_n + I_n$. The following assumptions are used to construct the mathematical model of DHF transmission:

1. Humans are born into the susceptible population at a constant rate.
2. Mosquitoes are born into the aquatic stage, with their population growth regulated by a logistic growth rate to account for density-dependent factors such as resource limitations.
3. Susceptible humans can become infected with DHF if bitten by an infected mosquito, and susceptible mosquitoes can become infected if they bite an infected human.
4. The incubation period is ignored, allowing the infected population to immediately transmit DHF upon infection.
5. Mosquito populations do not recover from infection.
6. There is no reinfection of humans with DHF.
7. The incidence rate is modeled using the standard formulation.
8. Death due to DHF is considered for infected humans.

The mathematical model also includes a detailed description of parameters and their roles, which are summarized in Table 1.

Table 1. Parameters description.

Parameters	Description	Unit
Λ_m	Human birth rate	Individual $\times$ Time^{-1}
φ	Oviposition rate of mosquitoes	Individual $\times$ Time^{-1}
K	Carrying capacity of the mosquito population	Individual
b	Probability of a mosquito biting a human in a single interaction	-
β_m	Transmission rate of DHF from infected mosquitoes to susceptible humans	Individual $^{-1}$ $\times$ Time^{-1}
β_n	Transmission rate of DHF from infected humans to susceptible mosquitoes	Individual $^{-1}$ $\times$ Time^{-1}
μ_m	Natural death rate of humans	Time^{-1}
μ_n	Natural death rate of adult mosquitoes	Time^{-1}
μ	Natural death rate of pre-adult mosquitoes	Time^{-1}
η	Transition rate of mosquitoes from the pre-adult stage to the adult stage	Time^{-1}
δ_m	Mortality rate of humans due to DHF	Time^{-1}

Based on the previously explained assumptions, as well as the descriptions of the variables and parameters, the transmission diagram of the model is presented in Figure 1.

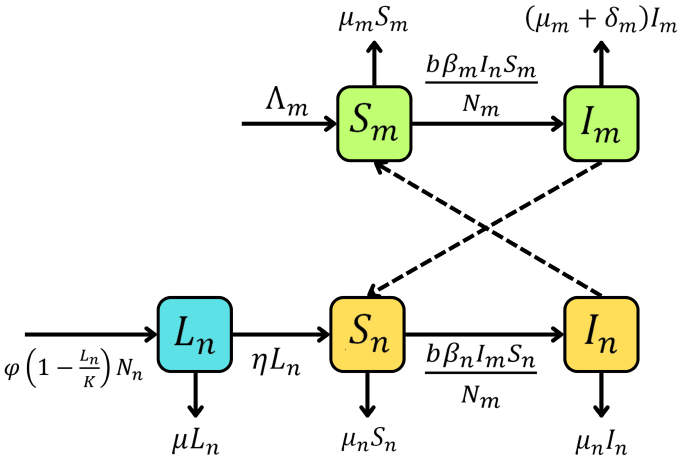

Figure 1. DHF transmission diagram.

The DHF transmission model is constructed as a five-dimensional nonlinear autonomous system of ordinary differential equations, as presented in Equation (1).

$$\begin{aligned}
\frac{dS_m}{dt} &= \Lambda_m - \frac{b\beta_m I_n S_m}{N_m} - \mu_m S_m \\
\frac{dI_m}{dt} &= \frac{b\beta_m I_n S_m}{N_m} - (\mu_m + \delta_m) I_m \\
\frac{dL_n}{dt} &= \varphi \left(1 - \frac{L_n}{K}\right) N_n - (\eta + \mu) L_n \\
\frac{dS_n}{dt} &= \eta L_n - \frac{b\beta_n I_m S_n}{N_m} - \mu_n S_n \\
\frac{dI_n}{dt} &= \frac{b\beta_n I_m S_n}{N_m} - \mu_n I_n
\end{aligned} \tag{1}$$

The model (1), subject to the initial values $S_m(0)$, $I_m(0)$, $L_n(0)$, $S_n(0)$, $I_n(0) \geq 0$, ensures that the solutions of the system (1) remain non-negative for all time $t > 0$. The solutions are assigned within a closed and non-negativity invariant set Ω, as given in:

$$\Omega = \Omega_m \cup \Omega_l \cup \Omega_n \subset \mathbb{R}^2_+ \times \mathbb{R}_+ \times \mathbb{R}^2_+,$$

with

$$\begin{aligned}
\Omega_m &= (S_m(t), I_m(t)) \in \mathbb{R}^2_+, N_m \leq \frac{\Lambda_m}{\mu_m}, \\
\Omega_l &= L_n(t) \in \mathbb{R}_+, L_n = K\left(\frac{\varphi N_n}{\varphi N_n + K(\eta + \mu)}\right) \text{ or } L_n = K\left(1 - \frac{\mu_n(\eta + \mu)}{\eta\varphi}\right), \\
\Omega_n &= (S_n(t), I_n(t)) \in \mathbb{R}^2_+, N_n = \frac{\eta}{\mu_n} L_n \text{ or } N_n = \frac{K\left(\eta\varphi - \mu_n\left(\eta + \mu\right)\right)}{\eta\varphi}.
\end{aligned}$$

In this case, $\mathbb{R}^n_+$ represents the n-dimensional non-negative real space where all components are non-negative. Next, we show the non-negativity of the solution to system (1) based on the following theorem.

Theorem 2.1
Let $S_m(0), I_m(0), L_n(0), S_n(0)$, and $I_n(0)$ be the initial values of the system. If $S_m(0) \geq 0, I_m(0) \geq 0, L_n(0) \geq 0, S_n(0) \geq 0$, and $I_n(0) \geq 0$ then all solutions are non-negative for every $t > 0$.

Proof
To ensure that the solutions remain non-negative, we show that each vector field is non-negative on the boundary of $\mathbb{R}^5_+$. Evaluating system (1) at the respective boundaries, we obtain:

$$\begin{aligned}
\left.\frac{dS_m}{dt}\right|_{S_m=0} &= \Lambda_m > 0 \\
\left.\frac{dI_m}{dt}\right|_{I_m=0} &= \frac{b\beta_m I_n S_m}{N_m} \geq 0 \\
\left.\frac{dL_n}{dt}\right|_{L_n=0} &= \varphi\left(1 - \frac{L_n}{K}\right) N_n \geq 0 \\
\left.\frac{dS_n}{dt}\right|_{S_n=0} &= \eta L_n \geq 0 \\
\left.\frac{dI_n}{dt}\right|_{I_n=0} &= \frac{b\beta_n I_m S_n}{N_m} \geq 0
\end{aligned}$$

It is proven that all the vector directions related to system (1) are non-negative. Therefore, if the initial value starts within the interior of the non-negative region of $\mathbb{R}^5_+$, the system will remain in this region since the vector field always points inward on the bounded planes. As a yield, the non-negativity of all solutions to system (1) is confirmed. □

3. Model analysis

In this section, we elaborate the local and global stability of the equilibria of model (1). The analysis involves determining the equilibrium points, their conditions of existence, and the basic reproduction number, which provides insight into the potential for disease transmission within the population. From model (1), three equilibria are obtained: the disease-free without presence of mosquito equilibrium, disease-free with presence of mosquito equilibrium and the endemic equilibrium.

The disease-free without mosquito presence equilibrium is given by:

$$E_0 = (S_{m0}, I_{m0}, L_{n0}, S_{n0}, I_{n0}) = \left(\frac{\Lambda_m}{\mu_m}, 0, 0, 0, 0\right).$$

This equilibrium represents a disease-free state where mosquitoes are absent. The components S_{m0}, I_{m0}, L_{n0}, S_{n0}, and I_{n0} respectively denote the equilibrium values of the susceptible human population, infected human population, aquatic-stage mosquito population, susceptible mosquito population, and infected mosquito population under disease-free conditions without mosquito presence. This equilibrium is a trivial solution for the mosquito population in model (1), and its stability analysis is typically not biologically relevant. Thus, it is not further considered in this study.

Next, the disease-free with mosquito presence equilibrium is given by:

$$E_1 = (S_{m1}, I_{m1}, L_{n1}, S_{n1}, I_{n1}) = \left(\frac{\Lambda_m}{\mu_m}, 0, \frac{\mu_n}{\eta} S_{n1}, \frac{K(\eta+\mu)}{\varphi}(R_n - 1), 0\right).$$

where $R_n = \frac{\varphi\eta}{\mu_n(\eta+\mu)}$ serves as a threshold parameter for mosquito presence. This equilibrium corresponds to a disease-free state where mosquitoes are present. The components S_{m1}, I_{m1}, L_{n1}, S_{n1}, and I_{n1} respectively represent the equilibrium values of the susceptible human population, infected human population, aquatic-stage mosquito population, susceptible mosquito population, and infected mosquito population under disease-free conditions with mosquito presence. The disease-free equilibrium with mosquito presence exists when $R_n > 1$. Furthermore, the basic reproduction number (R_0) measures the potential for disease spread within the population. Using the Next Generation Matrix (NGM) approach [12], the matrices F (transmission terms) and Z (transition terms) are evaluated at the disease-free equilibrium with mosquito presence (E_1):

$$F(E_1) = \begin{pmatrix} 0 & b\beta_m \\ \frac{b\beta_n\mu_m K(\eta+\mu)}{\Lambda_m} & 0 \end{pmatrix} \text{ and } Z(E_1) = \begin{pmatrix} \mu_m + \delta_m & 0 \\ 0 & \mu_n \end{pmatrix}.$$

The basic reproduction number is defined as the spectral radius of the matrix FZ^{-1}. Consequently, R_0 for model (1) is expressed as:

$$R_0 = \sqrt{\frac{b^2\beta_m\beta_n\mu_m K(\eta+\mu)}{\Lambda_m\varphi\mu_n(\mu_m+\delta_m)}(R_n - 1)}.$$

The basic reproduction number is always positive when $R_n > 1$, indicating that the presence of mosquitoes significantly contributes to the potential for disease transmission.

4. Local stability of the disease-free with mosquito presence equilibrium

The local stability of the disease-free with mosquito presence equilibrium (E_1) is obtained by substituting the value of E_1 into the Jacobian matrix of the system. The Jacobian matrix at E_1 is given by:

$$J(E_1) = \begin{pmatrix} -\mu_m & 0 & 0 & 0 & -b\beta_m \\ 0 & -(\mu_m+\delta_m) & 0 & 0 & b\beta_m \\ 0 & 0 & J_{33} & J_{34} & J_{35} \\ 0 & J_{42} & \eta & -\mu_n & 0 \\ 0 & J_{52} & 0 & 0 & -\mu_n \end{pmatrix},$$

where

$$\begin{aligned} J_{33} &= -(\eta+\mu)(R_n-1)-(\eta+\mu), \\ J_{34} &= \varphi\left(1-\frac{\mu_n(\eta+\mu)(R_n-1)}{\varphi\eta}\right), \\ J_{35} &= \varphi\left(1-\frac{\mu_n(\eta+\mu)(R_n-1)}{\varphi\eta}\right), \\ J_{42} &= \frac{-b\beta_n K(\eta+\mu)(R_n-1)\mu_m}{\varphi\Lambda_m}, \\ J_{52} &= \frac{-b\beta_n K(\eta+\mu)(R_n-1)\mu_m}{\varphi\Lambda_m}. \end{aligned}$$

To determine the stability of E_1, we calculatee the characteristic equation of the matrix $J(E_1)$, given by $|\lambda I - J(E_1)| = 0$. The resulting characteristic equation is:

$$(\lambda+\mu_m)(\lambda^2+b_1\lambda+b_2)(\lambda^2+c_1\lambda+c_2)=0, \tag{2}$$

where

$$\begin{aligned} b_1 &= \mu_m+\delta_m+\mu_n, \\ b_2 &= \mu_n(\mu_m+\delta_m)(1-R_0^2), \\ c_1 &= \eta+\mu+\mu_n+(\eta+\mu)(R_n-1), \\ c_2 &= \mu_n(\eta+\mu)(R_n-1). \end{aligned}$$

From Equation (2), one eigenvalue is clearly $\lambda_1 = -\mu_m < 0$. The remaining eigenvalues are the roots of the equations:

$$\lambda^2+b_1\lambda+b_2=0 \text{ and } \lambda^2+c_1\lambda+c_2=0. \tag{3}$$

Using the Routh-Hurwitz criteria, the roots of Equation (3) will have negative real parts if and only if b_1, b_2, c_1, and $c_2 > 0$.

1. It is evident that $b_1 > 0$, as all parameters value are positive.
2. The coefficient $b_2 > 0$ if $R_0^2 < 1$, which implies $R_0 < 1$.
3. Since the condition for the existence of E_1 requires $R_n > 1$, it is clear that both $c_1 > 0$ and $c_2 > 0$.

The foregoing discussion could be represented in the following theorem.

Theorem 4.1
The disease-free with mosquito presence equilibrium (E_1) of the system (1) is locally asymptotically stable in region of interest Ω if $R_0 < 1$ and unstable if $R_0 > 1$.

5. Global stability of disease-free with mosquito presence equilibrium

The global stability of the disease-free with mosquito presence equilibrium is examined using the method established by Castillo-Chavez et al. [13]. Let $X = (S_m, L_n, S_n)^T \in \mathbb{R}^3_+$ and $Z = (I_m, I_n)^T \in \mathbb{R}^2_+$, then the system (1) can be rewritten as:

$$\begin{aligned} \frac{dX}{dt} &= F(X,Z), \\ \frac{dZ}{dt} &= G(X,Z), \quad G(X,0) = 0, \end{aligned} \tag{4}$$

where $E_1 = (X_1, 0)$ with $X_1 = (S_{m1}, I_{n1}, S_{n1})$ states the disease-free with mosquito presence equilibrium.

By using [13], the fixed point $E_1 = (X_1, 0)$ is globally asymptotically stable provided that $R_0 < 1$ and the two conditions bellow are fulfilled:

(H1) For $\dfrac{dX}{dt} = F(X,0)$, X_1 is globally asymptotically stable,

(H2) The matrix $G(X,Z) = AZ - \hat{G}(X,Z)$,
fullfills $\hat{G}(X,Z) \geq 0$ for $(X,Z) \in \Omega$, where $A = D_Z G(X_1, 0)$.

From the system (1), we have the form of Equation (4) as follows:

$$\begin{aligned} F(X,Z) &= \begin{pmatrix} \Lambda_m - \frac{b\beta_m I_n S_m}{N_m} - \mu_m S_m \\ \varphi\left(1 - \frac{L_n}{K}\right) N_n - (\eta + \mu) L_n \\ \eta L_n - \frac{b\beta_n I_m S_n}{N_m} - \mu_n S_n \end{pmatrix}, \\ Z(X,Z) &= \begin{pmatrix} \frac{b\beta_m I_n S_m}{N_m} - (\mu_m + \delta_m) I_m \\ \frac{b\beta_n I_m S_n}{N_m} - \mu_n I_n \end{pmatrix}. \end{aligned} \tag{5}$$

Furthermore, based on Equation (5), when $Z = 0$, the function $F(X,0)$ can be derived as follows:

$$F(X,0) = \begin{pmatrix} \Lambda_m - \mu_m S_m \\ \varphi\left(1 - \frac{L_n}{K}\right) S_n - (\eta + \mu) L_n \\ \eta L_n - \mu_n S_n \end{pmatrix},$$

Solving $\frac{dX}{dt} = F(X,0)$, we get:

$$\begin{pmatrix} S_m(t) \\ L_n(t) \\ S_n(t) \end{pmatrix} = \begin{pmatrix} \frac{\Lambda_m}{\mu_m} + \left(S_m(0) - \frac{\Lambda_m}{\mu_m}\right) e^{-\mu_m t} \\ \frac{K\varphi S_n}{(\eta+\mu)K + \varphi S_n} + \left(L(0) - \frac{K\varphi S_n(0)}{(\eta+\mu)K + \varphi S_n(0)}\right) e^{-\left(\eta + \mu + \frac{\varphi}{K} S_n\right) t} \\ \frac{\eta L_n}{\mu_n} + \left(S_n(0) - \frac{\eta L_n(0)}{\mu_n}\right) e^{\mu_n t} \end{pmatrix}. \tag{6}$$

Hence, from Equation (6), when $t \to \infty$ and some algebra simplification, we obtain

$$\lim_{t\to\infty} \begin{pmatrix} S_m(t) \\ L_n(t) \\ S_n(t) \end{pmatrix} = \begin{pmatrix} \frac{\Lambda_m}{\mu_m} \\ K\left(\frac{\varphi\eta - \mu_n(\eta+\mu)}{\varphi\eta}\right) \\ \frac{\eta}{\mu_n} K\left(\frac{\varphi\eta - \mu_n(\eta+\mu)}{\varphi\eta}\right) \end{pmatrix} = \begin{pmatrix} S_{m1} \\ L_{n1} \\ S_{n1} \end{pmatrix}. \tag{7}$$

Equation (7) confirms that equilibrium point:

$$X_1 = \left(\frac{\Lambda_m}{\mu_m}, K\left(\frac{\varphi\eta - \mu_n(\eta+\mu)}{\varphi\eta}\right), \frac{\eta}{\mu_n} K\left(\frac{\varphi\eta - \mu_n(\eta+\mu)}{\varphi\eta}\right)\right),$$

is globally asymptotically stable, ensuring that H1 is satisfied.

In addition, from Equation (5) and through algebra calculations, we obtain the matrix A and $\hat{G}(X,Z)$, which satisfy $G(X,Z) = AZ - \hat{G}(X,Z)$, as follows:

$$A = \begin{pmatrix} -(\mu_m+\gamma) & \frac{b\beta_m S_{m1}}{N_{m1}} \\ \frac{b\beta_n S_{n1}}{N_{m1}} & -\mu_n \end{pmatrix} \text{ and } \hat{G}(X,Z) = \begin{pmatrix} \frac{b\beta_m I_n S_{m1}}{N_{m1}}\left(1-\frac{S_m N_{m1}}{N_m S_{m1}}\right) \\ \frac{b\beta_n I_m S_{n1}}{N_{m1}}\left(1-\frac{S_n N_{m1}}{N_m S_{n1}}\right) \end{pmatrix}.$$

Next, it is clear that:

$$S_m \le N_m \le \frac{\Lambda_m}{\mu_m} = S_{m1} \text{ and } S_n \le N_n \le \frac{\eta}{\mu_n} K\left(\frac{\varphi\eta - \mu_n(\eta+\mu)}{\varphi\eta}\right) = S_{n1}.$$

Hence, we have $S_m \le S_{m1}$ and $S_n \le S_{n1}$. However, to yield $\hat{G}_1(X,Z) \ge 0$ and $\hat{G}_2(X,Z) \ge 0$, some conditions are involved. For example, we could let the total human population be at an equilibrium level $\left(N_m = \frac{\Lambda_m}{\mu_m} = N_{m1}\right)$ and this condition will be obtained when we assume to omit the disease-induced death rate $(\delta_m = 0)$. Under this assumption, the inequalities ensures that:

$$\left(1-\frac{S_m N_{m1}}{N_m S_{m1}}\right) \Leftrightarrow \left(1-\frac{S_m}{S_{m1}}\right) \ge 0 \text{ and } \left(1-\frac{S_n N_{m1}}{N_m S_{n1}}\right) \Leftrightarrow \left(1-\frac{S_n}{S_{n1}}\right) \ge 0.$$

Hence, H2 is satisfied. Since both conditions H1 and H2 are fulfilled under the assumption that the disease-induced death rate is omitted $(\delta_m = 0)$, then disease-free equilibrium with mosquito presence (E_1) is globally asymptotically stable when $R_0 < 1$. The previous discussion could be stated in the following theorem.

Theorem 5.1
Suppose the disease-induced death rate in system (1) is neglected $(\delta_m = 0)$. If $R_0 < 1$, then the disease-free with mosquito presence equilibrium point is globally asymptotically stable.

6. Endemic equilibrium

From the results of the analytical calculations, the endemic equilibrium point of the system (1) can be derived by considering the conditions for the force of infection (κ). In this context, we classify κ into two forms: the force of infection for humans (κ_m) and the force of infection for mosquitoes (κ_n), which are defined as follows:

$$\kappa_m = \frac{b\beta_m I_n}{N_m} \text{ and } \kappa_n = \frac{b\beta_n I_m}{N_m}. \tag{8}$$

Using these conditions, the endemic equilibrium point is expressed as:

$$E_2 = (S_{m2}, I_{m2}, L_{n2}, S_{n2}, I_{n2}),$$

where

$$\begin{aligned} S_{m2} &= \frac{\Lambda_m}{\kappa_{m2}+\mu_m}, \\ I_{m2} &= \frac{\kappa_{m2}}{\mu_m+\delta_m} S_{m2}, \\ L_{n2} &= \frac{K\mu_n(\eta+\mu)}{\eta\varphi}(R_n - 1), \\ S_{n2} &= \frac{\eta}{\kappa_{n2}+\mu_n} L_{n2}, \\ I_{n2} &= \frac{\kappa_{n2}}{\mu_n} S_{n2}. \end{aligned} \tag{9}$$

This equilibrium represents an endemic state where both humans and mosquitoes coexist with ongoing disease transmission. The components S_{m2}, I_{m2}, L_{n2}, S_{n2}, and I_{n2} respectively denote the equilibrium values of the susceptible human, infected human, aquatic-stage mosquito, susceptible mosquito, and infected mosquito populations under endemic conditions.

Substitute Equations (9) into (8) in steady state and after algebraic simplification we have:

$$\begin{aligned} \kappa_{n2} &= \frac{b\beta_n\Lambda_m\kappa_{m2}}{N_{m2}(\mu_m+\delta_m)(\kappa_{m2}+\mu_m)}, \\ \kappa_{m2} &= \frac{b^2\beta_n\beta_m\Lambda_m\eta L_{n2}-\mu_m\mu_n(\mu_m+\delta_m)N_{m2}}{N_{m2}\mu_n(b\beta_n\Lambda_m+\mu_n(\mu_m+\delta_m)N_{m2})}. \end{aligned} \tag{10}$$

The total number of human population in steady state condition is given by:

$$N_{m2} = S_{m2} + I_{m2} = \frac{\Lambda_m(\kappa_{m2}+\mu_m+\delta_m)}{(\mu_m+\delta_m)(\kappa_m+\mu_m)} \tag{11}$$

Subtitute Equation (11) into (10) and performing algebraic simplifications, κ_{m2} satisfying the quadratic equation of:

$$c_0\kappa_{m2}^2 + c_1\kappa_{m2} + c_2 = 0, \tag{12}$$

where

$$\begin{aligned} c_0 &= \mu_n\Lambda_m(b\beta_n+\mu_n), \\ c_1 &= \mu_n\Lambda_m(\mu_n(\mu_m+\delta_m)+(\mu_m+\delta_m)(b\beta_n+\mu_n)) - b^2\beta_m\beta_n\eta(\mu_m+\delta_m)L_{n2}, \\ c_2 &= \mu_n^2\Lambda_m(\mu_m+\delta_m)^2(1-R_0^2). \end{aligned}$$

Thus, we obtained the following results:

Theorem 6.1
The system (1) has the following endemic equilibrium points, depending on the conditions outlined below:

1. A unique endemic equilibrium exist in Ω if $c_2 < 0$ $(i.e. R_0 > 1)$.
2. A unique endemic equilibrium exist in Ω if $c_1 < 0$ and either $c_2 = 0$ $(i.e. R_0 = 1)$ or $c_1^2 - 4c_0c_2 = 0$.
3. Two endemic equilibria exist in Ω if $c_1 < 0$, $c_2 > 0$ $(i.e. R_0 < 1)$, and $c_1^2 - 4c_0c_2 > 0$.
4. No endemic equilibrium otherwise.

Proof
It is clear that the coefficient c_0 is positive since all the parameters are positive.

1. If $c_2 < 0$:
   Using the formula for the product of the roots of a quadratic equation, we obtain $\kappa_{m2_1} \times \kappa_{m2_2} = \frac{c_2}{c_0}$. Since $c_0 > 0$ and $c_2 < 0$, it follows that $\frac{c_2}{c_0} < 0$. The product of the two roots is negative, which implies that one root is positive and the other is negative. Therefore, a unique endemic equilibrium exists in this case.
2. If $c_1 < 0$ and $c_2 = 0$:
   Using the quadratic formula for the roots of a quadratic equation, we get:
   $$\kappa_{m2_{1,2}} = \frac{-c_1 \pm c_1}{2c_0}.$$
   This gives $\kappa_{m2_1} = 0$ and $\kappa_{m2_2} = -\frac{c_1}{c_0}$. Since $c_0 > 0$ dan $c_1 < 0$, it is clear that $\kappa_{m2_2} > 0$. Therefore, a unique endemic equilibrium exists in this case.
3. If $c_1 < 0$ and $c_1^2 - 4c_0c_2 = 0$:
   Using the quadratic formula for the roots of a quadratic equation, we get:
   $$\kappa_{m2_{1,2}} = \frac{-c_1}{2c_0}.$$
   Thus, the two roots are equal: $\kappa_{m2_1} = \kappa_{m2_2} = -\frac{c_1}{2c_0}$. Since $c_0 > 0$ dan $c_1 < 0$, it is clear that $\kappa_{m2_1} = \kappa_{m2_2} > 0$. Therefore, a unique endemic equilibrium exists in this case.

Table 2. Parameters value for the backward bifurcation case.

Parameters	Value	Parameters	Value
Λ_m	10	δ_m	0.25
b	0.05	φ	5
β_m	0.2	K	1000
β_n	0.2	η	0.7
μ_m	0.14	μ	0.08
μ_n	0.05		

4. If $c_1 < 0$, $c_2 > 0$, and $c_1^2 - 4c_0c_2 > 0$:
The positive discriminant ensures that the quadratic equation has two distinct real roots. Using the quadratic formula, we obtain:

$$\kappa_{m2_1} = \frac{-c_1 + \sqrt{c_1^2 - 4c_0c_2}}{2c_0} \text{ and } \kappa_{m2_2} = \frac{-c_1 - \sqrt{c_1^2 - 4c_0c_2}}{2c_0}.$$

- Considering κ_{m2_1}, since $c_1 < 0$, we have $-c_1 + \sqrt{c_1^2 - 4c_0c_2} > 0$. Thus, the numerator of κ_{m2_1} is positive, and since $c_0 > 0$, it follows that $\kappa_{m2_1} > 0$.
- Considering κ_{m2_2}, since $c_0, c_2 > 0$, we have $\sqrt{c_1^2 - 4c_0c_2} < \sqrt{c_1^2}$. Since $c_1 < 0$, we have $\sqrt{c_1^2} = -c_1$ which implies that $\sqrt{c_1^2 - 4c_0c_2} < -c_1$. Thus, the numerator of κ_{m2_2} is positive, and since $c_0 > 0$, it follows that $\kappa_{m2_2} > 0$.

Therefore, two endemic equilibria exist in this case.

□

7. Existence of backward bifurcation

According to Theorem 6.1, case 3 confirms the existence of multiple equilibria, indicating the possibility of a backward bifurcation. A backward bifurcation occurs when a locally asymptotically stable of the disease-free equilibrium (DFE) coexists with a locally asymptotically stable endemic equilibrium, even when $R_0 < 1$. To determine the threshold for this bifurcation, the discriminant of Equation (12) is set to zero, leading to:

$$c_1^2 - 4c_0\mu_n^2\Lambda_m(\mu_m + \delta_m)^2(1 - R_0^2) = 0.$$

This yields the critical reproduction number:

$$R_0^{critical} = \sqrt{1 - \frac{c_1^2}{4c_0\mu_n^2\Lambda_m(\mu_m + \delta_m)^2}}. \tag{13}$$

Equation (13) provides an analytical expression for the threshold value, indicating that a backward bifurcation occurs when $R_0^{critical} < R_0 < 1$. Using the parameter values listed in Table 2, we calculate $R_0 = 0.997$ and $R_0^{critical} = 0.966$, fulfilling the condition $R_0^{critical} < R_0 < 1$. This confirms that the parameter selection in Table 2 for model (1) causes a backward bifurcation.

Based on Figure 2, we classify the regions according to the number and stability of equilibria as follows:

- For $R_0 < R_0^{critical}$, the system exhibits only the disease-free equilibrium, which is globally stable, and no endemic equilibrium exists
- At $R_0 = R_0^{critical}$ marks the threshold for backward bifurcation. The system transitions from a single equilibrium to multiple equilibria.

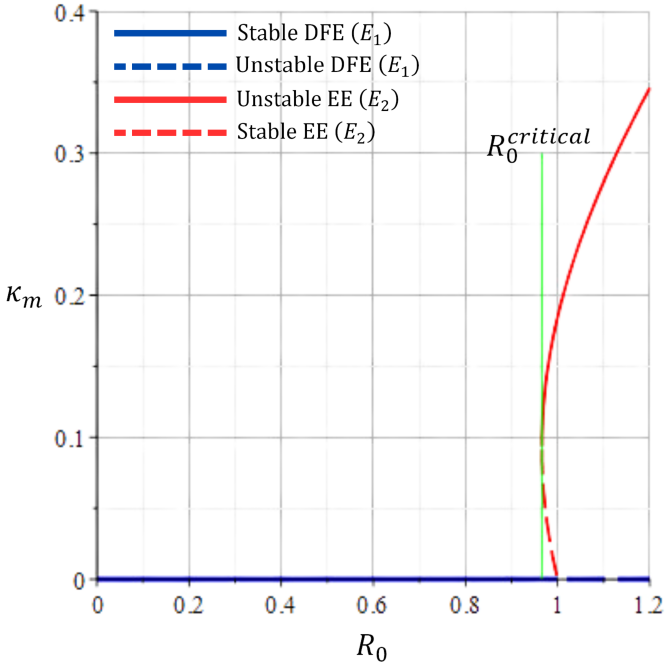

Figure 2. Backward bifurcation plot.

- For $R_0^{critical} < R_0 < 1$, the system maintains three equilibria: the disease-free equilibrium becomes locally stable but loses global stability, one unstable endemic equilibrium, and one locally stable endemic equilibrium.
- For $R_0 \geq 1$, the system transitions to having only two equilibria: the disease-free equilibrium and one endemic equilibrium. The disease-free equilibrium becomes unstable, while the endemic equilibrium becomes globally stable.

To illustrate this backward bifurcation, we simulate model (1) using the parameters from Table 2 and two distinct initial conditions. The numerical simulations are carried out using the classical fourth-order Runge–Kutta (RK4) method. The results, presented in Figure 3, demonstrate how these different initial conditions cause variations in the stability properties of the solutions to system (1).

Based on Figures 3, it is evident that the same model and parameter values, under different initial conditions, result in distinct system behaviors. This is attributed to the occurrence of backward bifurcation. Specifically:

- Under the first initial condition, the solution of system asymptotically stable at the disease-free equilibrium with mosquito presence (E_1).
- Under the second initial condition, the solution of system asymptotically stable at the endemic equilibrium (E_2).

Interestingly, the aquatic-stage mosquito population remains the same in both E_1 and E_2, as this population is unaffected by the bifurcation. Next, by subtituting the parameters value in Table 2 into model (1), the following equilibrium points are obtained:

1. $(S_{m0};\ I_{m0};\ L_{n0};\ S_{n0};\ I_{n0}) = (71.43;\ 0;\ 0;\ 0;\ 0)$ is the disease-free without mosquito presence equilibrium (E_0) which is unstable.
2. $(S_{m1};\ I_{m1};\ L_{n1};\ S_{n1};\ I_{n1}) = (71.43;\ 0;\ 988.86;\ 13844;\ 0)$ is the disease-free with mosquito presence equilibrium (E_1) which is asymptotically stable.

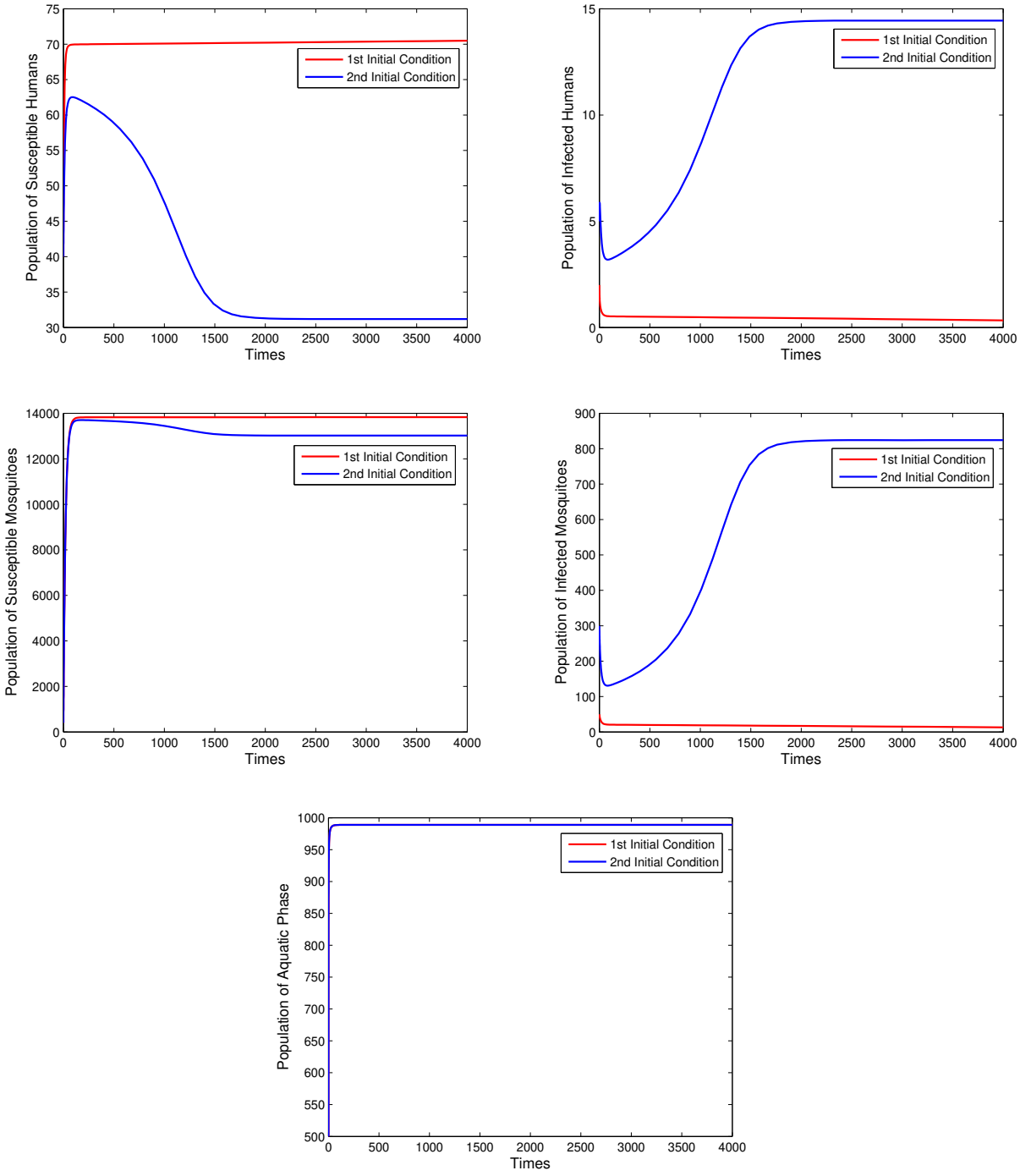

Figure 3. Numerical simulation graph based on first initial condition $(S_m(0) = 40, I_m(0) = 2, L_n(0) = 500, S_n(0) = 400, I_n(0) = 50)$ and second intial condition $(S_m(0) = 40, I_m(0) = 5, L_n(0) = 500, S_n(0) = 400, I_n(0) = 300)$.

3. $(S_{m2};\ I_{m2};\ L_{n2};\ S_{n2};\ I_{n2}) = (69.32;\ 0.76;\ 988.86;\ 13814.14;\ 29.86)$ is the first endemic equilibrium (E_2) which is unstable.

4. $(S_{m2};\ I_{m2};\ L_{n2};\ S_{n2};\ I_{n2}) = (31.19;\ 14.44;\ 988.86;\ 13019.83;\ 824.17)$ is the second endemic equilibrium (E_2) which is asymptotically stable.

The occurrence of a backward bifurcation in model (1) has significant epidemiological implications. Specifically, the conventional criterion of $R_0 < 1$ is no longer sufficient to guarantee disease eradication, although it remains necessary. In such cases, the success of disease eradication depends on the initial population sizes in the model. This highlights that controlling dengue fever (DHF) when $R_0 < 1$ may require careful consideration of initial population conditions.

8. Special case of endemic equilibrium

As a continuation of Theorem 5.1, which states that the disease-free with mosquito presence equilibrium point (E_1) is globally asymptotically stable when the disease-induced death rate is ignored, we define the special case here as the scenario where the disease-induced mortality rate is neglected $(\delta_m = 0)$. Under this condition, we demonstrate that backward bifurcation disappears from the system, ensuring the global stability of E_1 when $R_0 < 1$. This global stability of E_1 is guaranteed as long as the endemic equilibrium is unique.

Neglecting the disease-induced death rate allows the total human population at equilibrium to be approximated as:

$$N_{m2} = \frac{\Lambda_m}{\mu_m} \tag{14}$$

Substituting Equation (14) and (9) into (8) and performing the necessary calculations, we obtain the explicit form of:

$$\kappa_{m2} = \frac{\mu_n\mu_m(\mu_m + \delta_m)}{b\beta_n\mu_m + \mu_n(\mu_m + \delta_m)}(R_0^2 - 1).$$

It is evident that κ_{m2} is unique and exist if $R_0^2 > 1 \Leftrightarrow R_0 > 1$, resulting in a single endemic equilibrium. Consequently, under these conditions, backward bifurcation is eliminated from the system.

In conclusion, this analysis indicates that the inclusion of disease-induced mortality in the model influences the emergence of backward bifurcation. Neglecting this mortality simplifies the system dynamics, removing backward bifurcation and ensuring the global stability of the disease-free equilibrium when $R_0 < 1$. The foregoing discussion could be summarized in the following theorem.

Theorem 8.1
Suppose that the disease-induced death rate of the system (1) is ignored $(\delta_m = 0)$. Then the system (1) has a unique endemic equilibrium that exists in Ω if $R_0 > 1$.

9. Global stability analysis of endemic equilibrium in special case

Consider the set:

$$\Omega_0 = \{M \in \Omega : I_m = I_n = 0\}$$

where $M = (S_m(t), I_m(t), L_n(t), S_n(t), I_n(t))$. The set Ω_0 represents the stable manifold of the disease-free equilibria E_1. The global stability of the endemic equilibrium is described in the following theorem:

Theorem 9.1
Suppose that the disease-induced death rate of the system (1) is ignored $(\delta_m = 0)$. The endemic equilibrium (E_2) of this special case is globally asymptotically stable in the interior of region $\Omega\backslash\Omega_0$ if $R_0 > 1$.

Proof
We use Goh-Volterra type Lyapunov function $\mathcal{L} : \Omega \backslash \Omega_0 \to \mathbb{R}$ defined as:

$$\begin{aligned}\mathcal{L} &= \left(S_m - S_{m2} - S_{m2}\ln\frac{S_m}{S_{m2}}\right) + \left(I_m - I_{m2} - I_{m2}\ln\frac{I_m}{I_{m2}}\right)\\ &\quad +k\left(S_n - S_{n2} - S_{n2}\ln\frac{S_n}{S_{n2}}\right) + k\left(I_n - I_{n2} - I_{n2}\ln\frac{I_n}{I_{n2}}\right)\end{aligned}$$

with $k = \frac{\beta_m S_{m2} I_{n2}}{\beta_n S_{n2} I_{m2}}$.
The time derivative of $\mathcal{L}$ is:

$$\begin{aligned}\frac{d\mathcal{L}}{dt} &= \left(\frac{dS_m}{dt} - \frac{S_{m2}}{S_m}\frac{dS_m}{dt}\right) + \left(\frac{dI_m}{dt} - \frac{I_{m2}}{I_m}\frac{dI_m}{dt}\right) + k\left(\frac{dS_n}{dt} - \frac{S_{n2}}{S_n}\frac{dS_n}{dt}\right) + k\left(\frac{dI_n}{dt} - \frac{I_{n2}}{I_n}\frac{dI_n}{dt}\right)\\ \frac{d\mathcal{L}}{dt} &= \left(1 - \frac{S_{m2}}{S_m}\right)\frac{dS_m}{dt} + \left(1 - \frac{I_{m2}}{I_m}\right)\frac{dI_m}{dt} + k\left(1 - \frac{S_{n2}}{S_n}\right)\frac{dS_n}{dt} + k\left(1 - \frac{I_{n2}}{I_n}\right)\frac{dI_n}{dt} \qquad (15)\end{aligned}$$

Substituting the equations from system (1) into Equation (15) yields:

$$\begin{aligned}\frac{d\mathcal{L}}{dt} &= \left(1 - \frac{S_{m2}}{S_m}\right)\left[\Lambda_m - \frac{b\beta_m I_n S_m}{N_m} - \mu_m S_m\right] + \left(1 - \frac{I_{m2}}{I_m}\right)\left[\frac{b\beta_m I_n S_m}{N_m} - (\mu_m + \delta_m) I_m\right]\\ &\quad +k\left(1 - \frac{S_{n2}}{S_n}\right)\left[\eta L_n - \frac{b\beta_n I_m S_n}{N_m} - \mu_n S_n\right] + k\left(1 - \frac{I_{n2}}{I_n}\right)\left[\frac{b\beta_n I_m S_n}{N_m} - \mu_n I_n\right]. \qquad (16)\end{aligned}$$

At equilibrium, from system (1) we have relation:

$$\begin{aligned}\Lambda_m &= \frac{b\beta_m I_{n2} S_{m2}}{N_{m2}} + \mu_m S_{m2},\\ \mu_m + \delta_m &= \frac{b\beta_m I_{n2} S_{m2}}{I_{m2} N_{m2}}\\ \eta &= \frac{b\beta_n I_{m2} S_{n2}}{L_{n2} N_{m2}} + \frac{\mu_n S_{n2}}{L_{n2}}\\ \mu_n &= \frac{b\beta_n I_{m2} S_{n2}}{I_{n2} N_{m2}}\end{aligned} \qquad (17)$$

Replacing relation at steady state (17) into Equation (16) and after some simplification we have:

$$\begin{aligned}\frac{d\mathcal{L}}{dt} &= \frac{b\beta_m I_{n2} S_{m2}}{N_{m2}}\left(2 - \frac{S_{m2}}{S_m} - \frac{I_n S_m N_{m2} I_{m2}}{I_{n2} S_{m2} N_m I_m} + \frac{I_n N_{m2}}{I_{n2} N_m} - \frac{I_m}{I_{m2}}\right) + \mu_m S_{m2}\left(2 - \frac{S_m}{S_{m2}} - \frac{S_{m2}}{S_m}\right)\\ &\quad +k\frac{b\beta_n I_{m2} S_{s2}}{N_{m2}}\left(2 - \frac{S_{n2}}{S_n} - \frac{I_m S_n N_{m2} I_{n2}}{I_{m2} S_{n2} N_m I_n} + \frac{I_m N_{m2}}{I_{m2} N_m} - \frac{I_n}{I_{n2}}\right) + k\mu_n S_{n2}\left(2 - \frac{S_m}{S_{m2}} - \frac{S_{m2}}{S_m}\right).\end{aligned}$$

Subtitute $k = \frac{\beta_m S_{m2} I_{n2}}{\beta_n S_{n2} I_{m2}}$, we get:

$$\begin{aligned}\frac{d\mathcal{L}}{dt} &= \frac{b\beta_m I_{n2} S_{m2}}{N_{m2}}\left(4 - \frac{S_{m2}}{S_m} - \frac{I_n S_m N_{m2} I_{m2}}{I_{n2} S_{m2} N_m I_m} - \frac{S_{n2}}{S_n} - \frac{I_m S_n N_{m2} I_{n2}}{I_{m2} S_{n2} N_m I_n} + \frac{I_n N_{m2}}{I_{n2} N_m} - \frac{I_m}{I_{m2}} + \frac{I_m N_{m2}}{I_{m2} N_m} - \frac{I_n}{I_{n2}}\right)\\ &\quad +\mu_m S_{m2}\left(2 - \frac{S_m}{S_{m2}} - \frac{S_{m2}}{S_m}\right) + \frac{\mu_n \beta_m S_{m2} I_{n2}}{\beta_n I_{m2}}\left(2 - \frac{S_m}{S_{m2}} - \frac{S_{m2}}{S_m}\right).\end{aligned}$$

Neglecting the disease-induced death rate in special case allows the total human population at equilibrium to be approximated as $N_m = N_{m2} = \frac{\Lambda_m}{\mu_m}$, hence we have:

$$\begin{aligned}\frac{d\mathcal{L}}{dt} &= \frac{b\beta_m I_{n2} S_{m2}}{N_{m2}}\left(4 - \frac{S_{m2}}{S_m} - \frac{I_n S_m I_{m2}}{I_{n2} S_{m2} I_m} - \frac{S_{n2}}{S_n} - \frac{I_m S_n I_{n2}}{I_{m2} S_{n2} I_n}\right)\\ &\quad +\mu_m S_{m2}\left(2 - \frac{S_m}{S_{m2}} - \frac{S_{m2}}{S_m}\right) + \frac{\mu_n \beta_m S_{m2} I_{n2}}{\beta_n I_{m2}}\left(2 - \frac{S_m}{S_{m2}} - \frac{S_{m2}}{S_m}\right).\end{aligned}$$

Since arithmetic mean is greater than or equal to geometric mean, then this is guaranteed:

$$\left(4-\frac{S_{m2}}{S_m}-\frac{I_nS_mI_{m2}}{I_{n2}S_{m2}I_m}-\frac{S_{n2}}{S_n}-\frac{I_mS_nI_{n2}}{I_{m2}S_{n2}I_n}\right)\leq 0 \text{ and } \left(2-\frac{S_m}{S_{m2}}-\frac{S_{m2}}{S_m}\right)\leq 0.$$

Therefore, $\frac{d\mathcal{L}}{dt}\leq 0$ since all the parameters are positive, with $\frac{d\mathcal{L}}{dt}=0$ if only if $S_m=S_{m2}$, $I_m=I_{m2}$, $L_n=L_{n2}$, $S_n=S_{n2}$, and $I_n=I_{n2}$. The endemic equilibrium point E_2 in special case is unique and exists if only if $R_0>1$ and the singleton set $\{E_2\}$ is the biggest compact invariant set in $\{(S_m,I_m,L_n,S_n,I_n)\in\Omega \mid \frac{d\mathcal{L}}{dt}=0\}$. According to LaSalle's invariance principle [14] endemic equilibrium point E_2 in special case is globally asymptotically stable in the interior of region $\Omega\backslash\Omega_0$ if $R_0>1$. □

10. Sensitivity Analysis

This section presents the sensitivity analysis of the basic reproduction number (R_0) to identify the parameters that have the most significant influence, following the methodology outlined in [15]. Sensitivity analysis quantifies how variations in model parameters affect the outcome of interest, in this case, R_0. The sensitivity index of R_0 with respect to a given parameter a is defined as:

$$\Upsilon_a^{R_0}=\frac{\partial R_0}{\partial a}\times\frac{a}{R_0}.$$

Using the parameter values listed in Table 2, the sensitivity indices of R_0 with respect to each parameter are computed and summarized in Table 3.

Table 3. Sensitivity indices of the parameters involved in R_0.

Parameter	Sensitivity Index	Parameter	Sensitivity Index
Λ_m	-0.50	δ_m	-0.32
b	$+1.00$	φ	$+0.01$
β_m	$+0.50$	K	$+0.50$
β_n	$+0.50$	η	$+0.50$
μ_m	$+0.32$	μ	-0.001
μ_n	-1.01		

As shown in Table 3, a positive sensitivity index implies that an increase in the corresponding parameter leads to an increase in R_0, whereas a negative index indicates that increasing the parameter will decrease R_0. Among the parameters, the biting rate (b) exhibits the highest positive sensitivity index of $+1.00$, indicating it has the strongest direct impact on increasing R_0. Conversely, the natural death rate of adult mosquitoes (μ_n) has the most significant negative influence, with a sensitivity index of -1.01. These findings suggest that control strategies targeting the biting rate and increasing the mortality rate of adult mosquitoes could be particularly effective in reducing disease transmission.

Furthermore, although the sensitivity index of the parameter δ_m is relatively small and thus does not significantly affect changes in the basic reproduction number R_0, variations in this parameter may influence the occurrence of bifurcation phenomena. Therefore, a trajectory simulation is carried out using the parameter values listed in Table 2, except for δ_m, which is varied at three values: 0, 0.25, and 0.5, to observe the presence or absence of backward bifurcation in the system, as illustrated in Figure 4 .

Based on Figure 4, when $\delta_m=0$, the value of R_0 is 1.664, which corresponds to the endemic case. In this scenario, only a single endemic equilibrium exists, leading to the global asymptotic stability of the endemic state. When $\delta_m=0.25$, the value of R_0 decreases to 0.997, falling within the range where a backward bifurcation occur. Both the disease-free and endemic equilibria coexist, and each exhibits local asymptotic stability. This indicates the presence of a backward bifurcation, where the disease may persist even though $R_0<1$. Lastly, when $\delta_m=0.5$,

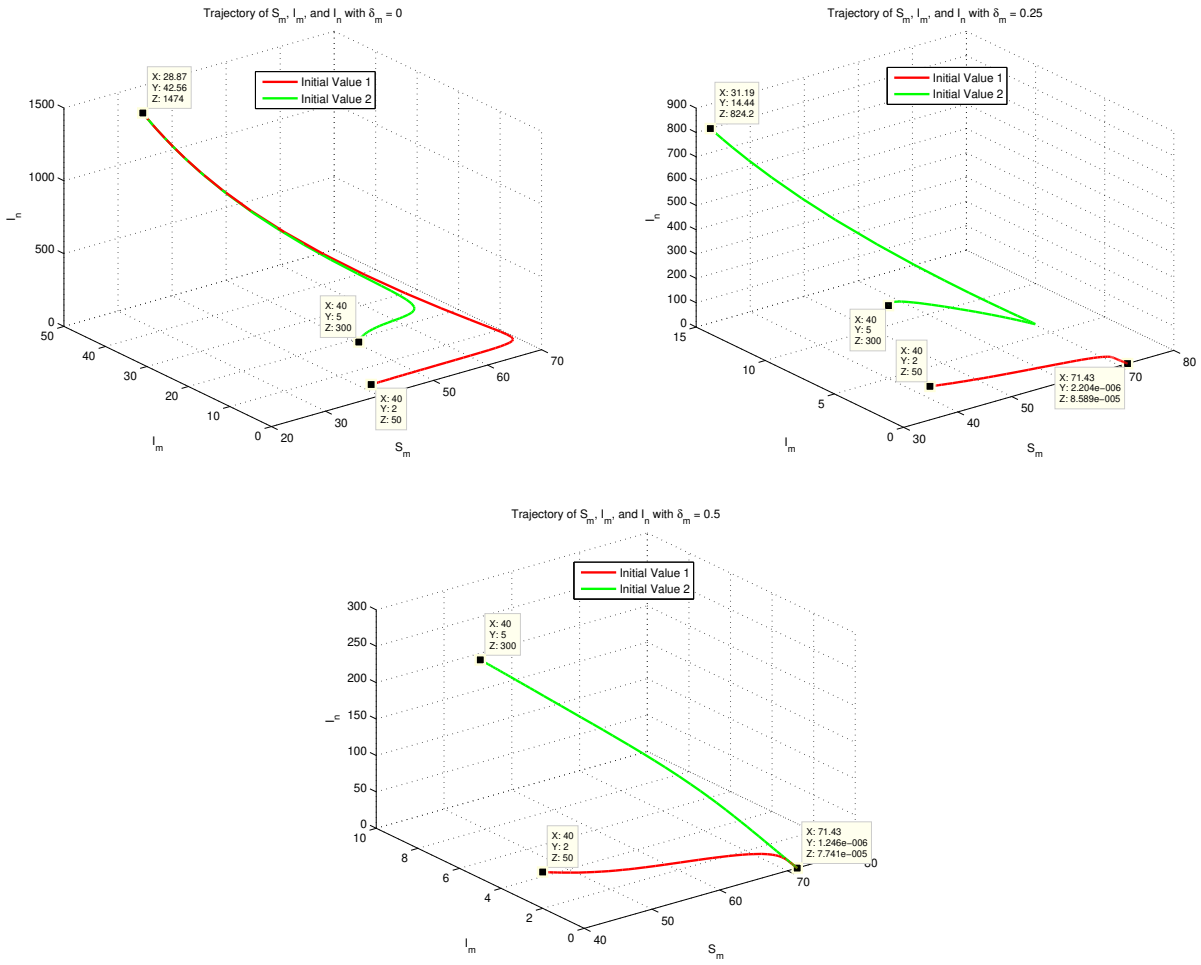

Figure 4. Trajectory simulations of the system for different values of δ_m based on first initial condition $(S_m(0) = 40, I_m(0) = 2, L_n(0) = 500, S_n(0) = 400, I_n(0) = 50)$ and second intial condition $(S_m(0) = 40, I_m(0) = 5, L_n(0) = 500, S_n(0) = 400, I_n(0) = 300)$.

the value of R_0 is further reduced to 0.778, representing a disease-free scenario without bifurcation. In this case, only the disease-free equilibrium exists and exhibits global asymptotic stability, implying that the infection will eventually be eradicated from the population.

11. Conclusion

This work presented a comprehensive analysis of an epidemiological model incorporating the mosquitoes population in aquatic phase and logistic growth rate for mosquitoes. Our findings reveal that the system exhibits backward bifurcation when disease-induced mortality is present, meaning that reducing R_0 below one may not be sufficient to eradicate the disease. This highlights the importance of intervention strategies beyond just lowering R_0. A key result of our study is that when disease-induced mortality is ignored, the model no longer exhibits backward bifurcation, and the disease-free equilibrium becomes globally stable when $R_0 < 1$. This implies that disease mortality significantly influence the system's dynamical behavior. Additionally, we have shown that the

endemic equilibrium is globally asymptotically stable when $R_0 > 1$. Our theoretical results are supported by numerical simulations that illustrate different stability outcomes under varying initial conditions. These findings emphasize the need for targeted control measures, as small changes in initial conditions can lead to different long-term disease dynamics. Future work may extend this model to incorporate additional behavioral and environmental factors influencing DHF transmission.

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