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MODELING DENGUE TRANSMISSION WITH HUMAN AWARENESS AND STAGNANT WATER INDEX: ANALYSIS AND SIMULATION

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Abstract

Dengue fever remains a major vector-borne health threat, particularly in regions where climatic conditions and human activities such as improper waste management and water storage support mosquito breeding. This paper improves the classical nonlinear $SIR-SI$ host-vector framework by introducing an environmentally dependent mosquito recruitment function, $\lambda(\mathcal{A}) = \lambda_0 + \lambda_1 \mathcal{A}$, where $\mathcal{A}$ denotes a dimensionless Stagnant Water Index (SWI). This modification addresses a key limitation of earlier models, which assumed constant mosquito recruitment and therefore could not capture seasonal or ecological variability. By coupling the environmentally responsive recruitment term with human awareness (ϕ) and vector-control efforts (ψ), the proposed model captures dengue transmission dynamics more realistically under diverse environmental scenarios. We examine the existence and stability of both the disease-free equilibrium (DFE) and endemic equilibrium (EE), and compute the basic reproduction number $\mathcal{R}_0$ using the next-generation matrix approach. Numerical simulations establish that reducing stagnant-water accumulation (lower $\mathcal{A}$), together with enhanced community awareness, considerably curbs peak infection and reduces $\mathcal{R}_0$. The results highlight the combined importance of ecological management and human behavioral responses in controlling dengue transmission.

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1 Introduction

Dengue fever is a viral disease transmitted by mosquitoes, primarily the female *Aedes aegypti*, and is a major public-health concern in tropical and subtropical regions worldwide. Environmental factors play a crucial role in the disease's transmission, particularly the availability of stagnant water that enables mosquito breeding, as well as social and behavioral factors within the human population [7, 11]. Mathematical models have long played an important role in understanding dengue transmission, with several classical host-vector frameworks developed to analyze epidemic patterns [4, 5, 8]. However, many existing formulations depend on fixed mosquito recruitment rates or purely biological assumptions, and therefore do not capture environmental variability or community-driven behavioral responses [1, 11, 16].

Recent research has incorporated human awareness as a factor influencing transmission dynamics. For instance, Phaijoo and Gurung [12] demonstrated that increased public awareness can substantially reduce infection levels. In parallel, several models have focused on clinical and patient-level predictions, aiming to assess disease severity and outcomes using statistical and machine-learning approaches [2]. These studies highlight the growing need to integrate behavioral, clinical, and environmental factors into dengue modeling. A number of works have explored advanced computational and numerical techniques for analyzing infectious disease systems [9, 14, 17, 18, 19], underscoring the relevance of improved modelling frameworks for complex biological dynamics.

Building on these contributions, the present study extends the standard $SIR-SI$ model by integrating three key components: human awareness (ϕ), vector-control interventions (ψ), and an environment-dependent

mosquito recruitment rate regulated by the stagnant-water index $\mathcal{A}$. The major contribution and motivation of this study involve incorporating both human behavior and environmental influences into the recruitment function,

$$\lambda(\mathcal{A}) = \lambda_0 + \lambda_1 \mathcal{A},$$

where λ_0 represents the baseline recruitment in low-risk conditions, and λ_1 captures the sensitivity of mosquito population growth to environmental change. Unlike earlier dengue models, including the widely used frameworks of Esteva and Vargas [4, 5] and the awareness-based model of Phaijoo and Gurung [12], the present formulation replaces the traditional constant mosquito recruitment rate with an explicit environmental term. This modification provides a direct and biologically meaningful mechanism for assessing how ecological variability—such as dry versus monsoon conditions—influences dengue transmission. The stagnant-water index $\mathcal{A}$ serves as a practical environmental indicator, enabling the model to assess how ecological interventions that reduce stagnant water can lower recruitment and limit transmission. By coupling $\mathcal{A}$ with ϕ and ψ , the model provides a unified framework for analyzing the combined effects of environmental conditions, human behavior, and control strategies.

Using this extended SIR – SI formulation, we determine the disease-free equilibrium (DFE), calculate the basic reproduction number $\mathcal{R}_0$ via the next-generation method, and examine the local stability of both the DFE and endemic equilibrium (EE). Numerical experiments further show how changes in $\mathcal{A}$, awareness levels, and vector-control efforts jointly influence the resulting epidemic dynamics.

2 Model Formulation

We develop a hostvector model to capture the spread of dengue fever between humans and mosquitoes. The human host population follows an SIR (Susceptible-Infected-Recovered) structure, reflecting the fact that individuals who recover from dengue get temporary immunity. For mosquitoes, an SI (Susceptible-Infected) formulation is employed, since infected mosquitoes do not recover; therefore, a recovered class is biologically unnecessary.

The human population is divided into three epidemiological classes: susceptible ($\mathcal{H}_S$), infected ($\mathcal{H}_I$), and recovered ($\mathcal{H}_R$). Similarly, the mosquito population is represented by susceptible ($\mathcal{M}_S$) and infected ($\mathcal{M}_I$) classes. The interaction between these compartments and the flow of infection in the system are illustrated in the following diagram.

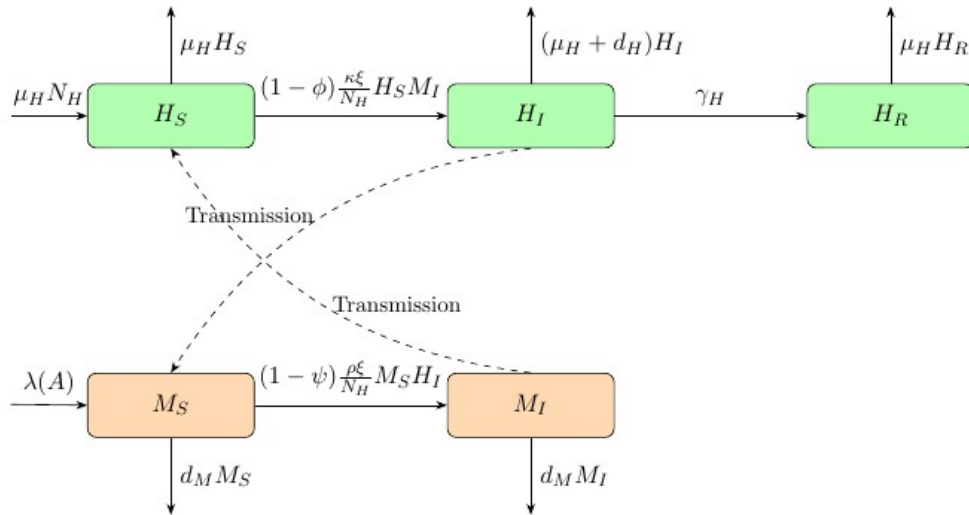


Figure 2.1: Flowchart representing the compartmental structure of the SIR – SI dengue model, showing the transitions between human hosts and mosquito classes and the corresponding epidemiological parameters.

Table 2.1: Description of the state variables used in the model.

Symbol	Description
$\mathcal{H}_S$	The population of susceptible humans
$\mathcal{H}_I$	The population of infected humans
$\mathcal{H}_R$	The population of recovered humans
$\mathcal{M}_S$	The population of susceptible mosquitoes
$\mathcal{M}_I$	The population of infected mosquitoes
N_H	Total human population ($N_H = \mathcal{H}_S + \mathcal{H}_I + \mathcal{H}_R$)

Table 2.2: Description of parameters used in the model.

Symbol	Description
μ_H	Human birth rate / natural death rate of humans
κ	Transmission probability from mosquito to human per bite
ρ	Transmission probability from human to mosquito per bite
ξ	Average mosquito biting rate per day
ϕ	Proportion of aware susceptible humans (reduces exposure by $(1 - \phi)$)
ψ	Proportion of mosquitoes under control (reduces biting by $(1 - \psi)$)
γ_H	Recovery rate of infected humans
d_H	Disease-induced mortality rate in humans
d_M	Natural death rate of mosquitoes
$\lambda(\mathcal{A})$	Mosquito recruitment rate depending on stagnant water index $\mathcal{A} \in [0, 1]$

Using the flow structure (Figure 2.1) and the above compartment descriptions (Tables 2.1-2.2), the *SIR-SI* dengue model equations are given by:

$$\begin{aligned}
\frac{d\mathcal{H}_S}{dt} &= \mu_H N_H - (1 - \phi) \frac{\kappa \xi}{N_H} \mathcal{H}_S \mathcal{M}_I - d_H \mathcal{H}_S = f_1(\mathcal{H}_S, \mathcal{H}_I, \mathcal{H}_R, \mathcal{M}_S, \mathcal{M}_I), \\
\frac{d\mathcal{H}_I}{dt} &= (1 - \phi) \frac{\kappa \xi}{N_H} \mathcal{H}_S \mathcal{M}_I - (\gamma_H + \mu_H + d_H) \mathcal{H}_I = f_2(\mathcal{H}_S, \mathcal{H}_I, \mathcal{H}_R, \mathcal{M}_S, \mathcal{M}_I), \\
\frac{d\mathcal{H}_R}{dt} &= \gamma_H \mathcal{H}_I - \mu_H \mathcal{H}_R = f_3(\mathcal{H}_S, \mathcal{H}_I, \mathcal{H}_R, \mathcal{M}_S, \mathcal{M}_I), \\
\frac{d\mathcal{M}_S}{dt} &= \lambda(\mathcal{A}) - (1 - \psi) \frac{\rho \xi}{N_H} \mathcal{M}_S \mathcal{H}_I - d_M \mathcal{M}_S = f_4(\mathcal{H}_S, \mathcal{H}_I, \mathcal{H}_R, \mathcal{M}_S, \mathcal{M}_I), \\
\frac{d\mathcal{M}_I}{dt} &= (1 - \psi) \frac{\rho \xi}{N_H} \mathcal{M}_S \mathcal{H}_I - d_M \mathcal{M}_I = f_5(\mathcal{H}_S, \mathcal{H}_I, \mathcal{H}_R, \mathcal{M}_S, \mathcal{M}_I).
\end{aligned} \tag{2.1}$$

The recruitment rate of mosquitoes, incorporating the environmental influence, is:

$$\lambda(\mathcal{A}) = \lambda_0 + \lambda_1 \mathcal{A}, \tag{2.2}$$

which increases linearly with the stagnant water index $\mathcal{A} \in [0, 1]$. Here, $\lambda_0 > 0$ denotes the baseline daily mosquito recruitment in the absence of environmental influence, while $\lambda_1 > 0$ accounts for the additional recruitment arising from human-generated stagnant-water breeding sites.

3 Model Analysis

3.1 Positivity and Well-Posedness of the Model

Theorem 3.1 (Positivity of Solutions). *Assume that all parameters in system (2.1) are non-negative and the initial conditions satisfy*

$$(\mathcal{H}_S(0), \mathcal{H}_I(0), \mathcal{H}_R(0), \mathcal{M}_S(0), \mathcal{M}_I(0)) \in \mathbf{R}_+^5.$$

Then the non-negative orthant $\mathbf{R}_+^5$ is positively invariant under the dynamics of system (2.1). That is, the solutions remain in $\mathbf{R}_+^5$ for all $t \geq 0$, ensuring the model is biologically valid.

Proof. Consider the *SIR-SI* dengue system given in (2.1) with initial conditions

$$(\mathcal{H}_S(0), \mathcal{H}_I(0), \mathcal{H}_R(0), \mathcal{M}_S(0), \mathcal{M}_I(0)) \in \mathbf{R}_+^5.$$

Step 1: Boundary Analysis. We examine each compartment at its zero boundary, assuming all other variables are non-negative:

- At $\mathcal{H}_S = 0$, we have:

$$\left. \frac{d\mathcal{H}_S}{dt} \right|_{\mathcal{H}_S=0} = \mu_H N_H \geq 0.$$

- At $\mathcal{H}_I = 0$, we have:

$$\left. \frac{d\mathcal{H}_I}{dt} \right|_{\mathcal{H}_I=0} = (1 - \phi) \frac{\kappa \xi}{N_H} \mathcal{H}_S \mathcal{M}_I \geq 0.$$

- At $\mathcal{H}_R = 0$, we have:

$$\left. \frac{d\mathcal{H}_R}{dt} \right|_{\mathcal{H}_R=0} = \gamma_H \mathcal{H}_I \geq 0.$$

- At $\mathcal{M}_S = 0$, we have:

$$\left. \frac{d\mathcal{M}_S}{dt} \right|_{\mathcal{M}_S=0} = \lambda(\mathcal{A}) \geq 0.$$

- At $\mathcal{M}_I = 0$, we have:

$$\left. \frac{d\mathcal{M}_I}{dt} \right|_{\mathcal{M}_I=0} = (1 - \psi) \frac{\rho \xi}{N_H} \mathcal{M}_S \mathcal{H}_I \geq 0.$$

Step 2: Invariance of the Non-negative Orthant. Since the derivative of each variable is non-negative at the corresponding zero boundary, no state variable can become negative. Hence, the non-negative orthant $\mathbf{R}_+^5$ is invariant, and

$$\mathcal{H}_S(t), \mathcal{H}_I(t), \mathcal{H}_R(t), \mathcal{M}_S(t), \mathcal{M}_I(t) \geq 0, \quad \forall t \geq 0.$$

The standard invariance arguments discussed in [6, 23] lead to this conclusion

Step 3: Biological Relevance. All compartments represent population counts. Positivity ensures that the model respects natural biological constraints, preventing negative populations.

Therefore, the solutions of system (2.1) remain non-negative for every $t \geq 0$. $\square$

3.2 Equilibria of the System

Equilibrium points of a system are determined by setting all time derivatives to zero, representing a state in which the populations in all compartments remain constant. For system (2.1), this condition implies:

$$\frac{d\mathcal{H}_S}{dt} = \frac{d\mathcal{H}_I}{dt} = \frac{d\mathcal{H}_R}{dt} = \frac{d\mathcal{M}_S}{dt} = \frac{d\mathcal{M}_I}{dt} = 0.$$

3.2.1 Disease-Free Equilibrium (DFE)

The disease-free equilibrium (DFE), denoted by E^0 , corresponds to an equilibrium state in which the disease is absent from the population. In this scenario, the number of infected humans ($\mathcal{H}_I^0$) and infected mosquitoes ($\mathcal{M}_I^0$) is zero:

$$\mathcal{H}_I^0 = 0, \quad \mathcal{M}_I^0 = 0.$$

By applying these conditions to the system's differential equations, (2.1) we can determine the steady-state values for the remaining variables.

- Susceptible humans: From the first equation of (2.1),

$$0 = \mu_H N_H - \mu_H \mathcal{H}_S^0 \Rightarrow \mathcal{H}_S^0 = N_H.$$

- Recovered humans: From the third equation of (2.1),

$$0 = \gamma_H \mathcal{H}_I^0 - \mu_H \mathcal{H}_R^0 \Rightarrow \mathcal{H}_R^0 = 0.$$

- Susceptible mosquitoes: From the fourth equation of (2.1),

$$0 = \lambda(\mathcal{A}) - d_M \mathcal{M}_S^0 \Rightarrow \mathcal{M}_S^0 = \frac{\lambda(\mathcal{A})}{d_M}.$$

Hence, the DFE is

$$E^0 = \left(N_H, 0, 0, \frac{\lambda(\mathcal{A})}{d_M}, 0 \right). \quad (3.1)$$

3.3 Basic Reproduction Number ($\mathcal{R}_0$)

The basic reproduction number, $\mathcal{R}_0$, measures the average number of new infections generated by a single infected individual in a population where all individuals are susceptible. To compute $\mathcal{R}_0$, we apply the next-generation matrix method, considering only the infected compartments $(\mathcal{H}_I, \mathcal{M}_I)$.

In this framework, we define $\mathcal{F}$ as the rate of appearance of new infections and $\mathcal{V}$ as the rate of transfer or removal from the infected compartments.

$$\begin{aligned}\mathcal{F}_1 &= (1 - \phi) \frac{\kappa \xi}{N_H} \mathcal{H}_S \mathcal{M}_I, & \mathcal{V}_1 &= (\gamma_H + \mu_H + d_H) \mathcal{H}_I \\ \mathcal{F}_2 &= (1 - \psi) \frac{\rho \xi}{N_H} \mathcal{M}_S \mathcal{H}_I, & \mathcal{V}_2 &= d_M \mathcal{M}_I\end{aligned}$$

The Jacobian matrices of $\mathcal{F}$ and $\mathcal{V}$, evaluated at the DFE E^0 given by (3.1), with respect to $(\mathcal{H}_I, \mathcal{M}_I)$ are:

$$\begin{aligned}F &= \begin{pmatrix} \frac{\partial \mathcal{F}_1}{\partial \mathcal{H}_I} & \frac{\partial \mathcal{F}_1}{\partial \mathcal{M}_I} \\ \frac{\partial \mathcal{F}_2}{\partial \mathcal{H}_I} & \frac{\partial \mathcal{F}_2}{\partial \mathcal{M}_I} \end{pmatrix}_{E^0} = \begin{pmatrix} 0 & \frac{(1 - \phi) \kappa \xi \mathcal{H}_S^0}{N_H} \\ \frac{(1 - \psi) \rho \xi \mathcal{M}_S^0}{N_H} & 0 \end{pmatrix}, \\ V &= \begin{pmatrix} \frac{\partial \mathcal{V}_1}{\partial \mathcal{H}_I} & \frac{\partial \mathcal{V}_1}{\partial \mathcal{M}_I} \\ \frac{\partial \mathcal{V}_2}{\partial \mathcal{H}_I} & \frac{\partial \mathcal{V}_2}{\partial \mathcal{M}_I} \end{pmatrix}_{E^0} = \begin{pmatrix} \delta_H & 0 \\ 0 & d_M \end{pmatrix}, \quad \text{where } \delta_H := \gamma_H + \mu_H + d_H.\end{aligned}$$

The next-generation matrix is $K = FV^{-1}$, giving

$$K = \begin{pmatrix} 0 & \frac{(1 - \phi) \kappa \xi \mathcal{H}_S^0}{N_H d_M} \\ \frac{(1 - \psi) \rho \xi \mathcal{M}_S^0}{N_H \delta_H} & 0 \end{pmatrix}.$$

The basic reproduction number $\mathcal{R}_0$ is the spectral radius of K , $\mathcal{R}_0 = \rho(K)$.

$$\mathcal{R}_0 = \sqrt{\left(\frac{(1 - \phi) \kappa \xi \mathcal{H}_S^0}{N_H d_M} \right) \cdot \left(\frac{(1 - \psi) \rho \xi \mathcal{M}_S^0}{N_H \delta_H} \right)}$$

Substituting the DFE values for $\mathcal{H}_S^0$ and $\mathcal{M}_S^0$:

$$\mathcal{H}_S^0 = N_H, \quad \mathcal{M}_S^0 = \frac{\lambda(\mathcal{A})}{d_M}.$$

Thus, the basic reproduction number is:

$$\boxed{\mathcal{R}_0 = \sqrt{\frac{(1 - \phi)(1 - \psi) \kappa \rho \xi^2 \lambda(\mathcal{A})}{N_H d_M^2 \delta_H}}}. \quad (3.2)$$

Letting

$$C = (1 - \phi) \kappa \xi, \quad B = \frac{(1 - \psi) \rho \xi \lambda(\mathcal{A})}{N_H d_M},$$

we can write

$$\mathcal{R}_0 = \sqrt{\frac{CB}{\delta_H d_M}}. \quad (3.3)$$

3.4 Stability Analysis at Disease Free Equilibrium point

Local stability of the disease-free equilibrium E^0 is ensured when the Jacobian J at E^0 has eigenvalues with strictly negative real components, under classical stability theory [15] and the Routh-Hurwitz criterion.

Theorem 3.2. *The disease-free equilibrium point E^0 of the system given in (2.1) is:*

- (i) **Locally asymptotically stable** if $\mathcal{R}_0 < 1$,
- (ii) **Unstable** if $\mathcal{R}_0 > 1$.

Proof. The Jacobian matrix of system (2.1) is

$$J = \begin{pmatrix} \frac{\partial f_1}{\partial \mathcal{H}_S} & \frac{\partial f_1}{\partial \mathcal{H}_I} & \frac{\partial f_1}{\partial \mathcal{H}_R} & \frac{\partial f_1}{\partial \mathcal{M}_S} & \frac{\partial f_1}{\partial \mathcal{M}_I} \\ \frac{\partial f_2}{\partial \mathcal{H}_S} & \frac{\partial f_2}{\partial \mathcal{H}_I} & \frac{\partial f_2}{\partial \mathcal{H}_R} & \frac{\partial f_2}{\partial \mathcal{M}_S} & \frac{\partial f_2}{\partial \mathcal{M}_I} \\ \frac{\partial f_3}{\partial \mathcal{H}_S} & \frac{\partial f_3}{\partial \mathcal{H}_I} & \frac{\partial f_3}{\partial \mathcal{H}_R} & \frac{\partial f_3}{\partial \mathcal{M}_S} & \frac{\partial f_3}{\partial \mathcal{M}_I} \\ \frac{\partial f_4}{\partial \mathcal{H}_S} & \frac{\partial f_4}{\partial \mathcal{H}_I} & \frac{\partial f_4}{\partial \mathcal{H}_R} & \frac{\partial f_4}{\partial \mathcal{M}_S} & \frac{\partial f_4}{\partial \mathcal{M}_I} \\ \frac{\partial f_5}{\partial \mathcal{H}_S} & \frac{\partial f_5}{\partial \mathcal{H}_I} & \frac{\partial f_5}{\partial \mathcal{H}_R} & \frac{\partial f_5}{\partial \mathcal{M}_S} & \frac{\partial f_5}{\partial \mathcal{M}_I} \end{pmatrix}.$$

The Jacobian matrix at DFE point E^0 is:

$$J(E^0) = \begin{pmatrix} -\mu_H & 0 & 0 & 0 & -C \\ 0 & -\delta_H & 0 & 0 & C \\ 0 & \gamma_H & -\mu_H & 0 & 0 \\ 0 & -B & 0 & -d_M & 0 \\ 0 & B & 0 & 0 & -d_M \end{pmatrix}.$$

The eigenvalues are obtained from the characteristic equation $\det(J(E^0) - \lambda I) = 0$. This yields:

$$\lambda_1 = -\mu_H, \quad \lambda_2 = -\mu_H, \quad \lambda_3 = -d_M,$$

and the remaining two satisfy the quadratic equation derived from the lower right 2×2 block of the matrix:

$$\lambda^2 + (\delta_H + d_M)\lambda + \delta_H d_M - CB = 0.$$

Using $CB = \mathcal{R}_0^2 \delta_H d_M$ from (3.3), the quadratic can be written as

$$\lambda^2 + (\delta_H + d_M)\lambda + \delta_H d_M(1 - \mathcal{R}_0^2) = 0.$$

Let $c_1 = \delta_H + d_M$ and $c_2 = \delta_H d_M(1 - \mathcal{R}_0^2)$. Since $c_1 > 0$:

- If $\mathcal{R}_0 < 1$, then $c_2 > 0$. By the Routh–Hurwitz criterion, both roots have negative real parts. Together with $\lambda_1, \lambda_2, \lambda_3 < 0$, all eigenvalues are negative, and E^0 is *locally asymptotically stable*.
- If $\mathcal{R}_0 > 1$, then $c_2 < 0$. Since the product of the roots is negative, the quadratic has one positive and one negative real root. Thus E^0 is *unstable*.

□

3.5 Endemic Equilibrium (E^*): Existence and Stability

An endemic equilibrium, denoted E^* , represents a state where the disease persists in both human and mosquito populations, with the number of infected individuals remaining positive and constant, i.e., $\mathcal{H}_I^* > 0$ and $\mathcal{M}_I^* > 0$. The existence and stability of E^* are governed by the basic reproduction number $\mathcal{R}_0$.

Theorem 3.3 (Existence of Endemic Equilibrium). *The system (2.1) possesses a unique endemic equilibrium*

$$E^* = (\mathcal{H}_S^*, \mathcal{H}_I^*, \mathcal{H}_R^*, \mathcal{M}_S^*, \mathcal{M}_I^*)$$

with all components positive if and only if $\mathcal{R}_0 > 1$. Here, let

$$\alpha = 1 + \frac{\gamma_H}{\mu_H}, \quad K = \frac{(1 - \phi)\kappa\xi}{\delta_H N_H}, \quad L = \frac{(1 - \psi)\rho\xi}{d_M N_H}, \quad N_M = \frac{\lambda(\mathcal{A})}{d_M}.$$

Note that $\mathcal{R}_0^2 = KLN_H N_M$. The equilibrium components are:

$$\mathcal{H}_I^* = \frac{N_H(\mathcal{R}_0^2 - 1)}{LN_H + \alpha\mathcal{R}_0^2}, \tag{3.4}$$

$$\mathcal{H}_S^* = \frac{N_H(LN_H + \alpha)}{LN_H + \alpha\mathcal{R}_0^2}, \quad (3.5)$$

$$\mathcal{H}_R^* = \frac{\gamma_H N_H (\mathcal{R}_0^2 - 1)}{\mu_H (LN_H + \alpha\mathcal{R}_0^2)}, \quad (3.6)$$

$$\mathcal{M}_I^* = \frac{LN_M N_H (\mathcal{R}_0^2 - 1)}{\mathcal{R}_0^2 (LN_H + \alpha)}, \quad (3.7)$$

$$\mathcal{M}_S^* = \frac{N_M (\alpha\mathcal{R}_0^2 + LN_H)}{\mathcal{R}_0^2 (LN_H + \alpha)}. \quad (3.8)$$

Proof. At equilibrium, setting the derivatives in (2.1) to zero and solving for the infected classes gives:

$$(1 - \phi) \frac{\kappa_S^{\xi}}{N_H} \mathcal{H}_S^* \mathcal{M}_I^* = \delta_H \mathcal{H}_I^*, \quad \text{or } \mathcal{H}_I^* = K \mathcal{H}_S^* \mathcal{M}_I^*$$

$$(1 - \psi) \frac{\rho_S^{\xi}}{N_H} \mathcal{M}_S^* \mathcal{H}_I^* = d_M \mathcal{M}_I^*, \quad \text{or } \mathcal{M}_I^* = L \mathcal{M}_S^* \mathcal{H}_I^*.$$

The total human population N_H remains constant at equilibrium. Solving $\frac{d\mathcal{H}_S}{dt} = \frac{d\mathcal{H}_I}{dt} = \frac{d\mathcal{H}_R}{dt} = 0$ along with $N_H = \mathcal{H}_S^* + \mathcal{H}_I^* + \mathcal{H}_R^*$ implies:

$$\mathcal{H}_S^* = N_H - \alpha\mathcal{H}_I^*, \quad \text{where } \alpha = 1 + \frac{\gamma_H}{\mu_H}.$$

Similarly, the total number of mosquitoes N_M is $N_M^* = \mathcal{M}_S^* + \mathcal{M}_I^* = N_M$, implying:

$$\mathcal{M}_S^* = N_M - \mathcal{M}_I^*.$$

Substituting $\mathcal{M}_S^*$ into the mosquito infection balance and eliminating $\mathcal{M}_I^*$:

$$\mathcal{M}_I^* = L(N_M - \mathcal{M}_I^*)\mathcal{H}_I^* \Rightarrow \mathcal{M}_I^* = \frac{LN_M \mathcal{H}_I^*}{1 + L\mathcal{H}_I^*}.$$

Substituting this into the human infection balance ($\mathcal{H}_I^* = K \mathcal{H}_S^* \mathcal{M}_I^*$) and dividing both sides by $\mathcal{H}_I^* > 0$ yields:

$$1 = K \cdot (N_H - \alpha\mathcal{H}_I^*) \cdot \left(\frac{LN_M}{1 + L\mathcal{H}_I^*} \right).$$

Rearranging to collect terms in $\mathcal{H}_I^*$:

$$1 + L\mathcal{H}_I^* = KLN_M N_H - KLN_M \alpha\mathcal{H}_I^*$$

$$\mathcal{H}_I^* (L + KLN_M \alpha) = KLN_M N_H - 1.$$

Using the relation $\mathcal{R}_0^2 = KLN_H N_M$, we simplify the expression for $\mathcal{H}_I^*$:

$$\mathcal{H}_I^* = \frac{\mathcal{R}_0^2 - 1}{L + \alpha KLN_M} = \frac{N_H(\mathcal{R}_0^2 - 1)}{LN_H + \alpha\mathcal{R}_0^2}.$$

This proves (3.4). The remaining components, (3.5)-(3.8), follow from the conservation and relation equations:

$$\mathcal{H}_S^* = N_H - \alpha\mathcal{H}_I^*, \quad \mathcal{H}_R^* = \frac{\gamma_H}{\mu_H} \mathcal{H}_I^*, \quad \mathcal{M}_I^* = \frac{LN_M^0 \mathcal{H}_I^*}{1 + L\mathcal{H}_I^*}, \quad \mathcal{M}_S^* = N_M - \mathcal{M}_I^*.$$

□

Positivity: For the endemic equilibrium E^* is biologically relevant, all state variables must be strictly positive. From (3.4), the numerator of $\mathcal{H}_I^*$, $N_H(\mathcal{R}_0^2 - 1)$, is positive if and only if $\mathcal{R}_0 > 1$, while the denominator $LN_H + \alpha\mathcal{R}_0^2$ is always positive. Therefore, $\mathcal{H}_I^* > 0$ precisely when $\mathcal{R}_0 > 1$. Since $\mathcal{H}_R^*$ is proportional to $\mathcal{H}_I^*$, and both $\mathcal{M}_I^*$ and $\mathcal{M}_S^*$ remain positive under the same condition, a unique positive endemic equilibrium exists if and only if $\mathcal{R}_0 > 1$.

Theorem 3.4 (Stability of Endemic Equilibrium). *If $\mathcal{R}_0 > 1$, the endemic equilibrium E^* is locally asymptotically stable.*

To simplify interpretation, the system can also be expressed in terms of normalized population proportions. In this normalized form, the basic reproduction number takes the compact expression

$$\mathcal{R}_0 = \sqrt{\frac{(1-\phi)(1-\psi)\kappa\rho\xi^2 m_S}{\delta_H d_M}}, \quad (3.9)$$

where

$$m_S = \frac{N_M}{N_H} = \frac{\lambda(\mathcal{A})}{d_M N_H}, \quad \delta_H = \gamma_H + \mu_H + d_H.$$

This normalized form reduces to the reproduction number of Phaijoo and Gurung [12] when the mosquito recruitment rate $\lambda(\mathcal{A})$ is constant and the disease-induced human death rate d_H is assumed negligible. In contrast, by allowing λ to depend on the stagnant water index $\mathcal{A}$, our model explicitly incorporates environmental effects.

4 Numerical Simulation and Interpretation

4.1 Numerical Methodology

The compartmental model (2.1) is formulated as a system of nonlinear ordinary differential equations. This system, given in (2.1), was solved numerically using the classical fourth-order Runge–Kutta (RK4) method implemented in Python.

4.2 Parameter Justification and Initial Conditions

To ensure the biological relevance of our numerical experiments, we adopt parameter values drawn from the literature wherever available, complemented by biologically reasonable assumed values.

Table 4.1: *Parameter values, definitions, and sources/assumptions.*

Parameter	Value	Unit	Definition	Source/Assumption
κ	0.75	(unitless)	Human infection rate parameter	[13]
ρ	0.75	(unitless)	Mosquito infection rate parameter	[13]
ξ	1/3	day ⁻¹	Human biting/contact rate	[10]
γ_H	0.14286	day ⁻¹	Human recovery rate (7 days)	[10]
μ_H	0.0000457	day ⁻¹	Human natural death rate	[10]
d_M	0.14286	day ⁻¹	Mosquito natural death rate (7 days lifespan)	[10]
d_H	0.00143	day ⁻¹	Disease-induced death rate	Assumed
λ_0	5000	day ⁻¹	Baseline mosquito recruitment	Assumed
λ_1	5000	day ⁻¹	SWI-dependent recruitment coefficient	Assumed
$\mathcal{A}$	0.1, 0.7	(dimensionless)	Stagnant Water Index (dry/monsoon)	Assumed

The disease-induced mortality rate for humans (d_H) is taken as 0.00143 day⁻¹. This value corresponds to an assumed case fatality proportion of approximately 1% relative to the human recovery rate (γ_H), which is consistent with typical clinical outcomes for dengue patients receiving adequate medical care. The baseline mosquito recruitment rate (λ_0) and the environmentally driven recruitment coefficient (λ_1) are both assigned the value 5000 day⁻¹. These choices ensure that the mosquito population attains a stable, high endemic level while also exhibiting a substantial increase in recruitment as environmental conditions become more favorable (i.e., as the stagnant water index $\mathcal{A}$ increases). This setup effectively captures strong ecological sensitivity in mosquito proliferation.

For environmental comparison, the Stagnant Water Index ($\mathcal{A}$) is evaluated at two representative levels: 0.1 and 0.7. The value $\mathcal{A} = 0.1$ corresponds to a dry, low-risk setting with minimal stagnant water, whereas $\mathcal{A} = 0.7$ represents a monsoon-driven, high-risk environment characterized by abundant breeding sites and favorable conditions for vector growth.

Initial Conditions:

1. $H_S(0) = 9900$, $H_I(0) = 100$, $H_R(0) = 0$,
2. $M_S(0) = 34750$, $M_I(0) = 350$.

These conditions correspond to a human population of $N_H = 10,000$ with 1% initial infection, and a mosquito population of 35,000 with 1% infected vectors.

4.3 Comparison with the Phaijoo and Gurung (2015) Model

4.3.1 Full Model of Phaijoo and Gurung (2015):

Phaijoo and Gurung ([12]) proposed an *SIR-SI* dengue model incorporating human awareness (ϕ) and vector control (ψ). Denoting total human population by

$$N_H = H_S + H_I + H_R,$$

their system is given by:

Human Population Equations

$$\begin{aligned} \frac{dH_S}{dt} &= \mu_H N_H - (1 - \phi) \frac{\xi \kappa}{N_H} H_S M_I - \mu_H H_S, \\ \frac{dH_I}{dt} &= (1 - \phi) \frac{\xi \kappa}{N_H} H_S M_I - (\mu_H + \gamma_H) H_I, \\ \frac{dH_R}{dt} &= \gamma_H H_I - \mu_H H_R. \end{aligned} \quad (4.1)$$

Vector Population Equations

$$\begin{aligned} \frac{dM_S}{dt} &= \lambda_0 - (1 - \psi) \frac{\rho \xi}{N_H} M_S H_I - d_M M_S, \\ \frac{dM_I}{dt} &= (1 - \psi) \frac{\rho \xi}{N_H} M_S H_I - d_M M_I. \end{aligned} \quad (4.2)$$

Basic Reproduction Number:

$$\mathcal{R}_0^{PG} = \sqrt{\frac{(1 - \phi)(1 - \psi) \kappa \rho \xi^2 \lambda_0}{(\mu_H + \gamma_H) d_M^2 N_H}}. \quad (4.3)$$

4.3.2 Extended Model with Environment-Dependent Recruitment

In our extended framework, mosquito recruitment incorporates stagnant-water effects:

$$\lambda(\mathcal{A}) = \lambda_0 + \lambda_1 \mathcal{A}.$$

This relationship reflects that greater availability of stagnant water (represented by $\mathcal{A}$) increases the mosquitoes recruitment rate. From the normalized reproduction number (3.9), the extended reproduction number is:

$$R_0^{\text{ext}}(\mathcal{A}) = \mathcal{R}_0^{PG} \sqrt{\left(1 + \frac{\lambda_1 \mathcal{A}}{\lambda_0}\right) \cdot \left(\frac{\mu_H + \gamma_H}{\delta_H}\right)}. \quad (4.4)$$

If we assume no disease-induced death (i.e., $d_H = 0$, implying $\delta_H = \mu_H + \gamma_H$) and equate the recruitment parameter ($\lambda_0 = \lambda_1$), the expression simplifies to a direct relationship with the environmental factor:

$$R_0^{\text{ext}}(\mathcal{A}) = \mathcal{R}_0^{PG} \sqrt{1 + \mathcal{A}}. \quad (4.5)$$

This shows that increasing stagnant water ($\mathcal{A}$) directly increases the basic reproduction number by the factor:

$$\sqrt{1 + \mathcal{A}}.$$

4.4 Interpretation and Validation of $\mathcal{R}_0$

Table 4.2: Comparison of $\mathcal{R}_0$ under varying stagnant-water conditions.

Scenario	Awareness-only Model	Extended Model ($\mathcal{A} = 0.1$)	Extended Model ($\mathcal{A} = 0.7$)	Outcome
No control ($\phi = 0, \psi = 0$)	3.2733	3.4160	4.2467	Epidemic
High control ($\phi = 0.8, \psi = 0.8$)	0.6547	0.6833	0.8495	Disease Eradication

Environmental influence. For both control regimes, $\mathcal{R}_0$ increases as $\mathcal{A}$ rises from 0.1 (dry) to 0.7 (monsoon). For example, under no control, $\mathcal{R}_0$ grows from 3.4160 to 4.2467, showing that favorable breeding conditions sharply enhance transmission potential.

Comparison with the baseline model. The awareness-only model assumes fixed mosquito recruitment, yielding a constant $\mathcal{R}_0$. The extended model provides a more realistic seasonal range:

- $\mathcal{A} = 0.1$: $\mathcal{R}_0 = 3.4160$ (dry season risk lower than baseline),
- $\mathcal{A} = 0.7$: $\mathcal{R}_0 = 4.2467$ (approaches baseline during monsoon).

Effectiveness of control measures. High awareness ($\phi = 0.8$) and strong vector control ($\psi = 0.8$) push all values of $\mathcal{R}_0$ below one, even for high $\mathcal{A}$. This demonstrates that public health interventions can effectively counteract environmental risk.

Overall, these results confirm that incorporating the environmental index $\mathcal{A}$ is essential to capture seasonal variation in dengue transmission, and that the combination of awareness and vector control remains effective across all environmental conditions.

4.5 Comparative Evaluation of Control Methods in High Transmission Risk Environments

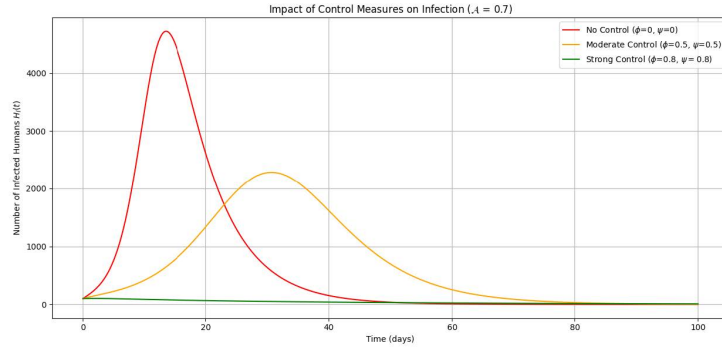


Figure 4.1: Time series of $\mathcal{H}_I$ (Infected Humans) under high stagnant-water index ($\mathcal{A} = 0.7$) for different levels of awareness (ϕ) and vector control (ψ). The curves correspond to: $(\phi = 0, \psi = 0)$, $(\phi = 0.5, \psi = 0.5)$, and $(\phi = 0.8, \psi = 0.8)$.

Interpretation: Figure 4.1 demonstrates that in the absence of awareness or vector control ($\phi = \psi = 0$), the number of infected humans rises sharply and reaches its maximum peak. Even under high-risk environmental conditions ($\mathcal{A} = 0.7$), the combined application of awareness and vector-control interventions markedly suppresses transmission. When both measures are strong ($\phi = \psi = 0.8$), infection levels remain low and decline rapidly, highlighting the effectiveness of integrated public-health strategies.

4.6 Influence of Stagnant Water Index on Infection Peaks

To investigate the role of environmental conditions, the model is simulated for two values of the stagnant-water index $\mathcal{A}$.

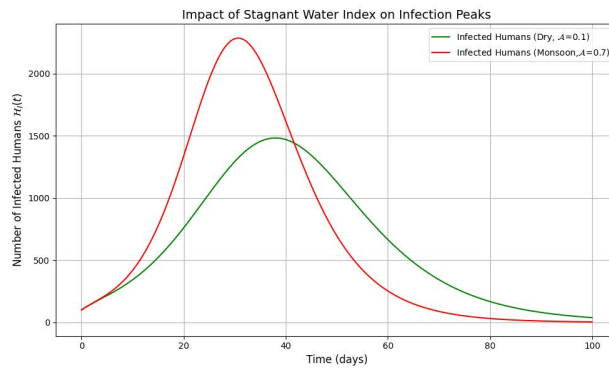


Figure 4.2: Time series of $\mathcal{H}_I$ (Infected Humans) for dry-season conditions ($\mathcal{A} = 0.1$) and monsoon-like conditions ($\mathcal{A} = 0.7$), with moderate awareness ($\phi = 0.5$) and vector control ($\psi = 0.5$).

Interpretation: Figure 4.2 compares infection dynamics during dry-season ($\mathcal{A} = 0.1$) and monsoon-season ($\mathcal{A} = 0.7$) scenarios. A higher stagnant-water index substantially enhances mosquito recruitment, resulting in larger and more persistent infection peaks. The comparison underscores that environmental factors—particularly water accumulation—play a critical role in shaping outbreak intensity, even when awareness and vector control are moderately applied.

4.7 Contour and Threshold Plots with Respect to ϕ and $\mathcal{A}$

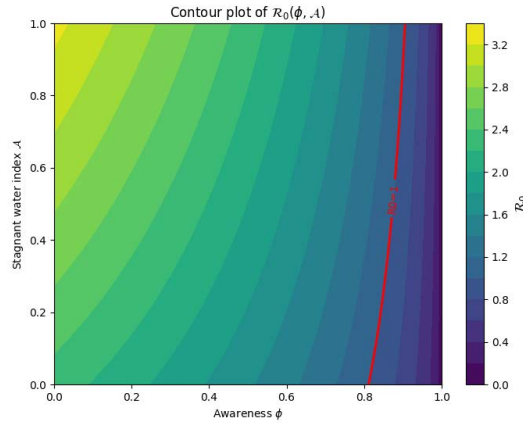


Figure 4.3: Contour plot of $\mathcal{R}_0(\phi, \mathcal{A})$, illustrating level curves of constant basic reproduction number. Values increase toward high $\mathcal{A}$ and low ϕ .

Interpretation: The contour map in Figure 4.3 illustrates how awareness (ϕ) and stagnant water index ($\mathcal{A}$) jointly affect $\mathcal{R}_0$. The highest transmission risk occurs in regions of high $\mathcal{A}$ and low awareness. The $\mathcal{R}_0 = 1$ boundary (pink line) shows the combined level of ϕ and $\mathcal{A}$ required to eliminate the disease. This confirms that environmental sanitation and behavioral interventions act synergistically in reducing dengue transmission.

4.8 Peak Infection vs. Awareness and Stagnant Water

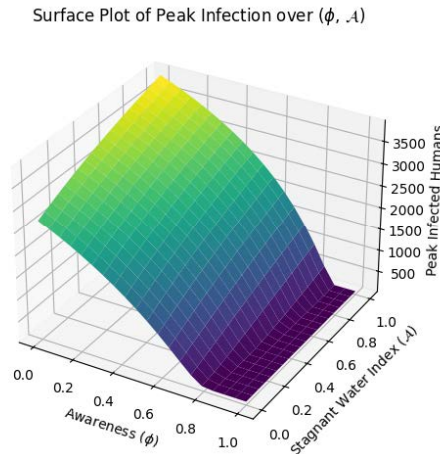


Figure 4.4: Surface plot of peak infection (maximum $\mathcal{H}_I$) as a function of awareness (ϕ) and stagnant-water index ($\mathcal{A}$). Higher awareness and lower $\mathcal{A}$ sharply decrease peak infections.

Interpretation: The surface plot in Figure 4.4 shows that peak infection levels decline sharply as awareness (ϕ) increases and stagnant water ($\mathcal{A}$) decreases. This reinforces the importance of combining public awareness campaigns with environmental sanitation.

4.9 Sensitivity Analysis

The influence of key parameters on $\mathcal{R}_0$ is examined using the normalized forward sensitivity index:

$$\Upsilon_p^{\mathcal{R}_0} = \frac{\partial \mathcal{R}_0}{\partial p} \cdot \frac{p}{\mathcal{R}_0}, \quad (4.6)$$

which measures the proportional change in $\mathcal{R}_0$ caused by a proportional change in the parameter p .

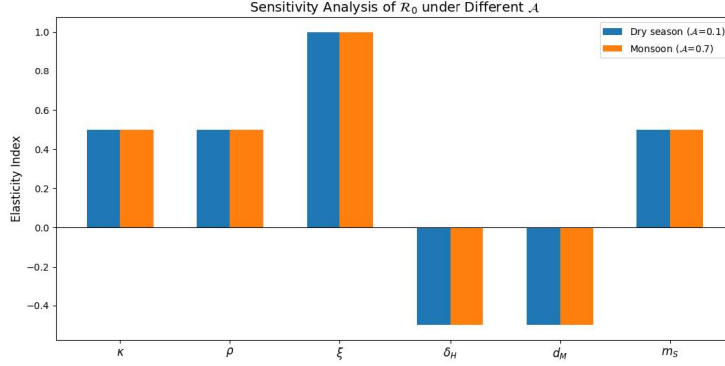


Figure 4.5: Sensitivity of $\mathcal{R}_0$ to key parameters ($\xi, \kappa, \rho, \delta_H, d_M, m_S$) under dry-season ($\mathcal{A} = 0.1$) and monsoon-season ($\mathcal{A} = 0.7$) conditions.

Interpretation: The sensitivity analysis (Figure 4.5) shows that the mosquito biting rate ξ has the strongest positive effect on $\mathcal{R}_0$, followed by m_S , κ , and ρ . Conversely, human removal δ_H and mosquito death d_M exert strong negative effects. These results highlight that interventions targeting mosquito survival and biting behavior are the most effective for controlling transmission.

Table 4.3: Sensitivity indices for $\mathcal{R}_0$ (see Figure 4.5).

Parameter	Sign	Interpretation
ξ	Positive (Strong)	An increase in the mosquito biting rate ξ substantially raises $\mathcal{R}_0$ by exposing more humans per unit time.
κ	Positive (Moderate)	The mosquito-to-human transmission probability moderately increases $\mathcal{R}_0$.
ρ	Positive (Moderate)	Increased human-to-mosquito transmission probability ρ per bite sustains the infection cycle and elevates $\mathcal{R}_0$.
δ_H	Negative (Strong)	Higher human removal rate δ_H reduces $\mathcal{R}_0$ by shortening the infectious period.
d_M	Negative (Strong)	Increased mosquito mortality d_M strongly limits vector lifespan and reduces $\mathcal{R}_0$.
m_S	Positive (Moderate)	Higher equilibrium susceptible mosquito-to-human ratio m_S increases $\mathcal{R}_0$, reflecting the role of environmental recruitment.

5 Conclusion

This study presents an extended mathematical model (2.1) to evaluate the combined effects of stagnant water accumulation ($\mathcal{A}$), public awareness (ϕ), and vector-control (ψ) on vector-borne disease transmission. By incorporating $\mathcal{A}$ linearly into mosquito recruitment $\lambda(\mathcal{A})$, the model extends the awareness-only framework of Phaijoo and Gurung [12]. The unique contribution of this model lies in its ability to quantify the synergistic

interaction between socio-behavioral responses and ecological conditions. Specifically, by replacing the standard constant mosquito recruitment with dynamic recruitment function based on the Stagnant Water Index (SWI), we demonstrate that environmental management acts as a crucial force-multiplier for human awareness, directly determining the baseline effort required for effective disease suppression.

Key findings include:

1. Higher stagnant water levels ($\mathcal{A} = 0.7$) increase mosquito breeding and intensify outbreaks (Figure 4.2).
2. Public awareness (ϕ) mitigates infections by promoting preventive behavior, lowering peak incidence and shortening outbreak duration (Figure 4.1).
3. The basic reproduction number ($\mathcal{R}_0$) rises with stagnant water $\mathcal{A}$ but decreases with increasing awareness ϕ (Figure 4.3).
4. Sensitivity analysis (Figure 4.5) identifies the mosquito biting rate ξ and mosquito death rate d_M as the most influential parameters for $\mathcal{R}_0$, confirming that vector-targeted interventions are paramount.

Effective disease control requires combined strategies addressing both environmental management (reducing $\mathcal{A}$) and community awareness (increasing ϕ), especially during high-risk periods. Future work in our research direction could incorporate spatial heterogeneity, demographic structure, or stochastic elements to further improve predictive accuracy and intervention planning. Furthermore, solving these complex extensions, which often involve time-delay or fractional-order dynamics, will require highly advanced numerical techniques. For instance, methods employing wavelet operational matrices are promising computational directions for future research, including those used to solve complex Fredholm integro-differential equations [20], singular value problems [21], and advanced biological models like the *HIV*-infected cells model [22].

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