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Mathematical Model for Dengue Fever with Vertical Transmission and Control Measures

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Abstract

Dengue Fever is one of the infectious vector-borne diseases transmitted to humans through the biting of Aedes mosquito species. Recently, Dengue Fever is known as the most infectious disease with 5.2 million infection case. In this article, we formulate a deterministic mathematical model to simulate and study dengue fever transmission between humans and vectors. In the model, we considered vertical transmission of Dengue virus in the vectors population and control measures to prevent Dengue virus transmission. We analyze the model and determine the basic reproduction number using the next-generation matrix approach. Also, we found the model equilibrium points and stability analysis of the model equilibrium points determined, and we obtained a forward bifurcation. We deduced that when $\mathcal{R}_0 < 1$ Dengue Fever die out and at $\mathcal{R}_0 > 1$ Dengue Fever spread. Sensitivity analysis of the basic reproduction number achieved local and global results, and we determined the important parameters for dengue fever transmission. The model's numerical simulation was found by using the Runge-Kutta fourth-order method. We investigated the effects of the control measures on the model compartments, and the results are shown in graphical forms. Advice for eradicating and reducing Dengue Fever transmission is provided.

Keywords: Dengue Fever, Mathematical Model, Stability Analysis, Sensitivity Analysis.
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1. Introduction

Dengue Fever is vector–borne viral disease affected people in the tropical and subtropical regions in the world. Dengue virus transmitted into humans through biting of female of *Aedes* mosquitoes species and primarily by *Aedes aegypti* and secondary by other *Aedes* mosquitoes. Dengue Fever caused by four virus serotypes: DENV–1, DENV–2, DENV–3, and DENV–4 and recovering from infection by one serotype provide lifelong immunity from that serotype but temporary immunity against the others three serotypes. Dengue Fever infection cause severe symptoms for infected individual and sometimes fatal diseases known as Dengue Hemorrhagic Fever(DHF) and Dengue Shock Syndrome(DSS) [1, 2, 3].

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World Health Organization(WHO) reported 5.2 million dengue infection case in 2019. Moreover, Dengue Fever is currently endemic in more than 100 couturiers in Africa, the Americas, the Eastern Mediterranean, South–East Asia, and the Western Pacific, and recently, it is spread to the European region. The most affected regions by Dengue Fever disease are The Americas, Asia, and the Western Pacific, where 70% of Dengue cases were reported [3].

Ordinary differential equations have been used for simulating different science phenomena, including simulating and studying infectious disease transmission dynamics. Many authors have been developed mathematical models for Dengue Fever transmission between humans and vectors. Boutayeb et al. and many other authors have used SIR models for simulating Dengue Fever transmission in [4, 5, 6, 7]. In Syafruddin and Noorin [8], and Phaijoo et al. [9] SEIR model was utilized for studying Dengue Fever transmission, but in [9], control measures implemented to the model and the results show that the control measures have great effect in eradicating and control Dengue Fever spread. In the models developed by Vargas–De–león et al. [10], and Dwivedi and Keval [11] different types of susceptible humans considered in their models according to age or risk of gain Dengue Fever infection, respectively. The fact of vertical transmission of Dengue virus in the vector population considered in some models see [12, 13, 14]. For instance, Optimal control methods were used by many authors to study Dengue Fever transmission in [15, 16, 17]. In Pongsumpun et al. [18], the optimal control method used and vaccination considered in the model. Pongsumpun et al. results show that focusing on Dengue Fever control intervention instead of treatment measures. In Rodrigues et al. [20], and Reyes and Escaner [21] works, the authors search for parameters that influence the Dengue Fever transmission through sensitivity analysis of the basic reproduction number.

This study used a novel deterministic SEIR model for modeling Dengue Fever transmission between humans and vectors. We considered a vertical transmission for the Dengue virus in vector population, and we added two control measures Insecticide–Treated bed Nets(ITN) and Indoor Residual Spraying(IRS). We analyzed the model and determined the important parameters for Dengue Fever transmission. The effects of the control measures in the model were investigated and expressed good effect for reducing and eradicating Dengue Fever transmission.

The next section is organized as follows. In Section 2 we formulate a mathematical model for Dengue Fever transmission and analyze the model in Section 3. In Section 4, we provide numerical results about the sensitivity analysis of the basic reproduction number and numerical simulation of the model. Lastly, in Section 5 we conclude the article.

2. Model Formulation

This section proposes a mathematical model for Dengue fever transmission between humans and vectors. We use the SEIR model for the human population and employ vertical transmission for the vector population. The human population divided into four compartment at time t *Susceptible* $S(t)$, *Exposed* $E(t)$, *Infected* $I(t)$, and *Recovered* $R(t)$. For vector population, we used a model similar to the SEI model because we divided it into three compartments at time t *Susceptible* $A(t)$, *Exposed* $W(t)$, and *Infected* $V(t)$. Furthermore, we add two control measures, Insecticide–Treated bed Nets(ITN) ψ and Indoor

Residual Spraying(IRS) γ to the model. Figure 1 shows the flow diagram of Dengue Fever transmission dynamics between humans and vectors. The total human population is given

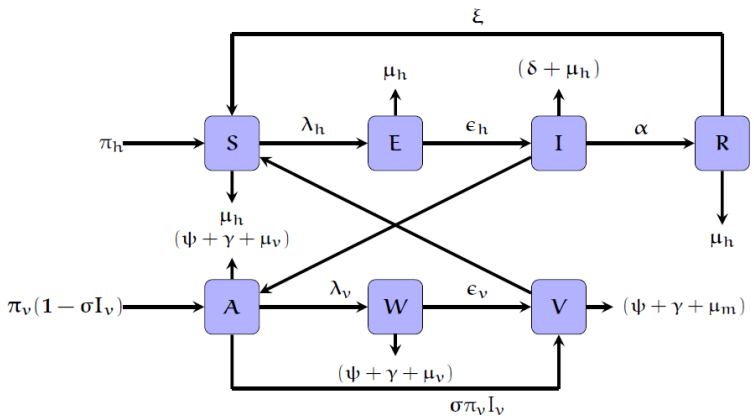

Figure 1: Flow diagram of Dengue Fever transmission between humans and vectors

by

$$N_h(t) = S(t) + E(t) + I(t) + R(t). \tag{2.1}$$

The total of vector population is given by

$$N_v(t) = A(t) + W(t) + V(t). \tag{2.2}$$

We define the force of infection functions for Dengue virus transmission between humans and vectors λ_h and λ_v as follows

$$\lambda_h(t) = \frac{\theta(1-\psi)\beta_h V(t)}{N_h}, \tag{2.3}$$

$$\lambda_v(t) = \frac{\theta(1-\psi)\beta_v I(t)}{N_h}. \tag{2.4}$$

The following assumptions are considered in our model: The human and vector populations are constant, the Dengue virus is transmitted vertically in the vector population, and all new recruitment for human populations is susceptible to Dengue Fever.

From Figure 1 and the above assumptions the mathematical model for Dengue Fever transmission represented by the following system of nonlinear ordinary differential equa-

tions

$$\begin{aligned}
\frac{dS}{dt} &= \pi_h - \lambda_h S - \mu_h S + \xi R,\\
\frac{dE}{dt} &= \lambda_h S - (\epsilon_h + \mu_h)E,\\
\frac{dI}{dt} &= \epsilon_h E - (\alpha + \delta + \mu_h)I,\\
\frac{dR}{dt} &= \alpha I - (\xi + \mu_h)R,\\
\frac{dA}{dt} &= \pi_v(1-\sigma V) - \lambda_v A - (\psi + \gamma + \mu_v)A,\\
\frac{dW}{dt} &= \lambda_v A - (\epsilon_v + \psi + \gamma + \mu_v)W,\\
\frac{dV}{dt} &= \epsilon_v W - (\psi + \gamma + \mu_v - \sigma\pi_v)V.
\end{aligned} \tag{2.5}$$

Subject to initial conditions

$$\begin{aligned}
&S(0) \geqslant 0, \quad E(0) \geqslant 0, \quad I(0) \geqslant 0, \quad R(0) \geqslant 0,\\
&A(0) \geqslant 0, \quad W(0) \geqslant 0, \quad V(0) \geqslant 0.
\end{aligned} \tag{2.6}$$

The variables and parameters in the model (2.5) are positive or non–negative.

Table 1: Table show the parameters of the model (2.5) and their descriptions.

parameter	Description	Value	Source
π_h	**Recruitment rate of susceptible humans population**	**2500**	[22]
π_v	**Recruitment rate of susceptible vectors population**	**100**	[19]
μ_h	**Humans natural death rate**	**0.00004212**	[25]
δ	**Humans death rate due to Dengue Fever**	**0.0003454**	[25]
μ_v	**Vectors death rate**	**0.1**	[24]
θ	**Rate of vectors biting humans**	**18.0**	[22]
β_h	**Rate of Dengue virus transmission from infected vectors into susceptible humans**	**0.375**	[8]
β_v	**Rate of Dengue virus transmission from infected humans into susceptible vectors**	**0.75**	[8]
ϵ_h	**Rate of humans progression from *Exposed* compartment into *Infected* compartment**	**0.5550**	[15]
ϵ_v	**Rate of vectors progression from *Exposed* compartment into *Infected* compartment**	**0.7186**	[15]
α	**Rate of humans recovered from Dengue Fever**	**0.0840**	[15]
ξ	**Rate of humans losing immunity**	**0.57500**	[5]
σ	**Rate of vector gain Dengue virus due to vertical transmission**	**0.002**	[19]
ψ	**Rate of using ITN**	**0.1030**	[23]
γ	**Rate of using IRS**	**0.0270**	[23]

3. Model Analysis

In this section, we will find invariant region of the Dengue Fever model (2.5), positivity of the model (2.5) solutions, the model (2.5) equilibrium points, the basic reproduction number, and stability analysis of the model (2.5) equilibrium points.

3.1. Invariant Region and Postivity of Solution

Theorem 3.1. *There is exist of an invariant region* Φ *such that all solutions of the model* (2.5) *contained and bounded.*

Proof. The total of human population given by equation (2.1) then

$$\begin{aligned}\frac{N_h(t)}{dt} &= \frac{d}{dt}(S(t)+E(t)+I(t)+R(t)) = \pi_h - \delta I - \mu_h N_h(t),\\ \frac{N_h(t)}{dt} &\leqslant \pi_h - \mu_h N_h(t).\end{aligned} \tag{3.1}$$

The solution of the differential equation (3.1) given by $N_h(t) = \frac{\pi_h}{\mu_h} + \left(N_h(0) - \frac{\pi_h}{\mu_h}\right) e^{-\mu_h t}$. Thus the invariant region for humans population given as following

$$\Phi_h = \{(S(t),E(t),I(t),R(t)) \in \mathbb{R}^4_+ : S(t)+E(t)+I(t)+R(t) \leqslant \frac{\pi_h}{\mu_h}\}. \tag{3.2}$$

Similarly, following the same manner for vectors population then we obtain the invariant region

$$\Phi_v = \{(A(t),W(t),V(t)) \in \mathbb{R}^3_+ : A(t)+W(t)+V(t) \leqslant \frac{\pi_v}{(\psi+\gamma+\mu_v)}\}. \tag{3.3}$$

The model (2.5) have an invariant region obtained form the equations (3.2) and (3.3) as $\Phi = \Phi_h \times \Phi_v$. □

Theorem 3.2. *The solutions of the model* (2.5) *with the initial data* (2.6) *are remain non–negative for all time* $t > 0$.

Proof. As shown in Theorem B1 in [26] lets suppose that there is exist t^* such that $S(t^*) = 0$ and $S'(t^*) \leqslant 0$. And $S(t) > 0, E(t) > 0, I(t) > 0, R(t) > 0, A(t) > 0, W(t) > 0, V(t) > 0$ for $0 < t < t^*$. Form the *Susceptible* humans equation in model(2.5) yield

$$\begin{aligned}\frac{dS}{dt^*} &= \pi_h - \lambda_h(t^*)S(t^*) - \mu_h S(t^*) + \xi R(t^*),\\ \frac{dS}{dt^*} &= \pi_h + \xi R(t^*) > 0.\end{aligned}$$

And that is a contradiction then $S(t) > 0$.

Suppose that there exits $t_1 > 0$ and $E(t_1) = 0$ for $t_1 > 0$ and $E(t) > 0$ for $t \in [0, t_1)$. By integrating the *Exposed* human equation in the model (2.5) hence

$$E(t_1) = e^{-(\epsilon_h+\mu_h)t_1} \times \int_0^{t_1} \lambda_h(\tau)S(\tau)e^{(\epsilon_h+\mu_h)\tau}d\tau + E(0)e^{-(\epsilon_h+\mu_h)t_1} > 0.$$

Thus we contradict $E(t_1) = 0$. By following the same manner we can prove that the rest of the model (2.5) compartments equations solutions are positive for all time $t > 0$. □

3.2. Disease Free Equilibrium Point $\mathcal{P}_{dfe}$

The disease free equilibrium point for the model(2.5) it is the steady state whenever there is no infection cases in the host and vector populations hence

$$\mathcal{P}_{dfe} = \left(\frac{\pi_h}{\mu_h}, 0, 0, 0, \frac{\pi_v}{(\psi+\gamma+\mu_v)}, 0, 0\right). \tag{3.4}$$

3.3. The Basic Reproduction Number $\mathcal{R}_0$

In P. van den Driessche et al. [27] the basic reproduction number $\mathcal{R}_0$ defined as the expected number of secondary infected cases that produced in completely susceptible population by one infected case. By using the next generation matrix approach yield

$$\mathcal{F} = \begin{bmatrix} 0 & 0 & 0 & \frac{\theta\beta_h\pi_h}{N_h\mu_h} \\ 0 & 0 & 0 & 0 \\ 0 & \frac{\theta(1-\psi)\beta_v\pi_v}{N_h(\psi+\gamma+\mu_m)} & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

$$\mathcal{V} = \begin{bmatrix} (\epsilon_h+\mu_h) & 0 & 0 & 0 \\ -\epsilon_h & (\alpha+\delta+\mu_h) & 0 & 0 \\ 0 & 0 & (\epsilon_v+\psi+\gamma+\mu_v) & 0 \\ 0 & 0 & -\epsilon_v & (\psi+\gamma+\mu_v-\sigma\pi_v) \end{bmatrix}$$

The basic reproduction number $\mathcal{R}_0$ determined by spectral radius of the matrix $\mathcal{F}\mathcal{V}^{-1}$ hereby $\mathcal{R}_0 = \rho(\mathcal{F}\mathcal{V}^{-1})$. Also, for simplicity lets consider the following
$l_1 = (\epsilon_h+\mu_h)$, $l_2 = (\alpha+\delta+\mu_h)$, $l_3 = (\psi+\gamma+\mu_v)$, $l_4 = (\epsilon_v+\psi+\gamma+\mu_v)$, and $l_5 = (\psi+\gamma+\mu_v-\sigma\pi_v)$.

$$\mathcal{R}_0 = \sqrt{\frac{\theta^2(1-\psi)^2\beta_h\beta_v\epsilon_h\epsilon_v\pi_v\mu_h}{\pi_h l_1 l_2 l_3 l_4 l_5}} \tag{3.5}$$

The basic reproduction number $\mathcal{R}_0$ can be written as $\mathcal{R}_0 = \sqrt{\mathcal{R}_{0h}\mathcal{R}_{0v}}$. Where $\mathcal{R}_{0h} = \frac{\theta(1-\psi)\epsilon_h\beta_h\mu_h}{\pi_h l_1 l_2}$ is the number of humans infected by Dengue Fever due to one infected vector. Beside, $\mathcal{R}_{0v} = \frac{\theta(1-\psi)\epsilon_v\beta_v\pi_v}{l_3 l_4 l_5}$ is the number of infected vectors by Dengue virus because of one infected human.

3.4. Locally Asymptotically Stability of $\mathcal{P}_{dfe}$

Theorem 3.3. *The Dengue Fever model (2.5) disease free equilibrium point $\mathcal{P}_{dfe}$ is locally asymptotically stable if $\mathcal{R}_0 < 1$ and unstable if $\mathcal{R}_0 > 1$.*

3.5. Globally Asymptotically Stability of $\mathcal{P}_{dfe}$

Theorem 3.4. *The Dengue Fever model(2.5) disease free equilibrium point $\mathcal{P}_{dfe}$is globally asymptotically stable if $\mathcal{R}_0 \leqslant 1$ and unstable if $\mathcal{R}_0 > 1$.*

Proof. Define Lyapunov function as follows

$$\mathcal{L} = a_1 E(t) + a_2 I(t) + a_3 W(t) + a_4 V(t)$$

Whereby $a_1 = \frac{\epsilon_h}{N_h l_1 l_2}, a_2 = \frac{1}{N_h l_2}, a_3 = \frac{l_3}{\theta(1-\psi)\beta_v \pi_v}$, and $a_4 = \frac{l_3 l_4}{\theta(1-\psi)\epsilon_v \beta_v \pi_v}$.

$$\begin{aligned}
\dot{\mathcal{L}} &= a_1 \dot{E}(t) + a_2 \dot{I}(t) + a_3 \dot{W}(t) + a_4 \dot{V}(t), \\
&= \frac{\theta(1-\psi)\epsilon_h \beta_h V(t) S(t)}{N_h^2 l_1 l_2} - \frac{\epsilon_h I(t)}{l_1} + \frac{l_3 I(t) A(t)}{N_h \pi_v} - \frac{l_3 l_4 l_5 V(t)}{\theta(1-\psi)\epsilon_v \beta_v \pi_v}, \\
\dot{\mathcal{L}} &\leqslant \frac{\theta(1-\psi)\epsilon_h \beta_h V(t)}{N_h l_1 l_2} - \frac{l_3 l_4 l_5 V(t)}{\theta(1-\psi)\epsilon_v \beta_v \pi_v}, \\
&= \frac{\theta(1-\psi)\epsilon_v \beta_v \pi_v V(t)}{l_3 l_4 l_5} [\mathcal{R}_0^2 - 1].
\end{aligned}$$

Therefore, $\dot{\mathcal{L}} \leqslant 0$ at $\mathcal{R}_0 < 1$ and $\dot{\mathcal{L}} = 0$ at $V(t) = 0$ or $\mathcal{R}_0 = 1$. Furthermore, the largest compact invariant set in Φ is the singleton $\{\mathcal{P}_{dfe}\}$. Then, by LaSalle's Invariance Principle [28], the $\mathcal{P}_{dfe}$ is globally asymptotically stable whenever $\mathcal{R}_0 \leqslant 1$. □

3.6. *Existence of Endemic Equilibrium Point* $\mathcal{P}_{ee}$

The Dengue Fever model (2.5) endemic equilibrium point $\mathcal{P}_{ee}$ it is the steady state when infection cases by Dengue Fever existing in the host and vectors population hence

$$S^* = \frac{\mathcal{A}_1 \pi_h I^* + \mathcal{A}_2}{(\mathcal{A}_3 \epsilon_v \pi_v + \mu_h \mathcal{A}_1) I^* + \mu_h \mathcal{A}_2}, \tag{3.6}$$

$$E^* = \frac{l_2 I^*}{\epsilon_h}, \tag{3.7}$$

$$R^* = \frac{\alpha I^*}{l_6}, \tag{3.8}$$

$$A^* = \frac{N_h \pi_v l_4 l_5}{\mathcal{A}_1 I^* + \mathcal{A}_2}, \tag{3.9}$$

$$W^* = \frac{l_5 V^*}{\epsilon_v}, \tag{3.10}$$

$$V^* = \frac{\epsilon_v \pi_v I^*}{\mathcal{A}_1 I^* + \mathcal{A}_2}. \tag{3.11}$$

Whereby

$$\begin{aligned}
l_6 &= (\xi + \mu_h), \\
\mathcal{A}_1 &= \theta(1-\psi)\beta_v (l_4 l_5 + \epsilon_v \sigma \pi_v), \\
\mathcal{A}_2 &= N_h l_3 l_4 l_5, \\
\mathcal{A}_3 &= \frac{\theta(1-\psi)\beta_h}{N_h l_1 l_2 l_6} (l_1 l_2 l_6 - \epsilon_h \alpha \xi).
\end{aligned}$$

While I^* well be the positive root of the equation

$$\mathcal{B}_1 I^{*2} + \mathcal{B}_2 I^* = 0. \tag{3.12}$$

Whereby

$$\mathcal{B}_1 = N_h l_1 l_2(\mathcal{A}_3\epsilon_v\pi_v + \mu_h\mathcal{A}_1) > 0, \tag{3.13}$$

$$\mathcal{B}_2 = \pi_h N_h l_1 l_2 l_3 l_4 l_5(1-\mathcal{R}_0^2). \tag{3.14}$$

Since $\mathcal{B}_1 > 0$ and $\mathcal{B}_2 < 0$ if $\mathcal{R}_0 > 1$. Therefore, there is existence of positive endemic equilibrium point $\mathcal{P}_{ee}$ whenever $\mathcal{R}_0 > 1$.

Theorem 3.5. *The Dengue Fever model* (2.5) *has a unique endemic equilibrium point if* $\mathcal{R}_0 > 1$*, and no endemic equilibrium point otherwise.*

3.7. Locally Asymptotically Stability of $\mathcal{P}_{ee}$

Theorem 3.6. *The Dengue Fever model* (2.5) *endemic equilibrium point* $\mathcal{P}_{ee}$ *is locally asymptotically stable if* $\mathcal{R}_0 > 1$ *and unstable if* $\mathcal{R}_0 < 1$.

Proof. The proof will obtain by using Center Manifold Theory [Theorem 4.1 ,[29]]. The Dengue Fever model (2.5) will be written in the form $\frac{dX}{dt} = F(X)$ where $X = (x_1, x_2, x_3, x_4, x_5, x_6, x_7)^T$ and $F = (f_1, f_2, f_3, f_4, f_5, f_6, f_7)^T$. Therefore, $S = x_1, E = x_2, I = x_3, R = x_4, A = x_5, W = x_6, V = x_7$ and the model (2.5) becomes

$$\begin{aligned}
\frac{dx_1}{dt} &= f_1 := \pi_h - \lambda_h x_1 - \mu_h x_1 + \xi x_4,\\
\frac{dx_2}{dt} &= f_2 := \lambda_h x_1 - (\epsilon_h + \mu_h)x_2,\\
\frac{dx_3}{dt} &= f_3 := \epsilon_h x_2 - (\alpha + \delta + \mu_h)x_3,\\
\frac{dx_4}{dt} &= f_4 := \alpha x_3 - (\xi + \mu_h)x_4,\\
\frac{dx_5}{dt} &= f_5 := \pi_v(1-\sigma x_7) - \lambda_v x_5 - (\psi + \gamma + \mu_v)x_5,\\
\frac{dx_6}{dt} &= f_6 := \lambda_v x_5 - (\epsilon_v + \psi + \gamma + \mu_v)x_6,\\
\frac{dx_7}{dt} &= f_7 := \epsilon_v x_6 - (\psi + \gamma + \mu_v - \sigma\pi_v)x_7.
\end{aligned} \tag{3.15}$$

We chose β_h as a bifurcation parameter and $\mathcal{R}_0 = 1$ at (3.5) hence we find $\beta_h = \beta_h^* = \frac{\pi_h l_1 l_2 l_3 l_4 l_5}{\theta^2(1-\psi)^2\epsilon_h\epsilon_v\beta_v\pi_v\mu_h}$. The linearization matrix of the system (3.15) at $\mathcal{P}_{dfe}$ and $\beta_h = \beta_h^*$ is given by

$$D_x f = \begin{bmatrix}
-\mu_h & 0 & 0 & \xi & 0 & 0 & -\theta(1-\psi)\beta_h^*\\
0 & -l_1 & 0 & 0 & 0 & 0 & \theta(1-\psi)\beta_h^*\\
0 & \epsilon_h & -l_2 & 0 & 0 & 0 & 0\\
0 & 0 & \alpha & -l_6 & 0 & 0 & 0\\
0 & 0 & -\frac{\theta(1-\psi)\beta_v\pi_v}{N_h l_3} & 0 & -l_3 & 0 & 0\\
0 & 0 & \frac{\theta(1-\psi)\beta_v\pi_v}{N_h l_3} & 0 & 0 & -l_4 & 0\\
0 & 0 & 0 & 0 & 0 & \epsilon_v & -l_5
\end{bmatrix} \tag{3.16}$$

It is obvious that the matrix (3.16) has one zero eigenvalue and six eigenvalues with negative real part. The right eigenvectors corresponding to the zero eigenvalue is given by $\omega = (\omega_1, \omega_2, \omega_3, \omega_4, \omega_5, \omega_6, \omega_7)^T$ whereby

$$\omega_1 = \frac{\pi_h l_3 l_4}{\theta(1-\psi)\beta_v \pi_v \mu_h^2}\left(\frac{\xi\alpha\epsilon_h - l_1 l_2 l_6}{\epsilon_h l_6}\right)\omega_6 < 0, \quad \omega_2 = \frac{\pi_h l_2 l_3 l_4 l_5}{\theta(1-\psi)\epsilon_h \epsilon_v \beta_v \pi_v \mu_h}\omega_7 > 0,$$
$$\omega_3 = \frac{N_h l_3 l_4}{\theta(1-\psi)\beta_v \pi_v}\omega_6 > 0, \quad \omega_4 = \frac{\alpha}{l_6}\omega_3 > 0, \quad \omega_5 = -\frac{\theta(1-\psi)\beta_v \pi_v}{N_h l_3^2}\omega_3 < 0,$$
$$\omega_6 = \omega_6 > 0,, \quad \omega_7 = \frac{\epsilon_v}{l_5}\omega_6 > 0.$$

The left eigenvectors corresponding to the zero eigenvalue given by $v = (v_1, v_2, v_3, v_4, v_5, v_6, v_7)$ is obtained as

$$v_1 = v_4 = v_5 = 0$$
$$v_2 = \frac{\pi_h l_1 l_2 l_3 l_4}{\theta(1-\psi)\epsilon_h \epsilon_v \beta_v \pi_v \mu_h}v_7 > 0, \quad v_3 = \frac{l_1}{\epsilon_h}v_2 > 0,$$
$$v_6 = \frac{l_4}{\epsilon_v}v_7 > 0, \quad v_7 = v_7 > 0.$$

Now, we need to compute a and b in [Theorem 4.1 ,[29]], therefore we need to compute non–vanishing partial derivatives of f_2 and f_6. Firstly, compute the value of a and the non–vanishing partial derivatives are

$$\frac{\partial^2 f_2}{\partial x_1 \partial x_7} = \frac{\partial^2 f_2}{\partial x_7 \partial x_1} = \frac{\theta(1-\psi)\beta_h^* \mu_h}{\pi_h},$$
$$\frac{\partial^2 f_6}{\partial x_3 \partial x_5} = \frac{\partial^2 f_6}{\partial x_5 \partial x_3} = \frac{\theta(1-\psi)\beta_v \mu_h}{\pi_h}.$$

It follows that

$$a = \sum_{k,j,i=1}^{n} v_k \omega_i \omega_j \frac{\partial^2 f_k}{\partial x_i \partial x_j}(\mathcal{P}_{dfe}, \beta_h^*) = \frac{\theta(1-\psi)\mu_h}{\pi_h}[v_2\omega_1\omega_7\beta_h^* + v_6\omega_3\omega_5\beta_v] < 0.$$

For computing b we only need to compute the non–vanishing partial derivative of f_2. Thus $\frac{\partial^2 f_2}{\partial x_7 \partial \beta_h^*} = \theta(1-\psi)$ and we obtain

$$b = \sum_{k,i=1}^{n} v_k \omega_i \frac{\partial^2 f_k}{\partial x_i \partial \beta_h^*}(\mathcal{P}_{dfe}, \beta_h^*) = v_2\omega_7\theta(1-\psi) > 0.$$

Since $a < 0$ and $b > 0$ according to the item (iv) in Theorem 4.1 in [29] the endemic equilibrium point $\mathcal{P}_{ee}$ is locally asymptotically stable at $\mathcal{R}_0 > 1$. Also, a forward bifurcation occurred for the model (2.5) which mean the Dengue Fever transmission eradicate at $\mathcal{R}_0 < 1$ and propagate whenever $\mathcal{R}_0 > 1$. □

4. Numerical Results

In this section, sensitivity analysis of the basic reproduction number $\mathcal{R}_0$ and numerical simulation of the model (2.5) will accomplish.

4.1. Sensitivity Analysis of $\mathcal{R}_0$

The basic reproduction number $\mathcal{R}_0$ determined as important threshold for control the Dengue Fever transmission. Therefore, the sensitivity analysis of $\mathcal{R}_0$ lead to determine important parameters for Dengue Fever transmission.

4.1.1. Local Sensitivity Analysis

Driving the local sensitivity analysis of $\mathcal{R}_0$ by using normalized forward sensitivity index approach as shown in [30]. Obtain the sensitivity index of $\mathcal{R}_0$ with respect ot the parameter p we evaluate $\Upsilon_p^{\mathcal{R}_0} = \frac{\partial \mathcal{R}_0}{\partial p} \times \frac{p}{\mathcal{R}_0}$. We evaluate $\mathcal{R}_0$ sensitivity index by using the parameters values in the Table 1 and the obtained results presented in Table 2. We obtained the parameters $\theta, \mu_v, \psi, \sigma$, and π_v have highly index values for $\mathcal{R}_0$ sensitivity. Therefore, if θ increase(or decrease) then $\mathcal{R}_0$ increase (or decrease) by 10% and as μ_v increase(or decrease) then $\mathcal{R}_0$ decrease(or increase) by 19.369%.

4.1.2. Global Sensitivity Analysis

To carryout the global sensitivity analysis of $\mathcal{R}_0$ we will use the Partial Ranking Correlation Coefficient(PRCC) method as described in [31]. The PRCC method preform partial correlation between the input x_i and the output y whereby the other inputs considered in baseline values. The PRCC method depend on the Latin Hypercube Sampling(LHS) in [31, 32] and it is a sampling method based on Monte Carol simulation. LHS sampling method used for generating samples for $\mathcal{R}_0$ uncertain parameters and then determine PRCC values for each uncertain parameter. The obtained results presented in the Table 2 and we obtained the parameters $\beta_v, \pi_v, \beta_h, \theta$ and μ_v has highly PRCC ranking for $\mathcal{R}_0$. Figure 2 show the PRCC values for $\mathcal{R}_0$ with respect to the composite parameters.

Table 2: Table shows sensitivity indices and PRCC values of $\mathcal{R}_0$.

parameter	$\Upsilon_p^{\mathcal{R}_0}$	**PRCC**
π_h	-0.5	-0.4157
π_v	3.8333	0.4522
μ_h	0.4997	0.2672
δ	-0.0020	-0.0379
μ_v	-1.9368	-0.7974
θ	1.0	0.7687
β_h	0.5	0.5460
β_v	0.5	0.4360
ϵ_h	0.000037943	0.0348
ϵ_v	0.1212	0.0485
α	-0.00004574	-0.4746
σ	3.3333	0.0439
ψ	-2.1097	-0.0510
γ	-0.5229	-0.0040

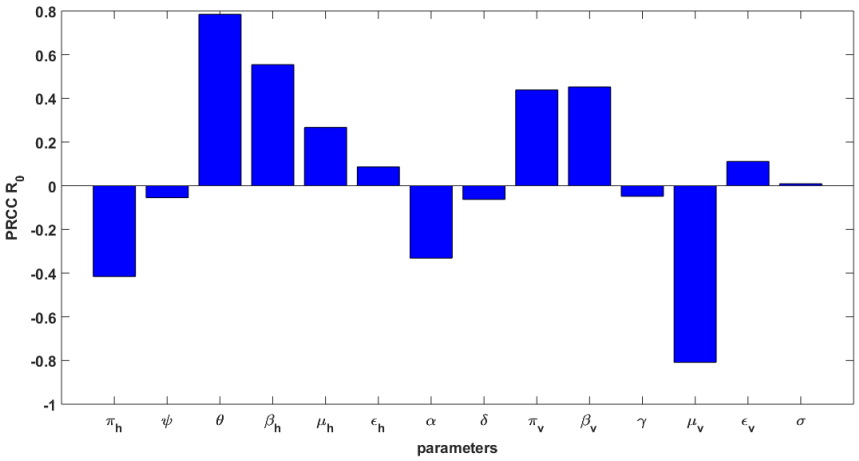

Figure 2: PRCC values of $\mathcal{R}_0$.

From the sensitivity analysis of $\mathcal{R}_0$ we deduce avoiding contact between humans and vectors, shorting lifespan of vectors, and effective treatment will lead to reduce Dengue Fever transmission. Moreover, employing of control measures ψ and γ also reduce Dengue Fever transmission since ψ and γ cause decrease of $\mathcal{R}_0$.

4.2. Numerical Simulation

In this subsection, we will simulate the model (2.5) numerically by using Runge–Kutta fourth order method in MATLAB. In the numerical simulations we examined two scenarios for Dengue Fever transmission. Dengue Fever die out scenario and Dengue Fever endemic scenario. The Dengue Fever die out scenario parameters found in the Table 1 whereby $\mathcal{R}_0 = 0.4009$. For the endemic scenario we use the parameters values form table 1 with replacing $\theta = 28$, $\beta_h = 0.75$, $\mu_v = 0.083$,$\psi = 0.1230$ and $\mu_h = 0.0004212$ and we obtain $\mathcal{R}_0 = 2.5722$. Particularly, we are interested in investigate the effects of control measures ITN and IRS in the Dengue Fever model (2.5) compartments.

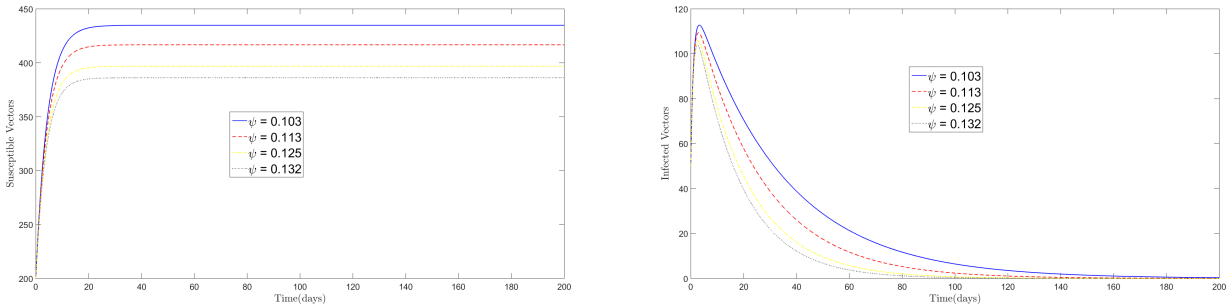

Figure 3: The effects of ψ on *Susceptible* and *Infected* vectors at $\mathcal{R}_0 = 0.4009$.

Figure 3 show that increase of ψ cause decrease on *Susceptible* and *Infected* vectors. Using of ITN lead to reduce the amount of vectors per capita. The same effect appeared in Figure 4 as γ increase then the *Susceptible* and *Infected* vectors numbers decreases.

Figure 5 show that as increase of ψ the *Susceptible* and *Infected* vectors decrease. We observe that the increase of ψ lead to decrease the vectors population. Also, in Figure 6 we obtain that as γ increase then *Susceptible* and *Infected* vectors decrease. Using ITN and IRS lead to avoiding contact between humans and vectors, and reduce the amount of vectors per capita.

Figure 7 show that as ψ and γ increase the *Infected* humans numbers decrease. Using ψ and γ reduce Dengue Fever infection cases in the humans populations by preventing the Dengue virus transmission.

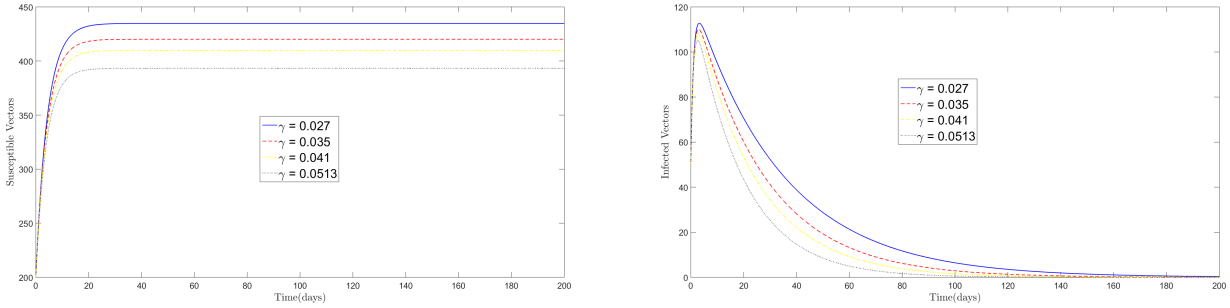

Figure 4: The effects of γ on *Susceptible* and *Infected* vectors at $\mathcal{R}_0 = 0.4009$.

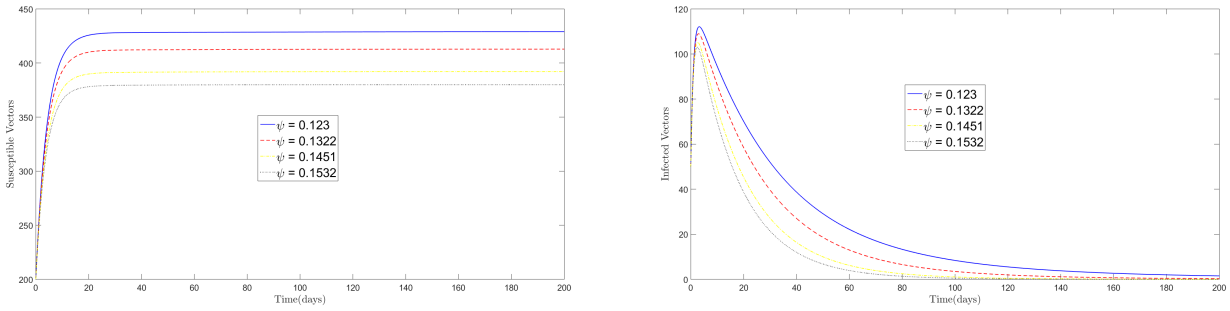

Figure 5: The effects of ψ on *Susceptible* and *Infected* vectors at $\mathcal{R}_0 = 2.5722$.

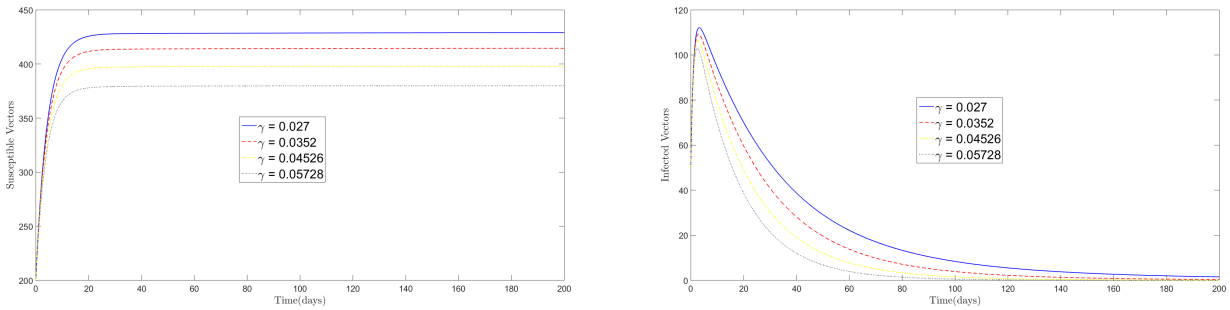

Figure 6: The effects of γ on *Susceptible* and *Infected* vectors at $\mathcal{R}_0 = 2.5722$.

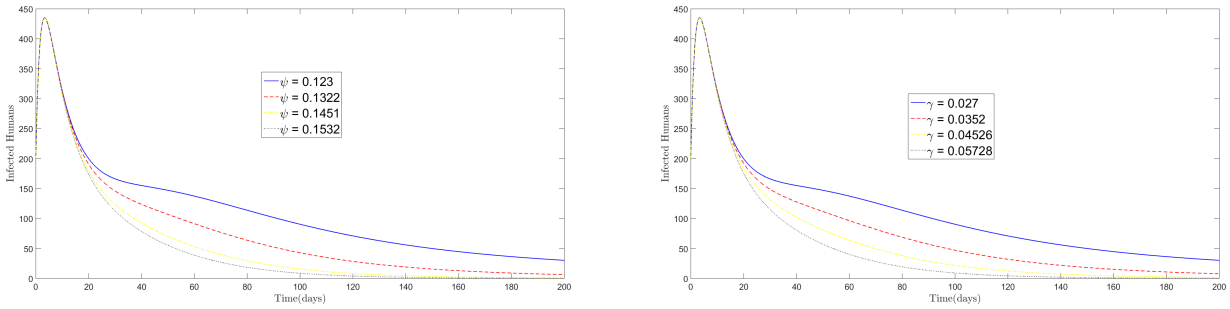

Figure 7: The effects of ψ and γ on *Infected* humans at $\mathcal{R}_0 = 2.5722$.

From the numerical simulation, we can say that the control measures ψ and γ help reduce and eradicate Dengue Fever transmission between humans and vectors. Using ψ and γ greatly reduces Dengue Fever transmission by controlling the contact rate between humans and vectors and the number of vectors. Furthermore, additional control measures such as Insecticide Space Spray and Larva Control can be applied to reduce the number of vectors and prevent Dengue Fever transmission [33].

Therefore, advice for eradicating Dengue Fever transmission, shortening the life span of vectors, avoiding the contact between humans and vectors, and effective treatment. Furthermore, applying the different types of control measures against the vector populations has great impact on preventing Dengue Fever transmission.

5. Conclusion

In this article, we have formulated a deterministic mathematical model for Dengue Fever transmission between humans and vectors. We considered the vertical transmission of the Dengue virus in the vector population and added two control measures, ITN and IRS, to the model. We discussed in detail the invariant region, the positivity of solutions, the model equilibrium points, and the basic reproduction number. The stability analysis of the model equilibrium points was performed, and the forward bifurcation was exhibited for the model. We found that the Dengue Fever transmission die out at $\mathcal{R}_0 < 1$ and spread whenever $\mathcal{R}_0 > 1$. The sensitivity analysis of the basic reproduction number accomplished local and global results, and we determined the important parameters for dengue fever transmission. We found that the parameters for Dengue Fever transmission are $\theta, \mu_v, \beta_v, \beta_h$, and π_v. Beside, increase of the parameters ψ, γ cause reducing on $\mathcal{R}_0$, but increase of σ increment $\mathcal{R}_0$. The model's numerical simulation was obtained using the Runge–Kutta fourth-order method, and we investigated the effects of the control measures in the Dengue Fever model (2.5). The effects of the control measures are noticed clearly, and we can say that employing control measures helps reduce and eradicate Dengue Fever transmission. Also, we provide advice for reducing and eradicating Dengue Fever transmission.

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