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GLOBAL STABILITY OF HOST-VECTOR MODEL FOR VECTOR-BORN DISEASE

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Abstract

The purpose of this research is to examine a biological model of vector-borne disease. The paper's research demonstrates that its dynamics are solely dependent on the basic reproduction number R_0. Our investigation is consisted on stability theory and numerical simulations. The Routh-Hurwitz Criteria and the Lyapunov approach are used to determine the local and global asymptotic stability of the disease-free equilibrium. In this paper, we use the work of McCluskey and van den Driessche to show that endemic equilibrium is stable locally. We also use the geometric approach method developed by Li and Muldowney to show that endemic equilibrium is stable at the global level, where the disease stays latent if it already exists. If $R_0 \leq 1$, the disease-free equilibrium is globally asymptotically stable, and the disease will vanish, and a unique endemic equilibrium exists if $R_0 > 1$.

Keywords: Biological model, Stability theory, Routh-Hurwitz Criteria, Endemic equilibrium.

1 Introduction

Vector-borne diseases that emerge or re-emerge pose a worldwide health concern [1]. These diseases are transmitted through vectors, animal hosts, climate factors, pathogens, and vulnerable humans under favourable conditions [2]. Viruses are the primary cause of a significant fraction of new infectious illnesses, which are transmitted by vectors. In the last twenty years, there has been a significant rise in vector-borne infections and an increase in endemic diseases. Certain indigenous infections exhibit controlled proliferation in response to alterations in their natural habitats, regardless of the isolation between their introductions and occurrences. According to a previous study [3], yellow fever and dengue are more widespread globally. The correlation between vector-borne diseases and climate change is a subject of ongoing dispute. The reality of global warming is universally acknowledged, and it has far-reaching effects on all aspects of the natural world. The impact of climate change in the 21st century is substantial. Current research suggests that there will be a temperature increase of 1.0-3.5◦C worldwide by the year 2100. This temperature change could potentially lead to a higher likelihood of vector-borne diseases. Weather and climate impact the behavior of vectors and the transmission of viruses. The construction of dams and irrigation systems can enhance the food and energy requirements of developing nations. Nevertheless, emerging vector-borne infectious diseases have the potential to propagate [4]. The expansion of water resources and population growth can lead to ecological changes that facilitate the spread of schistosomiasis to previously unaffected areas [5, 6]. Gaining comprehension of the resurgence of vector-borne diseases is crucial in mitigating their detrimental impact. This is of utmost importance as infectious diseases sometimes go undiagnosed. Hence, it is imperative to closely monitor the advancements in infectious disease surveillance and control to facilitate timely public health interventions [7]. Mathematical modeling is a highly efficient approach for investigating the progression of different diseases. Through the utilization of these models and the implementation of investigations, we may optimize our planning and formulate efficient control strategies. The study was conducted to evaluate the global stability of a host-vector system.

The following structure describes how this paper is organized. Section 2 explains how the mathematical model was constructed. The dimensionless formulation of the prescribe model is shown in section 3. Section 4 reveals the basic reproduction number R_0, the presence of a disease-free equilibrium, and the stability of that equilibrium. The presence and uniqueness of endemic equilibrium, as well as the stability of that equilibrium, are presented in sections 5 and 6, respectively. Section 7 contains the results of the discussion and simulations, whereas section 8 contains the appendices.

2 Model Formulation

In this model, we divide a total host population N_h into few distinct compartments individually who are susceptible S_h, infectious I_h and recovered R_h. Most likely, the total number of vectors N_v is also split into two groups: vectors that are susceptible (size S_v) and vectors that can spread disease (size I_v). Immune class approximately does not exits in vector class. Their death concludes their infectious phase. Consequently, the disease divides the host population into classes of susceptible, infectious, and recovered individuals, whereas the vector population divides into classes of susceptible and infectious individuals. At time t, the total populations of both humans and vectors are, respectively: $N_h = S_h + I_h + R_h$ and $N_v = S_v + I_v$. So, the following set of differential equations can be used to state a host-vector model:

$$\begin{aligned}
\frac{ds_h}{dt} &= \Lambda_h N_H - \frac{b\beta_h i_v s_h}{N_V} + \mu_h s_h,\\
\frac{di_h}{dt} &= \frac{b\beta_h i_v s_h}{N_V} - (\delta_h + \mu_h + \gamma_h) i_h,\\
\frac{dr_h}{dt} &= \gamma_h i_h - \Lambda_h r_h, \qquad\qquad (2.1)\\
\frac{ds_v}{dt} &= \Lambda_v N_V - \frac{b\beta_v i_h s_v}{N_H} + \mu_v s_v,\\
\frac{di_v}{dt} &= \frac{b\beta_v i_h s_v}{N_H} - (\delta_v + \mu_v) i_v.
\end{aligned}$$

S is susceptible, I is infected and R is recovered individual. The birth rate of those who are considered to be in the susceptible class is represented in model (2.1) by Λ_h. There are two main ways in which infected organisms are spread throughout a population of susceptible hosts: direct contact with an infected person or a bite from an infectious vector. The infection rate of susceptible people caused by the biting of infected vectors is equal to the infection rate of suffering people caused by forced contact with an irresistible person, or $b\beta_h$. The occurrence of new contamination of transmission is given by the frequency shape $b\beta_h(i_v s_h/N_V)$. Natural mortality in humans occurs at a rate known as μ_h. We suppose that the rate at which susceptible people develop lifelong immunity is γ_h. Disease-related mortality in humans is denoted by the rate δ_h. For the vector population, Λ_v is the birth rate and μ_v is the mortality rate due to natural causes. The rate of recently tainted vectors is again given by the frequency frame $b\beta_v(i_h s_v/N_H)$. The following equation describes the entire host population:

$$\frac{dN_H}{dt} = (\Lambda_h - \mu_h)N_H - \delta_h i_h. \tag{2.2}$$

3 Dimensionless Formulation

Where $S_h = \frac{s_h}{N_H}$, $R_h = \frac{r_h}{N_H}$, $I_h = \frac{i_h}{N_H}$, $I_v = \frac{i_v}{N_V}$, and $S_v = \frac{s_v}{N_V}$ represents. S_h, R_h, I_h, I_v and S_v should satisfy the becoming system. In this paper, we devote all of our attention to the system's dynamic behavior

$\Phi = \{(S_h, I_h, R_h, S_v, I_v) \in R_+^5 | S_h \geq 0, I_h \geq 0, R_h \geq 0, S_v \geq 0, I_v \geq 0\}$.

All model parameters are taken to be non-negative in our analysis $\Lambda_h \geq 0, b \geq 0, \beta_h \geq 0, \delta_h \geq 0 \Lambda_v \geq 0, \beta_v \geq 0, \delta_v \geq 0$;

(for more detail see Appendix):

$$\begin{aligned}
\frac{dS_h}{dt} &= \Lambda_h(1 - S_h) - b\beta_h I_v S_h + \delta_h I_h S_h,\\
\frac{dI_h}{dt} &= b\beta_h I_v S_h - (\delta_h + \Lambda_h + \gamma_h)I_h + \delta_h I_h^2,\\
\frac{dR_h}{dt} &= \gamma_h I_h - \Lambda_h R_h + \delta_h I_h R_h,\\
\frac{dS_v}{dt} &= \Lambda_v(1 - S_v) - b\beta_v I_h S_v + \delta_v I_v S_v,\\
\frac{dI_v}{dt} &= b\beta_v I_h S_v - (\delta_v + \Lambda_v)I_v + \delta_v I_v^2.
\end{aligned} \tag{3.1}$$

where the solution is to be $S_h + R_h + I_h = 1$, $S_v + I_v = 1$. The value of S_v is given by $S_v = 1 - I_v$. Assuming the scale-normalized system (3.1), we can examine the reduced system (3.2) that explains all the dynamics in the same way throughout this paper.

$$\begin{aligned}
\frac{dS_h}{dt} &= \Lambda_h(1 - S_h) - b\beta_h I_v S_h + \delta_h I_h S_h,\\
\frac{dI_h}{dt} &= b\beta_h I_v S_h - (\delta_h + \Lambda_h + \gamma_h)I_h + \delta_h I_h^2,\\
\frac{dI_v}{dt} &= b\beta_v I_h(1 - I_v) - (\delta_v + \Lambda_v)I_v + \delta_v I_v^2.
\end{aligned} \tag{3.2}$$

System (3.2) has a remarkably invariant set of viable regions: $\Gamma = \{(S_h, I_h, I_v) \in R_+^3 \quad | \quad 0 \leq S_h + I_h \leq 1, 0 \leq I_v \leq 1\}$, where R_+^3 denotes the lower-dimensional cone of R_+^3 which is nonnegative.

Table 1: For simulation analysis, the model parameters are shown below. As for system (3.2), we establish the following theorem.

Theorem 1. *Let* (S_h, I_h, I_v) *be the solution of the system (3.2) with initial conditions of* $S_h(0) = S_h^0$, $I_h(0) = I_h^0$, $I_v(0) = I_v^0$, *then* Γ *is positively invariant set with respect to system (3.2) and attracting under the flow represented by system (2.2).*

Symbol	Description of parameter
Λ_h	The recruitment and natural fatality rate of humans
Λ_v	The recruitment and natural fatality rate of vectors
β_h	The rate of new infection to human
β_v	The rate of new infection to vector
δh	Disease mortality rates among humans
δv	Death rates of vector due to disease
γ_h	The rate of infectious individuals acquire permanent immunity

4 Stability theory to Disease-Free Equilibrium

In this paper, we use direct calculations to show that the system (3.2) contains disease-free equilibrium points in steady-state solutions in which there is no infection. For the diseasefree equilibrium point, $S_h = 1$, $I_h = 0$, $I_v = 0$ that is, $E_0 = (1,0,0)$. The term "basic reproduction number" is used to refer to the quantity that describes the entire disease dynamics $R_0 = b\sqrt{\frac{\beta_h\beta_v}{(\delta_v+\Lambda_v)(\delta_h+\Lambda_h+\gamma_h)}}$. In model (3.2), R_0 represents the critical threshold of the epidemic model and serves as its foundational reproduction number. We can tell if an infectious disease has the potential to spread throughout a population by looking at the basic reproduction number. Using second Theorem of [8], by assuming that

$E = (S_h, I_h, I_v)^T$

$$\frac{dE}{dt} = \mathbb{F}(E) - \mathbb{V}(E), \tag{4.1}$$

where

$$\mathbb{F}(E) = \begin{bmatrix} 0 \\ b\beta_h I_v S_h \\ b\beta_v I_h S_v \end{bmatrix}, \quad \mathbb{V}(E) = \begin{bmatrix} -\Lambda_h(1-S_h) + b\beta_h I_v S_h - \delta_h I_h S_h \\ (\delta_h + \Lambda_h + \gamma_h)I_h - \delta_h I_h^2 \\ (\delta_v + \Lambda_v)I_v - \delta_v I_v^2 \end{bmatrix}$$

$$F_1 = b\beta_h I_v S_h \quad \text{and} \quad V_1 = (\delta_h + \Lambda_h + \gamma_h)I_h - \delta_h I_h^2$$
$$F_2 = b\beta_v I_h(1 - I_v) \quad \text{and} \quad V_2 = (\delta_v + \Lambda_v)I_v - \delta_v I_v^2.$$

All new infections are represented by the Jacobian matrix F(E). V(E) is a representation of the net transition rates aside from the corresponding compartment, where

$$D\mathbb{F}(E_0) = \begin{bmatrix} F & 0 \\ 0 & 0 \end{bmatrix}, \quad D\mathbb{V}(E_0) = \begin{bmatrix} V & 0 \\ J_1 & J_2 \end{bmatrix},$$

where F and V are a 2 × 2 matrix and therefor, by linearization at

$X_0 = E^*(1,0,0)$, we get

$$F = \begin{bmatrix} \frac{\partial F_1}{\partial I_h} & \frac{\partial F_1}{\partial I_v} \\ \frac{\partial F_2}{\partial I_h} & \frac{\partial F_2}{\partial I_v} \end{bmatrix} \text{ and } V = \begin{bmatrix} \frac{\partial V_1}{\partial I_h} & \frac{\partial V_1}{\partial I_v} \\ \frac{\partial V_2}{\partial I_h} & \frac{\partial V_2}{\partial I_v} \end{bmatrix}$$

$$F = \begin{bmatrix} 0 & b\beta_h \\ b\beta_v & 0 \end{bmatrix}, \quad V = \begin{bmatrix} (\delta_h + \Lambda_h + \gamma_h) & 0 \\ 0 & (\delta_v + \Lambda_v) \end{bmatrix}$$

$$\text{as} \quad V^{-1} = \frac{1}{|V|}Adj(V), \text{ then} \quad V^{-1} = \begin{bmatrix} \frac{1}{(\delta_h+\Lambda_h+\gamma_h)} & 0 \\ 0 & \frac{1}{(\delta_v+\Lambda_v)} \end{bmatrix},$$

hence FV^{-1} contains the next generation matrix of the system (3.2);

$$FV^{-1} = \begin{bmatrix} 0 & \frac{b\beta_h}{(\delta_v+\Lambda_v)} \\ \frac{b\beta_v}{(\delta_h+\Lambda_h+\gamma_h)} & 0 \end{bmatrix}$$

As a result, the spectral radius $R_0 = \rho(FV^{-1})$ provides the basic reproduction number of the system (2.1) as shown below.

$$R_0 = b\sqrt{\frac{\beta_h\beta_v}{(\delta_h + \Lambda_h + \gamma_h)(\delta_v + \Lambda_v)}}.$$

Theorem 2. *System (3.2) disease-free equilibrium E_0 is locally stable if and only if $R_0 < 1$, and is unstable otherwise if $R_0 > 1$.*

Proof. We evaluate the Jacobian matrix of the system (3.2) at the disease-free equilibrium point E_0 and is given by

$$J(E_0) = \begin{bmatrix} -\Lambda_h & \delta_h & -b\beta_h \\ 0 & -(\delta_h + \Lambda_h + \gamma_h) & b\beta_h \\ 0 & b\beta_v & -(\delta_v + \Lambda_v) \end{bmatrix}.$$

The Jacobian matrix has a characteristic equation of $det(\lambda I - J(E_0)) = 0$ based on the Routh-Hurwitz criterion.

$$\lambda^3 + a_1\lambda^2 + a_2\lambda + a_3 = 0, \qquad (4.2)$$

where

$$\begin{aligned} &a_1 = \delta_h + 2\Lambda_h + \gamma_h + \delta_v + \Lambda_v > 0, \\ &a_2 = \Lambda_h(\delta_h + \Lambda_h + \gamma_h + \delta_v + \Lambda_v) + (\delta_h + \Lambda_h + \gamma_h)(\delta_v + \Lambda_v)(1 - R_0^2) > 0, \\ &a_3 = \Lambda_h(\delta_h + \Lambda_h + \gamma_h)(\delta_v + \Lambda_v)(1 - R_0^2) > 0. \end{aligned}$$

Now we should check the said criteria. If the criteria is satisfied then all the eigenvalues have negative real part,

$$\text{Routh-Hurwitz Criteria: } a_1 > 0, a_2 > 0, a_3 > 0, \quad then \quad a_1a_2 > a_3.$$

$$\begin{aligned} a_1a_2 - a_3 &= (\delta_h + 2\Lambda_h + \gamma_h + \delta_v + \Lambda_v)[\Lambda_h(\delta_h + \Lambda_h + \gamma_h + \delta_v + \Lambda_v) + (\delta_h + \Lambda_h + \gamma_h) \\ &\quad (\delta_v + \Lambda_v)(1 - R_0^2)] - \Lambda_h(\delta_h + \Lambda_h + \gamma_h)(\delta_v + \Lambda_v)(1 - R_0^2) \\ &= \Lambda_h + (\delta_h + \Lambda_h + \gamma_h + \delta_v + \Lambda_v)[\Lambda_h(\delta_h + \Lambda_h + \gamma_h + \delta_v + \Lambda_v) + (\delta_h + \Lambda_h + \gamma_h) \\ &\quad (\delta_v + \Lambda_v)(1 - R_0^2)] - \Lambda_h(\delta_h + \Lambda_h + \gamma_h)(\delta_v + \Lambda_v)(1 - R_0^2) \\ &= \Lambda_h^2(\delta_h + \Lambda_h + \gamma_h + \delta_v + \Lambda_v) + \Lambda_h(\delta_h + \Lambda_h + \gamma_h + \delta_v + \Lambda_v)^2 + (\delta_h + \Lambda_h + \gamma_h + \delta_v + \Lambda_v) \\ &\quad (\delta_h + \Lambda_h + \gamma_h)(\delta_v + \Lambda_v)(1 - R_0^2) > 0. \end{aligned}$$

Thus, E_0 is locally asymptotically stable in model (3.2). □

The global stability of an equilibrium free of disease for system (3.2) is now being studied.

Theorem 3. *For* $b\beta_hI_v > \delta_hI_h$, $b\beta_vI_h > \delta_vI_v$, *The disease-free equilibrium* E_0 *is globally asymptotically stable in* Γ *of the model if and only if* $R_0 \leq 1$. *In contrast,* E_0 *is unstable if* $R_0 > 1$.

Proof. For globally stability we construct Lyapunov function as.

$$L(t) = a_1I_h + a_2I_v, \qquad (4.3)$$

where,

$$a_1 = (\delta_v + \Lambda_v), \qquad a_2 = b\beta_h.$$

Taking the derivative of L along the system (3.2) solutions yields

$$\begin{aligned} L^{\cdot}(t) &= a_1I_h^{\cdot} + a_2I_v^{\cdot} \\ &= a_1\Big[b\beta_hI_vS_h - (\delta_h + \Lambda_h + \gamma_h)I_h + \delta_hI_h^2\Big] + a_2\Big[b\beta_vI_h(1 - I_v) - (\delta_v + \Lambda_v)I_v + \delta_vI_v^2\Big] \\ &= (\delta_v + \Lambda_v)\Big[b\beta_hI_vS_h - (\delta_h + \Lambda_h + \gamma_h)I_h + \delta_hI_h^2\Big] + b\beta_h\Big[b\beta_vI_h(1 - I_v) - (\delta_v + \Lambda_v)I_v + \delta_vI_v^2\Big] \\ &= \Big[b\beta_h(\delta_v + \Lambda_v)I_vS_h - (\delta_h + \Lambda_h + \gamma_h)(\delta_v + \Lambda_v)I_h + \delta_h(\delta_v + \Lambda_v)I_h^2\Big] \\ &\quad + \Big[b^2\beta_h\beta_vI_h(1 - I_v) - b\beta_h(\delta_v + \Lambda_v)I_v + b\beta_h\delta_vI_v^2\Big] \\ &= \Big[b\beta_h(\delta_v + \Lambda_v)I_v(1 - I_h) - (\delta_h + \Lambda_h + \gamma_h)(\delta_v + \Lambda_v)I_h + \delta_h(\delta_v + \Lambda_v)I_h^2\Big] \\ &\quad + \Big[b^2\beta_h\beta_vI_h(1 - I_v) - b\beta_h(\delta_v + \Lambda_v)I_v + b\beta_h\delta_vI_v^2\Big] \\ &= -\Big[(\delta_h + \Lambda_h + \gamma_h)(\delta_v + \Lambda_v)(1 - R_0^2)\Big]I_h - b^2\beta_h\beta_vI_hI_v + b\beta_h(\delta_v + \Lambda_v)I_v \\ &\quad + \delta_h(\delta_v + \Lambda_v)I_h^2 - b\beta_h(\delta_v + \Lambda_v)I_vI_h - b\beta_h(\delta_v + \Lambda_v)I_v + b\beta_h\delta_vI_v^2 \\ &= -\Big[(\delta_h + \Lambda_h + \gamma_h)(\delta_v + \Lambda_v)(1 - R_0^2) + (\delta_v + \Lambda_v)(b\beta_hI_v - \delta_hI_h)\Big]I_h - b\beta_h(b\beta_vI_h - \delta_vI_v)I_v \leq 0 \end{aligned}$$

.

Thus here if $R_0 \leq 1$ then $L'(t)$ is negative. Further along the solution of the system $L > 0$ and $L = 0$ iff $I_h = I_v = 0$. That is $L'(t) \leq 0$ if $R_0 \leq 1$, then $L'(t) = 0$ when and only when $I_h = I_v = 0$. Consequently, our endemic equilibrium point is the singelton set E_0, which is the biggest compact invariant set in $\{(S_h, I_h, I_v) \in \Phi \mid L'(t) = 0\}$ when $R_0 \leq 1$. Consequently, we infer that E_0 is globally asymptotically stable in Φ by applying Lasalle's Invariance Principle [9]. □

5 Stability theory of the Endemic Equilibrium

In this part, we investigate the occurrence and stability of endemic equilibrium points. A unique endemic equilibrium $E^* = (I_h^*, I_h^*, I_v^*)$ in Γ exists in the host-vector model (2.4) if and only if $R_0 > 1$, with

$$\begin{aligned}
&\Lambda_h(1-S_h) - b\beta_h I_v S_h + \delta_h I_h S_h = 0,\\
&b\beta_h I_v S_h = (\delta_h + \Lambda_h + \gamma_h)I_h - \delta_h I_h^2,\\
&\Lambda_h(1-S_h) - (\delta_h + \Lambda_h + \gamma_h)I_h + \delta_h I_h^2 + \delta_h I_h S_h = 0,\\
&(\delta_h I_h - \Lambda_h)S_h = (\delta_h + \Lambda_h + \gamma_h)I_h - \delta_h I_h^2 - \Lambda_h,
\end{aligned}$$

$$\begin{aligned}
S_h^* &= \frac{\Lambda_h - (\delta_h + \Lambda_h + \gamma_h)I_h^* + \delta_h I_h^{*2}}{(\Lambda_h - \delta_h I_h^*)},\\
I_v^* &= \frac{b\beta_v I_h^* + (\delta_v + \Lambda_v) + \sqrt{\Delta}}{2\delta_v},
\end{aligned}$$

where $\Delta = b^2\beta_v^2 I_h^{*2} + 2b\beta_v(\Lambda_v - \delta_v)I_h^* + (\delta_v + \Lambda_v)^2$,
and I_h^* is the root of the following equation:

$$C_0 I_h^{*6} + C_1 I_h^{*5} + C_2 I_h^{*4} + C_3 I_h^{*3} + C_4 I_h^{*2} + C_5 I_v^* + C_6 = 0, \tag{5.1}$$

where

$$\begin{aligned}
C_0 = {}& 4\delta_h^4\delta_v^2 - 4b^2\beta_h\beta_v\delta_h^3\delta_v, C_1\\
& - \left(2b^3\beta_h^2\beta_v\delta_h^2(\Lambda_v - \delta_v) - 2b^4\beta_h^2\beta_v^2\delta_h(\delta_h + \Lambda_h + \gamma_h)\right),
\end{aligned}$$

$$\begin{aligned}
C_2 = {}& \left(2\delta_h\delta_v\Lambda_h - b^2\beta_h\beta_v(\delta_h + \Lambda_h + \gamma_h) + 2\delta_h\delta_v(\delta_h + \Lambda_h + \gamma_h) + b\beta_h\delta_h(\delta_v + \Lambda_v)\right)^2 +\\
& 2\left(b^2\beta_h\beta_v\delta_h - 2\delta_h^2\delta_v\right)\left(b^2\beta_h\beta_v\Lambda_h - 2\delta_v\Lambda_h(\delta_h + \Lambda_h + \gamma_h) - b\beta_h(\delta_h + \Lambda_h + \gamma_h)(\delta_v + \Lambda_v)\right) -\\
& \left(b^2\beta_h^2\delta_h^2(\delta_v + \Lambda_v)^2 - 4b^3\beta_h^2\beta_v\delta_h(\delta_h + \Lambda_h + \gamma_h)(\Lambda_v - \delta_v) + b^4\beta_h^2\beta_v^2(\delta_h + \Lambda_h + \gamma_h)^2 + 2b^4\beta_h^2\beta_v^2\Lambda_h\delta_h\right),\\
C_3 = {}& 2\left(b^2\beta_h\beta_v\delta_h - 2\delta_h^2\delta_v\right)\left(b\beta_h\Lambda_h(\delta_v + \Lambda_v)\right) + 2\Big(2\delta_h\delta_v\Lambda_h - b^2\beta_h\beta_v(\delta_h + \Lambda_h + \gamma_h) + 2\delta_h\delta_v(\delta_h + \Lambda_h + \gamma_h)\\
& + b\beta_h\delta_h(\delta_v + \Lambda_v)\Big)\left(b^2\beta_h\beta_v\Lambda_h - 2\delta_v\Lambda_h(\delta_h + \Lambda_h + \gamma_h) - b\beta_h(\delta_h + \Lambda_h + \gamma_h)(\delta_v + \Lambda_v)\right) +\\
& 2b^2\beta_h^2\delta_h(\delta_h + \Lambda_h + \gamma_h)(\delta_v + \Lambda_v)^2 - 2b^3\beta_h^2\beta_v(\delta_h + \Lambda_h + \gamma_h)^2(\Lambda_v - \delta_v) - 4b^3\beta_h^2\beta_v\Lambda_h\delta_h(\Lambda_v - \delta_v) +\\
& 2b^4\beta_h^2\beta_v^2\Lambda_h(\delta_h + \Lambda_h + \gamma_h),\\
C_4 = {}& 2\left(2\delta_h\delta_v\Lambda_h - b^2\beta_h\beta_v(\delta_h + \Lambda_h + \gamma_h) + 2\delta_h\delta_v(\delta_h + \Lambda_h + \gamma_h) + b\beta_h\delta_h(\delta_v + \Lambda_v)\right)\left(b\beta_h\Lambda_h(\delta_v + \Lambda_v)\right)\\
& + \left(b^2\beta_h\beta_v\Lambda_h - 2\delta_v\Lambda_h(\delta_h + \Lambda_h + \gamma_h) - b\beta_h(\delta_h + \Lambda_h + \gamma_h)(\delta_v + \Lambda_v)\right)^2 - b^4\beta_h^2\beta_v^2\Lambda_h^2\\
& - b^2\beta_h^2(\delta_h + \Lambda_h + \gamma_h)^2(\delta_v + \Lambda_v)^2 - 2b^2\beta_h^2\Lambda_h\delta_h(\delta_v + \Lambda_v)^2 + 4b^3\beta_h^2\beta_v\Lambda_h(\delta_h + \Lambda_h + \gamma_h)(\Lambda_v - \delta_v)\\
C_5 = {}& 2\left(b^2\beta_h\beta_v\Lambda_h - 2\delta_v\Lambda_h(\delta_h + \Lambda_h + \gamma_h) - b\beta_h(\delta_h + \Lambda_h + \gamma_h)(\delta_v + \Lambda_v)\right)\left(b\beta_h\Lambda_h(\delta_v + \Lambda_v)\right) +\\
& 2b^2\beta_h^2\Lambda_h(\delta_h + \Lambda_h + \gamma_h)(\delta_v + \Lambda_v)^2 - 2b^3\beta_h^2\beta_v\Lambda_h^2(\Lambda_v - \delta_v),\\
C_6 = {}& 0.
\end{aligned}$$

Thus we obtain the polynomial function of the degree six in (5.1). Which represents the presence of few endemic equilibrium points. This shows that there are six possible roots for I_h^*, which further means that there are at most six possible endemic equilibrium points.
As in [10,11], we employ the additive compound matrices method to determine endemic equilibrium. The following Jacobian matrix is obtained by linearizing system (3.2) about the endemic equilibrium point E^*.

$$J(E^*) = \begin{bmatrix} -\Lambda_h - b\beta_h I_v^* + \delta_h I_h^* & \delta_h S_h^* & -b\beta_h S_h^* \\ b\beta_h I_v^* & -(\delta_h + \Lambda_h + \gamma_h) + 2\delta_h I_h^* & b\beta_h S_h^* \\ 0 & b\beta_v(1 - I_v^*) & -b\beta_v I_h^* - (\delta_v + \Lambda_v) + 2\delta_v I_v^* \end{bmatrix}$$

The Jacobian matrix $J(E^*)$ has an additive compound matrix $J^{[2]}(E^*)$, which is given by

$$J^{[2]}(E^*) = \begin{bmatrix} M_{11} & b\beta_h S_h^* & b\beta_h S_h^* \\ b\beta_v(1 - I_v^*) & M_{22} & \delta_h S_h^* \\ 0 & b\beta_h I_v^* & M_{33} \end{bmatrix}$$

Where

$$\begin{aligned} M_{11} &= -(\delta_h + 2\Lambda_h + \gamma_h) - b\beta_h I_v^* + 3\delta_h I_h^*, \\ M_{22} &= -(\Lambda_h + \delta_v + \Lambda_v) - b\beta_v I_h^* - b\beta_h I_v^* + \delta_h I_h^* + 2\delta_v I_v^*, \\ M_{33} &= -(\delta_h + \Lambda_h + \gamma_h + \delta_v + \Lambda_v) - b\beta_v I_h^* + 2(\delta_h I_h^* + \delta_v I_v^*). \end{aligned}$$

we know that if the Jacobian of our dynamical system with negative real part, then the system will be asymptotically stable.

Lemma 1. *Consider Z to be a real matrix with the dimensions* $3 \times 3)$. *If tr(Z), det(Z), and det($Z^{[2]}$) are all negative, then all eigenvalues of Z have negative real part.*
For the stability of endemic equilibrium we use the above lemma.

Theorem 4. *If $R_0 > 1$, then the endemic equilibrium E^* is locally asymptotically stable.*
Proof. We get the following from the Jacobian matrix $J(E^*)$

$$tra(J(E^*)) = -\Big((\delta_h + 2\Lambda_h + \gamma_h + \delta_v + \Lambda_v) + b\beta_h I_v^* + b\beta_v I_h^*\Big) + 3\delta_h I_h^* + 2\delta_v I_v^*$$

$$tra(J(E^*)) = -\Big(\delta_h + 2\Lambda_h + \gamma_h + \delta_v + \Lambda_v\Big) - I_v^*\Big(b\beta_h - 2\delta_v\Big) - I_h^*\Big(b\beta_v - 3\delta_h\Big)$$

If $b\beta_h \geq 2\delta_v$ and $b\beta_v \geq 3\delta_h$, then

$$tra(J(E^*)) = -\Big(\delta_h + 2\Lambda_h + \gamma_h + \delta_v + \Lambda_v\Big) - I_v^*\Big(b\beta_h - 2\delta_v\Big) - I_h^*\Big(b\beta_v - 3\delta_h\Big) \leq 0.$$

$$det(J(E^*)) = \begin{vmatrix} -\Lambda_h - b\beta_h I_v^* + \delta_h I_h^* & \delta_h S_h^* & -b\beta_h S_h^* \\ b\beta_h I_v^* & -(\delta_h + \Lambda_h + \gamma_h) + 2\delta_h I_h^* & b\beta_h S_h^* \\ 0 & b\beta_v(1 - I_v^*) & -b\beta_v I_h^* - (\delta_v + \Lambda_v) + 2\delta_v I_v^* \end{vmatrix}$$

$$
\begin{aligned}
&det(J(E^*))\\
&= (-\Lambda_h - b\beta_h I_v^* + \delta_h I_h^*)\Bigg[\bigg(-(\delta_h + \Lambda_h + \gamma_h) + 2\delta_h I_h^*\bigg)\bigg(-b\beta_v I_h^* - (\delta_v + \Lambda_v) + 2\delta_v I_v^*\bigg)\\
&\quad - b\beta_v(1 - I_v^*)(b\beta_h S_h^*)\Bigg] - b\beta_h I_v^*\Bigg[\delta_h S_h^*\bigg(-b\beta_v I_h^* - (\delta_v + \Lambda_v) + 2\delta_v I_v^*\bigg) + b\beta_v(1 - I_v^*)b\beta_h S_h^*\Bigg]\\
&= \frac{-\Lambda_h}{S_h^*}\left[\bigg(-(\delta_h + \Lambda_h + \gamma_h) + 2\delta_h I_h^*\bigg)\left(\frac{-b\beta_v I_h^*}{I_v^*} + \delta_v I_v^*\right) - b\beta_v(1 - I_v^*)(b\beta_h S_h^*)\right]\\
&\quad - b\beta_h I_v^*\left[\delta_h S_h^*\left(\frac{-b\beta_v I_h^*}{I_v^*} + \delta_v I_v^*\right) + b\beta_v(1 - I_v^*)b\beta_h S_h^*\right]\\
&= \frac{-\Lambda_h}{S_h^*}\Bigg[(\delta_h + \Lambda_h + \gamma_h)\frac{b\beta_v I_h^*}{I_v^*} - (\delta_h + \Lambda_h + \gamma_h)\delta_v I_v^* - 2b\beta_v\delta_h\frac{I_h^{*2}}{I_v^*} + 2\delta_h\delta_v I_h^* I_v^*\\
&\quad - b^2\beta_h\beta_v S_h^* + b^2\beta_h\beta_v I_v^* S_h^*\Bigg] + b^2\beta_h\beta_v\delta_h S_h^* I_h^* - b\beta_h\delta_v\delta_h S_h^* I_v^{*2} - b^3\beta_h^2\beta_v I_v^* S_h^* + b^3\beta_h^2\beta_v I_v^{*2} S_h^*\\
&= -\frac{(\delta_h + \Lambda_h + \gamma_h)b\beta_v\Lambda_h I_h^*}{I_v^* S_h^*} + \frac{(\delta_h + \Lambda_h + \gamma_h)\delta_v\Lambda_h I_v^*}{S_h^*} + \frac{2b\beta_v\delta_h\Lambda_h I_h^{*2}}{I_v^* S_h^*} - \frac{2\delta_h\delta_v\Lambda_h I_h^* I_v^*}{S_h^*}\\
&\quad + b^2\beta_h\beta_v\Lambda_h - b^2\beta_h\beta_v\Lambda_h I_v^* + b^2\beta_h\beta_v\delta_h S_h^* I_h^* - b\beta_h\delta_v\delta_h S_h^* I_v^{*2} - b^3\beta_h^2\beta_v I_v^* S_h^* + b^3\beta_h^2\beta_v I_v^{*2} S_h^*\\
&= -\Bigg[\left(\frac{(\delta_h + \Lambda_h + \gamma_h)b\beta_v\Lambda_h I_h^*}{I_v^* S_h^*} + \frac{2\delta_h\delta_v\Lambda_h I_h^* I_v^*}{S_h^*} + b^2\beta_h\beta_v\Lambda_h I_v^* + b\beta_h\delta_v\delta_h S_h^* I_v^{*2} + b^3\beta_h^2\beta_v I_v^* S_h^*\right)\\
&\quad - \left(\frac{(\delta_h + \Lambda_h + \gamma_h)\delta_v\Lambda_h I_v^*}{S_h^*} + \frac{2b\beta_v\delta_h\Lambda_h I_h^{*2}}{I_v^* S_h^*} + b^2\beta_h\beta_v\Lambda_h + b^2\beta_h\beta_v\delta_h S_h^* I_h^* + b^3\beta_h^2\beta_v I_v^{*2} S_h^*\right)\Bigg].
\end{aligned}
$$

If

$$
\begin{aligned}
&\left(\frac{(\delta_h + \Lambda_h + \gamma_h)b\beta_v\Lambda_h I_h^*}{I_v^* S_h^*} + \frac{2\delta_h\delta_v\Lambda_h I_h^* I_v^*}{S_h^*} + b^2\beta_h\beta_v\Lambda_h I_v^* + b\beta_h\delta_v\delta_h S_h^* I_v^{*2} + b^3\beta_h^2\beta_v I_v^* S_h^*\right) >\\
&\quad\left(\frac{(\delta_h + \Lambda_h + \gamma_h)\delta_v\Lambda_h I_v^*}{S_h^*} + \frac{2b\beta_v\delta_h\Lambda_h I_h^{*2}}{I_v^* S_h^*} + b^2\beta_h\beta_v\Lambda_h + b^2\beta_h\beta_v\delta_h S_h^* I_h^* + b^3\beta_h^2\beta_v I_v^{*2} S_h^*\right),
\end{aligned}
$$

then

$$
\begin{aligned}
&= -\Bigg[\left(\frac{(\delta_h + \Lambda_h + \gamma_h)b\beta_v\Lambda_h I_h^*}{I_v^* S_h^*} + \frac{2\delta_h\delta_v\Lambda_h I_h^* I_v^*}{S_h^*} + b^2\beta_h\beta_v\Lambda_h I_v^* + b\beta_h\delta_v\delta_h S_h^* I_v^{*2} + b^3\beta_h^2\beta_v I_v^* S_h^*\right)\\
&\quad - \left(\frac{(\delta_h + \Lambda_h + \gamma_h)\delta_v\Lambda_h I_v^*}{S_h^*} + \frac{2b\beta_v\delta_h\Lambda_h I_h^{*2}}{I_v^* S_h^*} + b^2\beta_h\beta_v\Lambda_h + b^2\beta_h\beta_v\delta_h S_h^* I_h^* + b^3\beta_h^2\beta_v I_v^{*2} S_h^*\right)\Bigg] < 0.
\end{aligned}
$$

For the compound matrix, the determinant of $J^{[2]}(E^*)$, we have

$$
det(J^{[2]}(E^*)) = \begin{vmatrix} M_{11} & b\beta_h S_h^* & b\beta_h S_h^* \\ b\beta_v(1 - I_v^*) & M_{22} & \delta_h S_h^* \\ 0 & b\beta_h I_v^* & M_{33} \end{vmatrix},
$$

Where

$$
\begin{aligned}
M_{11} &= -(\delta_h + 2\Lambda_h + \gamma_h) - b\beta_h I_v^* + 3\delta_h I_h^*,\\
M_{22} &= -(\Lambda_h + \delta_v + \Lambda_v) - b\beta_v I_h^* - b\beta_h I_v^* + \delta_h I_h^* + 2\delta_v I_v^*,\\
M_{33} &= -(\delta_h + \Lambda_h + \gamma_h + \delta_v + \Lambda_v) - b\beta_v I_h^* + 2(\delta_h I_h^* + \delta_v I_v^*).
\end{aligned}
$$

$$
\begin{aligned}
&det(J^{[2]}(E^*))\\
&= M_{11}\big(M_{22}M_{33} - b\beta_h\delta_h I_v^* S_h^*\big) - b\beta_v(1 - I_v^*)\big(b\beta_h S_h^* M_{33} - b^2\beta_h^2 I_v^* S_h^*\big)\\
&= -\Big((\delta_h + 2\Lambda_h + \gamma_h) + b\beta_h I_v^* - 3\delta_h I_h^*\Big)\Big[\Big((\Lambda_h + \delta_v + \Lambda_v) + b\beta_v I_h^* + b\beta_h I_v^* - \delta_h I_h^* - 2\delta_v I_v^*\Big)\\
&\quad \Big((\delta_h + \Lambda_h + \gamma_h + \delta_v + \Lambda_v) + b\beta_v I_h^* - 2(\delta_h I_h^* + \delta_v I_v^*)\Big) - b\beta_h\delta_h I_v^* S_h^*\Big]\\
&\quad - b\beta_v(1 - I_v^*)\Big[\Big(b\beta_h S_h^*\Big)\Big(- (\delta_h + \Lambda_h + \gamma_h + \delta_v + \Lambda_v) - b\beta_v I_h^* + 2(\delta_h I_h^* + \delta_v I_v^*)\Big) - b^2\beta_h^2 I_v^* S_h^*\Big]
\end{aligned}
$$

If $\delta_h = 0$ and $\delta_v = 0$, then

$$
\begin{aligned}
&= -\Big((\delta_h + 2\Lambda_h + \gamma_h) + b\beta_h I_v^* - 3\delta_h I_h^*\Big)\Big[\Big((\Lambda_h + \delta_v + \Lambda_v) + b\beta_v I_h^* + b\beta_h I_v^* - \delta_h I_h^* - 2\delta_v I_v^*\Big)\\
&\quad \Big((\delta_h + \Lambda_h + \gamma_h + \delta_v + \Lambda_v) + b\beta_v I_h^* - 2(\delta_h I_h^* + \delta_v I_v^*)\Big) - b\beta_h\delta_h I_v^* S_h^*\Big]\\
&\quad - b\beta_v(I_v^* - 1)\Big[\Big(b\beta_h S_h^*\Big)\Big((\delta_h + \Lambda_h + \gamma_h + \delta_v + \Lambda_v) + b\beta_v I_h^* - 2(\delta_h I_h^* + \delta_v I_v^*)\Big) + b^2\beta_h^2 I_v^* S_h^*\Big] < 0 .
\end{aligned}
$$

Consequently, the endemic equilibrium $E*$ of the model (3.2) is locally asymptotically stable in Γ, in accordance with lemma (1). □

6 Stability of Endemic Equilibrium on a Global Scale

Now we show that when $R_0 > 1$, the endemic equilibrium is globally stable. For this, we introduce some important result.

Lemma 2. *System (3.2) is uniformly persistent if* $R_0 > 1$*, and there exist* $c > 0$ *(Algorithmic independence of initial values), such that* $\liminf_{x\to\infty} S_h(t) \geq c$ *,* $\liminf_{x\to\infty} I_h(t) \geq c$ *and*
$\liminf_{x}{\to\infty}\, I_v(t) \geq c$*.*

Proof. Let Π be a semi-dynamical system (3.2) in $(R_0^+)^3$, X a locally compact metric space and $\Gamma_0 = \{(S_h,I_h,I_v) \in \Gamma \mid I_v = 0\}$. In system (3.2) Γ_0 set is a compact subset of Γ and Γ/Γ_0 set is positively invariant. Let a mapping $P : X \to R_0^+$ be defined by $P(S_h,I_h,I_v) = I_v$ and set $S = \{(S_h,I_h,I_v) \in \Gamma \mid P(S_h,I_h,I_v) < \rho\}$, where ρ is sufficiently small constant so that $R_0(1 - (\Lambda_v/\Lambda_v)\rho) > 1$. Assuming that $x \in S$ is a solution such that, for all $t > 0$, we find $P(\Pi(x,t)) < P(x) < \rho$. Considering Lyapunov function and let δ be the minimum of function, then finally the result becomes:

$$L^{'}(t) \geq \delta L(t). \tag{6.1}$$

The inequality (6.1) means that if $t \to \infty$ then $L(t) \to \infty$. In contrast, $L(t)$ is constrained by the set Γ. This completes the proof of Lemma 2 in [12], which follows from Theorem 1. □

Using Li MY and Muldowney JS's geometrical technique in the feasible region Φ, we analyze the global stability of the endemic equilibrium E^*. We sum up this method as follows (see [9,13,14]). Each solution $y(t,y_0)$ of the differential equation is a $f : y\ 7\!\!\longrightarrow f(y)$ on the E^1 map from the open set $F \subset R^n$ to R^n.

$$y^{'} = f(y) \tag{6.2}$$

is individually defined by the initial value $y(0,y_0)$.

The following are our assumptions: (H_1) D is simply connected;

(H_2) there exists a compact absorbing set $K \subset F$;

(H_3) has unique equilibrium $\bar{y}$ in F. Let $p : y \to p(y)$ be a nonsingular $\binom{n}{2} \times \binom{n}{2}$ matrix valued function which is E^1 in F and a vector norm | . | on R^N, where $N = \binom{n}{2}$.

Let μ be the *Lozinskiˇi* measure with respect to the | . |, then define a quantity $\overline{q_2}$ as

$$\overline{q_2} = \lim_{t \to \infty} \sup \sup \frac{1}{t} \int_0^t \mu(B(y(s, y_0)))ds,$$

where $B = p_f p^{-1} + pj^{[2]}p^{-1}$, $J^{[2]}$ is the Jacobian matrix's J second additive compound matrix. Li and Muldowney have proven the following theorem.

Theorem 5. *Assuming $H_1 - H_3$ holds, the unique endemic equilibrium E^* is globally stable in Φ if and only if $\overline{q_2} < 0$.*

In this case, we employ a matrix-valued function with a norm of $|\cdot|$ in R^3 and 3×3,

$$p(x) = \begin{pmatrix} 1 & 0 & 0 \\ 0 & \frac{I_h}{I_v} & 0 \\ 0 & 0 & \frac{I_h}{I_v} \end{pmatrix}.$$

In the interior of Φ, it is clear that p is E^1 and nonsingular. To obtain the following Jacobian matrix, we linearize system (3.2) about the endemic point E^*.

$$J(E) = \begin{bmatrix} -\Lambda_h - b\beta_h I_v + \delta_h I_h & \delta_h S_h & -b\beta_h S_h \\ b\beta_h I_v & -(\delta_h + \Lambda_h + \gamma_h) + 2\delta_h I_h & b\beta_h S_h \\ 0 & b\beta_v(1 - I_v) & -b\beta_v I_h - (\delta_v + \Lambda_v) + 2\delta_v I_v \end{bmatrix}$$

Also the second additive compound matrix is:

$$J^{[2]}(E) = \begin{bmatrix} M_{11} & b\beta_h S_h & b\beta_h S_h \\ b\beta_v(1 - I_v) & M_{22} & \delta_h S_h \\ 0 & b\beta_h I_v & M_{33} \end{bmatrix},$$

where

$$\begin{aligned} M_{11} &= -(\delta_h + 2\Lambda_h + \gamma_h) - b\beta_h I_v + 3\delta_h I_h, \\ M_{22} &= -(\Lambda_h + \delta_v + \Lambda_v) - b\beta_v I_h - b\beta_h I_v + \delta_h I_h + 2\delta_v I_v, \\ M_{33} &= -(\delta_h + \Lambda_h + \gamma_h + \delta_v + \Lambda_v) - b\beta_v I_h + 2(\delta_h I_h + \delta_v I_v). \end{aligned}$$

The matrix $B = p_f p^{-1} + pj^{[2]}p^{-1}$ can be interpreted as a block matrix

$$B = \begin{bmatrix} B_{11} & B_{12} \\ B_{21} & B_{22} \end{bmatrix},$$

where

$$\begin{aligned} B_{11} &= -(\delta_h + 2\Lambda_h + \gamma_h) - b\beta_h I_v + 3\delta_h I_h, \\ B_{12} &= \left(b\beta_h S_h \frac{I_v}{I_h}, b\beta_h S_h \left(\frac{I_v}{I_h} \right) \right), \\ B_{21} &= \begin{pmatrix} \left(\frac{I_h}{I_v} \right) b\beta_v(1 - I_v) \\ 0 \end{pmatrix}, \\ B_{22} &= \begin{pmatrix} A_{11} & A_{12} \\ A_{21} & A_{22} \end{pmatrix}, \end{aligned}$$

where

$$\begin{aligned} A_{11} &= \frac{I_h'}{I_h} - \frac{I_v'}{I_v} - (\Lambda_h + \delta_v + \Lambda_v) - b\beta_v I_h - b\beta_h I_v + \delta_h I_h + 2\delta_v I_v, \\ A_{12} &= \delta_h S_h, \\ A_{21} &= b\beta_h I_v, \\ A_{22} &= \frac{I_h'}{I_h} - \frac{I_v'}{I_v} - (\delta_h + \Lambda_h + \gamma_h + \delta_v + \Lambda_v) - b\beta_v I_h + 2(\delta_h I_h + \delta_v I_v). \end{aligned}$$

Take into account the norm in R^3, which is defined as $|(u,v,w)| = max(|u|,|v| + |w|)$, where (u,v,w) denotes the vector in R^3. With regards to the define norm, the *Lozinskiĭ* measure is

$\mu(B) \leq \sup(g_1, g_2)$, (6.3)

with
$g1 = \mu 1(B11) + |B12|, g2 = \mu 1(B22) + |B21|$.
From system (3.2), we write down

$$\frac{I_h'}{I_h} = \frac{b\beta_h I_v S_h}{I_h} - (\delta_h + \Lambda_h + \gamma_h) + \delta_h I_h$$
$$\frac{I_v'}{I_v} = \frac{b\beta_v I_h}{I_v} - b\beta_v I_h - (\delta_v + \Lambda_v) + \delta_v I_v.$$
,

whereas B_{11} is a scalar quantity, (therefore, each R^1 vector norm has a *Lozinskiˇi* measure equal to B_{11}. Therefor

$$\mu_1(B_{11}) = B_{11} = -(\delta_h + 2\Lambda_h + \gamma_h) - b\beta_h I_v + 3\delta_h I_h$$
$$|B_{12}| = b\beta_h S_h \frac{I_v}{I_h},$$
,

also g_1 will become

$$\begin{aligned} g_1 &= -(\delta_h + 2\Lambda_h + \gamma_h) - b\beta_h I_v + 3\delta_h I_h + b\beta_h S_h \frac{I_v}{I_h} \\ &= -(\delta_h + \Lambda_h + \gamma_h) - b\beta_h I_v + \delta_h I_h + b\beta_h S_h \frac{I_v}{I_h} - \Lambda_h + 2\delta_h I_h \\ &= \frac{I_h'}{I_h} - \Lambda_h - b\beta_h I_v + 2\delta_h I_h \\ &\le \frac{I_h'}{I_h} - \Lambda_h + 2\delta_h I_h. \end{aligned} \tag{6.4}$$

Further, $|B_{21}| = b\beta_v(1 - I_v)\left(\frac{I_h}{I_v}\right)$. The norm operators of $|B_{12}|$, which map from R^2 to R, are denoted by the notation B_{12}, and $|B_{21}|$ are the norm operator of B_{21} which are mapping from R to R^2, as well as the $\imath_1$ norm being a part of R^2. Furthermore, B_{22} is 2×2 matrix and $\mu_1(B_{22})$ is its *Lozinskiˇı* measure with regard to $\imath_1$ norm in R^2. Consider the following

$$\begin{aligned} \mu_1(B_{22}) = \sup \Bigg[& \frac{I_h'}{I_h} - \frac{I_v'}{I_v} - (\Lambda_h + \delta_v + \Lambda_v) - b\beta_v I_h - b\beta_h I_v + \delta_h I_h + 2\delta_v I_v + b\beta_h I_v, \\ & \frac{I_h'}{I_h} - \frac{I_v'}{I_v} - (\delta_h + \Lambda_h + \gamma_h + \delta_v + \Lambda_v) - b\beta_v I_h + 2(\delta_h I_h + \delta_v I_v) - \delta_h S_h \Bigg] \\ = {} & \frac{I_h'}{I_h} - \frac{I_v'}{I_v} - (\Lambda_h + \delta_v + \Lambda_v) - b\beta_v I_h + \delta_h I_h + 2\delta_v I_v. \end{aligned}$$
,

Hence,

$$\begin{aligned} g_2 &= \mu_1(B_{22}) + |B_{21}| \\ &= \frac{I_h'}{I_h} - \frac{I_v'}{I_v} - (\Lambda_h + \delta_v + \Lambda_v) - b\beta_v I_h + \delta_h I_h + 2\delta_v I_v + \frac{I_h}{I_v} b\beta_v(1 - I_v) \\ &= \frac{I_h'}{I_h} - \frac{I_v'}{I_v} - \Lambda_h - (\delta_v + \Lambda_v) - b\beta_v I_h + \delta_h I_h + 2\delta_v I_v + \frac{b\beta_v I_h}{I_v} - b\beta_v I_h \\ &= \frac{I_h'}{I_h} - \frac{I_v'}{I_v} - \Lambda_h + \frac{b\beta_v I_h}{I_v} - b\beta_v I_h - (\delta_v + \Lambda_v) + \delta_v I_v - b\beta_v I_h + \delta_h I_h + \delta_v I_v \qquad (6.5) \\ &= \frac{I_h'}{I_h} - \frac{I_v'}{I_v} + \frac{I_v'}{I_v} - \Lambda_h - b\beta_v I_h + \delta_h I_h + \delta_v I_v \\ &= \frac{I_h'}{I_h} - \Lambda_h - b\beta_v I_h + \delta_h I_h + \delta_v I_v \\ &\le \frac{I_h'}{I_h} - \Lambda_h + \delta_h I_h + \delta_v I_v. \end{aligned}$$

Thus,

$$\mu(B) = sup(g_1, g_2) \le \left(\frac{I_h'}{I_h}\right) - \Lambda_h. \tag{6.6}$$

Because the system (3.2) is consistently persistent for $R_0 > 1$, and consequently when $t > 0$, such that $t > T$, implies that $S_h(t) \geq c$, $I_h(t) \geq c$, $I_v(t) \geq c$ and $\frac{\log I_h(t)}{t} < -\frac{\Lambda_h}{2}$, for all $(S_h(0), I_h(0), I_v(0)) \in K$. Thus,

$$\frac{1}{t}\int_a^b \mu(B)\mathrm{d}t < \frac{\log I_h(t)}{t} - \Lambda_h < -\frac{\Lambda_h}{2}, \tag{6.7}$$

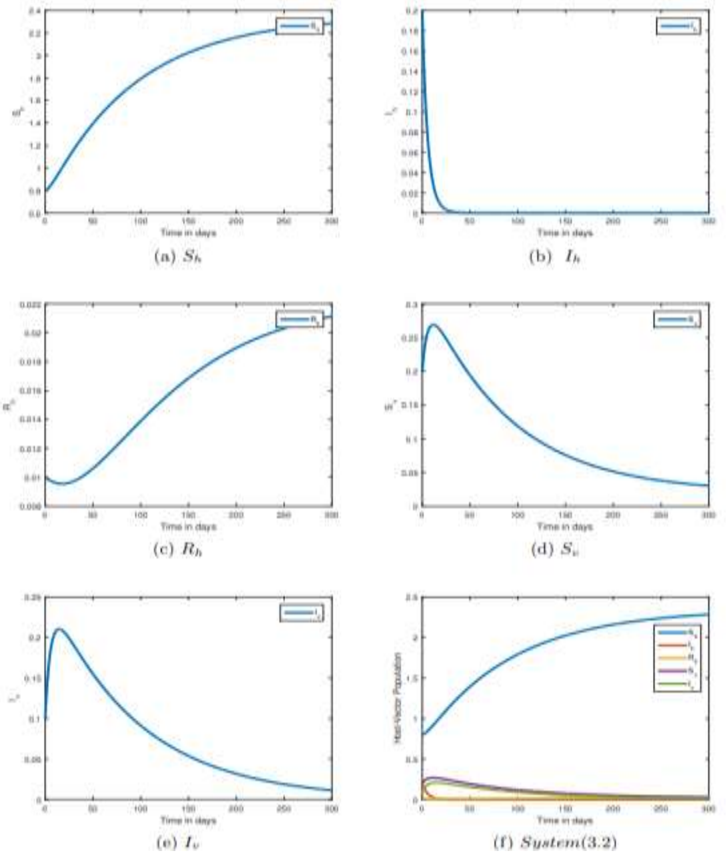
for all $(S_h(0), I_h(0), I_v(0)) \in K$. In addition, this implies that $q_2 < \overline{0}$. This proves that Theorem 5 holds true. This indicates that E^* is globally asymptotically stable in Γ.

7 Numerical simulations

In this section, the transmission processes of Vector-Born Disease with Linear Incidence Rate has been presented with the help of a numerical scheme to elaborate the dynamical behavior of the system. Our simulation has been performed by applying the well-known MATLAB 2020 a and Runge Kutta order 4th MATLAB 2020a method. Different scenarios are accomplished with different assumptions of input values. For these numerical simulations, we considered the values of input factors of the system of dengue from Table 1. Moreover, the values of state variables are taken as follows: $S_h = 0.8, I_h = 0.2, R_h = 0.1, S_v = 0.2$ and $V_v = 0.1$.

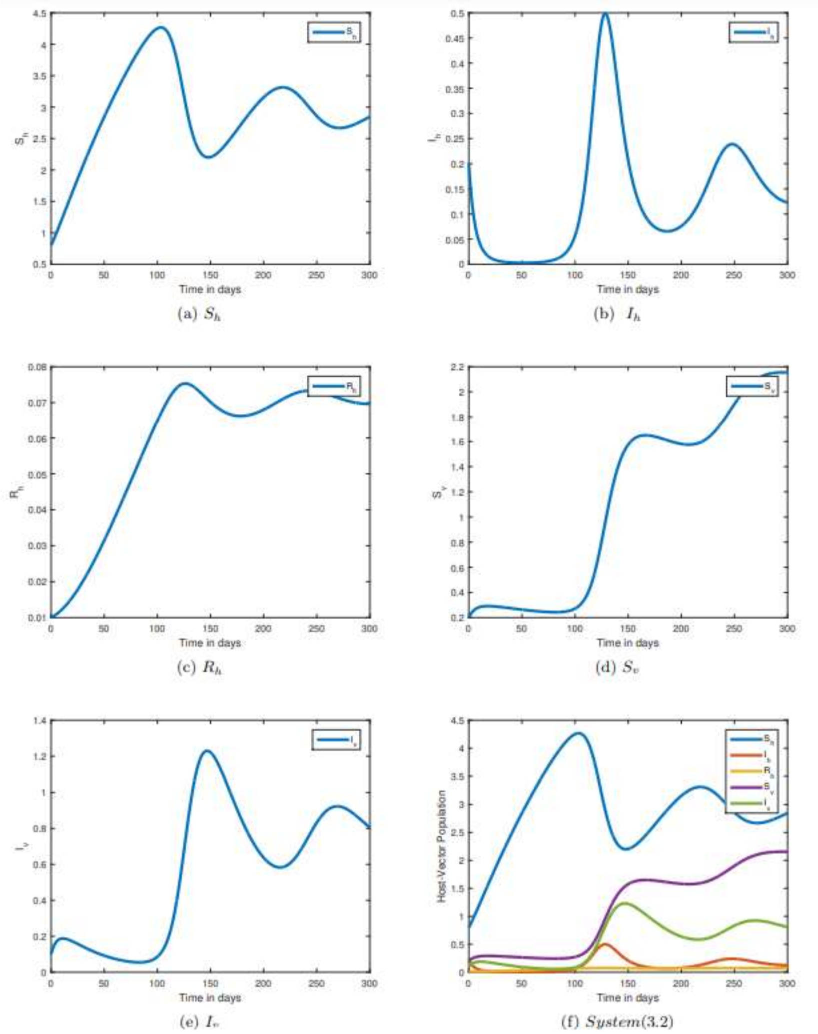
Symbol	Description of parameter	X1	X2	
Λ_h	The recruitment and natural fatality rate of humans	0.01	0.1	
Λ_v	The recruitment and natural fatality rate of vectors	0.02	0.2	
β_h	The rate of new infection to human	0.24	0.23	
β_v	The rate of new infection to vector	0.13	0.34	
δh	Disease mortality rates among humans	0.5	0.5	
δv	Death rates of vector due to disease	0.14	0.17	
γ_h	The rate of infectious individuals acquire permanent immunity	0.01	0.1	

Table 1: The duration of incubation for some epidemic illnesses.



(a) S_h (b) I_h
(c) R_h (d) S_v
(e) I_v (f) $System(3.2)$

Figure 1: The dynamics of each state variable for the system (3.2).



(a) S_h (b) I_h

(c) R_h (d) S_v

(e) I_v (f) $System(3.2)$

Figure 2: The dynamics of each state variable for the system (3.2).

8 Conclusion

In this paper, we present a host-vector model for vector-borne diseases that accounts for direct transmission and a dynamic human population. It refers to conditions that have a high mortality rate over a prolonged period of time (e.g., dengue fever or malaria). A mosquito model carrying a disease vector is numerically analyzed. In this model, the new infection rate in both human and vector populations is represented by a single number, R_0. The basic reproduction number R_0 governs the model's (3.2) local and global dynamics. By developing Lyapunov work, we demonstrated that the disease-free equilibrium E_0 is globally asymptotically stable in Γ, if $R_0 \leq 1$ and thus the disease are reach to ends always. If $R_0 > 1$, then the unique endemic equilibrium exists and endemic equilibrium E^* is globally asymptotically stable in Γ and thus the disease alloy at the endemic equilibrium if it is initially present.

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9 Appendix

Utilizing the transformation $I_h = \frac{i_h}{N_H}$, $S_h = \frac{s_h}{N_H}$, $S_v = \frac{s_v}{N_V}$, $R_h = \frac{r_h}{N_H}$ and $I_v = \frac{i_v}{N_V}$ for scaling, their differentials:

$\frac{dS_h}{dt} = \frac{1}{N_H}\left[\frac{ds_h}{dt} - S_h\frac{dN_H}{dt}\right]$, $\frac{dI_h}{dt} = \frac{1}{N_H}\left[\frac{di_h}{dt} - I_h\frac{dN_H}{dt}\right]$, $\frac{dR_h}{dt} = \frac{1}{N_H}\left[\frac{dr_h}{dt} - R_h\frac{dN_H}{dt}\right]$,
$\frac{dS_v}{dt} = \frac{1}{N_V}\left[\frac{ds_v}{dt} - S_v\frac{dN_V}{dt}\right]$, $\frac{dI_v}{dt} = \frac{1}{N_V}\left[\frac{di_v}{dt} - I_v\frac{dN_V}{dt}\right]$, and from the system (2.1) and (2.2), we acquire the dimensionless form (3.1). If $\delta_h = 0$ and $\Lambda_h = \mu_h$, then $N'_H(t)$ becomes vanish and so $N_H(t)$ remains constant at its initial value N_{H0}. In this case, the system (2.1) becomes the model with constant populace whose dynamics are the similar as the transform system (3.1). Hence, all the solutions with initial condition $s_{h0}+i_{h0}+r_{h0} = N_{H0}$ tends to $(N_{H0},0,0)$, if $R_0 \leq 1$, and the $N_{H0}(s^*_h, i^*_h, r^*_h)$, if $R_0 > 1$. In the other rest part of this section, we assume that $\delta_h > 0$.