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Modeling Dynamical Interactions between Leptospirosis Infected Vector and Human Population

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Abstract

In this paper, we combined two non-linear models of human and vector (rats) population. First, we present the local asymptotic stability of disease-free equilibria. Then, we present the endemic equilibrium and backward bifurcation for several parameters. We also show the global asymptotical stability of both disease-free and endemic equilibrium by using the Lyapunov function theory. Finally, we present the numerical simulations of a real leptospirosis epidemic for justification of our work.

Mathematics Subject classification: 92D25, 49J15, 93D20

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1 Introduction

Leptospirosis disease has emerged as a globally important infectious disease, in the past decade. This kind of infection occurs in urban areas of industrialized and the developed countries, as well as in rural regions worldwide. The people belong to the city area slums who wade through dirty water are mostly infected. Rice planters, sewer cleaners, workers cleaning canals, agriculture labor easily contract this disease. Mortality remains significant, related both to delays in diagnosis due to lack of infrastructure and adequate clinical suspicion, and the poorly reason that may include pathogenicity of some leptospiral strains or genetically determined host immunopathological responses. Many models have been proposed to represents the compartmental dynamics of both susceptible, infected and recovered human and vector population [1, 2, 3]. Pongsuumpun et al. [4] developed mathematical models to study the behavior of leptospirosis disease. In their work, they represent the rate of change for both rats and human population. The human population is further divided into two main groups Juveniles and adults. Triampo et al. [5] considered a deterministic models for the transmission of leptospirosis disease presented in [5]. In their work they considered a number of leptospirosis disease in Thailand and shown the numerical simulations. Zaman [6] considered the real data presented in [5] to studied the dynamical behavior and role of optimal control theory of this disease.

In this paper, we extend the model presented in [6] by taking into account the interaction of susceptible human with infected vector and disease related death rate in both infected human and vectors. First, we present the local asymptotic stability of disease-free equilibria of the extended model. Then, we present the endemic equilibrium and backward bifurcation for several parameters. We also introducing the basic reproduction number in the disease-free and endemic equilibrium. To find global stability of the disease-free and the endemic equilibrium we develop a Lyapunov function. In order to this, we first combining both system to develop a single system consisting of five differential equations and present the dynamical behavior. Finally, we present numerical simulation of our proposed model.

The paper is organized as follows. Section 2 is devoted to the mathematical formulation of Leptospirosis disease. We discuss the local asymptotical stability of both disease-free and endemic equilibrium in Section 3. In Section 4 we show global stability of both the disease-free and endemic equilibrium. In Section 5 we consider the real data for numerical simulations and discuss in detail our numerical results. Finally, we conclude our work.

2 Mathematical formulation

In this section, we extend the model presented in [6] by taking into account the interaction of susceptible human with infected vector and disease related death rate in both infected human and vectors. To understand the basic properties of the epidemic model, we first formulate the model in detail and define the parameter involve in the model. To this end, we assume that $S_h(t)$ represents number of susceptible human at time t; $I_h(t)$ represents number of human in the population, which is infected from the leptospirosis disease at time t; $R_h(t)$ represents number of human in the population which is recovered at time t; we denote the total population size by N_h, with $N_h(t) = S_h(t) + I_h(t) + R_h(t)$. For vector population, let $S_v(t)$ are susceptible vector and $I_v(t)$ are infectious vector at time t. The total population size of vector population is denoted by N_v with $N_v(t) = S_v(t) + I_v(t)$. By the interaction of both human and vector population we get the following system of five differential equations is given by:

$$\begin{aligned}
\tfrac{dS_h}{dt} &= b_1 - \mu_h S_h - \beta_2 S_h I_v - \beta_1 S_h I_h + \lambda_h R_h, \\
\tfrac{dI_h}{dt} &= \beta_2 S_h I_v + \beta_1 S_h I_h - \mu_h I_h - \delta_h I_h - \gamma_h I_h, \\
\tfrac{dR_h}{dt} &= \gamma_h I_h - \mu_h R_h - \lambda_h R_h, \\
\tfrac{dS_v}{dt} &= b_2 - \gamma_v S_v - \beta_3 S_v I_h, \\
\tfrac{dI_v}{dt} &= \beta_3 S_v I_h + \mu_v I_v - \gamma_v I_v - \delta_v I_v,
\end{aligned} \tag{1}$$

with initial conditions

$$S_h(0) \geq 0, \qquad I_h(0) \geq 0, \qquad R_h(0) \geq 0, \qquad S_v(0) \geq 0, \qquad I_v(0) \geq 0. \tag{2}$$

Here b_1 is the recruitment rate of human population, susceptible human can be infected by two ways of transmission, β_1 which represents the direct transmission from infected human and β_2 is the rate of transmission from infected vector. μ_h is the natural mortality rate of human, γ_h is the recovery rate of human. In this work, we assumed that disease may be fatal to some infectious host, so δ_h represents the disease related death rate of infected individuals. b_2 is the recruitment rate of vector population. μ_v is the natural mortality rate of vector population. The infectious vector die due to disease at a rate of δ_v, β_3 represents the disease carrying of susceptible vector per host per unit time. γ_v is the death rate of vector. The complete flow chart which show the interaction of both human and vector are represented in Figure 1. The total dynamics of human population is given by

$$\frac{dN_h}{dt} = b_1 - \mu_h N_h - \delta_h I_h. \tag{3}$$

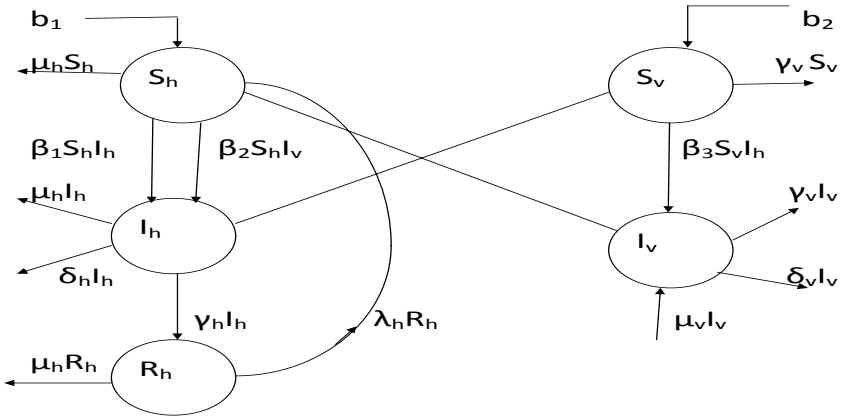

Figure 1: The plot represents the interaction of both human and vector population.

The initials conditions (2) ensures that $N_h(0) \geq 0$. Thus $N_h(t)$ is positive and bounded for all finite time t > 0. The total dynamics of vector population is

$$\frac{dN_v}{dt} = b_2 - N_v\gamma_v - \delta_v I_v, \tag{4}$$

using (3) and (4) we get

$$\frac{dN_h}{dt} \leq b_1 - \mu_h N_h, \qquad \frac{dN_v}{dt} \leq b_2 - \gamma_v N_v. \tag{5}$$

Then $\lim_{t\to\infty} SupN_h \leq \frac{b_1}{\mu_h}$ and $\lim_{t\to\infty} SupN_v \leq \frac{b_2}{\gamma_v}$.
The feasible region for system (1) is

$$\Omega = ((S_h, I_h, R_h, S_v, I_v) \in R^5_+, \qquad (N_h \leq \frac{b_1}{\mu_h}, N_v \leq \frac{b_2}{\gamma_v})).$$

Proposition 2.1. *Let $(S_h, I_h, R_h, S_v, I_v)$, be the solution of the system (1) with initial conditions (2) and closed set*
$\Omega = ((S_h, I_h, R_h, S_v, I_v) \in R^5_+, N_h \leq \frac{b_1}{\mu_h}, N_v \leq \frac{b_2}{\gamma_v})$, *then Ω is positively invariant and attracting under the flow described by the system (1).*
Proof. *Consider the Lyapunov function*

$$V(t) = (N_h(t), N_v(t)) = (S_h + I_h + R_h, S_v + I_v). \tag{6}$$

The time derivative of this equation is given by:

$$\frac{dV}{dt} = (b_1 - \mu_h N_h - \delta_h I_h \quad , \quad b_2 - \gamma_v N_v - \delta_v I_v). \tag{7}$$

Now it is easy to prove that

$$\begin{aligned} &\tfrac{dN_h}{dt} \leq b_1 - \mu_h N_h \leq 0 \qquad for \quad N_h \geq \tfrac{b_1}{\mu_h}, \\ &\tfrac{dN_v}{dt} \leq b_2 - \gamma_v N_v \leq 0 \qquad for \quad N_v \geq \tfrac{b_2}{\gamma_v}. \end{aligned} \tag{8}$$

Thus it follows that $\frac{dv}{dt} \leq 0$ *which implies that* Ω *is positively invariant set, and also a standard comparison theorem [11] is used to show that*

$$0 \leq (N_h, N_v) \leq ((N_h(0)e^{-\mu_h t} + \frac{b_1}{\mu_h}(1 - e^{-\mu_h t}), \quad N_v(0)e^{-\gamma_v t} + \frac{b_2}{\gamma_v}(1 - e^{-\gamma_v t})).$$

Thus as $t \to \infty$, $0 \leq (N_h, N_v) \leq (\frac{b_1}{\mu_h}, \frac{b_2}{\gamma_v})$ *and so* Ω *is an attracting set.*

3 Disease-free equilibrium

In this section first we present the dynamical behavior. For the dynamical behavior, we set left hand side of the system (1) equal to zero, and consider only the susceptible human and susceptible vector population such that E_1=$(S_h^o, 0, 0, S_v^o, 0)$, where $S_h^o = \frac{b_1}{\mu_h}$ and $S_v^o = \frac{b_2}{\gamma_v}$. The quantity R_0 is the threshold of the disease as follows:

$$R_0 = \frac{b_1}{\mu_h}(\frac{\beta_2\beta_3 b_2}{\gamma_v Q_1 Q_2} + \frac{\beta_1}{Q_2}),$$

where

$$Q_1 = (\delta_v + \gamma_v - \mu_v), \qquad Q_2 = (\mu_h + \delta_h + \gamma_h), \qquad Q_3 = \mu_h + \lambda_h.$$

The threshold quantity R_0 is also called the basic reproduction number of the disease [7, 8]. It shows the expected number of new infections which is produced directly and indirectly by a single infected individual by introducing into a completely susceptible population. For epidemic models, it is common that the basic reproduction number is the threshold quantity when $R_0 < 1$, the disease dies out which shows that an average of each infected individual infects fewer than one individual. On the other hand, we can expect the disease to spread in the community when $R_0 > 1$.

Theorem 3.1. *For $R_0 \geq 1$, then the disease free equilibrium point E_1 of the system (1) is locally asymptotically stable, if $Q_2 > \frac{\beta_1 b_1}{\mu_h}$, otherwise unstable.*
Proof. *The local stability of the disease-free equilibrium, solution can be examined by setting left hand side equal to zero of the system (1) around E_1. This gives the following Jacobian matrix*

$$J_1 = \begin{bmatrix} -\mu_h & -\beta_1 S_h^o & \lambda_h & 0 & -\beta_2 S_h^o \\ 0 & -Q_2 + \beta_1 S_h^o & 0 & 0 & \beta_2 S_h^o \\ 0 & \gamma_h & -Q_3 & 0 & 0 \\ 0 & -\beta_3 S_v^o & 0 & -\gamma_v & 0 \\ 0 & \beta_3 S_v^o & 0 & 0 & -Q_1 \end{bmatrix}.$$

Using some elementary row operations we get characteristics equation for the above matrix is

$$(-\mu_h - \lambda)(M_1 - \lambda)(-Q_3\beta_3 S_v^o - \lambda)(-\gamma_v - \lambda)(-M_1 Q_1 - \beta_2\beta_3 S_h^o S_v^o - \lambda) = 0,$$

where $M_1 = -Q_2 + \beta_1 S_h^o$. There are five eigenvalues corresponding to the above characteristics equation are given by $\lambda_1 = -\mu_h < 0$, $\lambda_2 = -\gamma_v < 0$, $\lambda_3 = -Q_3\beta_3 S_v^o < 0$, $\lambda_4 = -Q_2 + \beta_1 S_h^o$, $\lambda_5 = -M_1 Q_1 - \beta_2\beta_3 S_h^o S_v^o$ $\lambda_5 < 0 \Leftrightarrow -M_1 Q_1 - \beta_3\beta_2 S_h^o S_v^o < 0$. By using the value of M_1, S_h^o and S_v^o and a little rearrangement we get $\mu_h\gamma_v Q_1 Q_2(R_0 - 1) > 0$, $\lambda_4 = M_1$ $\lambda_4 < 0 \Leftrightarrow M_1 < 0$, using the value of M_1 we get $Q_2 > \frac{\beta_1 b_1}{\mu_h}$. Thus all the eigenvalues have negative real parts if $Q_2 > \frac{\beta_1 b_1}{\mu_h}$, so the above system is locally asymptotically stable. ■

Remark 1. *The Jacobian matrix around the trivial equilibrium $E_0 = (0, 0, 0, 0, 0)$*

$$J_0 = \begin{bmatrix} -\mu_h & 0 & \lambda_h & 0 & 0 \\ 0 & -Q_2 & 0 & 0 & 0 \\ 0 & \gamma_h & -Q_3 & 0 & 0 \\ 0 & 0 & 0 & -\gamma_v & 0 \\ 0 & 0 & 0 & 0 & -Q_1 \end{bmatrix}.$$

By elementary row operation we get the eigen values from the characteristics equation of the above Jacobian matrix. The eigen values around the trivial equilibrium $E_0 = (0, 0, 0, 0, 0)$ *are* $\lambda_1 = -\mu_h < 0$, $\lambda_2 = -Q_2 < 0$, $\lambda_3 = -Q_2Q_3 < 0$, $\lambda_4 = -\gamma_v < 0$ $\lambda_5 = -Q_1 < 0$.
All the eigenvalues have negative real part, which shows that the trivial equilibrium is locally stable.

Theorem 3.2. *The given system (1) around the disease-free equilibrium* $E_1 = (1, 0, 0, 0, 0)$ *is locally locally asymptotically stable if and only if* $Q_2 > \beta_1$.
Proof: *The disease-free equilibrium around* $E_1 = (1, 0, 0, 0, 0)$ *gives us the following Jacobian matrix.*

$$J_1 = \begin{bmatrix} -\mu_h & -\beta_1 & -\lambda_h & 0 & -\beta_2 \\ 0 & -Q_2 + \beta_1 & 0 & 0 & \beta_2 \\ 0 & \gamma_h & -Q_3 & 0 & 0 \\ 0 & 0 & 0 & -\gamma_v & 0 \\ 0 & 0 & 0 & 0 & -Q_1 \end{bmatrix}.$$

By some elementary row operation, we get the eigenvalues to the above matrix are $\lambda_1 = -\mu_h < 0$, $\lambda_2 = -Q_2+\beta_1$, $\lambda_3 = Q_2Q_3-\beta_1Q_3$, $\lambda_3 < 0 \Leftrightarrow -Q_2Q_3+\beta_1Q_3 > 0$, $Q_2 > \beta_1$. $\lambda_4 = -\gamma_v < 0$, $\lambda_5 = -Q_1 < 0$ *all the eigenvalues have negative real part if* $Q_2 > \beta_1$. ■

3.1 Endemic equilibria and bifurcation analysis

To find endemic equilibria of the system (1) where at least one of the infected components of the system (1) is non zero. For the endemic equilibrium of the system (1), we set left hand side of the system (1) equal to zero to get

$$S_h^* = \frac{Q_1Q_2(\gamma_v + \beta_3 I_h^*)}{\beta_2\beta_3 b_2 + \beta_1 Q_1(\gamma_v + \beta_3 I_h^*)}, S_v^* = \frac{b_2}{\gamma_v + \beta_3 I_h^*}, I_v^* = \frac{\beta_3 b_2 I_h^*}{Q_1(\gamma_v + \beta_3 I_h^*)}, R_h^* = \frac{\gamma_h}{Q_3} I_h^*.$$

In above expression for the endemic equilibria the infected component I_h^* is non zero. By using the value of S_h^* and I_v^* in first equation of the system (1), and setting left hand side equal to zero, we get

$$f(I_h^*) = aI_h^2 + bI_h + c = 0,$$

where $a = \beta_1\beta_3Q_1Q_2$, $b = (-\beta_1\beta_3Q_1b_1 + \beta_3\mu_hQ_1Q_2 + \beta_2\beta_3b_2Q_1Q_2 + \beta_1\gamma_vQ_1Q_2)$, $c = \mu_h\gamma_vQ_1Q_2(1 - R_0)$. Here the coefficients a is positive and

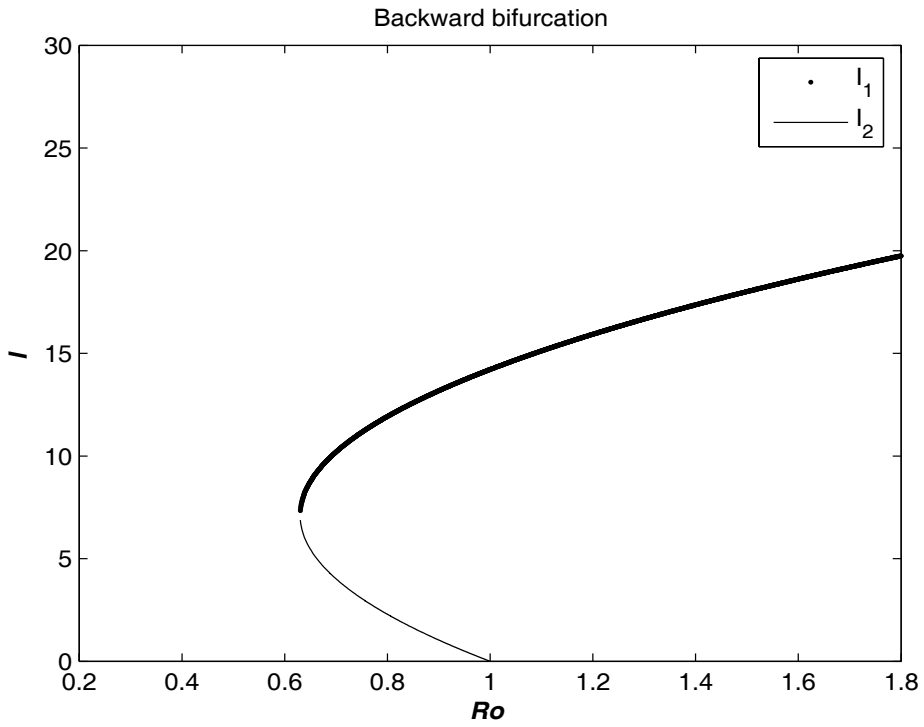

Figure 2: The plot shows the backward bifurcation.

can never be negative, c depends upon R_0, if $R_0 < 1$ then c is positive otherwise negative. Since $a > 0$, then the positive solution of the above equation depends upon b and c. For $R_0 > 1$ then the above equation gives us two roots, one is positive and the other one is negative. By substituting $R_0 = 1$, the equation have nonzero solution $I = -\frac{b}{a}$, which is positive in the case if and only if $b < 0$. For $b < 0$ there is a positive solution for $R_0 = 1$. It means that equilibria depends upon R_0, and there exists an open interval which have two positive roots $I_1 = \frac{-b-\sqrt{b^2-4ac}}{2a}$ and $I_2 = \frac{-b+\sqrt{b^2-4ac}}{2a}$. For $c > 0$ either $b^2 < 4ac$ or $b \geq 0$, then the above equation have no positive solution.

Now we find backward bifurcations, in order to do this we set $b^2 - 4ac = 0$, and $R_0 = R_c$ and solve for critical value of R_c is given by $R_c = 1 - \frac{b^2}{4a\mu_h\gamma_v Q_1 Q_2}$. Backward bifurcation occur when R_0 exists and $R_c < R_0$ with restriction that the discriminant is positive such that $R_c < R_0 < 1$. Figure 2 represents the backward bifurcation for the parameter values: $\mu_h = 0.2$, $\gamma_v = 0.0036$, $\delta_h = 0.002$, $\gamma_h = 0.003$, $\delta_v = 0.025$, $b_1 = 19$, $b_2 = 45$, $\beta_1 = 0.002026$, $\beta_2 = 0.00009$, $\beta_3 = 0.00002$, $\mu_v = 0.2$. The value of parameters satisfied the above conditions for the backward bifurcation. If we change the value of transmission coefficients β_1, β_2, β_3, the value of the basic reproduction number also change represents in Figure 3.

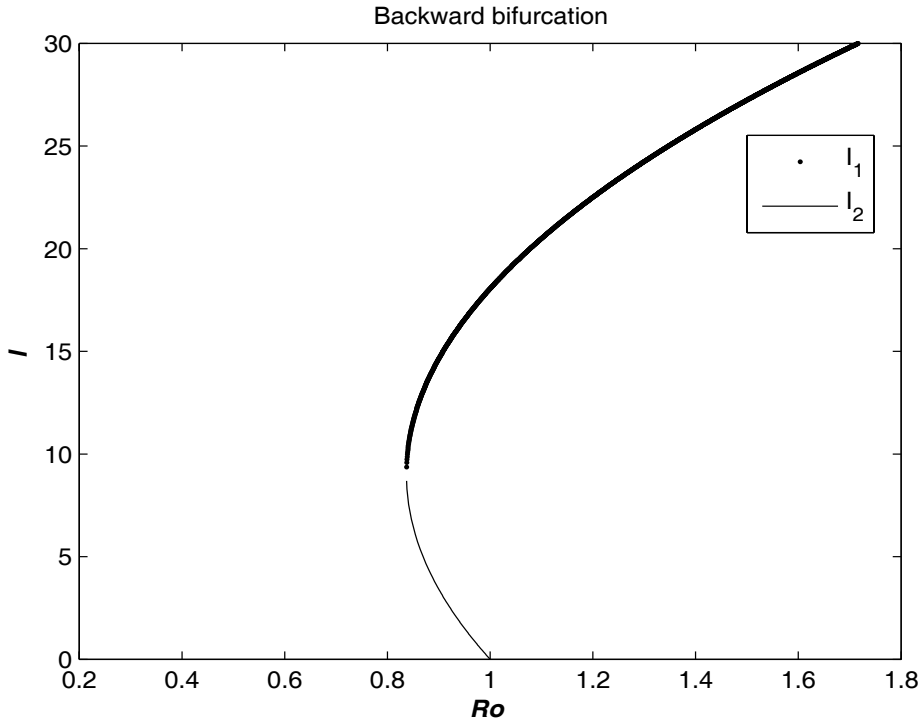

Figure 3: The plot shows the backward bifurcation for different values of b_1, b_2, β_1 and β_2.

Theorem 3.3. *When $R_0 > 1$, the endemic equilibrium state of the system (1) is locally asymptotically stable if $Q_1 > 1$.*

***Proof**: The Jacobian matrix of the system (1) around endemic equilibrium is given by*

$$J^* = \begin{bmatrix} -M_1 & -\beta_1 S_h^* & 0 & -\beta_h S_h^* \\ 0 & M_3 & 0 & M_4 \\ 0 & 0 & -\gamma_v & -Q_1 \\ 0 & 0 & 0 & \gamma_v M_5 - Q_1 M_3 \beta_3 I_h^* \end{bmatrix},$$

where $M_1 = \mu_h + \beta_1 I_h^* + \beta_2 I_v^*$, $M_2 = \beta_1 I_h^* + \beta_2 I_v^*$, $M_3 = -Q_2 + \frac{\mu_h \beta_1 S_h^*}{Q_1 M_1}$, $M_4 = \frac{\alpha_h \mu_h \beta_2 S_h^*}{Q_1 M_1}$, $M_5 = -M_3 Q_1 - M_4 \beta_3 S_v^*$.
The eigenvalues corresponding to the above Jacobian matrix are
$\lambda_1 = -M_1 < 0$, $\lambda_2 = -\gamma_v < 0$, $\lambda_4 = \gamma_v M_5 - Q_1 M_3 \beta_3 I_h^*$, $\lambda_4 < 0 \Leftrightarrow \gamma_v M_5 - Q_1 M_3 \beta_3 I_h^* < 0$,
$\gamma_v M_5 - Q_1 M_3 \beta_3 I_h^* < 0$.
By using the value of M_5, we get $\gamma_v(M_3 Q_1 + M_4 \beta_3 S_v^*) + Q_1 M_3 \beta_3 I_h^* > 0$,
$\lambda_3 = M_3$,
$\lambda_3 < 0 \Leftrightarrow M_3 < 0$. *For $M_3 < 0$, we have $Q_1 Q_2 M_1 - \mu_h \beta_h S_h^* > 0$.*

Now, we putting the value of M_1 and S_h^* and taking some rearrangement,

to get

$$(I_h^*)^2[b_1\mu_h\beta_1\beta_3^2Q_1(Q_1-1)+\beta_2\beta_3^2b_2b_1+\beta_1^2Q_1^2\beta_3^2b_1]$$

$$+I_h^*[2\beta_1\beta_3\mu_h\gamma_vQ_1b_1(Q_1-1)+\beta_2\beta_3b_2Q_1b_1(\beta_3\mu_h+\beta_1\beta_3)+2b_1\beta_1^2\beta_3Q_1^2\gamma_v+\beta_2\beta_3b_2\mu_h\gamma_vQ_1Q_2R_0]$$

$$+[\mu_h\gamma_vQ_1^2Q_2\beta_1\gamma_v(R_0-1)+\mu_h\gamma_vQ_1^2Q_2\beta_1\gamma_vR_0+\mu_h\gamma_vQ_1\beta_2\beta_3b_2b_1+\beta_1Q_1\gamma_v^2b_1\mu_h(Q_1-1)]>0.$$

All the coefficients of above expression are positive if $R_0>1$ and $Q_1>1$. Thus, all the eigenvalues have negative real parts so it is proved that the endemic equilibrium is locally asymptotically stable. ■

4 Global Stability analysis

To show that the system (1) is globally asymptotically stable, we use the Lyapunov functional theory for both disease-free and endemic equilibrium. First we present the globally stability of the disease-free equilibrium.

Theorem 4.1. *The disease-free equilibrium of the system (1) is globally asymptotically stable if $Q_3Q_2>\lambda_h\gamma_h$.*
Proof: *For the global stability of the disease-free we define he Lyapunov function in the following form*

$$V(t)=W_1(S_h-S_h^o)+W_2(S_v-S_v^o)+W_3I_v+W_4I_h+W_5R_h,$$

where W_1, W_2, W_3, W_4, W_5 are positive constants to be chosen later.
Taking the time derivative and using the system (1) we obtain

$$\begin{aligned}V'(t) &= W_1[b_1-\mu_hS_h-\beta_2S_hI_v-\beta_1S_hI_h+\lambda_hR_h]+W_2[b_2-\gamma_vS_v-\beta_3S_vI_h]\\ &\quad +W_3[\beta_3S_vI_h-Q_1I_v]+W_4[\beta_2S_hI_v+\beta_1S_hI_h-Q_2I_h]+W_5[\gamma_hI_h-Q_3R_h],\end{aligned}$$

where ($\prime$) denotes the derivative with respect to time. Using $b_1=\mu_hS_h^o$, $b_2=\gamma_vS_v^o$ and choosing the constant $W_1=W_4=Q_3$, $W_3=W_2=1$, $W_5=\lambda_h$ and after rearrangement, we get

$$V'(t)=-Q_3\mu_h(S_h-S_h^0)-\gamma_v(S_v-S_v^0)-Q_1Iv-I_h(Q_3Q_2-\lambda_h\gamma_h).$$

The disease-free equilibrium of the system (1) is globally asymptotically stable if $Q_3Q_2>\lambda_h\gamma_h$. $V'(t)$ is negative for $S_h=S_h^0$, $S_v=S_v^0$, and$I_h=R_h=I_v=0$. Thus by the asymptotical stability theorem [9] the disease-free equilibrium is globally stable on Ω. ■

To show that the endemic equilibrium is globally asymptotically stable, we define the following Lyapunov function.

Theorem 4.2. *The endemic equilibrium of the system (1) is globally asymptotically stable if* $Q_2 \geq \frac{\lambda_h \gamma_h \beta_3 S_v^*}{Q_3 \beta_1 S_h^*}$ *with* $\frac{S_h}{S_h^*} \geq 1$, *and* $\frac{S_v}{S_v^*} \geq 1$, *otherwise unstable.*
Proof: *We define the following Lyapunov function for the endemic equilibrium is given by*

$$P(t) = \frac{1}{\beta_1 S_h^*}[S_h - S_h^*] + \frac{1}{\beta_1 S_h^*} I_h + \frac{1}{\beta_3 S_v^*}[S_v - S_v^*] + \frac{1}{\beta_3 S_v^*} I_v + \frac{\lambda_h}{Q_3 \beta_1 S_h^*} R_h.$$

By taking the time derivative of the above equation and using the system (1) we get,

$$\begin{aligned} P'(t) &= \tfrac{1}{\beta_1 S_h^*}[b_1 - \mu_h S_h - \beta_2 S_h I_v - \beta_1 S_h I_h + \lambda_h R_h] + \tfrac{1}{\beta_1 S_h^*}[\beta_2 S_h I_v + \beta_1 S_h I_h - Q_2 I_h] \\ &\quad + \tfrac{1}{\beta_3 S_v^*}[b_2 - \gamma_v S_v - \beta_3 S_v I_h] + \tfrac{1}{\beta_3 S_v^*}[\beta_3 S_v I_h - Q_1 I_v] + \tfrac{\lambda_h}{Q_3 \beta_1 S_h^*}[\gamma_h I_h - Q_3 R_h] \end{aligned}$$

where $(\prime)$ *denotes derivative with respect to time. By using* $S_h^* = \frac{b_1}{\mu_h}$ *and* $S_v^* = \frac{b_2}{\gamma_v}$ *and after some rearrangement we obtain*

$$P'(t) = -\frac{\mu_h}{\beta_1}(\frac{S_h}{S_h^*} - 1) - \frac{\gamma_v}{\beta_3}(\frac{S_v}{S_v^*} - 1) - I_h(\frac{Q_2}{\beta_3 S_v^*} - \frac{\lambda_h \gamma_h}{Q_3 \beta_1 S_h^*}) - \frac{Q_1}{\beta_3 S_v^*} I_v.$$

$P'(t)$ *is negative for* $(S_h, I_h, R_h, S_v, I_v) \in \Omega$. *Also* $P'(t) = 0$ *only for* $S_h = S_h^*$, $S_v = S_v^*$, $I_h = I_h^*$, $I_v = I_v^*$, $R_h = R_h^*$.
Thus by condition used in [9] for global stability ensures that the system (1) is globally asymptotically stable. This completes the proof. ■

Remark 2. *By the above theorem, we have the following different possibilities for the global stability of the system (1)*

(i) $\frac{S_h}{S_h^*} = 1$, $\frac{S_v}{S_v^*} = 1 \Rightarrow S_h = S_h^*$, $S_v = S_v^*$,

(ii) $\frac{S_h}{S_h^*} > 1 \Rightarrow S_h > S_h^*$, $\frac{S_v}{S_v^*} > 1 \Rightarrow S_v > S_v^*$,

(iii) $S_h > S_h^*$, $S_v = S_v^*$,

(iv) $S_h = S_h^*$, $S_v > S_v^*$,

(v) $S_h > S_h^*$, $S_v > S_v^*$, $S_h < S_v$ *and* $S_h^* > S_v^*$,

(vi) $S_h > S_h^*$, $S_v > S_v^*$, $S_h < S_v^8$ *and* $S_h^* < S_v^*$,

(vii) $S_h > S_h^*$, $S_v > S_v^*$, $S_h \leq S_v$ *and* $S_h^* \neq S_v^*$

Now, we discuss the relation between human and vector population for the global stability.

Note: For the relationship between I_h, I_v, S_v, first we define the Lyapunov function is given by

$$L(t) = W_1(I_h - I_h^*) + W_2(I_v - I_v^*) + W_3(S_v - S_v^*).$$

Taking the derivative of this function, we obtain

$$L'(t) = W_1[\beta_2 S_h I_v + \beta_1 S_h I_h - Q_2 I_h] + W_2[\beta_3 S_v I_h - Q_1 I_v] + W_3[b_2 - \gamma_v S_v - \beta_3 S_v I_h].$$

After some rearrangement, we get

$$L'(t) = [W_1\beta_2 S_h - W_2 Q_1]I_v + (W_2 - W_3)\beta_3 S_v I_h + W_1\beta_1 S_h I_h - W_1 Q_2 I_h + W_3 b_2 - W_3\gamma_v S_v.$$

Now, we choose $W_1 = 1$, $W_2 = W_3 = \frac{\beta_2 S_h}{Q_1}$ with $\gamma_v S_v = b_2$, to get

$$L'(t) = -(\beta_1 S_h - Q_2)I_h$$

which show the relationship between S_h and I_h. For the relationship between S_h, S_v, I_v, we develop the following function

$$L(t) = \frac{1}{\beta_1 S_h^*}(S_h - S_h^*) + \frac{1}{\beta_3 S_v^*}(S_v - S_v^*) + \frac{1}{\beta_3 S_v^*}(I_v - I_v^*).$$

Taking the derivative and after simplifications, we get

$$L'(t) = -\frac{\mu_h}{\beta_3}(\frac{S_h - S_h^*}{S_h^*} - \frac{\beta_2 S_h}{\beta_1 S_h^*}I_v - \frac{S_h}{S_h^*}I_h - \frac{\gamma_v}{\beta_3}(\frac{S_v - S_v^*}{S_v^*}) - \frac{Q_1 I_v}{\beta_3 S_v^*}.$$

For the relation between I_h, I_v, S_h, we define the lyapunov function is given by

$$L(t) = W_1 I_h + W_2 I_v + W_3 S_h.$$

By taking derivative of the this function and simplifying we get

$$L'(t) = (W_1 - W_3)\beta_2 S_h I_v + \beta_1 S_h I_h(W_1 - W_3) + (-W_1 Q_2 + W_2\beta_3 S_v)I_h - W_2 Q_1 I_v + W_3 b_1 - W_3\mu_h S_h,$$

Now choosing the constant,$W_1 = W_3 = \beta_3 S_v$, $W_2 = Q_2$, with $b_1 = \mu_h S_h^*$, we obtain

$$L'(t) = -Q_1 Q_2 I_v - \beta_3 S_V \mu_h[S_h - S_h^*].$$

All the above functions show that the model is globally asymptotically stable, if the above interaction of these individuals exist in the community.

Table 1: Parameter values used in the numerical simulations

Notation	Parameter description	value
b	Recruitment rate	5×10^{-2}
β	Transmission rate	0.04
λ	Proportionality constant	2.85×10^{-3}
μ_1	Density-independent death rate	9×10^{-4}
μ_2	Proportionality constant	2×10^{-6}
γ	Recovery rate of the infected	21×10^{-3}
δ	Disease-induced death rate of infected	10^{-3}
α	Inhibitory effect	0.1

5 Numerical results and summary

In this section, we use some iterative method to find the numerical solution. First we choose reasonable parameter value. The work presented in [4, 6] was a case study of Leptospirosis disease in Thailand. But we extended the model by taking into account the interaction of susceptible human with infected vector and disease related death rate in both infected human and vectors. So, it is difficult to choose all parameter values from quantitative estimation, some hypothetical sets of parameters are used to verify our analytical results. For numerical simulation we considered the parameter values in Table 1. In fact we have considered different values of parameter for numerical simulation to observe biologically plausible different dynamical scenarios of the model. Parameters used in this model which represents the dynamics of Leptospirosis disease are rarely constant, because they depend on environmental conditions. We do not know, however, the detailed relationship between these parameters and environmental conditions may be available in some literature.

Figure 4 represents numerical simulation of human population. The susceptible human population sharply decreases while there is a sharp increase in infected human population. The recovered human individuals increase slowly when the infected human decreases. Figure 5 shows the susceptible and infected vector population. The infected vector population increases because the interaction of susceptible human.

In this paper, we extended the model by taking into account the interaction of susceptible human with infected vector and disease related death rate in both infected human and vectors. First, we shown the local asymptotic stability of disease-free equilibria. Then, we presented the endemic equilibrium and backward bifurcation for several parameters. We also introduced the basic reproduction number for both disease-free and endemic equilibrium. Further more, we shown that the model is globally asymptotically stable for both disease-free and the endemic equilibrium. We also presented numerical simulation of our proposed model.

There is still a tremendous amount of work need to be done in this area. In our proposed model which represents the interaction of both human and vector population may apply optimal control in the form of vaccination and treatment and can be useful in helping determine effective ways of controlling the spread of Leptospirosis disease.

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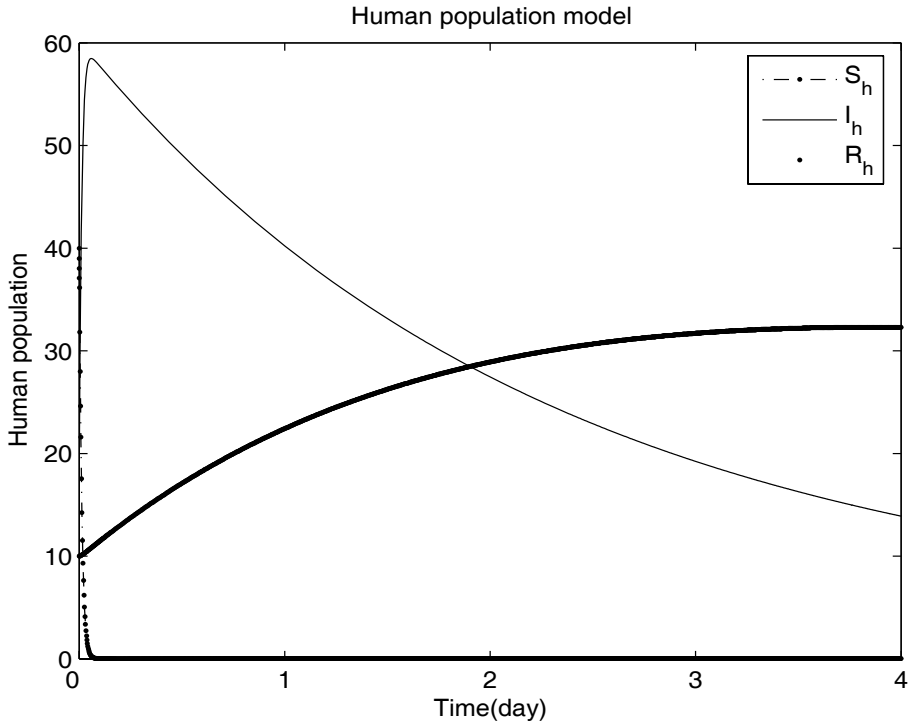

Figure 4: The plot shows the human population.

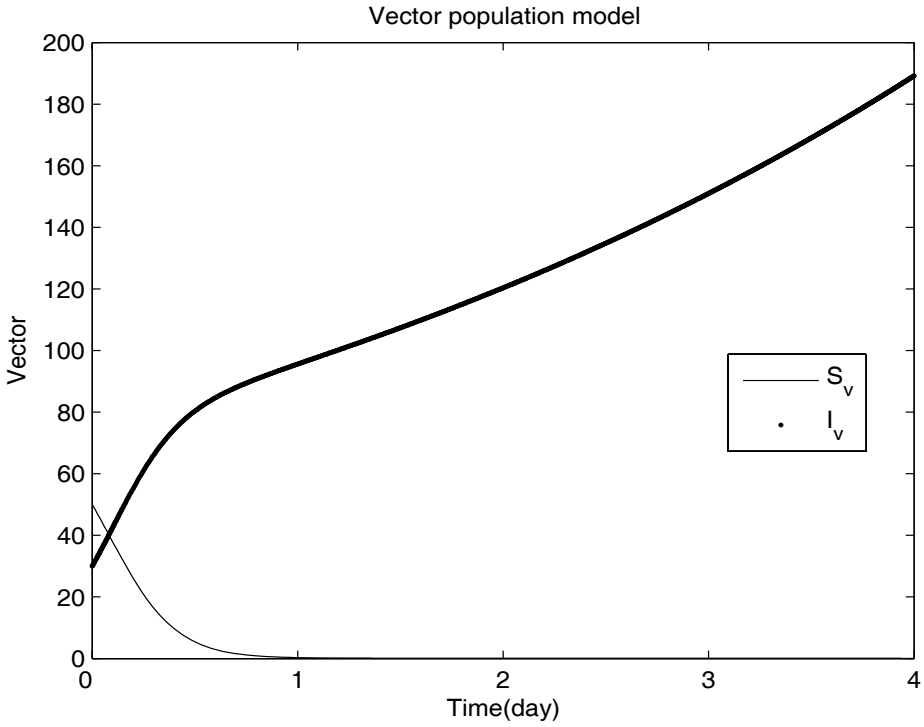

Figure 5: The plot represents the vector population.

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