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Mathematical Model of Leptospirosis: Linearized Solutions and Stability Analysis

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ABSTRACT

In this paper the transmission of leptospirosis, an infectious disease caused by bacteria, is studied. Leptospirosis is currently spreading in Thailand and worldwide. A Susceptible-Infected-Removed sir model is used to study the stability analysis, analytical solution and global behavior of the spreading of the disease. The model was analysed using the techniques of non-linear dynamical systems. Two equilibrium points were found and the stability conditions for these equilibrium points were established. It will be shown that the linearised solutions of the sir equations are in good agreement with numerical solutions.

Keywords: Technology; Preference for Quality; Volume of Trade; Vertical Intra-Industry Trade

1. Introduction

In Thailand, leptospirosis occurs mainly in the rainy season, with an increase in cases beginning in August, reaching a peak in October, and beginning to fall in November [1]. Leptospirosis in contaminated material may infect a person or other mammal. The bacteria penetrates the blood vessels, multiplies and infects several organs. Acute disease may be observed in several species, especially humans and dogs. In livestock sub-acute or even endemic, leptospirosis is generally observed. Infection induces antibody production in the animal renal carriers, shedding leptospirosis in their urine several weeks or even months after infection [2]. In humans, symptoms are generally flu-like, but the disease can result in liver damage and renal failure.

In this study, a compartmental model, with human susceptible-infective-removed-susceptible (sirs) model and vector susceptible-infective (si) model, [3-5] was used to examine the dynamical behaviour of the spread of leptospirosis, a vector borne disease. The sir model has been used to describe the transmission dynamics of many diseases. J Holt *et al.* 2006 [6] used this model to understand the behavior of infection in an African rodent of Tanzania. In Thailand, W. Triampo 2007 [1] introduced a deterministic sir model for the transmission of the spread of leptospirosis for the Thai population. In this work a modification of the sir model, which is used to describe the general transmission dynamics of leptospirosis, is proposed, and thresholds for changes in stability are found.

2. Model

The sir model has both human and vector populations. The vector in this case are rats. The human population is divided into three subgroups; susceptible humans S_H^*, infected humans I_H^*, and recovered humans R_H^*. The vector population is divided into two subgroups, susceptible vectors S_A^* and infected vectors I_A^* [1].

The following assumptions are considered in the model, as in Triampo [1], reproduced below:

- Newborns are not immunized and are therefore vulnerable instantly;
- All compartments of vector and human populations are well-mixed and therefore are spatially uniform;
- Humans can be infected by infected vectors but not by infected humans;

- Infected humans cannot infect susceptible vectors;
- Susceptible vectors S_A^* become infected vectors I_A^* instantly, with no incubation period needed for the infectious agents (leptospira) to develop.

In addition, we assume that:

- Perfect maternal transmission occurs, that is, new borns are susceptible if they are born to a susceptible mother and infective if they are born to an infective mother;
- Disease transmission is dependent on the product of the density of susceptibles and the infected (instead of the frequency of transmission: this difference disappears after normalisation);
- The total population remains constant.

Figure 1 shows the dynamics of the transmission of leptospirosis based on the assumptions above.

The law of mass action, where rates are proportional to the size (number) of each component, leads to the following set of coupled ordinary differential equations:

$$\frac{\mathrm{d}S_H^*}{\mathrm{d}t} = \mu_H N_H - \lambda_{HS} S_H^* - \gamma_H^* I_A^* S_H^* + r_2 R_H^*, \quad (1)$$

$$\frac{\mathrm{d}I_H^*}{\mathrm{d}t} = \gamma_H^* I_A^* S_H^* - \lambda_{HI} I_H^* - r_1 I_H^*, \quad (2)$$

$$\frac{\mathrm{d}R_H^*}{\mathrm{d}t} = r_1 I_H^* - \lambda_{HS} R_H^* - r_2 R_H^*, \quad (3)$$

$$\frac{\mathrm{d}S_A^*}{\mathrm{d}t} = \mu_{AS} S_A^* - \lambda_{AS} S_A^* - \gamma_A^* I_A^* S_A^*, \quad (4)$$

$$\frac{\mathrm{d}I_A^*}{\mathrm{d}t} = \mu_{AI} I_A^* - \lambda_{AI} I_A^* + \gamma_A^* I_A^* S_A^* \quad (5)$$

where * indicates a non-normalised variable.

The variables in (1)-(5) are normalised, giving proportions in each compartment, based on the assumption that the population remains constant, by letting

$$S_H = \frac{S_H^*}{N_H}, I_H = \frac{I_H^*}{N_H}, R_H = \frac{R_H^*}{N_H}, S_A = \frac{S_A^*}{N_A},$$

$$I_A = \frac{I_A^*}{N_A}, \gamma_H = \gamma_H^* N_A, \text{ and } \gamma_A = \gamma_A^* N_A.$$

Then Equations (1)-(5) become

$$\frac{\mathrm{d}S_H}{\mathrm{d}t} = \mu_H - \lambda_{HS} S_H - \gamma_H I_A S_H + r_2 R_H, \quad (6)$$

$$\frac{\mathrm{d}I_H}{\mathrm{d}t} = \gamma_H I_A S_H - \lambda_{HI} I_H - r_1 I_H, \quad (7)$$

$$\frac{\mathrm{d}R_H}{\mathrm{d}t} = r_1 I_H - \lambda_{HS} R_H - r_2 R_H, \quad (8)$$

$$\frac{\mathrm{d}S_A}{\mathrm{d}t} = \mu_{AS} S_A - \lambda_{AS} S_A - \gamma_A I_A S_A, \quad (9)$$

$$\frac{\mathrm{d}I_A}{\mathrm{d}t} = \mu_{AI} I_A - \lambda_{AI} I_A + \gamma_A I_A S_A. \quad (10)$$

By using the constraints $S_H + I_H + R_H = 1$ and $S_A + I_A = 1$ the above system of equations can be simplified to:

$$\frac{\mathrm{d}I_H}{\mathrm{d}t} = \gamma_H I_A (1 - I_H - R_H) - I_H (\lambda_{HI} + r_1), \quad (11)$$

$$\frac{\mathrm{d}R_H}{\mathrm{d}t} = r_1 I_H - R_H (\lambda_{HS} + r_2), \quad (12)$$

$$\frac{\mathrm{d}I_A}{\mathrm{d}t} = \mu_{AI} I_A - \lambda_{AI} I_A + \gamma_A I_A (1 - I_A). \quad (13)$$

Here we have omitted the equations involving S_H, S_A and used the constraints to make the system into only three compartments.

3. Equilibrium Points

Equilibrium points are found by setting the right hand sides of (11)-(13) equal to zero. This gives two equilibrium points in the feasible region. The disease-free equilibrium point $E_0 = (I_{H_E}, R_{H_E}, I_{A_E}) = (0,0,0)$ and the endemic equilibrium point $E_1 = (I_{H_E}, R_{H_E}, I_{A_E})$. After rearrangements this gives the endemic equlibrium point

$$I_{H_E} = \frac{\gamma_H (\mu_{AI} - \lambda_{AI} + \gamma_A)}{\left(\frac{\gamma_H r_1}{\gamma_{HH} + r_2} + \gamma_H\right)(\mu_{AI} - \lambda_{AI} + \gamma_A) + \gamma_A (\lambda_{HI} + r_1)}, \quad (14)$$

and

$$I_{A_E} = \frac{\mu_{AI} - \lambda_{AI} + \gamma_A}{\gamma_A}. \quad (16)$$

When $\mu_{AI} \le \lambda_{AI} < \mu_{AI} + \gamma_A$ then $I_{A_E} \in [0,1]$ and $\gamma_A \neq 0$. In this work the spreading of infection between human and vector is assumed to depend on rainfall. This means that the basic reproduction number $R_0(\gamma_A)$ depends on γ_A. Equations (14)-(16) can be simplified to:

$$R_{H_E} = \frac{r_1 \gamma_H (\mu_{AI} - \lambda_{AI} + \gamma_A)}{(\lambda_{HS} + r_2)\left(\left(\frac{\gamma_H r_1}{\lambda_{HS} + r_2} + \gamma_H\right)(\mu_{AI} - \lambda_{AI} + \gamma_A) + \gamma_A (\lambda_{HI} + r_1)\right)}, \quad (15)$$

$$I_{H_E} = \frac{\gamma_H \lambda_{AI}\left(R_0(\gamma_A)-1\right)\left(\lambda_{HS}+r_2\right)}{\gamma_H \lambda_{AI}\left(\lambda_{HS}+r_2+r_1\right)\left(R_0(\gamma_A)-1\right)+\gamma_A\left(\lambda_{HI}+r_1\right)\left(\lambda_{HS}+r_2\right)} \tag{17}$$

$$R_{H_E} = \frac{r_1\gamma_H \lambda_{AI}\left(R_0(\gamma_A)-1\right)}{\gamma_H \lambda_{AI}\left(\lambda_{HS}+r_2+r_1\right)\left(R_0(\gamma_A)-1\right)+\gamma_A\left(\lambda_{HI}+r_1\right)\left(\lambda_{HS}+r_2\right)}, \tag{18}$$

$$I_{A_E} = \frac{\lambda_{AI}\left(R_0(\gamma_A)-1\right)}{\gamma_A} \tag{19}$$

where $\frac{\mu_{AI}}{\gamma_{AI}} \le 1 < R_0(\gamma_A)$ and $R_0(\gamma_A) = \frac{\mu_{AI}+\gamma_A}{\lambda_{AI}}$ which is the basic reproduction number [1]. Infection in humans is described by an SIR model, but as animals do not recover, the disease in this vector is described by a SI process.

4. Local Stability Analysis

In this section the local stability analysis of (11)-(13) at steady-state is carried out. The Jacobian matrix of the system is given below:

$$J_{\left(I_{H_E},R_{H_E},I_{A_E}\right)} = \begin{bmatrix} -\gamma_H I_{A_E} - \left(\lambda_{HI}+r_1\right) & -\gamma_H I_{A_E} & \gamma_H\left(1-I_{H_E}-R_{H_E}\right) \\ r_1 & -\left(\lambda_{HS}+r_2\right) & 0 \\ 0 & 0 & \mu_{AI}-\lambda_{AI}+\gamma_A-2\gamma_A I_{A_E} \end{bmatrix} \tag{20}$$

The eigenvalues at E_0 are

$$\lambda_1 = -\lambda_{HI}-r_1, \lambda_2 = -\lambda_{HS}-r_2 \text{ and } \lambda_3 = \mu_{AI}-\lambda_{AI}+\gamma_A. \tag{21}$$

The eigenvalues of the Jacobian matrix in (19) of the disease-free steady state have negative roots which are independent of any parameter. These eigenvalues tell us that there is only one case of solution, *i.e.*, all eigenvalues are real and equal. The negative root condition is found by considering the eigenvalues (20). Now $\lambda_3 = \mu_{AI}-\lambda_{AI}+\gamma_A < 0$ when $\gamma_A < \lambda_{AI}-\mu_{AI}$ so $R_0(\gamma_A) = \frac{\mu_{AI}+\gamma_A}{\lambda_{AI}} < 1$. So the system is stable at the disease-free state since $R_0(\gamma_A) < 1$.

In the case of the endemic disease state, the eigenvalues at E_1 are

$$\lambda_1 = -\frac{\left(\gamma_H I_{A_E}+\lambda_{HI}+r_1+\lambda_{HS}+r_2\right)}{2} - \frac{\sqrt{\left(\gamma_H I_{A_E}+\lambda_{HI}+r_1-\lambda_{HS}-r_2\right)^2-4\left(\gamma_H I_{A_E} r_1\right)}}{2}, \tag{22}$$

$$\lambda_2 = -\frac{\left(\gamma_H I_{A_E}+\lambda_{HI}+r_1+\lambda_{HS}+r_2\right)}{2} + \frac{\sqrt{\left(\gamma_H I_{A_E}+\lambda_{HI}+r_1-\lambda_{HS}-r_2\right)^2-4\left(\gamma_H I_{A_E} r_1\right)}}{2}, \tag{23}$$

$$\lambda_3 = -\left(\mu_{AI}-\lambda_{AI}+\gamma_A\right) \tag{24}$$

The following three theorems follow immediately from [7]:

Theorem 1 The disease-free state at E_0 is locally asymptotically stable if $R_0(\gamma_A) < 1$ and unstable if $R_0(\gamma_A) > 1$.

Theorem 2 The endemic state at E_1 is locally asymptotically stable if $R_0(\gamma_A) > 1$ and unstable if $R_0(\gamma_A) < 1$.

From theorem 2 and theorem 2 $R_0(\gamma_A) = 1$ is a bifurcation point of the system where $R_0(\gamma_A) = \frac{\mu_{AI}+\gamma_A}{\lambda_{AI}}$. The expression above shows the relationships between $R_0(\gamma_A)$ and γ_A including bifurcations at E_0 and E_1 respectively. The parameters utilized in this calculation are $\lambda_{HI} = \frac{1}{18,000}$, $\lambda_{HS} = \frac{1}{21,900}$, $r_1 = \frac{1}{15}$, $r_2 = \frac{1}{360}$, $\mu_{AI} = 0.1$, $\lambda_{AI} = 0.7$ and $\gamma_H = 0.2$. Letting $\mu_{AI} = 0.1$ and $\lambda_{AI} = 0.7$ and using the above theorems the bifurcation point $R_0(\gamma_A) = 1$ occurs when $\gamma_A = 0.6$ as displayed in **Figures 2(a)-(c)** In the proof of the following theorem, the Liapunov function is used to show that the disease free state at E_0 is globally asymptotically stable.

Theorem 3 If $R_0(\gamma_A) < 1$, the existence of local stability implies its global stability [4].

Proof. Define the Liapunov function as $V(t) = I_A(t)$.

Then

$$\frac{\mathrm{d}V}{\mathrm{d}t}=\frac{\mathrm{d}I_A}{\mathrm{d}t}=\mu_{AI}I_A-\lambda_{AI}I_A+\gamma_A I_A\left(1-I_A\right)=I_A\left(\mu_{AI}-\lambda_{AI}+\gamma_A-\gamma_A I_A\right)$$
$$=\lambda_{AI}I_A\left(\frac{\mu_{AI}+\gamma_A}{\lambda_{AI}}-1-\frac{\gamma_A}{\lambda_{AI}}I_A\right)=\lambda_{AI}I_A\left(R_0\left(\gamma_A\right)-1-\frac{\gamma_A}{\lambda_{AI}}I_A\right)$$
$$\text{where } R_0\left(\gamma_A\right)<1 \text{ and } I_A\neq 0=\lambda_{AI}I_A\left(R_0\left(\gamma_A\right)-1-\frac{\gamma_A}{\lambda_{AI}}I_A\right)<0. \tag{25}$$

This concludes the proof.

Then from theorem 2 the disease-free state at E_0 using $\gamma_H=0.2$ is globally asymptotically stable since $R_0\left(\gamma_A\right)\approx 0.428<1$ as shown in **Figure 3**.

5. Numerical Solutions

Numerical calculations were utilized for solving (11) and (12), however, an analytical solution was found for (13). The solutions were used to analyze and examine the behavior of the model and determine whether the results converged.

From (13)

$$\frac{\mathrm{d}I_A}{\mathrm{d}t}=\mu_{AI}I_A-\lambda_{AI}I_A+\gamma_A I_A\left(1-I_A\right). \tag{26}$$

Divide both sides by I_A^2, then let $z=I_A^{-1}$ and $\frac{\mathrm{d}z}{\mathrm{d}t}=-I_A^{-2}\frac{\mathrm{d}I_A}{\mathrm{d}t}$. Then

$$\frac{\mathrm{d}z}{\mathrm{d}t}=-\left(\mu_{AI}-\lambda_{AI}+\gamma_A\right)z+\gamma_A. \tag{27}$$

Multiply both sides by $\mathrm{e}^{\left(\mu_{AI}-\lambda_{AI}+\gamma_A\right)t}$ to get

$$\mathrm{e}^{\left(\mu_{AI}-\lambda_{AI}+\gamma_A\right)t}\frac{\mathrm{d}z}{\mathrm{d}t}+\mathrm{e}^{\left(\mu_{AI}-\lambda_{AI}+\gamma_A\right)t}\left(\mu_{AI}-\lambda_{AI}+\gamma_A\right)z=\gamma_A\mathrm{e}^{\left(\mu_{AI}-\lambda_{AI}+\gamma_A\right)t}.$$

This simplifies to

$$\frac{\mathrm{d}}{\mathrm{d}t}\left(\mathrm{e}^{\left(\mu_{AI}-\lambda_{AI}+\gamma_A\right)t}z\right)=\frac{\gamma_A}{\left(\mu_{AI}-\lambda_{AI}+\gamma_A\right)}\frac{\mathrm{d}}{\mathrm{d}t}\left(\mathrm{e}^{\left(\mu_{AI}-\lambda_{AI}+\gamma_A\right)t}\right)$$

$$\mathrm{e}^{\left(\mu_{AI}-\lambda_{AI}+\gamma_A\right)t}z=\frac{\gamma_A}{\left(\mu_{AI}-\lambda_{AI}+\gamma_A\right)}\mathrm{e}^{\left(\mu_{AI}-\lambda_{AI}+\gamma_A\right)t}+c$$

$$z=\frac{\gamma_A}{\left(\mu_{AI}-\lambda_{AI}+\gamma_A\right)}+c\mathrm{e}^{-\left(\mu_{AI}-\lambda_{AI}+\gamma_A\right)t} \tag{28}$$

where c is a constant determined by the value of $I_A\left(t\right)$ at $t=t_0$.

Let

$$I_A\left(t\right)=\frac{I_A\left(t_0\right)\left(\mu_{AI}-\lambda_{AI}+\gamma_A\right)}{\gamma_A I_A\left(t_0\right)+\left(\mu_{AI}-\lambda_{AI}+\gamma_A-\gamma_A I_A\left(t_0\right)\right)\mathrm{e}^{-\left(\mu_{AI}-\lambda_{AI}+\gamma_A\right)\left(t-t_0\right)}}. \tag{29}$$

Here (29) is the analytical solution of (13).

The negative root condition is found by examining (24) and (29).

As the eigenvalues λ_1 and λ_2 from (22) and (23) must be real, the following inequality is required:

$$\left(\gamma_H I_{A_E}+\lambda_{HI}+r_1-\lambda_{HS}-r_2\right)^2-4\left(\gamma_H I_{A_E}r_1\right)\geq 0. \tag{30}$$

Then from (30)

$$\gamma_H\leq\frac{\left(\sqrt{\lambda_{HS}+r_2-\lambda_{HI}}-\sqrt{r_1}\right)^2}{I_{A_E}} \tag{31}$$

and

$$\gamma_H\geq\frac{\left(\sqrt{\lambda_{HS}+r_2-\lambda_{HI}}+\sqrt{r_1}\right)^2}{I_{A_E}} \tag{32}$$

when $\lambda_{HS}+r_2\geq\lambda_{HI}$. The cases are divided as will follow. The results correspond when using

$$\lambda_{HI}=\frac{1}{18,000},\quad \lambda_{HS}=\frac{1}{21,900},\quad r_1=\frac{1}{15},\quad r_2=\frac{1}{360},$$
$$\mu_{AI}=0.1,\quad \lambda_{AI}=0.7,\quad I_H\left(t_0\right)=0.02,\quad R_H\left(t_0\right)=0.01,$$
$$I_A\left(t_0\right)=0.02.$$

5.1. Case 1

All eigenvalues are real and distinct at the steady state E_0. When $\lambda_1,\lambda_2,\lambda_3<0$ since $\gamma_H,\mu_H,r_1,r_2,\gamma_A,\lambda_{HS},\lambda_{HI},\lambda_{AI}>0$, then the steady-state solution at $E_0=\left(0,0,0\right)$ is stable.

Figure 4(a) shows the stable steady state using a phase portrait. The graph of the numerical solution converges to the equilibrium point $E_0=\left(0,0,0\right)$. The parameters

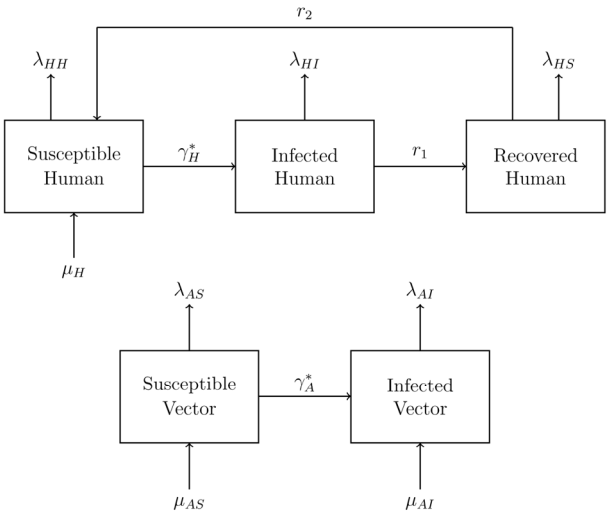


Figure 1. Flowchart of the transmission dynamics of leptospirosis.

used are $\gamma_A = 0.54, \gamma_H = 0.2$ and so $R_0(\gamma_A) \approx 0.91 < 1$. **Figure 5(a)** shows the solutions of I_H, R_H and I_A over time. The values of I_H, R_H and I_A are limited by $E_0 = (0,0,0)$.

At E_1

$$\gamma_H < \frac{\left(\sqrt{\lambda_{HS} + r_2 - \lambda_{HI}} - \sqrt{r_1}\right)^2}{I_{A_E}} = 0.1421, \qquad (33)$$

$$\gamma_H > \frac{\left(\sqrt{\lambda_{HS} + r_2 - \lambda_{HI}} + \sqrt{r_1}\right)^2}{I_{A_E}} = 0.3248, \qquad (34)$$

$$\text{when } \lambda_{HS} + r_2 \geq \lambda_{HI} \text{ and } so_0(\gamma_A) > 1. \qquad (35)$$

When $\lambda_1, \lambda_2, \lambda_3 < 0$ then $\gamma_H, \mu_H, r_1, r_2, \gamma_A, \lambda_{HS}, \lambda_{HI}, \lambda_{AI} > 0$ so the equilibrium point E_1 is stable.

Figure 4(b) is the phase portrait of the solution. The graph of the numerical solution converges to an equilibrium point $E_1 = (0.0372, 0.8792, 0.2974)$. The parameters are $\gamma_A = 0.854, \gamma_H = 0.1$ and so $R_0(\gamma_A) \approx 1.36 > 1$. So E_1 is stable. **Figure 5(b)** shows the solutions of I_H, R_H and I_A over time. The values for I_H, R_H and I_A are limited by $E_1 = (0.0372, 0.8792, 0.2974)$. In the following cases, these is no E_0 because the values of (20) can not be found.

5.2. Case 2

All eigenvalues λ_1, λ_2 and λ_3 from (21), (22) and (23) are real. Two eigenvalues are equal while the third is distinct.

Now

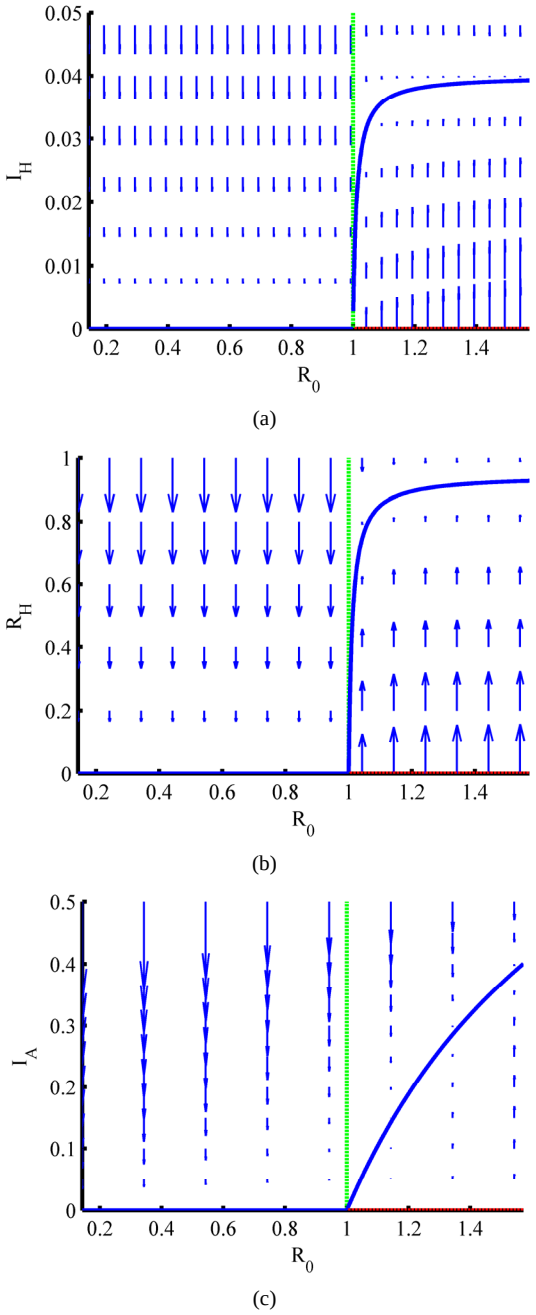


Figure 2. Equilibrium line between $R_0(\gamma_A)$ and (a) $I_H(t)$, (b) R_H (t), (c) $I_A(t)$ that shows the bifurcation at $R_0(\gamma_A)$. The heavy line represents the steady-state and the arrows represent the transient flow to the steady-states.

$$\gamma_H = \frac{\left(\sqrt{\lambda_{HS} + r_2 - \lambda_{HI}} - \sqrt{r_1}\right)^2}{I_{A_E}} = 0.1421 \qquad (36)$$

$$\text{and } \frac{\left(\sqrt{\lambda_{HS} + r_2 - \lambda_{HI}} + \sqrt{r_1}\right)^2}{I_{A_E}} = 0.3218 \qquad (37)$$

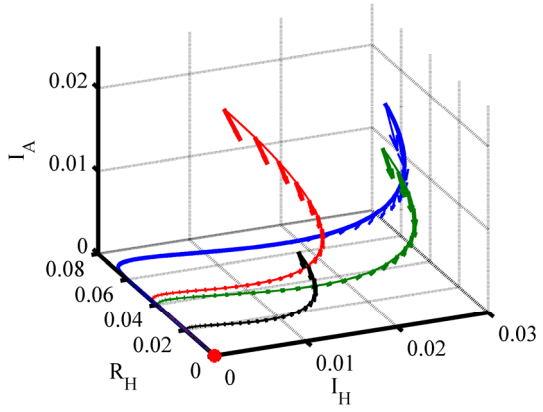
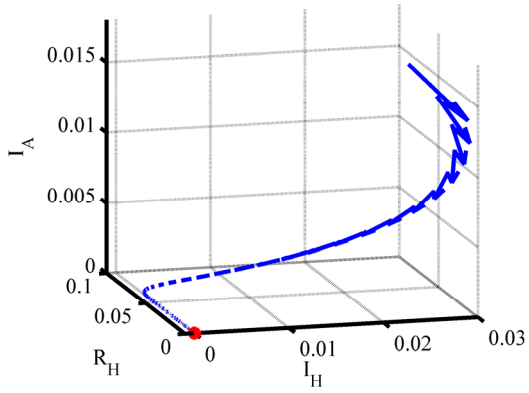
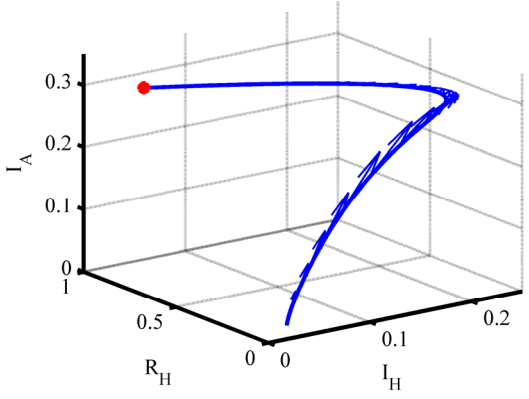


Figure 3. Graph shows global asymptotic stablity at $E_0 = (0,0,0)$.



(a)

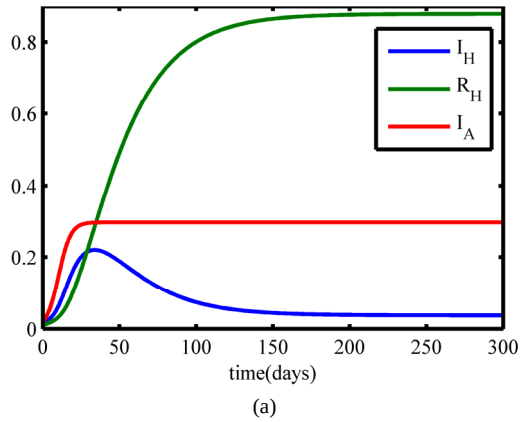


(b)

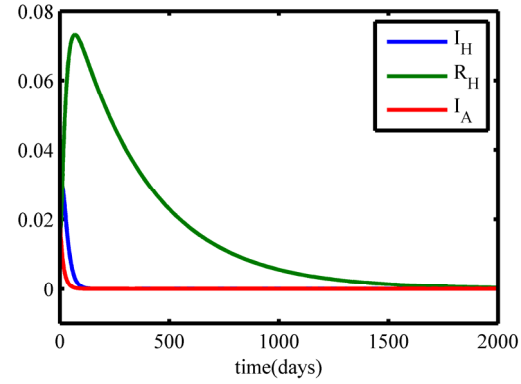
Figure 4. Phase portraits at (a) $E_0 = (0,0,0)$; (b) at steady state $E_1 = (0.0372, 0.8792, 0.2974)$.

when $\lambda_{HS} + r_2 \geq \lambda_{HI}$ and $so_0(\gamma_A) > 1$ (38)

Figure 6 shows the phase portrait for this case. The graph of the numerical solution converges to the equilibrium point $E_1 = (0.0382, 0.9015, 0.2974)$. The parameters used are $\gamma_A = 0.854, \gamma_H = 0.1421$ and so



(a)



(b)

Figure 5. Numerical solutions for I_H, R_H and I_A at (a) $E_0 = (0,0,0)$, (b) $E_1 = (0.0372, 0.8792, 0.2974)$.

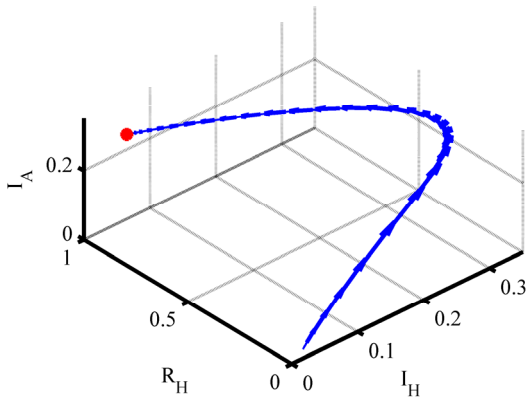


Figure 6. Phase portrait at $E_1 = (0.0382, 0.9015, 0.2974)$ when $\gamma_H = 0.1421$.

$R_0(\gamma_A) \approx 1.36 > 1$ so E_1 is stable. **Figure 7** shows the solutions of I_H, R_H and I_A over time. The values of I_H, R_H and I_A are limited by $E_1 = (0.0382, 0.9015, 0.2974)$.

5.3. Case 3

Two eigenvalues are complex while the third is real.

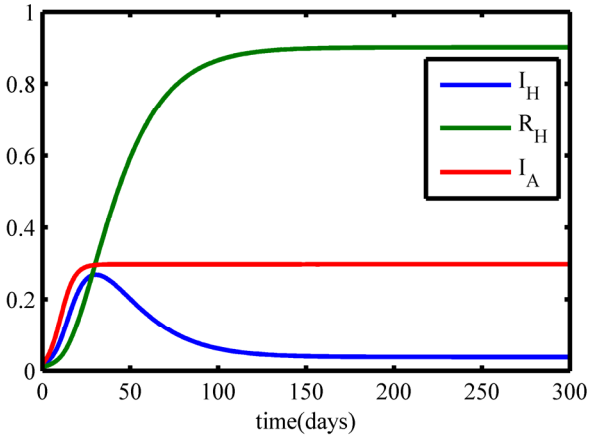


Figure 7. Numerical solution for I_H, R_H and I_A at $E_1 = (0.0382, 0.9015, 0.2974)$ when $\gamma_H = 0.1421$.

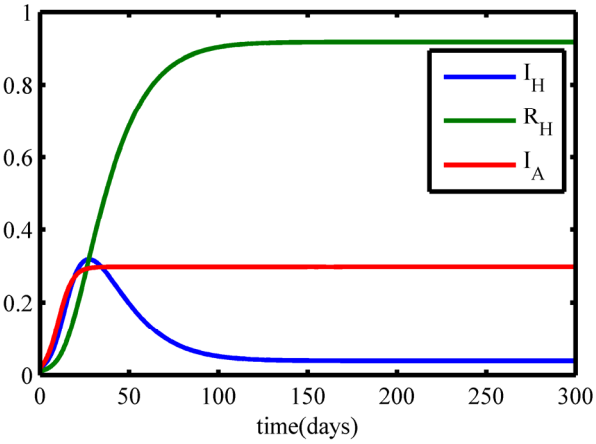


Figure 8. Numerical solutions for I_H, R_H and I_A at $E_1 = (0.0389, 0.9076, 0.2974)$ when $\gamma_H = 0.2$.

$$\frac{\left(\sqrt{\lambda_{HS}+r_2-\lambda_{HI}}-\sqrt{r_1}\right)^2}{I_{A_E}} < \gamma_H < \frac{\left(\sqrt{\lambda_{HS}+r_2-\lambda_{HI}}+\sqrt{r_1}\right)^2}{I_{A_E}} \tag{39}$$

$$\text{when } \lambda_{HS}+r_2 \geq \lambda_{HI} \text{ and } so_0(\gamma_A) > 1 \tag{40}$$

Figure 6 is the phase portrait of the solutions. The graph of the numerical solution converges to the equilibrium point $E_1 = (0.0389, 0.9076, 0.2974)$ where the parameters are $\gamma_A = 0.854, \gamma_H = 0.2$ and so $R_0(\gamma_A) \approx 1.36 > 1$ so E_1 is stable. **Figure 7** shows the solutions of I_H, R_H and I_A over time. The values of I_H, R_H and I_A approach the value of $E_1 = (0.0389, 0.9076, 0.2974)$.

6. Discussion and Conclusion

The important factors of the spreading of leptospirosis are the rate of transmission of leptospirosis from an infected vector to a susceptible human (γ_H) and the rate of transmission of leptospirosis from an infected vector to a susceptible vector (γ_A) [1]. These two factors depend on rainfall. A summary of the two factors is included here:

1) The spreading of leptospirosis has two states: the disease-free state and the endemic state. The occurence of a state depends on γ_A. If $R_0(\gamma_A) < 1$, then the disease-free state will occur but if $R_0(\gamma_A) > 1$ then the endemic state will occur as shown in **Figures 2(a)-(c)**.

2) For the disease-free state, a Liapunov function was used to prove that it is globally asymptotically stable. So for any initial population, over a long time, the population will converge to the disease-free steady state, as shown in **Figure 3**.

3) Two factors impact on the endemic state case: γ_A and γ_H. Before the convergence point

$$\gamma_H = \frac{\left(\sqrt{\lambda_{HS}+r_2-\lambda_{HI}}-\sqrt{r_1}\right)^2}{I_{A_E}} \tag{41}$$

when $\lambda_{HS}+r_2 \geq \lambda_{HI}$ then $R_0(\gamma_A) > 1$, $\lambda_{HS} = \frac{1}{18,000}$, $\lambda_{HI} = \frac{1}{21,900}$, $r_1 = \frac{1}{15}$, $r_2 = \frac{1}{360}$, $\mu_{AI} = 0.1$ and $\lambda_{AI} = 0.7$ which can be classified as below:

I. For $0.1421 \leq \gamma_H \leq 0.3218$ the number of infected humans initially increases before decreasing to the endemic state while the number of recovered humans increases to the endemic state. This is shown in **Figures 5(b)** and **7**.

II. For $0.1421 < \gamma_H < 0.3218$ the number of infected humans initially increases before decreasing to the endemic state while the number of recovered human initially increases before decreasing to the endemic state. This is shown in **Figure 8**.

4) The death rate of the infected vector population is equal to or greater than the natural birth rate of the infected vector population.

5) The time to convergence to the disease free state is longer than the time to convergence to the endemic state because the amount of time before the disease disappears is longer than that of the endemic state. This reflects what would happen in the real world.

7. Acknowledgements

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Nomenclature

S_H^* : number of humans susceptible (non-normalised).
I_H^* : number of humans infected (non-normalised).
R_H^* : number of humans recovered (non-normalised).
S_A^* : number of vectors susceptible (non-normalised).
I_A^* : number of vectors infected (non-normalised).
t : time measured in days.
μ_H : natural birth rate of human population.
N_H : human population.
λ_{HS} : natural death rate of susceptible and recovered humans.
γ_H^* : rate of transmission (non-normalised) of leptospirosis from an infected vector to a susceptible human, varying with rain fall.
r_2 : rate immune individuals become susceptible $\left(S_H^*\right)$ again.
λ_{HI} : natural death rate of infected humans plus the death rate due to the infection.
r_1 : rate infected humans can be cured by antibiotic medicines and become immune.
μ_{AS} : natural birth rate of susceptible vectors.
λ_{AS} : natural death rate of susceptible vectors.
μ_{AI} : constant natural birth rate of infected vectors.
λ_{AI} : natural death rate of infected vectors plus the death rate due to the infection.
γ_A^* : rate of transmission (non-normalised) of leptospirosis from an infected vector to a susceptible vector, varying with rain fall.
S_H : proportion of humans susceptible (normalised).
I_H : proportion of humans infected (normalised).
R_H : proportion of humans recovered (normalised).
S_A : proportion of vectors susceptible (normalised).
N_A : vector population.
I_A : proportion of vectors infected (normalised).
γ_H : rate of transmission of leptospirosis from an infected vector to a susceptible human, varying with rain fall.
γ_A : rate of transmission of leptospirosis from an infected vector to a susceptible vector, varying with rain fall.
E_0 : disease free equilibrium point.
I_{H_E} : proportion of humans infected at equilibrium point (normalised).
R_{H_E} : proportion of humans recovered at equilibrium point (normalised).
I_{A_E} : proportion of vectors infected at equilibrium point (normalised).
E_1 : endemic equilibrium point.
R_0 : basic reproduction number.
λ_i : $i = 1, 2, 3$ eigenvalues.

