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Stability Analysis of a Human-Mosquito Model of Malaria with Infective Immigrants

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***Abstract*—**In this paper, we analyse the stability of the SEIR model of malaria with infective immigrants which was recently formulated by the authors. The model consists of an SEIR model for the human population and SI Model for the mosquitoes. Susceptible humans become infected after they are bitten by infectious mosquitoes and move on to the Exposed, Infected and Recovered classes respectively. The susceptible mosquito becomes infected after biting an infected person and remains infected till death. We calculate the reproduction number R_0 using the next generation method and then discuss about the stability of the equilibrium points. We use the Lyapunov function to show the global stability of the equilibrium points.

***Keywords*—**Susceptible, exposed, infective, recovered, infective immigrants, reproduction number, Lyapunov function, equilibrium points, global stability.

I. Introduction

ONE of the diseases that have constantly had its presence in human population is malaria. It is caused by the entry of the malarial parasite, *Plasmodium* into the bloodstream, due to the bite of an infected female *Anopheles* mosquito. Years have been spent in finding ways to control and completely eradicate malaria from the human population, but all efforts have been in vain. The disease was once endemic and confined to certain parts of the world, but has now even spread to areas which were previously free of the disease. Even when eradicated for a period of time, it recurs in certain areas repeatedly. One major factor which has contributed to the wide spread nature of malaria is human migration and travel. An area with an uninfected population of mosquitoes can also get infected when an infected individual enters the area and is bitten by these mosquitoes. There are no dormant forms of malaria. If the parasite enters the body, it will surely cause a disease, unlike certain other conditions in which the diseased state does not occur even for years after infection.

It is logical to assume that infected humans will be unable to travel or migrate due to the symptoms brought on by the disease. However, there is a period of around 10 days to 4 weeks from the moment of infection to the actual onset of disease, and unaware people might travel during this time. During this period, the disease cannot be diagnosed by blood tests either as the parasite multiplies in the liver, thus allowing the infection to be carried to a new place. Such people will become infectious after a certain period of dormancy. As a result of this, immigration of infected people has a huge impact on the spread of malaria within, as well as, among populations.

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Even if the infected immigrants are not introducing the parasite to a new population, their entry into an already infected population will cause an increase in the infected mosquitoes of the area as they will be biting more number of infected people.

Several SEIR models for vector-borne diseases, with reference to malaria have been formulated [4], [8]-[10] and studied. The global stability of SEIR and SEIS models have been discussed in [1], [3], [5]-[7]. However, these models have not considered the impact of infective immigrants. In [14], an SIR model for malaria with infective immigrants has been studied. So far there were no specific SEIR models for malaria with infective immigrants until recently studied in [13]. In this paper, we calculate the disease-free equilibrium point and the endemic equilibrium point of the model formulated in [13] and analyse the local and global stability of these points.

The paper is organized in the following way: In Section II, we calculate the equilibrium points and the reproduction number R_0. In Section III, we have study the local stability of the equilibrium points and in Section IV, we have study the global asymptotical stability of the disease-free and unique endemic equilibrium points using the theory of Lyapunov function [11], [12].

A. Formulation of SEIR Model

Let us denote the total population of human hosts as $N_h(t)$ and the total population of the female mosquitoes as $N_m(t)$. The human population $N_h(t)$ is divided into the following epidemiological subclasses: Susceptible, Exposed, Infected and Recovered, denoted by $S_h(t), E_h(t), I_h(t)$ and $R_h(t)$ respectively. Thus,

$$N_h(t) = S_h(t) + E_h(t) + I_h(t) + R_h(t)$$

The mosquito population $N_m(t)$ is divided into two subclasses: Susceptible and Infected, and they are denoted by $S_m(t)$ and $I_m(t)$ respectively. We assume that the mosquito remains infectious for its entire lifespan. Thus,

$$N_m(t) = S_m(t) + I_m(t)$$

We now consider a model in which the new members that flow into the population are either infective or susceptible. This flow is assumed to occur through birth or immigration at constant rate Λ. We further assume that a fraction ϕ is infective and a fraction α is exposed and the remaining fraction$(1-\phi-\alpha)$ is susceptible.

The system of non-linear differential equations which describe the dynamics of malaria are formulated as:

$$\frac{dS_h}{dt} = (1-\phi-\alpha)\Lambda - \mu_h S_h - \beta_h S_h I_m$$

$$\frac{dE_h}{dt} = \alpha\Lambda + \beta_h S_h I_m - \mu_h E_h - \nu_h E_h$$

$$\frac{dI_h}{dt} = \phi\Lambda + \nu_h E_h - \gamma I_h - \alpha_h I_h - \mu_h I_h$$

$$\frac{dR_h}{dt} = \gamma I_h - \mu_h R_h$$

$$\frac{dN_h}{dt} = \Lambda - \mu_h N_h - \alpha_h I_h \quad (1)$$

$$\frac{dS_m}{dt} = \rho - \beta_m S_m I_h - \mu_m S_m - \alpha_m S_m$$

$$\frac{dI_m}{dt} = \beta_m S_m I_h - \mu_m I_m - \alpha_m I_m$$

$$\frac{dN_m}{dt} = \rho - \mu_m N_m - \alpha_m N_m$$

where β_h=Interaction coefficient of susceptible human with infectious mosquitoes, ν_h=Rate of progression of humans from the exposed to the infectious state, μ_h=Natural death rate of the human population, α_h=Disease related death rate of the human population, γ=Recovery rate of human population, β_m=Interaction coefficient of infected human with susceptible mosquitoes, α_m=Death rate due to control measures, μ_m=Natural death rate, ρ=Recruitment rate of mosquitoes.

II. Equilibrium Points and Basic Reproduction Number R_0

A. Disease-Free Equilibrium

We get the disease-free equilibrium points when we assume that the new recruits in the population are susceptible and do not consist of exposed or infected persons. Hence we have $\phi = \alpha = 0$..

In the absence of the disease, the diseased classes for the humans viz., Exposed, Infectious and Recovered and the diseased class for the mosquitoes viz., infectious mosquitoes do not exist. Hence we have $E_h = I_h = R_h = I_m = 0$. To find the steady state solution, we set the right hand side of the non-linear system of differential equations given by (1) to zero.

Using the two conditions, the system of equations given by (1) reduces to,
$\Lambda - \mu_h S_h = 0$
$\rho - \mu_m S_m - \alpha_m S_m = 0.$

This implies that $S_h = \frac{\Lambda}{\mu_h}$ and $S_m = \frac{\rho}{\mu_m+\alpha_m}$
Thus, the disease-free equilibrium point of malaria model (1) is given by;
$E_1 = (S_h^*, E_h^*, I_h^*, R_h^*, R_h^*, S_m^*, I_m^*)$
$= (\frac{\Lambda}{\mu_h}, 0, 0, 0, \frac{\rho}{\mu_m+\alpha_m}, 0, 0)$

We shall now calculate the basic reproduction number R_0.

B. Basic Reproduction Number R_0

The basic reproduction number R_0 is defined as the number of secondary infectious that one infectious individual would generate on average over the course of its infectious period. There are many methods to calculate R_0. We use the next generation operation approach as given in [2]. When $R_0 < 1$, the disease will decline and eventually die out. When $R_0 > 1$, the disease will spread in the population. Hence this means that the threshold quantity to be taken into account to eradicate the disease is to reduce the value of R_0 to be less than one.

According to [2], the matrix of FV^{-1} is called the next generation matrix for the model. The basic reproduction number R_0 is given by

$$R_0 = \sigma(FV^{-1})$$

where $\sigma(A)$ denotes the spectral radius of matrix A and the spectral radius is the biggest non-negative eigenvalue of the next generation matrix.

From the system, f_i and v_i are defined as

$$f_i = \begin{pmatrix} \beta_h S_h I_m \\ 0 \\ \beta_m S_m I_h \end{pmatrix} \quad (2)$$

and

$$v_i = \begin{pmatrix} (\mu_h+\nu_h)E_h \\ (\gamma+\alpha_h+\mu_h)I_h - \nu_h E_h \\ (\mu_m+\alpha_m)I_m \end{pmatrix} \quad (3)$$

The partial derivative of (2) with respect to (I_h, I_m) and the Jacobian matrix of f_i at the disease free equilibrium point is:

$$F = \begin{pmatrix} 0 & 0 & \beta_h S_h \\ 0 & 0 & 0 \\ 0 & \beta_m S_m & 0 \end{pmatrix}$$

Similarly partial derivative of (3) with respect to (E_h, I_h, I_m) and the Jacobian matrix of v_i is

$$V = \begin{pmatrix} \mu_h+\nu_h & 0 & 0 \\ -\nu_h & \gamma+\alpha_h+\mu_h & 0 \\ 0 & 0 & \mu_m+\alpha_m \end{pmatrix}$$

The inverse of V is given as:

$$V^{-1} = \begin{pmatrix} \frac{1}{\mu_h+\nu_h} & 0 & 0 \\ \frac{\nu_h}{(\mu_h+\nu_h)(\gamma+\alpha_h+\mu_h)} & \frac{1}{(\gamma+\alpha_h+\mu_h)} & 0 \\ 0 & 0 & \frac{1}{\mu_m+\nu_m} \end{pmatrix}$$

Now we have to find FV^{-1}.

$$FV^{-1} = \begin{pmatrix} 0 & 0 & \frac{\beta_h S_h}{(\mu_m+\alpha_m)} \\ 0 & 0 & 0 \\ \frac{\beta_m S_m \nu_h}{(\mu_h+\nu_h)(\gamma+\alpha_h+\mu_h)} & \frac{\beta_m S_m}{(\gamma+\alpha_h+\mu_h)} & 0 \end{pmatrix} \quad (4)$$

Thus

$$FV^{-1} = \begin{pmatrix} 0 & 0 & r \\ 0 & 0 & 0 \\ s & t & 0 \end{pmatrix}$$

where $r = \frac{\beta_h S_h}{(\mu_m+\nu_m)}$, $s = \frac{\beta_m \nu_h}{(\mu_h+\nu_h(\gamma+\alpha_h+\mu_h))}$ and $t = \frac{\beta_m}{(\gamma+\alpha_h+\mu_h)}$.

Now we calculate the eigenvalues of FV^{-1} and then consider the largest eigenvalue. Consider $|FV^{-1} - \lambda I| = 0$. Then, the corresponding matrix is

$$\begin{pmatrix} -\lambda & 0 & r \\ 0 & -\lambda & 0 \\ s & t & -\lambda \end{pmatrix}$$

The characteristic equation is $\lambda(\lambda^2 - rs) = 0$ and the eigenvalues are $\lambda = 0$ or $\lambda = \pm\sqrt{r}s$.

The dominant eigenvalue of the matrix FV^{-1} is $\lambda = +\sqrt{r}s$. Hence the reproduction number $R_0 = \sqrt{r}s$. Thus,

$$R_0 = \sqrt{\frac{\beta_h\beta_m\rho\nu_h\Lambda}{\mu_h(\mu_m+\alpha_m)^2(\mu_h+\nu_h)(\gamma+\alpha_h+\mu_h)}}.$$

C. Endemic Equilibrium Point

The set of non-linear differential equations given by (1) can be reduced to the set of equations using conditions that $S_h + E_h + I_h + R_h = N_h$ and $S_m + I_m = N_m$. The model (1) reduces to

$$\begin{aligned}
\frac{dE_h}{dt} &= \alpha\lambda + \beta_h(N_h - E_h - I_h - R_h)I_m - \mu_h E_h - \nu_h E_h \\
\frac{dI_h}{dt} &= \phi\lambda + \nu_h E_h - \gamma I_h - \alpha_h I_h - \mu_h I_h \\
\frac{dR_h}{dt} &= \gamma I_h - \mu_h R_h \\
\frac{dN_h}{dt} &= \lambda - \mu_h N_h - \alpha_h I_h \\
\frac{dI_m}{dt} &= \beta_m(N_m - I_m)I_h - \mu_m I_m - \alpha_m I_m \\
\frac{dN_m}{dt} &= \rho - \mu_m N_m - \alpha_m N_m
\end{aligned} \tag{5}$$

The endemic equilibrium point has been calculated in [13].

III. Local Stability of the Equilibrium Points

In this section, we analyse the stability of the disease-free equilibrium point and the endemic equilibrium point.

A. Disease-Free Equilibrium

The theorem tells us about the stability of the disease-free equilibrium point.

Theorem 1: The disease-free equilibrium point $E_1(\frac{\Lambda}{\mu_h}, 0, 0, 0, \frac{\rho}{\mu_m+\alpha_m}, 0, 0)$ of the model (1) is locally asymptotically stable if $R_0 < 1$, otherwise it is unstable.

Proof: Linearization of system (1) at disease-free equilibrium $E_1(\frac{\Lambda}{\mu_h}, 0, 0, 0, \frac{\rho}{\mu_m+\alpha_m}, 0, 0)$, gives the Jacobian matrix as,

$$J = \begin{pmatrix}
-\mu_h & 0 & 0 & 0 & 0 & -\frac{\beta_h\Lambda}{\mu_h} \\
0 & -B_1 & 0 & 0 & 0 & \frac{\beta_h\Lambda}{\mu_h} \\
0 & \nu_h & -B_2 & 0 & 0 & 0 \\
0 & 0 & \gamma & -\mu_h & 0 & 0 \\
0 & 0 & -\frac{\beta_m\rho}{\mu_m+\alpha_m} & 0 & -B_3 & 0 \\
0 & 0 & \frac{\beta_m\rho}{\mu_m+\alpha_m} & 0 & 0 & -B_3
\end{pmatrix}$$

where $B_1 = \mu_h + \nu_h$, $B_2 = \gamma + \alpha_h + \mu_h$ and $B_3 = \mu_m + \alpha_m$.

The characteristic equation corresponding to the matrix is $(\mu_h + \lambda)^2(B_3 + \lambda)(\lambda^3 + p_1\lambda^2 + p_2\lambda + p_3)$
where

$$p_1 = B_1 + B_2 + B_3$$

$$p_2 = B_1B_2 + B_1B_3 + B_2B_3$$

$$p_3 = B_1B_2B_3 - \frac{\beta_h\beta_m\nu_h\rho\Lambda}{\mu_h B_3}$$

The eigen values of characteristic equation are $-\mu_h, -B_3$ and roots of the polynomial $\lambda^3 + p_1\lambda^2 + p_2\lambda + p_3$.

By Routh-Hurwitz criterion, the polynomial $\lambda^3 + p_1\lambda^2 + p_2\lambda + p_3$ has roots with negative real part if $p_1p_2 - p_3 > 0$.
Since $p_1p_2 - p_3 = B_1^2B_2 + (B_2+B_3)(B_1B_2 + B_1B_3 + B_2B_3) + \frac{\beta_h\beta_m\nu_h\Lambda\rho}{\mu_h B_3} > 0$,
the disease-free equilibrium point is locally asymptotically stable. ■

B. Endemic Equilibrium Point

It has been proved in Theorem 3 of [13], that this endemic equilibrium point is locally asymptotically stable under certain conditions.

IV. Global Stabilty of the Equilibrium Points

The feasible region for the equilibrium points is given by

$$\Omega = \{(S_h, E_h, I_h, R_h, S_m, I_m) \in R_+^6 : 0 \le N_h \le \frac{\Lambda}{\mu_h};$$
$$0 \le N_m \le \frac{\rho}{\mu_m + \alpha_m}\}$$

A. Global Stability of Disease-Free Equilibrium

We now prove the global stability of the disease-free equilibrium point.

Theorem 2: Let

$$\mu_m = \beta_h S_h^* - \alpha_m, \mu_h = \beta_m S_m^* - \alpha_h \tag{6}$$

Then if $R_0 \le 1$ the disease-free equilibrium $E_1 = (S_h^*, E_h^*, I_h^*, R_h^*, S_m^*, I_m^*) = (\frac{\lambda}{\mu_h}, 0, 0, 0, \frac{\rho}{\mu_m+\alpha_m}, 0, 0)$ is globally asymptotically stable on Ω.

Proof: Consider the Lyapunov's function,

$$L_1(t) = (S_h - S_h^* ln S_h) + E_h + I_h + R_h + (S_m - S_m^* ln S_m) + I_m$$

Since we are considering the disease-free equilibrium, we have the condition that $\alpha = \phi = 0$.

Differentiating with respect to time,
$\dot{L_1}(t) = \dot{S_h}(1 - \frac{S_h^*}{S_h}) + \dot{E_h} + \dot{I_h} + \dot{R_h} + \dot{S_m}(1 - \frac{S_m^*}{S_m}) + \dot{I_m}$
$= (\Lambda - \mu_h S_h - \beta_h S_h I_m)(1 - \frac{S_h^*}{S_h}) + (\beta_h S_h I_m - \mu_h E_h - \nu_h E_h) + (\nu_h E_h - \gamma I_h - \alpha_h I_h - \mu_h I_h) + (\gamma I_h - \mu_h R_h) + (\rho - \beta_m S_m I_h - \mu_m S_m - \alpha_m S_m)(1 - \frac{S_m^*}{S_m}) + \beta_m S_m I_h -$

$\mu_m I_m - \alpha_m I_m$

$= \Lambda(1-\frac{S_h^*}{S_h}) - \mu_h S_h + \mu_h S_h + \beta_h S_h^* I_m - \mu_h E_h - \alpha_h I_h - \mu_h I_h - \mu_h R_h + \rho(1-\frac{S_m^*}{S_m}) - (\mu_m+\alpha_m)S_m + \beta_m S_m^* I_h + (\mu_m+\alpha_m)S_m^* - (\mu_m+\alpha_m)I_m.$

On Ω, we have $S_h^* = \frac{\Lambda}{\mu_h}$ and $S_m^* = \frac{\rho}{\mu_m+\alpha_m}$.

Substituting for S_h^* and S_m^* in the equation, we have

$\dot{L_1}(t) = \Lambda(2 - \frac{S_h^*}{S_h} - \frac{S_h}{S_h^*}) + I_m(\beta_h S_h^* - \mu_m - \alpha_m) - \mu_h R_h - \mu_h E_h - I_h(\alpha_h + \mu_h - \beta_m S_m^*) + \rho(2 - \frac{S_m^*}{S_m} - \frac{S_m}{S_m^*})$

Using condition (6), the equation reduces to

$\dot{L_1} = -\Lambda\frac{(S_h - S_h^*)^2}{S_h S_h^*} - \mu_h(E_h + R_h) - \rho\frac{(S_m - S_m^*)^2}{S_m S_m^*} - (\mu_m + \alpha_m)$

Hence $\dot{L_1}(t) \leq 0$

By using LaSalle's extension to Lyapunov's method, the limit set of each solution is contained in the largest invariant set for which $S_h = S_h^*$ and $S_m = S_m^*$ which is the singleton $E_1 = (S_h^*, E_h^*, I_h^*, R_h^*, S_m^*, I_m^*)$.This means that the disease-free equilibrium E_1 is globally asymptotically stable on Ω.

This prooves the theorem. ■

B. Global Stability of Endemic Equilibrium

We now prove global stability of the endemic equilibrium $E_2 = (S_h^{**}, E_h^{**}, I_h^{**}, S_m^{**}, I_m^{**})$ which satisfies the steady state equations:

$$(1-\phi-\alpha)\lambda - \mu_h S_h^{**} - \beta_h S_h^{**} I_m^{**} = 0$$

$$\alpha\lambda + \beta_h S_h^{**} I_m^{**} - \mu_h E_h^{**} - \nu_h E_h^{**} = 0$$

$$\phi\lambda + \nu_h E_h^{**} - \gamma I_h^{**} - \alpha_h I_h^{**} - \mu_h I_h^{**} = 0$$

$$\gamma I_h^{**} - \mu_h R_h^{**} = 0$$

$$\rho - \beta_m S_m^{**} I_h^{**} - \mu_m S_m^{**} - \alpha_m S_m^{**} = 0$$

$$\beta_m S_m^{**} I_h^{**} - \mu_m I_m^{**} - \alpha_m I_m^{**} = 0$$

Theorem 3: The unique endemic equilibrium E_2 is globally asymptotically stable in Ω whenever $R_0 > 1$.

Proof: We construct a Lyapunov function of the form,

$$L_2(t) = a_1(S_h - S_h^{**} ln S_h) + a_2(E_h - E_h^{**} ln E_h) + a_3(I_h - I_h^{**} ln I_h) + a_4(R_h - R_h^{**} ln R_h) + a_5(S_m - S_m^{**} ln S_m) + a_6(I_m - I_m^{**} ln I_m)$$

where a_1, a_2, a_3, a_4, a_5 and a_6 will be chosen later.

Differentiating L_2 with respect to time t along the solutions of (1), we have,

$$\dot{L_2}(t) = a_1\dot{S_h}(1-\frac{S_h^{**}}{S_h}) + a_2\dot{E_h}(1-\frac{E_h^{**}}{E_h}) + a_3\dot{I_h}(1-\frac{I_h^{**}}{I_h}) + a_4\dot{R_h}(1-\frac{R_h^{**}}{R_h}) + a_5\dot{S_m}(1-\frac{S_m^{**}}{S_m}) + a_6\dot{I_m}(1-\frac{I_m^{**}}{I_m})$$

Substituting the expressions from system (1) at the endemic steady state, we have

$$\dot{L_2}(t) = a_1[\mu_h S_h^{**}(2 - \frac{S_h}{S_h^{**}} - \frac{S_h^{**}}{S_h}) + \beta_h S_h^{**} I_m^{**}(1 - \frac{S_h^{**}}{S_h} + \frac{I_m}{I_m^{**}} - \frac{S_h I_m}{S_h^{**} I_m^{**}}) + a_2[\alpha\lambda(2 - \frac{E_h}{E_h^{**}} - \frac{E_h}{E_h^{**}}) + \beta_h S_h^{**} I_m^{**}(1 - \frac{E_h}{E_h^{**}} + \frac{S_h I_m}{S_h^{**} I_m^{**}} - \frac{S_h I_m E_h^{**}}{S_h^{**} I_m^{**} E_h})] + a_3[\phi\lambda(2 - \frac{I_h}{I_h^{**}} - \frac{I_h^{**}}{I_h}) + \nu_h E_h^{**}(1 - \frac{I_h}{I_h^{**}} + 4\frac{E_h}{E_h^{**}} - \frac{E_h I_h^{**}}{E_h^{**} I_h})] + a_4[\gamma I_h^{**}(1 + \frac{I_h}{I_h^{**}} - \frac{R_h}{R_h^{**}} - \frac{I_h R_h^{**}}{I_h^{**} R_h})] + a_5[(\mu_m+\alpha_m)S_m^{**}(2 - \frac{S_m}{S_m^{**}} - \frac{S_m^{**}}{S_m}) + \beta_m S_m^{**} I_h^{**}(1 - \frac{S_m^{**}}{S_m} + \frac{I_h}{I_h^{**}} - \frac{S_m I_h}{S_m^{**} I_h^{**}})] + a_6[\beta_m S_m^{**} I_h^{**}(1 - \frac{I_m}{I_m^{**}} + \frac{S_m I_h}{S_m^{**} I_h^{**}} - \frac{S_m I_h I_m^{**}}{S_m^{**} I_h^{**} I_m})]$$

.

We choose the coefficients, a_1, a_2, a_3, a_4, a_5 and a_6 as:

$$a_1 = a_2 = \frac{\beta_m S_m^{**} I_h^{**}}{\beta_h S_h^{**} I_m^{**}}, a_3 = \frac{\beta_m S_m^{**} I_h^{**}}{\nu_h E_h^{**}}, a_4 = 0,$$

and

$$a_5 = 1 = a_6$$

Then $\dot{L_2}$ becomes,

$$\dot{L_2}(t) = \frac{\beta_m\mu_h S_m^{**} I_h^{**}}{\beta_h I_m^{**}}(2 - \frac{S_h}{S_h^{**}} - \frac{S_h^{**}}{S_h}) + \beta_m S_m^{**} I_h^{**}(5 - \frac{S_h^{**}}{S_h} - \frac{S_m^{**}}{S_m} - \frac{E_h^{**} I_h^{**}}{E_h I_h} - \frac{S_h I_m E_h^{**}}{S_h^{**} I_m^{**} E_h} - \frac{S_m I_h I_m^{**}}{S_m^{**} I_h^{**} I_m}) + \frac{\alpha\lambda\beta_m S_m^{**} I_h^{**}}{\beta_h S_h^{**} I_m^{**}}(2 - \frac{E_h}{E_h^{**}} - \frac{E_h^{**}}{E_h}) + \frac{\phi\lambda\beta_m S_m^{**} I_h^{**}}{\nu_h E_h^{**}}(2 - \frac{I_h}{I_h^{**}} - \frac{I_h^{**}}{I_h}) + (\mu_m+\alpha_m)S_m^{**}(2 - \frac{S_m}{S_m^{**}} - \frac{S_m^{**}}{S_m})$$

Since

$$(2 - \frac{S_h}{S_h^{**}} - \frac{S_h^{**}}{S_h}) \leq 0,$$

$$(5 - \frac{S_h^{**}}{S_h} - \frac{S_m^{**}}{S_m} - \frac{E_h^{**} I_h^{**}}{E_h I_h} - \frac{S_h I_m E_h^{**}}{S_h^{**} I_m^{**} E_h} - \frac{S_m I_h I_m^{**}}{S_m^{**} I_h^{**} I_m}) \leq 0,$$

$$(2 - \frac{E_h}{E_h^{**}} - \frac{E_h^{**}}{E_h}) \leq 0,$$

$$(2 - \frac{I_h}{I_h^{**}} - \frac{I_h^{**}}{I_h}) \leq 0, \quad (7)$$

$$(2 - \frac{S_m}{S_m^{**}} - \frac{S_m^{**}}{S_m}) \leq 0,$$

We have $\dot{L_2}(t) \leq 0$. Hence, by Lyapunov's first theorem the endemic equilibrium

$E_2 = (S_h^{**}, E_h^{**}, I_h^{**}, R_h^{**}, S_m^{**}, I_m^{**})$ is globally asymptotically stable. ■

V. Conclusion and Future Work

In this paper, we found the disease free equilibrium point by assuming that the new immigrants in the population are susceptible and do not contain any exposed or infected individuals. The reproduction number R_0, was calculated using the Next Generation Method in order to find the number of secondary infections that one infectious individual would generate. The endemic equilibrium point has already been calculated in [13]. The disease free equilibrium and the endemic equilibrium were found to be stable and the global stability was found for these equilibrium points using the Lyapunov function.

In this paper, we have not carried out the numerical simulation and sensitivity analysis of the given system, which is necessary to understand the full extent of the effect of infective immigrants on the spread of malaria in a population. For future work, it would be interesting to note the change in parameters which would affect the epidemiology of this highly infectious disease, thus providing a way to combat the spread of the disease among new populations.

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