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MODELING, ANALYSIS AND OPTIMAL CONTROL OF VECTOR-BORNE DISEASES WITH AWARENESS FACTOR

NISHA KATARIA BUDHWAR[1], SUNITA DANIEL[2,*]

[1]Department of Mathematics, Suraj PG Degree College Gurugram-122001, India

[2]Information Technology Area, FORE School of Management, New Delhi - 110016, India

Abstract. In this paper we have developed an SEIRS model for vector borne diseases, taking awareness about the disease as a factor. The model has been formulated and analysed, along with assessment of creating awareness about preventive measures for the disease. The behaviour of the model, the effect of awareness and the effect of the control measures taken have been studied by carrying out numerical simulation using MATLAB.

Keywords: SEIRS model; reproduction number; local stability; optimal control theory; numerical simulation.

2010 AMS Subject Classification: 34G20, 34K20, 65L07, 49J15, 97N80.

1. INTRODUCTION

Vector borne diseases are transmitted through vectors which are organisms that transmit pathogens and parasites from one infected person (or animal) to another, causing serious diseases in human populations. These diseases are commonly found in tropical and sub-tropical regions and places where access to safe drinking-water and sanitation systems are problematic. Vector-borne diseases account for 17% of the estimated global burden of all infectious diseases [23]. According to the World Malaria Report (WMR) 2020 released by World Health

*Corresponding author

E-mail address: sunita@fsm.ac.in

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Organisation (WHO), there were 229 million malaria cases around the globe for the past four years [24]. The disease claimed around 409000 lives in 2019 alone. However, the world's fastest growing vector-borne disease is dengue, with a 30-fold increase in disease incidence over the last 50 years. There are many other vector borne diseases such as lymphatic filariasis, lyme disease, Chikungunya, Yellow fever etc.

One of the reasons for the transmission of these vector borne diseases is the lack of awareness among the human population. People need to know as to how these diseases spread and should take necessary precautions and use preventive measures to stop the spread of them. Hence different countries have been introducing various awareness programs to make the people aware of the cause of the disease and how to curb it. For example, April 25 is observed globally as Malaria Awareness Day and the theme for the year 2020 was "Zero malaria starts with me". India has launched the National Dengue Day and it is observed on May 16 every year. On this day efforts are taken by the government to spread awareness about dengue and how to take necessary precaution to prevent it. The National Vector Borne Disease Control Programme (NVBDCP) in India which was launched in the year 2003 also takes various measures to make people aware of these diseases. The effect of awareness in controlling the spread of the diseases has been modeled mathematically and studied for various diseases [7, 15, 20, 21]. Several SEIRS models for malaria and dengue have been modelled [2, 10, 13, 16, 18, 22] and the optimal strategies for controlling them have been studied [3, 6, 8, 9, 11, 12, 17]. However, none of them have considered the population as aware population and unaware population.

In this paper, we develop an SEIRS model by dividing the susceptible population into two classes-the aware susceptible and the unaware susceptible population. In Sections 3, 4 and 5, we analyse the model and establish the stability of the model. In Section 6, we use optimal control theory and derive necessary conditions by applying Pontryagin's Maximum Principle to control the transmission of the disease efficiently . Finally we carry out numerical simulation using MATLAB and study the behaviour of the model, the effect of awareness and the effect of the various control measures used to prevent the transmission of the disease.

2. MODEL FORMULATION

Let N_H denote the total human population which is divided into various components, Let us assume the susceptible human population to be of two classes where S_{H_1} denotes the susceptible human population who are unaware of the disease and S_{H_2} the susceptible human population who are aware of the disease. Let E_H and I_H denotes the exposed human population and the infected human population respectively. Then $N_H = S_{H_1} + S_{H_2} + E_H + I_H$ denotes the total human population.

Let S_M and I_M denote the susceptible and infected mosquito population respectively and $N_M = S_M + I_M$, the total mosquito population.

Based on the above classification of the human population and the mosquito population, the dynamics of vector borne diseases are modelled as a system of non-linear differential equations. The system of equations are as follows:

$$
\begin{cases}
\frac{dS_{H_1}}{dt} = \Lambda_1 - \beta_1 S_{H_1} I_M - \delta S_{H_1} - \mu_H S_{H_1} + (1-k)\gamma I_H \\
\frac{dS_{H_2}}{dt} = \delta S_{H_1} - \beta_2 S_{H_2} I_M - \mu_H S_{H_2} + k\gamma I_H \\
\frac{dE_H}{dt} = \beta_1 S_{H_1} I_M + \beta_2 S_{H_2} I_M - \mu_H E_H - \eta E_H \\
\frac{dI_H}{dt} = \eta E_H - \alpha_1 I_H - \mu_H I_H - \gamma I_H \\
\frac{dS_M}{dt} = \Lambda_2 - \beta_3 S_M I_H - \alpha_2 S_M - \mu_M S_M \\
\frac{dI_M}{dt} = \beta_3 S_M I_H - \alpha_2 I_M - \mu_M I_M
\end{cases} \tag{1}
$$

Adding the equations corresponding to $S_{H_1}, S_{H_2}, E_H, I_H$ and corresponding to S_M and I_M, we have

$$
\frac{dN_H}{dt} = \Lambda_1 - \mu_H N_H - \alpha_1 I_H \tag{2}
$$

$$
\frac{dN_M}{dt} = \Lambda_2 - (\mu_M + \alpha_2) N_M \tag{3}
$$

where Λ_1= birth rate of human population, β_1= contact rate of unaware susceptible humans with infective mosquitoes, δ=rate of transfer of unaware susceptible individual to aware susceptible class, μ_H= natural death rate of the human population, γ= rate of progression of humans from the infected class to the susceptible class after recovery, k= a fraction of recovered

persons going to the aware class, β_2= contact rate of aware susceptible humans with infective mosquitoes, η= rate of progression of humans from the exposed to the infectious class, α_1= disease induced death rate of humans, Λ_2= recruitment rate of mosquitoes, β_3= contact rate of infected human with susceptible mosquitoes, α_2 =death rate of mosquitoes due to control measures, μ_M= natural death rate of mosquitoes.

Figure 1 shows the variation of the human population based on the SEIRS model defined by (1) as a flow diagram.

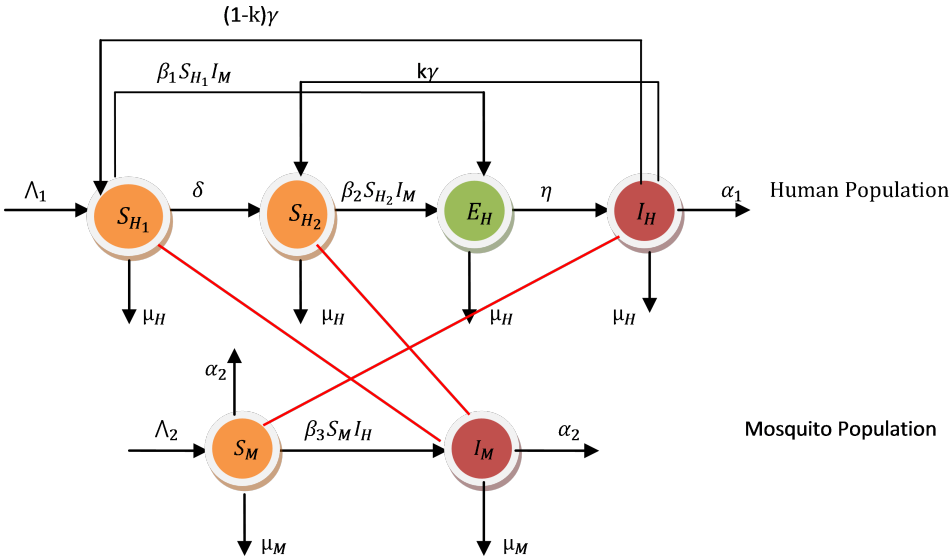


FIGURE 1. Variation in the total human population with time

3. FEASIBLE SOLUTION

In this section we show that the model governed by the system of non-linear equations given by (1) is epidemiologically and mathematically well-posed in a region Ω.

For the system to be epidemiologically meaningful, it is important to prove that all the variables are non-negative for $t \geq 0$. That is, the solutions of the model (1) with positive initial values

will remain positive for all time $t > 0$. Also the domain of the solution of the model should be a bounded set.

Theorem 1. *The feasible solution set for model (1) is given by,*
$\Omega = \{(S_{H_1}, S_{H_2}, E_H, I_H, S_M, I_M) \in R^6 : (S_{H_1}, S_{H_2}, E_H, I_H, S_M, I_M) \geq 0; 0 \leq N_H \leq \frac{\Lambda_1}{\mu_H}; 0 \leq N_M \leq \frac{\Lambda_2}{\alpha_2+\mu_M}\}$. *Moreover, it is positively invariant and mathematically well posed in the domain* Ω.

Proof. In order to prove the theorem, we need to prove the following:

(a) The total population and each population class remains bounded for all finite time $t \geq 0$.

(b) If the initial conditions are all positive i.e. $S_{H_1}(0) > 0, S_{H_2}(0) > 0, E_H(0) > 0, I_H(0) > 0, S_M(0) > 0, I_M(0) > 0$, then for all $t \in [0, t_0], S_{H_1}, S_{H_2}, E_H, I_H, S_M, I_M$ will remain positive in Ω.

In order to prove (a), making use of equations (2) and (3) we have,

$$\frac{dN_H}{dt} = \Lambda_1 - \mu_H N_H - \alpha_1 I_H \text{ and } \frac{dN_M}{dt} = \Lambda_2 - (\mu_M + \alpha_2) N_M.$$

$$\frac{dN_H}{dt} \leq \Lambda_1 - \mu_H N_H \text{ and } \frac{dN_M}{dt} \leq \Lambda_2 - (\mu_M + \alpha_2) N_M.$$

That is, $N_H(t) \leq N_h(0) e^{-\mu_H t} + \frac{\Lambda_1}{\mu_h}[1 - e^{-\mu_h t}]$ and

$$N_M(t) \leq N_M(0) e^{-(\mu_M+\alpha_2)(t)} + \frac{\Lambda_2}{(\mu_M+\alpha_2)}[1 - e^{-(\mu_M+\alpha_2)(t)}].$$

Taking limits as $t \to \infty$, we have

$\lim_{t\to\infty} sup N_H(t) \leq \frac{\Lambda_1}{\mu_H}$ and $\lim_{t\to\infty} sup N_M(t) \leq \frac{\Lambda_2}{(\mu_M+\alpha_2)}$.

This shows that the total population and each population class remains bounded for all finite time $t \geq 0$ in Ω.

We now prove the second part of the theorem. Since all the parameters used in the system and the initial values of the compartments are greater than zero, we can place lower bounds on each of the equations given in the model.

Thus $\frac{dS_{H_1}}{dt} = \Lambda_1 - \beta_1 S_{H_1} I_M - \delta S_{H_1} - \mu_H S_{H_1} + (1-k)\gamma I_H \geq -\mu_H S_{H_1} - \beta_1 S_{H_1} I_M$

$\frac{dS_{H_2}}{dt} = \delta S_{H_1} - \beta_2 S_{H_2} I_M - \mu_H S_{H_2} + k\gamma I_H \geq -\mu_H S_{H_2} - \beta_2 S_{H_2} I_M$

Through basic differential equations methods we have,

$$S_{H_1}(t) \geq e^{-\mu_H t - \beta_1 \int I_M(t)dt} \geq 0.$$

$$S_{H_2}(t) \geq e^{-\mu_H t - \beta_2 \int I_M(t)dt} \geq 0.$$

Similarly,

$$\frac{dE_H}{dt} = \beta_1 S_{H_1} I_M + \beta_2 S_{H_2} I_M - \mu_H E_H - \eta E_H \geq -\mu_H E_H - \eta E_H$$

which gives

$$E_H(t) \geq e^{-(\mu_H + \eta)t} \geq 0.$$

$$\frac{dI_H}{dt} = \eta E_H - \alpha_1 I_H - \mu_H I_H - \gamma I_H \geq -\gamma I_H(t) - \alpha_1 I_H(t) - \mu_H I_H(t)$$

and hence

$$I_H(t) \geq e^{-(\gamma + \alpha_1 + \mu_H)t} \geq 0$$

Proceeding similarly for $S_M(t)$ and $I_M(t)$, we have

$$S_M(t) \geq e^{-(\mu_M + \alpha_2)t + \beta_M \int I_H(t)dt} \geq 0 \text{ and } I_M(t) \geq e^{-(\mu_M + \alpha_2)t} \geq 0.$$

Thus, for all $t \in [0, t_0], S_{H_1}, S_{H_2}, E_H, I_H, S_M, I_M$ will be positive and remain in Ω. Hence this proves (b).

Combining (a) and (b), we conclude that the feasible solution is mathematically well posed in the region Ω. This proves the theorem.

□

We calculate the equilibrium points and discuss the local stability of the equilibrium points in the subsequent sections.

4. EXISTENCE OF EQUILIBRIUM POINTS

There are two equilibrium points for model (1) which are the disease free equilibrium point and the endemic equilibrium point. The existence of these points are given in the following theorem.

Theorem 2. *There exists two equilibrium points for the system (1) which are as follows:*

(1) The disease free equilibrium point is given by $P_0 = (S'_{H_1}, S'_{H_2}, E'_H, I'_H, S'_M, I'_M)$
$= (\frac{\Lambda_1}{\mu_H+\delta}, \frac{\delta\Lambda_1}{\mu_H(\mu_H+\delta)}, 0, 0, \frac{\Lambda_2}{\alpha_2+\mu_M}, 0)$.

(2) The endemic equilibrium point $P_1 = (S^*_{H_1}, S^*_{H_2}, E^*_H, I^*_H, S^*_M, I^*_M)$ *exists when* $R^*_0 > 1$, *where* $R^*_0 = \frac{\Lambda_2\eta\beta_3(\beta_1 S^*_{H_1}+\beta_2 S^*_{H_2})}{(\mu_M+\alpha_2)^2(\alpha_1+\gamma+\mu_H)(\mu_H+\eta)}$.

Proof. The equilibrium points are calculated by equating the equations of the system (1) to zero.

The disease-free equilibrium point exists in the absence of exposed humans, infected humans and infected vectors in the system. This means that $E_H = I_H = 0$ and $I_M = 0$. Solving the system (1) gives us the disease-free equilibrium point as $P_0 = (S'_{H_1}, S'_{H_2}, E'_H, I'_H, S'_M, I'_M) = (\frac{\Lambda_1}{\mu_H+\delta}, \frac{\delta\Lambda_1}{\mu_H(\mu_H+\delta)}, 0, 0, \frac{\Lambda_2}{\alpha_2+\mu_M}, 0)$. This proves the first part of the theorem.

To prove the second part, let $P_1 = (S^*_{H_1}, S^*_{H_2}, E^*_H, I^*_H, S^*_M, I^*_M)$ be the endemic equilibrium point of (1). Then all the components of P_1 should be positive. If we set the system of differential equations in (1) to zero, we get

$$S^*_{H_1} = \frac{\Lambda_1 + (1-k)\gamma I^*_H}{\mu_H + \beta_1 I^*_M + \delta} \tag{4}$$

$$S^*_{H_2} = \frac{\delta\Lambda_1 + \delta(1-k)\gamma I^*_H + k\gamma I^*_H(\beta_1 I^*_M + \mu_H + \delta)}{(\mu_H + \beta_2 I^*_M)(\beta_1 I^*_M + \mu_H + \delta)} \tag{5}$$

$$E^*_H = \frac{(\beta_1 S^*_{H_1} + \beta_2 S^*_{H_2}) I^*_M}{\eta + \mu_H} \tag{6}$$

$$I^*_H = \frac{\eta E^*_H}{\alpha_1 + \gamma + \mu_H} \tag{7}$$

$$S_M^* = \frac{\Lambda_2}{\beta_3 I_H^* + \mu_M + \alpha_2} \tag{8}$$

$$I_M^* = \frac{\beta_3 S_M^* I_H^*}{\alpha_2 + \mu_M} \tag{9}$$

Now putting the value of S_M^* from equation (8) in equation (9), we get

$$I_M^* = \frac{\beta_3 I_H^* \Lambda_2}{(\mu_M + \alpha_2)(\beta_3 I_H^* + \mu_M + \alpha_2)} \tag{10}$$

Putting the value of I_M^* from equation (10) in equation (4)

$$S_{H_1}^* = \frac{(\Lambda_1 + (1-k)\gamma I_H^*)(\mu_M + \alpha_2)(\beta_3 I_H^* + \mu_M + \alpha_2)}{(\mu_H + \delta)(\mu_M + \alpha_2)(\beta_3 I_H^* + \mu_M + \alpha_2) + \beta_1 \beta_3 \Lambda_2 I_H^*} \tag{11}$$

Substituting the value of I_M^* in equation (5), we have

$$S_{H_2}^* = \frac{[(\delta(\Lambda_1 + CI_H^*) + k\gamma I_H^* AB(\beta_3 I_H^* + B)\beta_1 \beta_3 \Lambda_2] + k\gamma I_H^{*2} B(\beta_3 I_H^* + B)}{[\mu_H B(\beta_3 I_H^* + B) + \beta_2 \beta_3 \Lambda_2 I_H^*][AB(\beta_3 I_H^* + B) + \beta_1 \beta_3 \lambda_2 I_H]}$$

where $A = \mu_H + \delta$, $B = \mu_M + \alpha_2$ and $C = (1-k)\gamma$

Substituting the value of E_H^* which is in terms of $S_{H_1}^*, S_{H_2}^*$ and I_M^* in (7),we have

$$I_H^* = \frac{\Lambda_2 \eta \beta_3 (\beta_1 S_{H_1}^* + \beta_2 S_{H_2}^*) - (\alpha_2 + \mu_M)^2 (\mu_H + \eta)(\alpha_1 + \gamma + \mu_H)}{\beta_3 (\alpha_2 + \mu_M)(\mu_H + \eta)(\alpha_1 + \gamma + \mu_H)} \tag{12}$$

The equilibrium P_1 exists if $I_H^* > 0$. That is, if

$$\frac{\Lambda_2 \eta \beta_3 (\beta_1 S_{H_1}^* + \beta_2 S_{H_2}^*)}{(\mu_M + \alpha_2)^2 (\alpha_1 + \gamma + \mu_H)(\mu_H + \eta)} = R_0^* > 1$$

where R_0^* can be called a threshold number.

□

We now calculate the basic reproduction number R_0.

5. BASIC REPRODUCTION NUMBER R_0

The basic reproduction number R_0 is defined as the number of secondary infections that one infectious individual would generate on an average over the course of the infectious period. There are many methods to calculate R_0. We use the next generation operation approach as given in [1]. 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.

F includes only infections that are newly arising, and V includes terms that describe the transfer of infectious from one infected compartment to another at the disease free equilibrium point. Then according to [1], the matrix of FV^{-1} is called the next generation matrix for the model. The basic reproduction number R_0 is given by $R_0 = \sigma(FV^{-1})$ which is the dominant eigenvalue of FV^{-1}. Corresponding to the model (1),

$$F = \begin{pmatrix} 0 & 0 & \beta_1 S_{H1} + \beta_2 S_{H2} \\ 0 & 0 & 0 \\ 0 & \beta_3 S_M & 0 \end{pmatrix}$$

and the partial derivative of (1) with respect to (E_H, I_H, I_M) and the Jacobian matrix is

$$V = \begin{pmatrix} \mu_H + \eta & 0 & 0 \\ -\eta & \alpha_1 + \gamma + \mu_H & 0 \\ 0 & 0 & \mu_M + \alpha_2 \end{pmatrix}$$

The inverse of V:

$$V^{-1} = \begin{pmatrix} \frac{1}{\mu_H+\eta} & 0 & 0 \\ \frac{\eta}{(\mu_H+\eta)(\alpha_1+\gamma+\mu_H)} & \frac{1}{\alpha_1+\gamma+\mu_H} & 0 \\ 0 & 0 & \frac{1}{\mu_M+\alpha_2} \end{pmatrix}.$$

The dominant eigenvalue of the matrix

$$FV^{-1} = \begin{pmatrix} 0 & 0 & \frac{\beta_1 S_{H_1} + \beta_2 S_{H_2}}{\mu_M+\alpha_2} \\ 0 & 0 & 0 \\ \frac{\eta\beta_3 S_M}{(\mu_H+\eta)(\alpha_1+\gamma+\mu_H)} & \frac{\beta_3 S_M}{\alpha_1+\gamma+\mu_H} & 0 \end{pmatrix} \text{ is}$$

$$\sqrt{\frac{\eta\beta_3 S_M^{'}(\beta_1 S_{H_1}^{'}+\beta_2 S_{H_2}^{'})}{(\mu_H+\eta)(\alpha_1+\gamma+\mu_H)(\mu_M+\alpha_2)}}.$$

Substituting for $S_{H_1}^{'}$, $S_{H_2}^{'}$ and $S_M^{'}$ the reproduction number is given by,

$$R_0=\sqrt{\frac{\eta\beta_3\Lambda_1\Lambda_2(\beta_1\mu_H+\beta_2\delta)}{\mu_H(\mu_H+\delta)(\mu_H+\eta)(\alpha_1+\gamma+\mu_H)(\mu_M+\alpha_2)^2}}. \tag{13}$$

6. Local Stability Analysis

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

Theorem 3. *The disease-free equilibrium* $P_0=(\frac{\Lambda_1}{\mu_H+\delta},\frac{\delta\Lambda_1}{\mu_H(\mu_H+\delta)},0,0,\frac{\Lambda_2}{\alpha_2+\mu_M},0)$ *is locally asymptotically stable if* $R_0<1$ *and unstable if* $R_0>1$.

Proof. Consider the Jacobian matrix L_0 of the system (1) at the disease free equilibrium point P_0

$$L_0=\begin{bmatrix}
-(\mu_H+\delta) & 0 & 0 & (1-k)\gamma & 0 & -\beta_1 S_{H_1}\\
\delta & -\mu_H & 0 & k\gamma & 0 & -\beta_2 S_{H_2}\\
0 & 0 & -(\mu_H+\eta) & 0 & 0 & (\beta_1 S_{H_1}+\beta_2 S_{H_2})\\
0 & 0 & \gamma & -(\mu_H+\gamma+\alpha_1) & 0 & 0\\
0 & 0 & 0 & -\beta_3 S_M & -(\mu_M+\alpha_2) & 0\\
0 & 0 & 0 & \beta_3 S_M & 0 & -(\mu_M+\alpha_2)
\end{bmatrix}$$

To calculate the eigenvalues, we consider the characteristic equation of L_0. It is given by

$$(\lambda+\mu_H)(\lambda+\mu_M+\alpha_2)(\lambda+\mu_H+\delta)(\lambda^3+a_1\lambda^2+a_2\lambda+a_3)=0 \tag{14}$$

where $a_1 = 2\mu_H + \eta + \alpha_1 + \gamma + \alpha_2 + \mu_M$,

$a_2 = \mu_H(\mu_H + \gamma + \alpha_1 + 2\mu_M + 2\alpha_2 + \eta) + (\mu_M + \alpha_2)(\gamma + \alpha_1) + (\gamma + \alpha_1)\eta + (\mu_M + \alpha_2)\eta$,

$a_3 = (\mu_M + \alpha_2)(\mu_H + \gamma + \alpha_1)(1 - \frac{\eta\beta_3 S'_M(\beta_1 S'_{H_1} + \beta_2 S'_{H_2})}{(\mu_H+\eta)(\alpha_1+\gamma+\mu_H)(\mu_M+\alpha_2)})$

$= (\mu_M + \alpha_2)(\mu_H + \gamma + \alpha_1)(\mu_H + \eta)[1 - R_0^2]$.

The eigenvalues of the matrix L_0 are $-\mu_H$, $-(\mu_M + \alpha_2)$, $-(\mu_H + \delta)$ and the roots of the cubic polynomial $\lambda^3 + a_1\lambda^2 + a_2\lambda + a_3 = 0$.

For the equilibrium point to be locally stable, the roots of the polynomial $\lambda^3 + a_1\lambda^2 + a_2\lambda + a_3$ have to be negative. We use Routh-Hurwitz criterion which states that if $a_i \geq 0$, $i = 1,2,3$ and $a_1a_2 - a_3 > 0$, the roots of the polynomial $\lambda^3 + a_1\lambda^2 + a_2\lambda + a_3$ are negative.

It is obvious that $a_1 > 0, a_2 > 0, a_3 > 0$ and $a_1a_2 - a_3 = (2\mu_H + \gamma + \alpha_1 + \eta)(\mu_M + \alpha_2)^2 + (\eta + \gamma + 2\mu_H)(\mu_H(\mu_H + \gamma + \alpha_1) + 2(\mu_M + \alpha_2)\mu_H + \mu_H\eta + (\mu_M + \alpha_2)(\gamma + \alpha_1) + \eta(\gamma + \alpha_1 + \mu_M + \alpha_2)) + \beta_3 S_M \eta(\beta_1 S_{H_1} + \beta_2 S_{H_2}) > 0$.

Since the criteria is satisfied, the roots of the polynomial are negative. Hence the disease free equilibrium point is locally stable. □

Theorem 4. *The equilibrium point* $P_1 = (S^*_{H_1}, S^*_{H_2}, E^*_H, I^*_H, S^*_M, I^*_M)$ *exists and is stable when* $R_0 > 1$.

Proof. Linearisation of the system (1), at the endemic equilibrium $(S^*_{H_1}, S^*_{H_2}, E^*_H, I^*_H, S^*_M, I^*_M)$ gives the Jacobian matrix as,

$$L_1 = \begin{bmatrix} -(\beta_1 I^*_M + \mu_H + \delta) & 0 & 0 \\ \delta & -(\mu_H + \beta_2 I^*_M) & 0 \\ \beta_1 I^*_M & \beta_2 I^*_M & -(\mu_H + \eta) \\ 0 & 0 & \gamma \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}$$

$$\begin{bmatrix} (1-k)\gamma & 0 & -\beta_1 S^*_{H_1} \\ k\gamma & 0 & -\beta_2 S^*_{H_2} \\ 0 & 0 & (\beta_1 S^*_{H_1} + \beta_2 S^*_{H_2}) \\ -(\mu_H + \gamma + \alpha_1) & 0 & 0 \\ -\beta_3 S^*_M & -(\beta_3 I^*_H + \mu_M + \alpha_2) & 0 \\ \beta_3 S^*_M & \beta_3 I^*_H & -(\mu_M + \alpha_2) \end{bmatrix}$$

Supposing $a = \beta_1 I^*_M + \mu_H + \delta$, $b = (1-k)\gamma$, $c = \beta_1 S^*_{H_1}$, $d = \delta$, $e = \beta_2 I^*_M + \mu_H$, $f = k\gamma$, $g = \beta_2 S^*_{H_2}$, $h = \beta_1 I^*_M$, $i = \beta_2 I^*_M$, $j = \mu_H + \eta$, $z = \gamma$, $l = \mu_H + \gamma + \alpha_1$, $m = \beta_3 S^*_M$, $p = \beta_3 I^*_H$, $q = \mu_M + \alpha_2$ we get

$$L_1 = \begin{bmatrix} -a & 0 & 0 & b & 0 & -c \\ d & -e & 0 & f & 0 & -g \\ h & i & -j & 0 & 0 & c+g \\ 0 & 0 & z & -l & 0 & 0 \\ 0 & 0 & 0 & -m & -p-q & 0 \\ 0 & 0 & 0 & m & p & -q \end{bmatrix}$$

Using the MAPLE software, the characteristic equation of the above matrix is

$(\lambda + q)\,(\lambda^5 + s_1\lambda^4 + s_2\lambda^3 + s_3\lambda^2 + s_4\lambda + s_5) = 0$

where $s_1 = a + e + j + l + p + q$,

$s_2 = l(e + j + a + p) + j(e + q + p + a) + qe + pe + ap + aq + ae$,

$s_3 = -qje + qlj + qle - kif + lje - mkg - mkc + plj + ple + pje + aej + ael + aep + aeq +$

$ajl + ajp + ajq + alq - bhk$,

$s_4 = -mkce + mkge + mkig - qkif + qlje - pkif + plje - ackm + aejl + aejp + aejq + aelp + aelq - agkm + ajlp + ajlq - bdik - behk - bhkp - bhkq + chkm$,

$s_5 = -pkidb - pkhbe - pkifa + pljea + mkidc - mkcea - mkgea + mkhce + mkiga - qkidb - qkhbe - qkifa + qljea$.

It is complicated to show the roots of the polynomial $\lambda^5 + s_1\lambda^4 + s_2\lambda^3 + s_3\lambda^2 + s_4\lambda + s_5 = 0$ are negative. The stability of the endemic equilibrium point is shown by numerical simulation in Section 8.

□

In the next section we use Optimal Control Theory to see the effect of awareness and the use of different control measures on the mosquito population.

7. Optimal Control Analysis of the Model

In this section we reformulate the model (1) to estimate the effect of the control strategies used to control the mosquitoes. The three main control strategies are: use of bed nets for personal protection denoted by $u_1(t)$, treatment of infected individuals with drugs denoted by $u_2(t)$ and the spraying of insecticides on the breeding ground of mosquitoes denoted by $u_3(t)$. Taking these controls into account, model (1) is reformulated as follows:

$$
\begin{cases}
\frac{dS_{H_1}}{dt} = \Lambda_1 - (1-u_1)\beta_1 S_{H_1} I_M - \delta S_{H_1} - \mu_H S_{H_1} + (1-k)\gamma I_H \\
\frac{dS_{H_2}}{dt} = \delta S_{H_1} - (1-u_1)\beta_2 S_{H_2} I_M - \mu_H S_{H_2} + k\gamma I_H \\
\frac{dE_H}{dt} = (1-u_1)\beta_H S_{H_1} I_M + (1-u_1)\beta_H S_{H_2} I_M - \mu_H E_H - \eta_H E_H \\
\frac{dI_H}{dt} = \eta_H E_H - \alpha I_H - \mu_H I_H - \gamma I_H - u_2 I_H \\
\frac{dS_M}{dt} = \Lambda_2 - (1-u_1)\beta_3 S_M I_H - \alpha_2 S_M - \mu_M S_M - (1-p)u_3 S_M \\
\frac{dI_M}{dt} = (1-u_1)\beta_3 S_M I_H - \alpha_2 I_M - \mu_M I_M - (1-w)u_3 I_M
\end{cases} \tag{15}
$$

where $1-w$ is the fraction of reduced mosquito population and hence the mosquitoes are reduced at the rate $u_3(1-w)$. Moreover, $0 \leq u_1 \leq 1$, $0 \leq u_2 \leq a_2$ where a_2 is the efficacy of the drug used for treatment, $0 \leq u_3 \leq a_3$ where a_3 is the efficacy of the insecticide at reducing

mosquito population.

Our objective is to minimize the number of infected individuals through the optimal control strategies $u_1(t)$, $u_2(t)$ and $u_3(t)$.

Define

$$J(u_1,u_2,u_3)=\int_0^{t_f}(lE_H+mI_H+nI_M+pu_1^2+qu_2^2+ru_3^2)dt \tag{16}$$

where t_f is final time and l,m,n are positive weights to balance the factor and p,q and r denote the weighting constants, mI_H is the cost of infection, pu_1^2 is the cost of use of bed nets, qu_2^2 is the cost of treatment efforts and ru_3^2 is the cost of use of insecticides.

We need to find an optimal control u_1^*, u_2^* and u_3^* such that,

$$J(u_1^*,u_2^*,u_3^*)=\min_{u_1,u_2,u_3}\{(u_1,u_2,u_3)/u_1,u_2,u_3\in\Omega_1\} \tag{17}$$

where the control set, $\Omega_1=\{(u_1,u_2,u_3)/u_i:[0,t_f]\to[0,1]$, Lebesgue measurable $i=1,2,3\}$

Theorem 5. *There exists an optimal control u_1^*,u_2^*,u_3^* and corresponding solutions S_{H_1},S_{H_2}, E_H,I_H,S_M,I_M of the system (15) that minimises $J(u_1,u_2,u_3)$ over Ω_1. Furthermore, there exists adjoint variables $\lambda_1,\lambda_2,\lambda_3,\lambda_4,\lambda_5,\lambda_6$ such that*

$$\begin{cases}
-\frac{d\lambda_1}{dt}=[-(1-u_1)\beta_1I_M-(\mu_H+\delta)]\lambda_1+\lambda_2[\delta-(1-u_1)\beta_2I_M]+\lambda_3(1-u_1)\beta_1I_M\\
-\frac{d\lambda_2}{dt}=-\lambda_2[(1-u_1)\beta_2I_M+\mu_H]+\lambda_3(1-u_1)\beta_2I_M\\
-\frac{d\lambda_3}{dt}=l-\lambda_3(\mu_H+\eta)+\lambda_4\eta\\
-\frac{d\lambda_4}{dt}=m-\lambda_4[\mu_H+\gamma+u_2+\alpha_2]+\lambda_1[(1-k)\gamma]+\lambda_2k\gamma\\
-\frac{d\lambda_5}{dt}=-\lambda_5[(1-u_1)\beta_3I_H+\mu_M+(1-p)u_3+\alpha_2]+\lambda_6(1-u_1)\beta_3I_H\\
-\frac{d\lambda_6}{dt}=n-\lambda_6[\mu_M+\alpha_2+(1-w)u_3]
\end{cases} \tag{18}$$

with transversality conditions,

$$\lambda_i(T)=0,i=1,2,...,6. \tag{19}$$

The controls u_1^*, u_2^* and u_3^* are given by

$$u_1^* = max\{0, min(1, \frac{\beta_1 S_{H_1}^* I_M^* (\lambda_3 - \lambda_1) + \beta_2 S_{H_2}^* I_M^* (\lambda_3 - \lambda_2) + \beta_3 S_M^* I_H^* (\lambda_6 - \lambda_5)}{2p})\}$$
$$u_2^* = max\{0, min(1, \frac{\lambda_4 I_H^*}{2q})\}$$
$$u_3^* = max\{0, min(1, \frac{\lambda_5 (1-w) S_M^* + \lambda_6 (2-w) I_M^*}{2r})\}$$

Proof. The optimal control exists since the integrand of J is convex with respect to u over a convex and closed control set Ω_1. Moreover the system satisfies Lipschitz property with respect to the state variables since the state solutions are bounded [4]. The Pontryagin's Maximum Principle [19] converts, (15), with (16) and (17) into a problem of minimising a Hamiltonian H, with respect to u_1, u_2 and u_3. Define

$$H = lE_H + mI_H + nI_M + pu_1^2 + qu_2^2 + ru_3^2 + \sum_{i=1}^{6} \lambda_i f_i \tag{20}$$

where $f_i, i = 1, 2, ..., 6$ are right hand side of the system (15).

We also have the adjoint equations

$$\begin{cases} \frac{d\lambda_1}{dt} = -\frac{\partial H}{\partial S_{H_1}}, \lambda_1(T) = 0 \\ \frac{d\lambda_2}{dt} = -\frac{\partial H}{\partial S_{H_2}}, \lambda_2(T) = 0 \\ \frac{d\lambda_3}{dt} = -\frac{\partial H}{\partial E_H}, \lambda_3(T) = 0 \\ \frac{d\lambda_4}{dt} = -\frac{\partial H}{\partial I_H}, \lambda_4(T) = 0 \\ \frac{d\lambda_5}{dt} = -\frac{\partial H}{\partial S_M}, \lambda_5(T) = 0 \\ \frac{d\lambda_6}{dt} = -\frac{\partial H}{\partial I_M}, \lambda_6(T) = 0 \end{cases} \tag{21}$$

Evaluating the six equations given by (21) at the optimal control and the corresponding states will give the adjoint system (18) and (19).

On the interior of the set Ω_1, where $0 < u_i < 1, i = 1, 2, 3$, we have

$$\frac{\partial H}{\partial u_1} = 0, \frac{\partial H}{\partial u_2} = 0, \frac{\partial H}{\partial u_3} = 0. \tag{22}$$

(22) gives the following three equations.

$$2pu_1^* + \beta_1 S_{H_1}^* I_M^* (\lambda_1 - \lambda_3) + \beta_2 S_{H_2}^* I_M^* (\lambda_2 - \lambda_3) + \beta_3 S_M^* I_H^* (\lambda_5 - \lambda_6) = 0,$$
$$2qu_2^* - \lambda_4 I_H^* = 0,$$

$2ru_3^* - \lambda_5(1-w)S_M^* - \lambda_6 I_M^* - \lambda_6(1-w)I_M^* = 0.$

Hence we have,

$$u_1^* = max\{0, min(1, \frac{\beta_1 S_{H_1}^* I_M^*(\lambda_3 - \lambda_1) + \beta_2 S_{H_2}^* I_M^*(\lambda_3 - \lambda_2) + \beta_3 S_M^* I_H^*(\lambda_6 - \lambda_5)}{2p})\}$$

$$u_2^* = max\{0, min(1, \frac{\lambda_4 I_H^*}{2q})\}$$

$$u_3^* = max\{0, min(1, \frac{\lambda_5(1-w)S_M^* + \lambda_6(2-w)I_M^*}{2r})\}$$

Hence the theorem. □

8. NUMERICAL SIMULATION

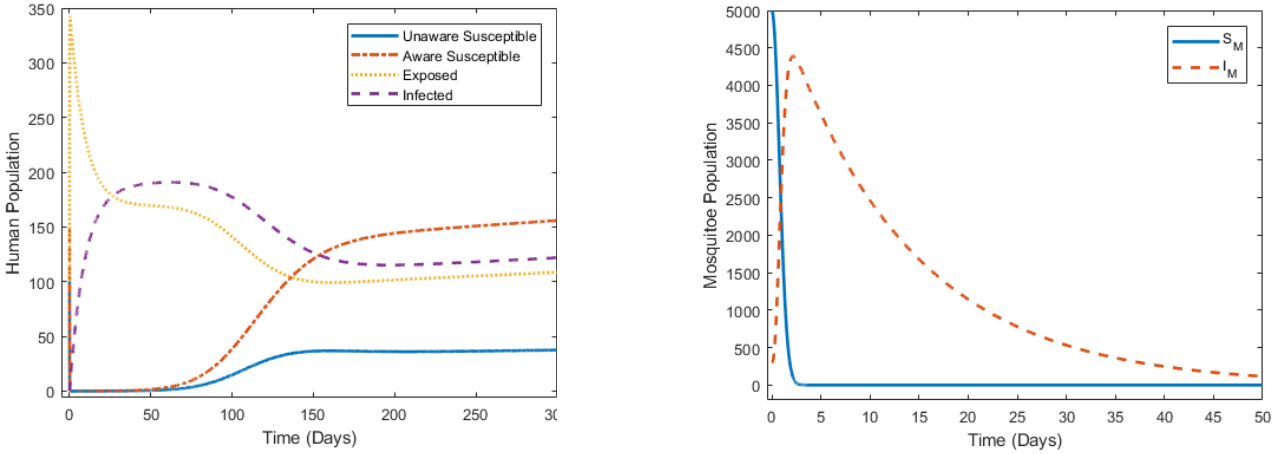
In this section, we use simulation and see how model (1) behaves. Further in order to see the effect of the various control measures on the model (15) for vector borne diseases, we carry out the simulations for malaria. The parameters for the model are taken from [14] and [5].

TABLE 1. Numerical values of the parameters for malaria $(days^{-1})$

Parameters	Symbols	Values $(days^{-1})$
Contact rate of unaware susceptible humans with infectious mosquitoes	β_1	0.05
Contact rate of aware susceptible humans with infectious mosquitoes	β_2	0.03
Rate of progression of humans from the exposed to the infectious state	η	0.058
Rate of progression of humans from the infected to the recovered state	γ	0.05
Disease induced death rate of humans	α_1	0.05
Contact rate of infected human with susceptible mosquitoes	β_3	0.09
Natural death rate of mosquitoes	μ_M	0.071
A fraction of mosquito population reduced	p	0.0667
Disease induced death rate of mosquitoes	α_2	0.05

We further assume that $\Lambda_1 = 0.405$, $\mu_H = 0.0000457, k = 0.6$, $\delta = 0.002$, $\Lambda_2 = 0.071$ and $p = 0.85$.

8.1. Behaviour of the model. Figures 2(a) and 2(b) show the behaviour of model (15) when no control measures are taken. In this case, we have $u_1 = u_2 = u_3 = 0$. It can be noted that when $u_1 = u_2 = u_3 = 0$, the model (15) reduces to the model given by (1). Figure 2 shows that the various compartments are stable after 150 days. Hence the endemic equilibrium point is stable.

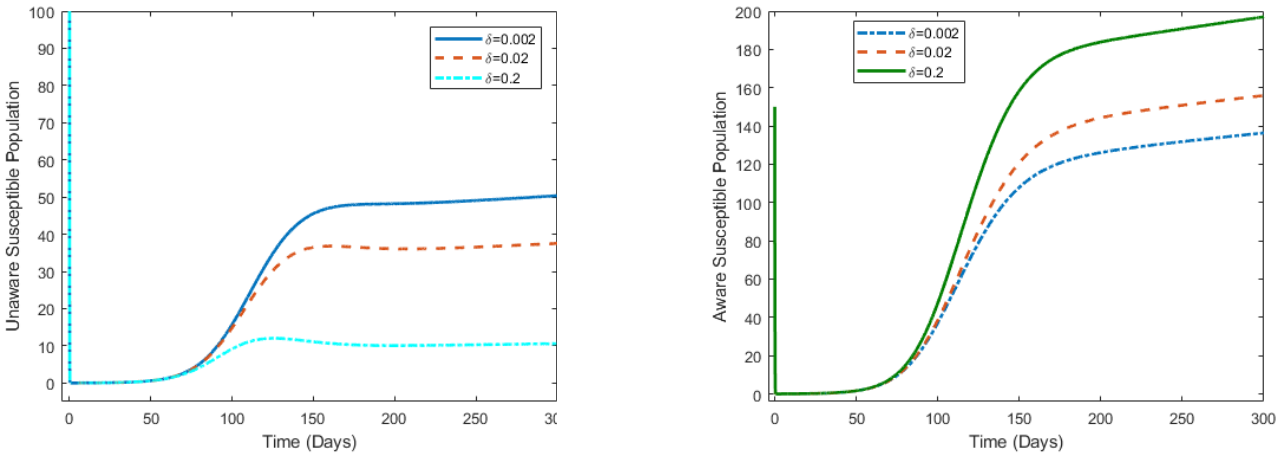


(a) (b)

FIGURE 2. Variation in the population with time of (a) Humans (b) Mosquitoes

The stability of the endemic equilibrium point can also be proved numerically by calculating the value of R_0. The expression for R_0 is given in (13). Using the above parameters, the value of R_0 is calculated and it is found to be 4.89 which is greater than 1. The eigenvalues of this matrix are -59.999, -0.558, -0.001, -0.0311, -0.074, -0.076 and they are all negative. Since the eigenvalues are negative, the system is stable.

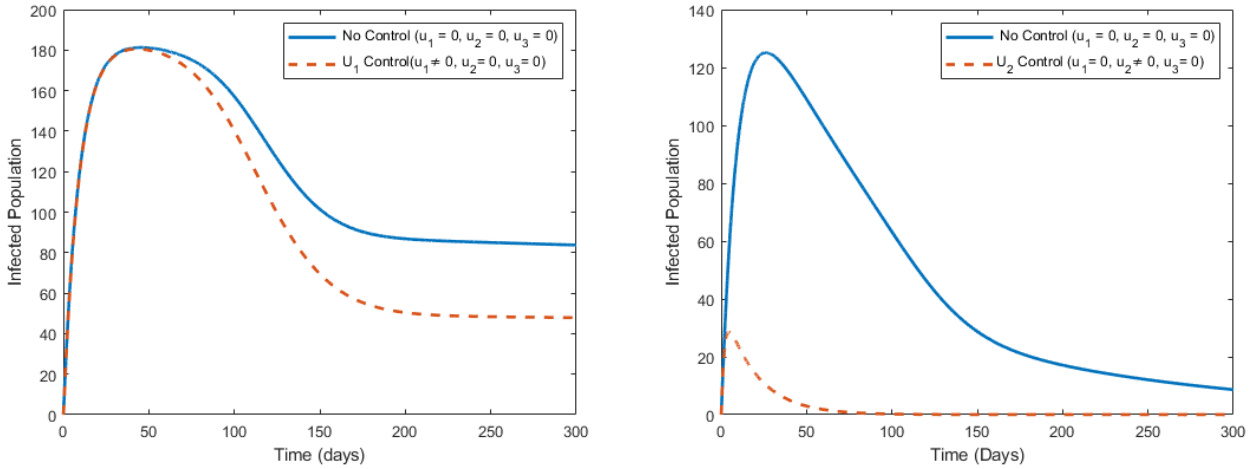
8.2. Effect of awareness. Figures 3(a) and 3(b) show the effect of varying δ where δ is the rate at which unaware susceptible population move into the aware susceptible population. As δ increases, the unaware susceptible population decreases and the aware susceptible population decreases. The same type of result also holds for the parameter k which is the fraction of recovered people going to the aware class.



(a) (b)

FIGURE 3. Variation in (a) Unaware susceptible population and (b) Aware susceptible population with time for different values of δ.

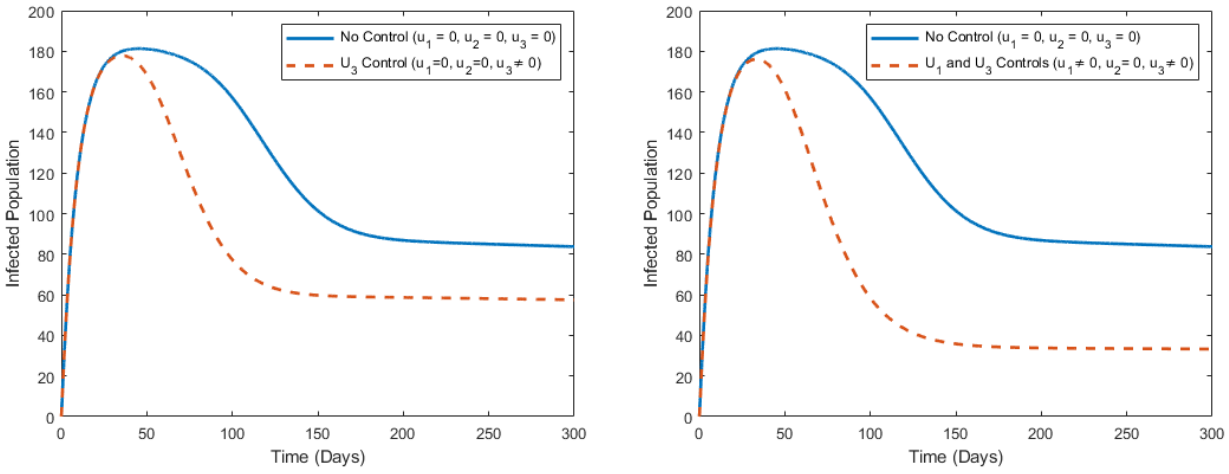
8.3. Effect of Control Measures. In this section, we analyse the effect of the various control measures on the infected human population. We compare the infected population when no control measures are taken along with the infected population when one or two or all the control measures are taken. We take the values of u_1, u_2 and u_3 as 0.5 for simulation.



(a) (b)

FIGURE 4. Comparison of infected population when no controls are applied with (a) infected population when $u_1(u_1 \neq 0, u_2 = u_3 = 0)$ control is applied (b) infected population when $u_2(u_1 = 0, u_2 \neq 0, u_3 = 0)$ control is applied

In Figures 4, 5 and 6 we apply the controls u_1, u_2 and u_3 respectively and compare the infected population along with the infected population when no controls are applied. It is observed that the treatment of patients with drugs brings down the number of infected persons drastically (Figure 4(b)). From Figures 4(a) and 5(b), it can be seen that using the bed nets is a better control measure than spraying of insecticides to reduce the interaction between mosquitoes and humans. However, from Figure 5(b) it can be seen that when both the control measures are used against the mosquitoes there is a considerable decrease in the mosquito population rather than using just one of them. Figure 6 compares the infected population when no control measures



(a) (b)

FIGURE 5. Comparison of infected population when no controls are applied with (a) infected population when $u_3(u_1 = 0, u_2 = 0, u_3 \neq 0)$ control is applied (b) infected population when control measures against mosquito are applied $(u_1 \neq 0, u_2 = 0, u_3 \neq 0)$

are taken with the infected population when all the three control measures are taken. It can be seen that these control measures are effective in decreasing the infected population.

9. CONCLUSION

In this paper we formulated an SEIRS model for the human population in which the susceptible population is divided into two compartments as those who are aware of the disease and those who are unaware of the disease. Moreover the various control measures were introduced in the model. These control measures were introduced to reduce the vector population as well

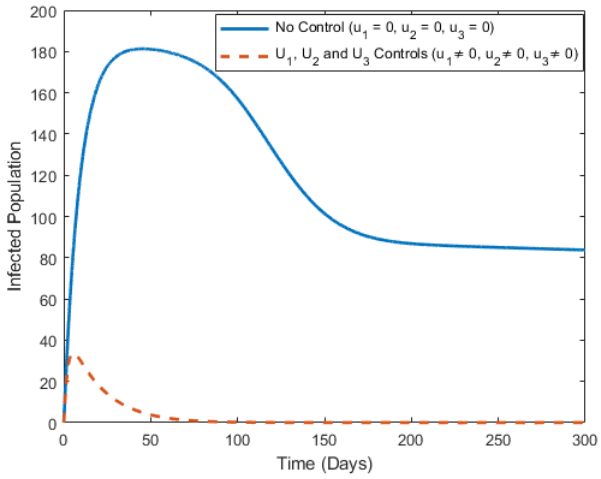


FIGURE 6. Comparison of infected population when no control measures are taken $(u_1 = u_2 = u_3 = 0)$ and when all the three control measures are taken $(u_1 \neq 0, u_2 \neq 0, u_3 \neq 0)$

as the treatment of the infected population by drugs. It was observed that the infected human population reduced drastically when treated whereas controlling the vector population did not have much effect on the infected population initially but later on slowly reduced it. In this model, we have included the parameter related to awareness only in the susceptible population and it showed that this parameter did not have much effect in reducing the infected population. Hence it remains to be seen whether the infected human population decreases if awareness of the disease among the human population is taken as a control measure.

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CONFLICT OF INTERESTS

The author(s) declare that there is no conflict of interests.

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