Int. J. Nonlinear Anal. Appl. 13 (2022) 2, 2999–3015
ISSN: 2008-6822 (electronic)
http://dx.doi.org/10.22075/ijnaa.2022.25189.2946

Vaccination and control measures on vector transmission dynamics: Modeling and simulation

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(Communicated by Haydar Akca)

Abstract

In this paper, a non-linear mathematical model is proposed and analyzed to study the role of vaccination and control measures on the spread of vector-borne diseases. It is assumed that susceptible hosts can be infected either directly or indirectly. In the modelling process, it is considered that only a susceptible person can be vaccinated. The existence of the control problem is proved and later used to investigate effective control efforts for the prevention of direct and indirect transmission of disease. The model is analyzed using Hurwitz and Sylvester's criterion. The analysis of the model reveals that, if the vaccination reproduction number $\mathcal{R}_v$ is less than one, the disease can be eradicated provided, and the vaccine is highly efficient.

Keywords: Vector-borne diseases, Control, Vaccination, Reproduction number, Stability
2020 MSC: 34D23, 34D35, 93D05

1 Introduction

Vector-borne diseases are human illnesses that are transmitted by vectors, such as: mosquitoes, ticks, sand flies, fleas etc. These vectors are capable of carrying infective pathogens like bacteria, protozoa and viruses, which they can transfer from one host to another. The significant vector-borne diseases account for around 17% of all infectious diseases [24]. The burden of vector-borne diseases is highest in tropical and subtropical areas. These diseases disproportionately affect the poorest population.

Various studies have been carried out to study the host-vector transmission dynamics of vector borne disease. The researchers mainly focused on the spread of disease in community with the help of vectors rather than by direct contact. Blayneh and Jag [4] proposed an SIS model for vector transmitted diseases by considering factors like transmission of disease from vector to vector and then to host via surrounding media. Cosner et al. [7] suggested that disease persists even in zero transmission when there is movement of humans between patches within heterogeneous environment. Tumwiine et al. [25] studied the effect of Infective human immigrants on the transmission dynamics of vector borne diseases. Vargas et al. [27] analysed two age structured model by assuming that host's physical age and susceptibility depends on this age. Further, Xu and Zhou [30] studied the behaviour of delayed epidemic model with partial immunity of reinfection on vector borne diseases model. Musso et al. [22] identified some additional features for the transmission

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Received: November 2021 *Accepted:* July 2022

of Zika virus (the transmission of infection may be direct (blood transfer, sexual contact) as well as through vectors. Fitzgibbon et al. [13] described infectious age structured model with incubation periods for population dynamics using reaction diffusion equation. Enduri et al. [11] studied the transmission of spatial and temporal dynamics (using reaction diffusion equation) by considering the mobility of both humans and environmental factors. Feng et al. [12] formulated a model by incorporating the impact of free pathogen and the effect of environment on the transmission of vector borne diseases.

Among all infectious diseases, vector borne diseases are the most complex to prevent and control. One of the effective methods in disease prevention is vaccination [16, 19, 9, 23]. However, for the major vector borne diseases the design of effective vaccine presents a great challenge. The difficulty with development of the malaria vaccine, for example, is the genetic complexity of the parasite and there are four distinct stereotypes in case of dengue [18]. The design of the vaccine, therefore, focuses on the development of a tetravalent vaccine for all stereotypes of the virus. Despite the above-mentioned challenges in developing effective vaccines for vector transmitted diseases, significant steps have been taken like; in recent years, international organisations have promoted increased vaccination programs to tackle the vector borne diseases like cholera and typhoid. Mathematical models have been used significantly to assess the efficacy of vaccination strategies. Various studies have been carried out, particularly for the direct transmitted diseases, for effective vaccination strategies [2, 10, 17, 14]. Since, there is no effective vaccine as yet for some common vector borne diseases, few models have specifically considered the possible impact of vaccination on such diseases. Billings et al. [3] analysed an ODE model to determine the impact of single-strain vaccine campaigns on the epidemic multistrain model dynamics. Coudeville and Garnett [8] studied the effect of vaccination on the age-structured, serotype-specific compartment model for dengue disease. Kar and Jana [20] analysed the combined control strategies on both host (treatment and vaccination controls) and vector (insecticide control). Recently, Abidemi et al. [1] proposed a two strain compartment model for the dengue transmission by considering the variable human and vector populations.

In this paper, we have formulated a mathematical model for vector born diseases with vaccination. Our aim is to explore the effect of vaccine and control measures on the spread of vector born diseases.

2 Mathematical Model

The total human host population at time t is denoted by $N_1(t)$ and total vector size at time t be denoted by $N_2(t)$. The human host population of size $N_1(t)$ is divided into five distinct classes: the susceptible population of size $S_h(t)$, the vaccinated population of size $V_h(t)$, the exposed population of size $E_h(t)$, the infectious population of size $I_h(t)$, and the recovered population of size $R_h(t)$. Thus $N_1(t)$=$S_h(t)$+$V_h(t)$+$E_h(t)$+$I_h(t)$+$R_h(t)$. The model is based on the following assumptions:

i) the susceptible host can be infected either directly (contact with infected person, possibly through blood transfusion) or through biting of an infectious vector [22].
ii) the vertical transmission in host as well as vector population is assumed to be negligible. Thus, all newly recureted hosts and vectors are susceptible host and susceptible vectors [28].
iii) the vaccination is assumed to be imperfect, vaccinated individuals can obtain breakthrough infection at a reduced rate $(1-\sigma)\lambda V_h I_h$ [15] .
iv) the recovered host acquire permanent immunity so as recovered host can not become susceptible again [21].
v) the infected vectors never recover from the infection and carry the pathogen until their death and hence there is no recovered class for the vectors [27].

The mathematical model can be represented by the following non-linear differential equations.

$$\begin{aligned}
\frac{dS_h}{dt} &= b_1 - \lambda S_h I_h - \beta S_h I_v - (\psi + \mu_1) S_h, \\
\frac{dV_h}{dt} &= \psi S_h - (1-\sigma)\lambda V_h I_h - \mu_1 V_h, \\
\frac{dE_h}{dt} &= \lambda S_h I_h + (1-\sigma)\lambda V_h I_h + \beta S_h I_v - (k + \mu_1) E_h, \\
\frac{dI_h}{dt} &= k E_h - d I_h - \delta I_h - \mu_1 I_h, \\
\frac{dR_h}{dt} &= \delta I_h - \mu_1 R, \qquad \frac{dS_v}{dt} = b_2 - \gamma S_v I_h - \mu_2 S_v, \qquad \frac{dI_v}{dt} = \gamma S_v I_h - \mu_2 I_v,
\end{aligned} \tag{2.1}$$

with initial conditions $S_h \geqslant 0$, $V_h \geqslant 0$, $E_h \geqslant 0$,$I_h \geqslant 0$,$R_h \geqslant 0$,$S_v \geqslant 0$,$I_v \geqslant 0$. Where b_1 and b_2 are the birth or immigrant rate for host and vector population respectively. λ is the rate of direct transmission. β is the rate of Infection spread by the pathogen-carrier vectors. ψ the vaccination rate of susceptible individuals. σ is the factor by which the vaccine reduces infection. k is transfer rate between the exposed and the infectious class. γ is the rate of incidence of newly infected vectors (after biting an infected host). δ is the per capita recovery of host population. d is disease induced death rate of host population. μ_1 and μ_2 natural death rates of host and vector population respectively.

Since the recovered population R_h appears only in fifth equation of system (2.1), therefore, the system (2.1) can be reduced as:

$$\begin{aligned}
\frac{dS_h}{dt} &= b_1 - \lambda S_h I_h - \beta S_h I_v - (\psi + \mu_1) S_h, \\
\frac{dV_h}{dt} &= \psi S_h - (1-\sigma)\lambda V_h I_h - \mu_1 V_h, \\
\frac{dE_h}{dt} &= \lambda S_h I_h + (1-\sigma)\lambda V_h I_h + \beta S_h I_v - (k + \mu_1) E_h, \\
\frac{dI_h}{dt} &= k E_h - d I_h - \delta I_h - \mu_1 I_h, \\
\frac{dS_v}{dt} &= b_2 - \gamma S_v I_h - \mu_2 S_v, \\
\frac{dI_v}{dt} &= \gamma S_v I_h - \mu_2 I_v.
\end{aligned} \tag{2.2}$$

The above system is equipped with initial conditions for host and vector population as : $S_h(0) = S_{h0}$, $V_h(0) = V_{h0}$, $E_h(0) = E_{h0}$, $I_h(0) = I_{h0}$, $S_v(0) = S_{v0}$, $I_v(0) = I_{v0}$.

It is worth to mention here that once the vector become carrier of micro-parasite, they carry it for life. The total population size can be determined by $N(t) = N_h(t) + N_v(t)$, where $N_h(t) = S_h(t) + V_h(t) + E_h(t) + I_h(t)$ is the total host population size and $N_v(t) = S_v(t) + I_v(t)$ is the total vector population.

Adding host population of model (2.2) gives that

$$\frac{dN_h}{dt} = b_1 - \mu_1 N_h - d I_h - \delta I_h. \tag{2.3}$$

It follows from equation (2.3) that if $N_h > \frac{b_1}{\mu_1}$, then $\frac{dN_h}{dt} < 0$. Clearly, $0 < I_h(t) < N_h(t)$, it follows that

$$b_1 - (\mu_1 + \delta + 2d)\, N_h(t) \leq \frac{dN_h(t)}{dt} \leq b_1 - \mu_1 N_h(t).$$

Thus,

$$\frac{b_1}{\mu_1 + 2d + \delta} \leq \liminf_{t\to\infty} N_h(t) \leq \limsup_{t\to\infty} N_h(t),$$

So that

$$\lim_{t\to\infty} N_h(t) = \frac{b_1}{\mu_1}.$$

Similarly, for vector population we have

$$\lim_{t\to\infty} N_v(t) = \frac{b_2}{\mu_2}.$$

From the first equation of model system (2.2), it follows that

$$0 < \limsup_{t\to\infty} S_h \leq \frac{b_1}{\mu_1 + \psi} \tag{2.4}$$

and then from the second equation of model system (2.2),

$$0 < \limsup_{t\to\infty} V_h \leq \frac{b_1 \psi}{\mu_1(\mu_1 + \psi)}. \tag{2.5}$$

It can be shown that $S_h > 0, V_h > 0, E_h > 0, I_h > 0, S_v > 0$ and $I_v > 0$ for all $t > 0$. Thus, all solutions of the model system (2.2), with non-negative initial data, remain non-negative for all $t > 0$. The system (2.2) will be analyzed in biologically feasible region Ω given as follows:

$$\Omega = \left\{ (S_h, V_h, E_h, I_h, S_v, I_v) \in \mathbf{R}^6_+ : 0 \leqslant S_h + V_h + E_h + I_h \leqslant \frac{b_1}{\mu_1}, 0 \leqslant S_v + I_v \leqslant \frac{b_2}{\mu_2}, S_h \leqslant \frac{b_1}{\mu_1 + \psi}, \right. \\ \left. V_h = \frac{b_1 \psi}{\mu_1(\mu_1 + \psi)} \right\}. \tag{2.6}$$

3 Disease Free Equilibrium and Reproduction number

The equilibria for the model (2.2), can be obtained by setting right hand side of model (2.2) equal to zero. The model clearly has a unique disease free equilibrium point E_0 in the region (2.6) given by $E_0 = (S_h^0, V_h^0, 0, 0, S_v^0, 0)$, where $S_h^0 = \frac{b_1}{\mu_1+\psi}, V_h^0 = \frac{\psi b_1}{\mu_1(\mu_1+\psi)}, S_v^0 = \frac{b_2}{\mu_2}$. We will discuss in detail the existence of endemic equilibrium E^*, before that we will obtain the expression of reproduction number. The reproduction number denoted by $\mathcal{R}_v$ and defined by the number of secondary infection produced when a single infectious host is introduced into a totally susceptible population. We use the next generation matrix method described in [26] to define the reproduction number $\mathcal{R}_v$ as:

Let $x = (S_h, V_h, E_h, I_h, S_v, I_v)^\mathsf{T}$. Then the model (2.2) can be written in the matrix form as:

$$\frac{dx}{dt} = \mathcal{F}(x) - \mathcal{V}(x),$$

where

$$\mathcal{F}(x) = \begin{pmatrix} \lambda S_h I_h + (1-\sigma)\lambda V_h I_h + \beta S_h I_v \\ 0 \\ 0 \end{pmatrix},$$

$$\mathcal{V}(x) = \begin{pmatrix} (k+\mu_1)E_h \\ (d+\delta+\mu_1)I_h - kE_h \\ \mu_2 I_v - \gamma S_v I_v \end{pmatrix}.$$

Now, we can get

$$\mathbf{F} = \begin{pmatrix} 0 & \lambda S_h^0 + (1-\sigma)\lambda S_v^0 & \beta S_h^0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}, \qquad \mathbf{V} = \begin{pmatrix} k+\mu_1 & 0 & 0 \\ -k & d+\delta+\mu_1 & 0 \\ 0 & -\gamma S_v^0 & \mu_2 \end{pmatrix},$$

we have

$$\mathbf{V}^{-1} = \begin{pmatrix} \frac{1}{k+\mu_1} & 0 & 0 \\ \frac{k}{(k+\mu_1)(d+\delta+\mu_1)} & \frac{1}{d+\delta+\mu_1} & 0 \\ \frac{k\gamma S_v^0}{\mu_2(k+\mu_1)(d+\delta+\mu_1)} & \frac{\gamma S_v^0}{\mu_2(d+\delta+\mu_1)} & \frac{1}{\mu_2} \end{pmatrix}.$$

The reproduction number $\mathcal{R}_v$, defined as the spatial radius $\mathbf{F}\mathbf{V}^{-1}$ is given as: $\rho\left(\mathbf{F}\mathbf{V}^{-1}\right) = \frac{k\lambda\left(S_h^0 + (1-\sigma)V_h^0\right)}{(k+\mu_1)(d+\delta+\mu_1)} + \frac{\beta k\gamma S_h^0 S_v^0}{\mu_2(k+\mu_1)(d+\delta+\mu_1)}$. According to [26] the vaccine reproduction number is given by:

$$\begin{aligned} \mathcal{R}_v &= \frac{k\lambda\left(S_h^0 + (1-\sigma)\,V_h^0\right)}{(k+\mu_1)\,(d+\delta+\mu_1)} + \frac{\beta k\gamma S_h^0 S_v^0}{\mu_2\,(k+\mu_1)\,(d+\delta+\mu_1)} \\ &= \frac{\mu_2^2 b_1 k\lambda\,(\mu_1 + (1-\sigma)\,\psi) + \beta k\gamma b_1 b_2 \mu_1}{\mu_1\mu_2^2\,(\mu_1+\psi)\,(k+\mu_1)\,(d+\delta+\mu_1)}. \end{aligned}$$

3.1 Stability of Disease free equilibrium with vaccination

The variational matrix at the disease free equilibrium point with vaccination E_v^0 of the model (2.2) is given as:

$$J_1 = \begin{pmatrix} -(\mu_1+\psi) & 0 & 0 & -\lambda S_h^0 & 0 & -\beta S_h^0 \\ \psi & -\mu_1 & 0 & -(1-\sigma)\lambda V_h^0 & 0 & 0 \\ 0 & 0 & -(\mu_1+k) & \lambda S_h^0 + (1-\sigma)\lambda V_h^0 & 0 & \beta S_h^0 \\ 0 & 0 & k & -(d+\delta+\mu_1) & 0 & 0 \\ 0 & 0 & 0 & -\gamma S_v^0 & -\mu_2 & 0 \\ 0 & 0 & 0 & \gamma S_v^0 & 0 & -\mu_2 \end{pmatrix}.$$

From the characteristic equation, we obtain three eigen values as $-(\mu_1+\psi)$, $-\mu_1$, $-\mu_2$ and the remaining three eigenvalue can be obtained from the following cubic equation

$$\zeta^3 + a_2\zeta^2 + a_1\zeta + a_0 = 0,$$

where

$$\begin{aligned}
a_2 =& \left[\mu_2 + (k+\mu_1) + (d+\delta+\mu_1)\right],\\
a_1 =& \left[\mu + \mu_2\,(d+\delta+\mu_1) + \beta k\gamma C + (k+\mu_1)\,(d+\delta+\mu_1)\,(1-\mathcal{R}_v)\right],\\
a_0 =& \mu_2(k+\mu_1)\,(d+\delta+\mu_1)\,(1-\mathcal{R}_v).
\end{aligned}$$

Here $\mu = \frac{\mu_2}{\mu_1}$ and $C = \frac{b_1}{\mu_2(\mu_1+\psi)}$. Since, $a_2 > 0$, and we can easily see that $a_0 > 0$ if $\mathcal{R}_v < 1$, $a_2a_1 > a_0$ if $\mathcal{R}_v < 1$. Hence, by using Hurwitz's criteria, we can state the following theorem.

Theorem 3.1. The Disease free equilibrium with vaccination is linearly asymptotically stable if $\mathcal{R}_v < 1$ and unstable if $\mathcal{R}_v > 1$.

4 Existence of Endemic equilibrium with vaccination

The endemic equilibrium of the model system (2.2) denoted by E^* is given by $E^* = (S_h^*, V_h^*, E_h^*, I_h^*, S_v^*, I_v^*)$. where $S_h^* = \frac{b_1\mu_2(\gamma I_h^*+\mu_2)}{\mu_2(\gamma I_h^*+\mu_2)(\lambda I_h^*+\mu_1+\psi)+\beta\gamma b_2 I_h^*}$, $E_h^* = \frac{1}{k}\,(d+\delta+\mu_1)\,I_h^*$, $V_h^* = \frac{\psi}{(1-\sigma)\lambda I_h^*+\mu_1}S_h^*$, $S_v^* = \frac{b_2}{\gamma I_h^*+\mu_2}$, $I_v^* = \frac{\gamma b_2}{\mu_2(\gamma I_h^*+\mu_2)}I_h^*$ and the value of I_h^* can be obtained from the following cubic equation

$$P\,(I_h^*) = b_0 I_h^{*3} + b_1 I_h^{*2} + b_2 I_h^* + b_3 = 0, \tag{4.1}$$

where,

$$\begin{aligned}
b_0 =& (k+\mu_1)(d+\delta+\mu_1)(1-\sigma)\gamma\mu_2\lambda^2,\\
b_1 =& (k+\mu_1)\,(d+\delta+\mu_1)\,(1-\sigma)\,\lambda\mu_2\left[\lambda\mu_2^2 + \gamma\beta b_2 + \mu_1\mu_2\gamma + \gamma\mu_2\,(\mu_1+\psi)\,(1-\mathcal{R}_v)\right]\\
&+ \frac{(1-\sigma)\,\lambda\gamma}{\mu_1\mu_2}\left[kb_1\lambda\mu_2^2\,(1-\sigma)\,\psi + \beta k\gamma b_1 b_2\mu_1\right],\\
b_2 =& (k+\mu_1)\,(d+\delta+\mu_1)\left[\lambda\mu_1\mu_2^2 + \mu_1\beta\gamma b_2 + \left(\gamma\mu_1\mu_2 + (1-\sigma)\,\lambda\mu_2^2\right)(1-\mathcal{R}_v)\right]\\
&+ \frac{kb_1}{\mu_1\mu_2}\left(\gamma\beta b_2\mu_1^2 + (1-\sigma)^2\,\lambda^2\mu_2^3\psi\right),\\
b_3 =& (k+\mu_1)\,(d+\delta+\mu_1)\,(\mu_1+\psi)\,\mu_1\mu_2^2 - \left[kb_1\mu_2^2\lambda\psi\,(1-\sigma) + kb_1b_2\mu_1\beta\gamma + k\lambda_1b_1\mu_1\mu_2^2\right]\\
=& \mu_1\mu_2^2\,(k+\mu_1)\,(d+\delta+\mu_1)\,(1-\mathcal{R}_v).
\end{aligned}$$

We state the theorem given in [6] to determine the existence of endemic equilibrium.

Theorem 4.1. Every equation of an odd degree has at least one real root of a sign opposite to that of its last term.

Since $0 < \sigma < 1$, therefore, $b_0 > 0$.
Now, two cases arise:

Case 1. when $\mathcal{R}_v > 1$, then using the theorem 4.1 equation (4.1) has atleast one positive root.

Again two cases arise:

Case 1a. when $\mathcal{R}_v > 1$, and if $b_1 < 0, b_2 < 0$ then using Descarts rule of signs, equation(4.1) has exactly one Positive root.

Case 1b. when $\mathcal{R}_v > 1$, and if $b_1 > 0, b_2 > 0$ then using Descarts rule of signs, equation(4.1) has atleast one Positive root.

Case 2. when $\mathcal{R}_v \leqslant 1$ then using Discart's rule of signs equation(4.1) has no positive root.

Thus, we summarize the result as:

Lemma 4.2. The system (2.2) has a unique endemic equilibrium point whenever $\mathcal{R}_v > 1$ and no positive endemic equilibrium when $\mathcal{R}_v \leqslant 1$.

4.1 Stability of endemic equilibrium with Vaccination

The endemic equilibrium $E^* = (S_h^*, V_h^*, E_h^*, I_h^*, S_v^*, I_v^*)$ is non-linearly asymptotically stable in the region Ω provided the following conditions are satisfied:

$$\begin{aligned}
&\left[a_1\left((\lambda I_h^* + \beta I_v^*) + (\mu_1+\psi) - \frac{\lambda b_1}{2\mu_1} - \frac{\beta b_1}{2\mu_1}\right) - a_3\left(\frac{\lambda b_1}{2\mu_1}\right)\right]\left[a_2\left((1-\sigma)\lambda I_h^* + \mu_1 - (1-\sigma)\frac{\lambda b_1}{2\mu_1}\right)\right.\\
&\qquad \left. -a_3\left((1-\sigma)\frac{\lambda b_1}{2\mu_1}\right)\right] > \frac{1}{2}a_2^2\psi^2\\
&\left[a_1\left((\lambda I_h^* + \beta I_v^*) + (\mu_1+\psi) - \frac{\lambda b_1}{2\mu_1} - \frac{\beta b_1}{2\mu_1}\right) - a_3\left(\frac{\lambda b_1}{2\mu_1}\right)\right] a_3\left((k+\mu_1) - \frac{\lambda b_1}{2\mu_1} - (1-\sigma)\frac{\lambda b_1}{2\mu_1}\right.\\
&\qquad \left. -\frac{\beta b_1}{2\mu_1}\right) > \beta^2 I_v^2\\
&a_3\left((k+\mu_1) - \frac{\lambda b_1}{2\mu_1} - \frac{\beta b_1}{2\mu_1} - (1-\sigma)\frac{\lambda b_1}{2\mu_1}\right)\left(a_4(d+\delta+\mu_1) - a_1\frac{\lambda b_1}{2\mu_1} - a_2(1-\sigma)\frac{\lambda b_1}{2\mu_1}\right)\\
&\qquad > \frac{3}{2}\left(a_3^2\left[(1-\sigma)\lambda V_h^*\right]^2 + a_4^2k^2\right)\\
&\left(a_4(d+\delta+\mu_1) - a_1\frac{\lambda b_1}{2\mu_1} - a_2(1-\sigma)\frac{\lambda b_1}{2\mu_1}\right)\left[a_5\left(\mu_2 + \frac{\gamma b_1}{\mu_1}\right) + a_6\left(-\frac{\gamma b_1}{2\mu_1}\right)\right] > \frac{3}{4}a_5^2\left(\gamma S_v^*\right)^2\\
&\left(a_4(d+\delta+\mu_1) - a_1\frac{\lambda b_1}{2\mu_1} - a_2(1-\sigma)\frac{\lambda b_1}{2\mu_1}\right)\left[a_6\left(\mu_1 - \frac{\gamma b_1}{2\mu_1}\right) - \frac{\beta b_1}{2\mu_1}(a_1+a_3)\right] > \frac{3}{4}a_6^2\left(\gamma S_v^*\right)^2
\end{aligned} \tag{4.2}$$

(For proof see Appendix-A)

5 The effect of vaccination

5.1 Analysis of vaccination-free model

Consider the system (2.2) in the absence of vaccination, obtained by setting $V_h = \psi = 0$ in system (2.2), given by

$$\begin{aligned}
\frac{dS_h}{dt} &= b_1 - \lambda S_h I_h - \beta S_h I_v - \mu_1 S_h,\\
\frac{dE_h}{dt} &= \lambda S_h I_h + \beta S_h I_v - (k+\mu_1)E_h,\\
\frac{dI_h}{dt} &= kE_h - dI_h - \delta I_h - \mu_1 I_h,\\
\frac{dS_v}{dt} &= b_2 - \gamma S_v I_h - \mu_2 S_v,\\
\frac{dI_v}{dt} &= \gamma S_v I_v - \mu_2 I_v.
\end{aligned} \tag{5.1}$$

We will consider the dynamic behaviour of system (5.1) on Ω_0 as:

$$\begin{aligned}
\Omega_0 = \Bigg\{ &(S_h, E_h, I_h, S_v, I_v) \in \mathbf{R}_+^6 : 0 \leqslant S_h + E_h + I_h \leqslant \frac{b_1}{\mu_1}, 0 \leqslant S_v + I_v \leqslant \frac{b_2}{\mu_2}, S_h \leqslant \frac{b_1}{\mu_1},\\
&S_v \leqslant \frac{b_2}{\mu_2}, S_h \geqslant 0, , E_h \geqslant 0, I_h \geqslant 0, S_v \geqslant 0, I_v \geqslant 0\Bigg\}.
\end{aligned} \tag{5.2}$$

It is easy to see that the region (5.2) is a positive invariant set of system (5.1).

5.2 Disease free equilibrium and reproduction number

The disease free equilibrium can be obtained by setting $I_h = I_v = 0$. The Disease free equilibrium of the system (5.1) in the region (5.2), is given by $E^0 = \left(S_h^0, E_h^0, I_h^0, S_v^0, I_v^0\right) = \left(\frac{b_1}{\mu_1}, 0, 0, \frac{b_2}{\mu_2}, 0\right)$.
Define

$$\mathcal{R}_0 = \frac{\mu_2^2 b_1 k\lambda + \beta k\gamma b_1 b_2}{\mu_1\mu_2^2(\mu_1+\psi)(k+\mu_1)(d+\delta+\mu_1)}.$$

The linearization of the system (5.1) at the equilibrium E^0 gives the following characteristic equation:

$$(-\eta-\mu_1)(-\eta-\mu_2)\left(\eta^3+c_2\eta^2+c_1\eta+c_0\right)=0.$$

From the characteristic equation, we obtain two eigen values as $-\mu_1$, $-\mu_2$ and the remaining eigenvalues can be obtained from the following cubic equation

$$\eta^3+c_2\eta^2+c_1\eta+c_0=0,$$

where

$$\begin{aligned}
c_2 &= [\mu_2+(k+\mu_1)+(d+\delta+\mu_1)],\\
c_1 &= [\mu_2(k+\mu_1)+(d+\delta+\mu_1)+\beta k\gamma D+(k+\mu_1)(d+\delta+\mu_1)(1-\mathcal{R}_0)],\\
c_0 &= \mu_2(k+\mu_1)(d+\delta+\mu_1)(1-\mathcal{R}_0).
\end{aligned}$$

Here $D=\frac{b_1b_2}{\mu_1\mu_2^2}$. Since, $c_2>0$, and $c_0>0$, $c_2c_1>c_0$ if $\mathcal{R}_0<1$.
Hence, by using Hurwitz's criteria, we can state the following theorem.

Theorem 5.1. The Disease free equilibrium (without vaccination) is linearly asymptotically stable if $\mathcal{R}_0<1$ and unstable if $\mathcal{R}_0>1$.

5.3 Existence of endemic equilibrium without vaccination

The endemic equilibrium of the system (5.1) without vaccination is given by $E^1=\left(\bar{S_h},\bar{E_h},\bar{I_h},\bar{S_v},\bar{I_v}\right)$ where $\bar{S_h}=\frac{b_2}{(\gamma\bar{I_h}+\mu_2)}$,$\bar{E_h}=\frac{d+\delta+\mu_1}{k}\bar{I_h}$,$\bar{S_v}=\frac{b_2}{(\gamma\bar{I_h}+\mu_2)}$,$\bar{I_v}=\frac{\gamma b_2}{\mu_2(\gamma\bar{I_h}+\mu_2)}\bar{I_h}$ and $\bar{I_h}$ is given by the quadratic equation

$$a_0\bar{I_h}^2+a_1\bar{I_h}+a_2=0, \tag{5.3}$$

where

$$\begin{aligned}
a_0 &= (k+\mu_1)(d+\delta+\mu_1)\mu_2^2\lambda\gamma,\\
a_1 &= (k+\mu_1)(d+\delta+\mu_1)\left[\left(\mu_2^2\lambda+\beta\gamma b_2\right)\mu_2+(1-\mathcal{R}_0)\right]+b_1b_2\beta\gamma^2,\\
a_2 &= (k+\mu_1)(d+\delta+\mu_1)\mu_1\mu_2^3(1-\mathcal{R}_0).
\end{aligned}$$

We state the following theorem to determine the existence of the endemic equilibrium:

Theorem 5.2. Every equation of an even degree, whose last term is negative, has at least two real roots, one positive and the other negative.

Since, $a_0>0$. Now two cases arise:

Case 1. when $\mathcal{R}_0>1$, then $a_2<0$, therefore, by Theorem 5.2 the Equation (5.3) has a unique positive real root.

Case 2. when $\mathcal{R}_0\leq 1$, then $a_1>0$ and $a_2>0$, therefore, by Descartes' rule of sign Equation (5.3) has no positive real root.

Thus, we can conclude that Equation (5.3) has unique positive real root. Hence system (5.1) a unique endemic equilibrium point whenever $\mathcal{R}_0>1$ and no positive endemic equilibrium $\mathcal{R}_0\leq 1$

5.4 Stability of endemic equilibrium without Vaccination

The endemic equilibrium $E^1=\left(\bar{S_h},\bar{E_h},\bar{I_h},\bar{S_v},\bar{I_v}\right)$ is non-linearly asymptotically stable in the region Ω_0 provided the following conditions are satisfied:

$$\begin{aligned}
&\left[c_1\left(\mu_1+(\lambda+\beta)\bar{I_h}-\frac{\lambda b_1}{2\mu_1}\right)-c_2\left(\frac{\beta b_2}{2\mu_1}\right)\right]\left[\left((k+\mu_1)-\frac{\lambda b_1}{2\mu_1}-\frac{\beta b_2}{2\mu_2}\right)\right]>\frac{3}{4}c_2\left(\lambda\bar{I_h}\right)^2\\
&c_2\left((k+\mu_1)-\frac{\lambda b_1}{2\mu_1}-\frac{\beta b_2}{2\mu_2}\right)\left[c_3(d+\delta+\mu_1)-(c_1+c_2)\frac{\lambda b_1}{2\mu_1}-(c_4+c_5)\frac{\gamma b_2}{2\mu_1}\right]>\frac{3}{4}(c_3k)^2\\
&\left((k+\mu_1)-\frac{\lambda b_1}{2\mu_1}-\frac{\beta b_2}{2\mu_2}\right)\left[c_5\left(\mu_2-\frac{\lambda b_2}{2\mu_2}\right)-c_1\frac{\beta b_1}{2\mu_1}\right]>\frac{3}{2}c_2\left(\beta\bar{S_h}\right)^2\\
&c_4\left(\mu_2+\gamma\bar{I_h}-\frac{1}{2}\gamma y_4^2\frac{b_2}{\mu_2}\right)\left[c_5\left(\mu_2-\frac{\lambda b_2}{2\mu_2}\right)-c_1\frac{\beta b_1}{2\mu_1}\right]>\frac{1}{2}\left(c_5\gamma\bar{I_h}\right)^2
\end{aligned} \tag{5.4}$$

(For proof see Appendix-B)

5.5 Dependence on vaccination rate

We will view ψ as a variable and consider all other parameters fixed. Practically, ψ is the easiest variable to control. Later, we will articulate our results in terms of an uncontrolled system with parameters $b_1, b_2, \mu_1, \mu_2, \lambda, \beta, \delta, \gamma$ and d fixed and analyze the impact of varying ψ. Keeping this in view, we will refer to the basic reproductive number $\mathcal{R}_v(\psi)$ of the model (2.2). The derivative of $\mathcal{R}_v(\psi)$ is given as:

$$\mathcal{R}_v'(\psi) = -\left[\frac{\mu_2^2 b_1 k\lambda\sigma\mu_1 + \beta k\gamma b_1 b_2\mu_1}{\mu_1\mu_2^2\left(k+\mu_1\right)\left(d+\delta+\mu_1\right)\left(\mu_1+\psi\right)^2}\right] \tag{5.5}$$

From equation (5.5) of $\mathcal{R}_v'(\psi)$, it is clear that $\mathcal{R}_v'(\psi) \leqslant 0$, therefore, $\mathcal{R}_v(\psi)$ is decreasing function in $\psi \geqslant 0$. This shows the effect of vaccination in reducing the vaccine reproduction number. Further, if there is no vaccination,i.e,

$$\psi = V = 0, \qquad \mathcal{R}_v(\psi) = \frac{\mu_2^2 b_1 k\lambda + \beta k\gamma b_1 b_2}{\mu_1\mu_2^2\left(k+\mu_1\right)\left(d+\delta+\mu_1\right)} = \mathcal{R}_0.$$

It is worth to mention here that the introduction of vaccination results $\mathcal{R}_v(\psi) \leqslant \mathcal{R}_0$, therefore, if $\mathcal{R}_0 < 1$ then $\mathcal{R}_v(\psi) < 1$ when $\sigma > 0$. Hence, E_0 is locally asymptotically stable provided that $\mathcal{R}_v(\psi) < 1$.

From the expression of $\mathcal{R}_0$, we have

$$(1-\sigma)\mathcal{R}_0 = \frac{(1-\sigma)(\mu_2^2 b_1 k\lambda + \beta k\gamma b_1 b_2)}{\mu_1\mu_2^2\left(k+\mu_1\right)\left(d+\delta+\mu_1\right)} \leqslant \mathcal{R}_v(\psi) \leqslant \mathcal{R}_0.$$

In order to find the critical value for vaccine-related reduction rate of infection. let us assume that $\frac{(1-\sigma)(\mu_2^2 b_1 k\lambda+\beta k\gamma b_1 b_2)}{\mu_1\mu_2^2(k+\mu_1)(d+\delta+\mu_1)} \geqslant 1$ then we have $\sigma > \sigma^*$ and

$$\sigma* = 1 - \frac{\mu_1\mu_2^2\left(k+\mu_1\right)\left(d+\delta+\mu_1\right)}{(\mu_2^2 b_1 k\lambda + \beta k\gamma b_1 b_2)}.$$

This implies that $\mathcal{R}_v(\psi) > 1$ and consequently, signifies that no amount of vaccine can now bring $\mathcal{R}_v(\psi) < 1$. Thus σ^* defines the critical value for vaccine-related reduction rate of infection. Suppose that $\lim_{\psi\to\infty}\mathcal{R}_v(\psi) = \frac{(1-\sigma)(\mu_2^2 b_1 k\lambda)}{\mu_1\mu_2^2(k+\mu_1)(d+\delta+\mu_1)} = \mathcal{R}^*$. Since $0 \leqslant \sigma < 1$, therefore, $\mathcal{R}^* \leqslant \mathcal{R}_0$. This implies that $\mathcal{R}^* < 1$ iff $\psi \to \infty$ and $\sigma \to 1$ i.e., in order to bring $\mathcal{R}^*$ is less than one, we have to significantly increase the vaccination rate provided the vaccine efficacy is high (almost 100% protective). Using $\mathcal{R}^*$ and $\mathcal{R}_0$, we can write $\mathcal{R}_v(\psi) = \frac{\mu_1\mathcal{R}_0+\psi\mathcal{R}^*}{\mu_1+\psi}$. Let us suppose that $\mathcal{R}_v(\psi) = 1$ and solving for ψ, we can obtain a threshold vaccination rate, $\psi^* = \frac{\mu_1(\mathcal{R}_0-1)}{1-\mathcal{R}^*}$.

Further, consider $\mathcal{R}^* < 1 < \mathcal{R}_0$, then we can get ψ^* positive. As $\mathcal{R}_v(\psi)$ is decreasing function for $\psi > 0$, in case $\psi > \psi^*$, then, $\mathcal{R}_v(\psi) < 1$. This shows that, if the rate of vaccination ψ is greater than the threshold ψ^*, the disease eradication is possible provided $\sigma \to 1$ (high vaccine efficacy).

From equation (2.2) we have

$$\frac{dV_h}{dt} = \psi S_h - (1-\sigma)\lambda V_h I_h - \mu_1 V_h.$$

When the population is at equilibrium we have $\psi^{**} = \frac{\mu_1 V_h^*}{S_h^*}$.

ψ^{**} is the critical rate of vaccination required for disease eradication, when the population is at equilibrium state. Thus, disease eradication is possible, if we choose ψ such that $\psi > max\left\{\psi^*, \psi^{**}\right\}$.

Remark 5.3. The model (2.2) has a stable disease-free equilibrium point for $\mathcal{R}_v < 1$, and it follows that the vaccination free model (5.1) also has a disease-free equilibrium point for $\mathcal{R}_0 < 1$. At the disease-free equilibrium the critical fraction that must be vaccinated can be determined. It is useful and informative to determine the elimination condition of the population that are vaccinated at equilibrium, given by $f = \frac{V_h(0)}{N_1(0)} = \frac{\psi}{\psi+\mu_1}$.

6 Optimal Control Problem

In this section, we formulate and analyse an optimal control problem applied to vector-host dynamics described by the system (2.2). We aim to find the optimal control $v^*(t) = \left(\psi(t), \beta(t), \mu_v(t)\right)^T \in \mathbb{R}^3$, which are represented as:

$\psi(t)$ for rate of vaccination, $\beta(t)$ is the control strategy that aims to limit the transmission of pathogen by reducing human contact with vector and $\mu_v(t)$ the control strategy for the elimination of vector population. The broad range of vector control tools that can be generally adopted are given in [29]. The control strategies are used to minimise the infected human population size, vector population size and the cost of this controlling efforts. We use Pontryagins Minimum Principle to investigate the optimal level of effort required to control the vector transmitted disease [5]. The ultimate preselected objective is to minimise the infected human population, reduce the human contact with vector and minimise the vector population at minimal cost over a finite time interval $[0, t_f]$. Thus, the objective function to be minimised is defined as:

$$J[(\psi(t), \beta(t), \mu_v(t)] = \frac{1}{2}\int_0^{t_f} \left[A_1 I_h^2 + A_2 I_v^2 + A_3\psi^2(t) + A_4\beta^2(t) + A_5\mu_v^2(t)\right] \mathrm{d}t. \tag{6.1}$$

The parameters $A_i > 0$ for $(i = 1, 2, 3, 4, 5)$ denote the dimensionless weight functions of the relative cost of the interventions over $[0, t_f]$. The aim of the optimal control problem is to search for optimum control functions $(\psi^*(t), \beta^*(t), \mu_v^*(t))$ such that

$$J(\psi^*, \beta^*, \mu_v^*) = min\{J(\psi, \beta, \mu_v) \mid \psi, \beta, \mu_v \in \mathcal{U}\}, \tag{6.2}$$

where $\mathcal{U} = \{(\psi, \beta, \mu_v) \mid \psi, \beta, \mu_v : [0, t_f] \to [0, 1], \forall\psi, \beta, \mu_v\}$ subject to system (2.6). Pontryagin's Minimum Principle is used to derive the necessary conditions that an optimal control must satisfy. This principle transforms system (2.2) and (6.1) into a minimisation problem. We determine the Hamiltonian function by introducing the costate vector also known as Lagrange multiplier $\lambda(t) \in \mathbb{R}^6$ as:

$$\begin{aligned} H =& A_1 I_h^2(t) + A_2 I_v^2(t) + A_3\psi^2(t) + A_4\beta^2(t) + A_5\mu_v^2(t) \\ &+ \lambda_1\left[b_h - \lambda S_h I_h - \beta S_h I_v - (\mu_h + \psi)\right] + \lambda_2\left[\psi S_h - (1-\sigma)\lambda V_h I_h - \mu_h V_h\right] \\ &+ \lambda_3\left[\lambda S_h I_h + (1-\sigma)\lambda V_h I_h + \beta S_h I_v - (k + \mu_h) E_h\right] + \lambda_4\left[kE_h - (d + \delta + \mu_h) I_h\right] \\ &+ \lambda_5\left[b_v - \gamma S_v I_h - \mu_v S_v\right] + \lambda_6\left[\gamma S_v I_h - \mu_v I_v\right]. \end{aligned} \tag{6.3}$$

We prove the existence of an optimal control for system (2.2) by the following theorem using the Pontragin's Minimum principle.

Theorem 6.1. Let ψ^*, β^* and μ_v^* be the optimal controls for the model system (2.2), χ^* the state space at equilibrium, and λ_i be positive semi-definite piecewise differentiable functions for all t and $i = 1, 2, ...6$. Supposes that, for all $t \in [0, t_f]$,

$$\begin{aligned} 0 =& H_\psi(t, \chi^*, \psi^*, \beta^*, \mu_v^*, \lambda(t)), \\ & H_\beta(t, \chi^*, \psi^*, \beta^*, \mu_v^*, \lambda(t)), \\ & H_{\mu_v}(t, \chi^*, \psi^*, \beta^*, \mu_v^*, \lambda(t)), \end{aligned} \tag{6.4}$$

then

$$H(t, \chi^*, \psi^*, \beta^*, \mu_v^*, \lambda(t)) \leq H(t, \chi, \psi, \beta, \mu_v, \lambda(t)) \tag{6.5}$$

holds for optimal control ψ^*, β^* and μ_v^*.

Proof . We differentiate the Hamiltonian with respect to each of the state variables; to find the differential equations with respect to the associated adjoint functions as:

$$\begin{aligned} \frac{d\lambda_1}{dt} =& \lambda_1\mu_h + \lambda_1\psi - \lambda_2\psi + \lambda_1\beta I_v - \lambda_3\beta I_v + \lambda_1\lambda I_h - \lambda_3\lambda I_h, \\ \frac{d\lambda_2}{dt} =& \lambda\mu_h + \lambda_2(1-\sigma)\lambda I_h - \lambda_3(1-\sigma)\lambda I_h, \\ \frac{d\lambda_3}{dt} =& \lambda_3\mu_h + \lambda_3 k - \lambda_4 k, \\ \frac{d\lambda_4}{dt} =& \lambda_4(d + \delta + \mu_h) - C_1 I_h + \lambda_1\lambda S_h - \lambda_3\lambda S_h + \lambda_2\lambda(1-\sigma)V_h - \lambda_3\lambda(1-\sigma)V_h \\ & + \lambda_5\gamma S_v - \lambda_6\gamma S_v, \\ \frac{d\lambda_5}{dt} =& \lambda_5\mu_v + \lambda_5\gamma I_h - \lambda_6\gamma I_h, \\ \frac{d\lambda_6}{dt} =& \lambda_6\mu_v + \lambda_1\beta S_h - C_2 I_v - \lambda_3\beta S_h, \end{aligned} \tag{6.6}$$

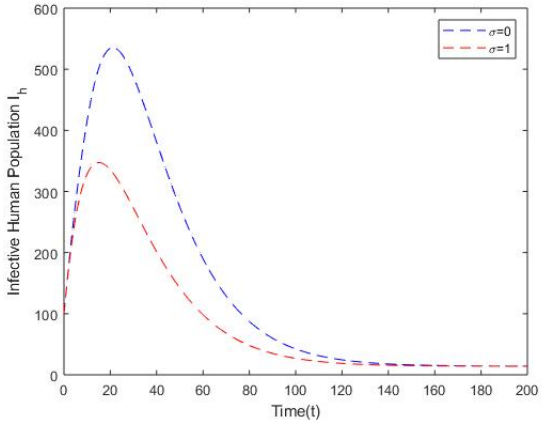

Figure 1: Variation of infective human(host) population for ($\sigma = 0$) and $\sigma = 1$) with respect to time t

with transversality condition

$$\lambda_1(t_f) = \lambda_2(t_f) = \lambda_3(t_f) = \lambda_4(t_f) = \lambda_5(t_f) = \lambda_6(t_f) = 0. \tag{6.7}$$

To determine the adjoint equations for given transversality condition (6.7), the following hold

$$\frac{d\lambda_1}{dt} = -\frac{\partial H}{\partial S_h}, \qquad \frac{d\lambda_2}{dt} = -\frac{\partial H}{\partial V_h} \qquad \frac{d\lambda_3}{dt} = -\frac{\partial H}{\partial E_h}, \qquad \frac{d\lambda_4}{dt} = -\frac{\partial H}{\partial I_h}, \tag{6.8}$$

$$\frac{d\lambda_5}{dt} = -\frac{\partial H}{\partial S_v}, \qquad \frac{d\lambda_6}{dt} = -\frac{\partial H}{\partial I_v}. \tag{6.9}$$

The following expressions describe the optimal control

$$\begin{aligned} \psi^*(t) &= max\left\{0, min\left(\bar{\psi}(t), 1\right)\right\}, \\ \beta^*(t) &= max\left\{0, min\left(\bar{\beta}(t), 1\right)\right\}, \\ \mu_v^*(t) &= max\left\{0, min\left(\bar{\mu_v}(t), 1\right)\right\}. \end{aligned} \tag{6.10}$$

By standard control arguments involving the bounds on the controls, we conclude

$$\psi^* = \begin{cases} 0, & \text{if } \bar{\psi} \le 0. \\ \bar{\psi}, & \text{if } 0 < \bar{\psi} < 0., \\ 1, & \text{if } \bar{\psi} \ge 1. \end{cases} \quad \beta^* = \begin{cases} 0, & \text{if } \bar{\beta} \le 0. \\ \bar{\beta}, & \text{if } 0 < \bar{\beta} < 0., \\ 1, & \text{if } \bar{\beta} \ge 1. \end{cases} \quad \mu_v^* = \begin{cases} 0, & \text{if } \bar{\mu_v} \le 0. \\ \bar{\mu}, & \text{if } 0 < \bar{\mu_v} < 0. \\ 1, & \text{if } \bar{\mu_v} \ge 1. \end{cases} \tag{6.11}$$

□

7 Numerical simulation

In this section our aim is to explore, through a non-linear model, the role of control strategies and impact of vaccination on the spread of vector borne diseases. To show the existence of equilibrium values of variables of the system (2.2) as well as the feasibility of stability conditions numerically, we integrate the systems by fourth order Runge-Kutta method using MATLAB. To study the dynamical behaviour of the system (2.2), numerical simulation of the system is done by using the following parameters.
$b_1 = 1, \lambda = 0.0004, \beta = 0.0586, \mu_1 = 0.006, \gamma = 0.000000256, \mu_2 = 0.006,\ d = 0.0023, \delta = 0.0553, k = 0.050, \sigma = 0.2, b_2 = 0.0023, \psi = 0.0003$ The equilibrium values are computed as follows:
$E^* = (105.35118, 4.19185, 6.12039, 4.81163, 0.36170, 0.02163)$.
The eigenvalues corresponding to variational matrix of endemic equilibrium E^* are:
$-0.0058 + 0.0042i, -0.0058 - 0.0042i, -0.0060, -0.0077, -0.0168, -0.1064$. It is noted here that all the eigenvalues corresponding to endemic equilibrium E^* are found to be negative or having negative real parts, therefore, endemic equilibrium E^* is locally asymptotically stable for the above set of parameter values. The results of numerical

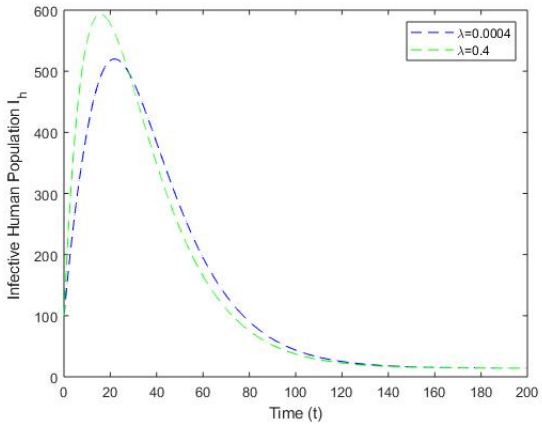

Figure 2: Variation of infective human(host) population for ($\lambda = 0.0004$) and $\lambda = 0.4$) with respect to time t

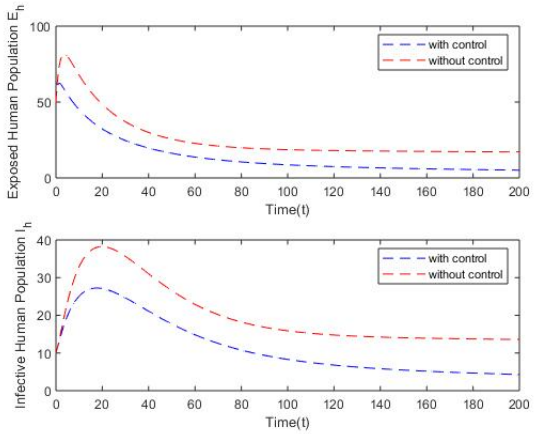

Figure 3: Variation of infective and exposed human(host) population for ψ with respect to time t

simulation are shown graphically in Figure. 1. In Figure. 1, the variation of infective human (host) population is shown for different values of vaccination efficacy σ. It is found that as vaccination efficacy (σ) increases, the infective human (host) population decreases. The graphic result displayed in Figure. 1 signifies that only by increasing the vaccination efficacy, spread of vector-borne disease cannot be significantly controlled. The effect of λ (rate of direct transmission) on the infective human (host) population is displayed in Figure. 2. It is seen that as the rate of direct transmission increases, the infective human population increases. This increase in infective human population is due to the increase in direct transmission (possibly through blood transfer or through sexual contact) of disease.

The primary aim of the present study is to investigate the impact of vaccination and control measures on the spread of vector borne disease. Therefore, we perform a comprehensive numerical study to analyse the impact of control related parameters on the disease dynamics. As explained earlier (in "Optimal Control 6" section), the optimal strategy is obtained by solving the state and adjoint systems and the transversality conditions. Three different control strategies are suggested analytically. Figure 3 show the variation of infective and exposed population with time for control parameter ψ^* , the vaccination rate of susceptible population. It is seen that without control, the infective and exposed population significantly increases as compared to when there is control. This is due to the reason that in presence of control the susceptible population will get vaccinated, so infected and exposed population will be reduced significantly. Figure 4 displays the impact of control variable β^* on infective and exposed human population. It is seen that infective and exposed population is decreased significantly with control variable. β. This decline in infective as well as exposed population is due to crubs on the spread of disease by pathogen carrier vectors using control measures. The impact of control strategy is displayed in Figure 5. It is found that with control parameter μ_2^*, the infective population as well as exposed population is sharply declined. This decrease in infective and exposed population is due to the decrease in vector population by using the vector control tools.

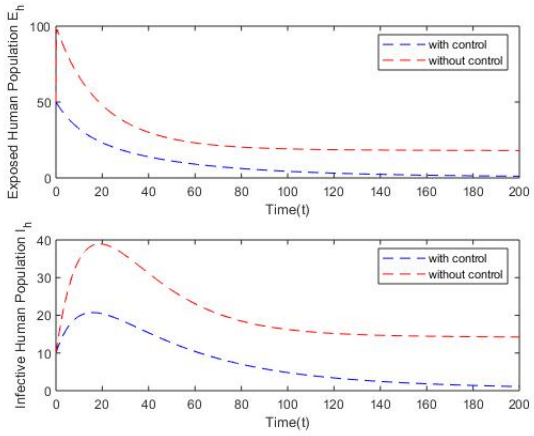

Figure 4: Variation of infective and exposed human(host) population for control parameter β with respect to time t

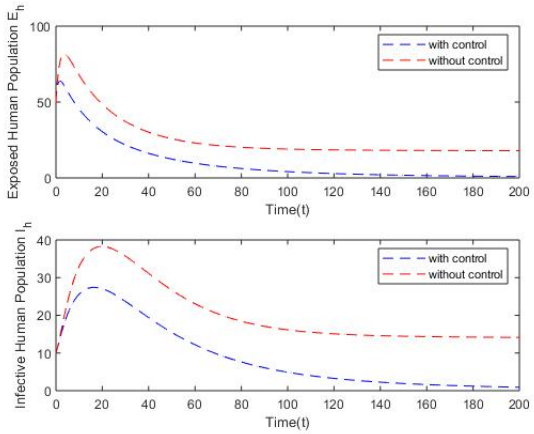

Figure 5: Variation of infective human (host) population for control parameter μ_2^* with respect to time t

8 Conclusion

In this paper, we developed and analyzed a mathematical model for vector borne diseases with vaccination and control measures. We assume that only a susceptible individual can be vaccinated and that the vaccine is imperfect i.e, not 100% protective. We analyzed the model with and without vaccination, formulated the vaccine reproduction number and discussed the stability of disease-free and endemic equilibrium. The analytical results suggests that, in order to eradicate the vector borne disease, the vaccination reproduction number $\mathcal{R}_v$ should be less than one. The increase in vaccination rate will be helpful to obtain the vaccination reproduction number $\mathcal{R}_v$ less than one. The study for vaccine reproduction number suggests that higher values of vaccination rate ψ reduce the infected population significantly.

We also considered the problem of optimal control of the transmission dynamics of a vector borne disease. The optimal control strategy presented involve three control parameters associated with rate of vaccination, human host protection and the vector reduction strategies are considered. The control graphs which we have plotted show that the infected and exposed population of infective and exposed human decreased. It also showed that in the optimality system, total number of vector population diminishes. For the existence of an optimal control, the control system is analyzed by using Pontryagin's Maximum Principle. Furthermore, to illustrate the effectiveness and efficiency of the proposed control problem, numerical simulations have been displayed. The results indicates that vector reduction is very effective in reducing the incidence of infectious hosts.

Appendix-A

We transform the system (2.2) by applying the transformation $S_h = S_h^* + x_1, V_h = V_h^* + x_2, E_h = E_h^* + x_3, I_h = I_h^* + x_4, S_v = S_v^* + x_5, I_v = I_v^* + x_5$, we have

$$\begin{aligned}
\frac{dx_1}{dt} =& -\lambda S_h^* x_4 - \lambda I_h^* x_1 - \lambda x_1 x_4 - \beta S_h^* x_6 - \beta I_v^* x_1 - \beta x_1 x_6 - (\mu_1 + \psi) x_1 \\
\frac{dx_2}{dt} =& \psi x_1 - (1-\sigma)\lambda I_h^* x_2 - (1-\sigma)\lambda x_2 x_4 - (1-\sigma)\lambda x_4 V_h^* - \mu_1 x_2 \\
\frac{dx_3}{dt} =& \lambda S_h^* x_4 + \lambda x_1 x_4 + (1-\sigma) V_h^* x_4 + (1-\sigma)\lambda x_2 x_4 + \beta S_h^* x_6 + \beta x_1 x_6 + \lambda I_h^* x_1 \\
& + \beta I_v^* x_1 + (1-\sigma)\lambda I_h x_2 - (k+\mu_1) x_3 \\
\frac{dx_4}{dt} =& k x_3 - (d + \delta + \mu_1) x_4 \\
\frac{dx_5}{dt} =& -\gamma S_v^* x_4 - \gamma I_h^* x_5 - \gamma x_4 x_5 - \mu_2 x_5 \\
\frac{dx_6}{dt} =& \gamma S_v^* x_4 + \gamma I_h^* x_5 - \gamma x_4 x_5 - \mu_2 x_6
\end{aligned}$$

Now, consider the Lyapunov function as

$$V_1 = \frac{1}{2}\left[a_1 x_1^2 + a_2 x_2^2 + a_3 x_3^2 + a_4 x_4^2 + a_5 x_5^2 + a_6 x_6^2\right]$$

we have

$$\begin{aligned}
\frac{dV_1}{dt} =& a_1\left[-\lambda x_1 x_4 (S_h^* + x_1) - (\lambda I_h^* + \beta I_v) x_1^2 - \beta x_1 x_6 (S_h^* + x_1) - (\mu_1 + \psi) x_1^2\right] \\
& + a_2\left[\psi x_1 x_2 - (1-\sigma)\lambda (V_h^* + x_2) x_2 x_4 - (1-\sigma)\lambda I_h^* x_2^2 - \mu_1 x_2^2\right] \\
& + a_3\left[\lambda (I_h^* + x_4) x_1 x_3 + (1-\sigma)\lambda (I_h^* + x_4) x_2 x_3 + \beta (S_h^* + x_1) x_3 x_6 + \lambda S_h^* x_3 x_4 + (1-\sigma)\lambda V_h^* x_3 x_4\right. \\
& \left. + \beta x_1 x_3 I_v^* - (k+\mu_1) x_3^2\right] + a_4\left[k x_4 x_3 - (d+\delta+\mu_1) x_4^2\right] + a_5\left[-\gamma (I_h^* + x_4) x_5^2 - \gamma S_v x_4 x_5 - \mu_2 x_5^2\right] \\
& + a_6\left[\gamma S_v^* x_4 x_6 + \gamma (I_h^* + x_4) x_5 x_6 - \mu_2 x_6^2\right]
\end{aligned}$$

Now using the inequality $\pm 2ab \leqslant \left(a^2 + b^2\right)$ and also using region Ω on the right hand side of the above equation, we get

$$\begin{aligned}
\frac{dV_1}{dt} =& a_1\left[-\lambda x_1 x_4\left(\frac{b_1}{\mu_1}\right) - (\lambda I_h^* + \beta I_v) x_1^2 - \beta x_1 x_6\left(\frac{b_1}{\mu_1}\right) - (\mu_1 + \psi) x_1^2\right] \\
& + a_2\left[\psi x_1 x_2 - (1-\sigma)\lambda\left(\frac{b_1}{\mu_1}\right) x_2 x_4 - (1-\sigma)\lambda I_h^* x_2^2 - \mu_1 x_2^2\right] \\
& + a_3\left[\lambda\left(\frac{b_1}{\mu_1}\right) x_3 x_4 + (\lambda I_h^* + \beta I_v^*) x_1 x_3 + \beta\left(\frac{b_1}{\mu_1}\right) x_3 x_6 + (1-\sigma)\lambda\left(\frac{b_1}{\mu_1}\right) x_2^2 + (1-\sigma)\lambda V_h^* x_4 x_3\right. \\
& \left. - (k+\mu_1) x_3^2\right] + a_4\left[k x_4 x_3 - (d+\delta+\mu_1) x_4^2\right] + a_5\left[-\gamma\left(\frac{b_2}{\mu_2}\right) x_5^2 - \gamma S_v x_4 x_5 - \mu_2 x_5^2\right] \\
& + \left[\gamma S_v^* x_4 x_5 + \gamma\left(\frac{b_2}{\mu_2}\right) x_5 x_6 - \mu_2 x_6^2\right] \\
=& a_1\left[\lambda\frac{b_1}{2\mu_1} x_1^2 + \frac{\lambda b_1}{2\mu_1} x_4^2 - x_1^2 (\lambda I_h + \beta I_v) + \frac{\beta b_1}{2\mu_1} x_1^2 + \frac{\beta b_1}{2\mu_1} x_6^2 - (\mu_1 + \psi) x_1^2\right] \\
& + a_2\left[\psi x_1 x_2 + (1-\sigma)\frac{\lambda b_1}{2\mu_1} x_2^2 + (1-\sigma)\frac{\lambda b_1}{2\mu_1} x_4^2 - (1-\sigma)\lambda I_h x_2^2 - \mu_2^2\right] \\
& + a_3\left[\frac{\lambda b_1}{2\mu_1} x_1^2 + \frac{\lambda b_1}{2\mu_1} x_3^2 + (1-\sigma)\lambda\frac{b_1}{2\mu_1} x_2^2 + (1-\sigma)\lambda\frac{b_1}{2\mu_1} x_3^2 + \beta\frac{b_1}{2\mu_1} x_3^2 + \beta\frac{b_1}{2\mu_1} x_6^2 + (1-\sigma)\lambda V_h^* x_3 x_4\right. \\
& \left. + \beta x_1 x_3 I_v^* - (k+\mu_1) x_3^2\right] + a_4\left[k x_3 x_4 - (d+\delta+\mu_1) x_4^2\right] + \left[-\gamma S_v^* x_4 x_5 - \gamma\frac{b_1}{\mu_1} x_5^2 - \mu_2 x_5^2\right] \\
& + a_6\left[\gamma S_v x_4 x_6 + \gamma\frac{b_1}{2\mu_1} x_5^2 + \gamma\frac{b_1}{2\mu_1} x_6 - \mu_2 x_6^2\right]
\end{aligned}$$

$$= -\left[\left(\frac{1}{2}a_{11}x_1^2 - a_{12}x_1x_2 + a_{22}x_2^2\right) + \left(\frac{1}{2}a_{11}x_1^2 - a_{13}x_1x_3 + \frac{1}{2}a_{33}x_3^2\right) + \left(\frac{1}{2}a_{33}x_3^2 - a_{34}x_3x_4 + \frac{1}{3}a_{44}x_4^2\right) + \left(\frac{1}{3}a_{44}x_4^2 - a_{45}x_4x_5 + a_{55}x_5^2\right) + \left(\frac{1}{3}a_{44}x_4^2 - a_{46}x_4x_6 + a_{66}x_6^2\right)\right]$$

where

$$\begin{aligned}
a_{11} =& a_1\left((\lambda I_h^* + \beta I_v^*) + (\mu_1 + \psi) - \frac{\lambda b_1}{2\mu_1} - \frac{\beta b_1}{2\mu_1}\right) - a_3\left(\frac{\lambda b_1}{2\mu_1}\right)\\
a_{22} =& a_2\left((1-\sigma)\lambda I_h^* + \mu_1 - (1-\sigma)\frac{\lambda b_1}{2\mu_1}\right) - a_3\left((1-\sigma)\frac{\lambda b_1}{2\mu_1}\right)\\
a_{33} =& a_3\left((k+\mu_1) - \frac{\lambda b_1}{2\mu_1} - (1-\sigma)\frac{\lambda b_1}{2\mu_1} - \frac{\beta b_1}{2\mu_1}\right)\\
a_{44} =& a_4(d+\delta+\mu_1) - a_1\frac{\lambda b_1}{2\mu_1} - a_2(1-\sigma)\frac{\lambda b_1}{2\mu_1}\\
a_{55} =& a_5\left(\frac{\gamma b_1}{\mu_1} + \mu_2\right) - a_6\frac{\gamma b_1}{2\mu_1}\\
a_{66} =& a_6\left(\mu_2 - \frac{\gamma b_1}{2\mu_1}\right) - a_3\frac{\beta b_1}{2\mu_1} - a_1\frac{\beta b_1}{2\mu_1}\\
a_{12} =& a_2\psi \qquad\qquad a_{13} = a_3(\beta I_v^*)\\
a_{34} =& a_3(1-\sigma)\lambda V_h^* + a_4 k, \qquad a_{45} = -\gamma S_v a_5, \qquad a_{46} = \gamma S_v a_6
\end{aligned}$$

Using Sylvester's criteria, it can be observed that $\frac{dV_1}{dt}$ is negative definite under the conditions (4.2).

Appendix-B

Applying the transformation $S_h = \bar{S}_h + y_1, E_h = \bar{E}_h + y_2, I_h = \bar{I}_h + y_3, S_v = \bar{S}_v + y_4, I_v = \bar{I}_v + y_5$ we have

$$\begin{aligned}
\frac{dy_1}{dt} &= -\lambda y_3\bar{S}_h - \lambda y_1\bar{I}_h - \lambda y_1y_3 - \beta y_5\bar{S}_h - \beta y_1\bar{I}_v - \beta y_1y_5 - \mu_1 y_1\\
\frac{dy_2}{dt} &= \lambda y_3\bar{S}_h + \lambda y_1\bar{I}_h + \lambda y_1y_3 + \beta y_5\bar{S}_h + \beta y_1\bar{I}_v + \beta y_1y_5 - (k+\mu_1)y_2\\
\frac{dy_3}{dt} &= ky_2 - dy_3 - \delta y_3 - \mu_1 y_3\\
\frac{dy_4}{dt} &= -\gamma y_3\bar{S}_v - \gamma y_4\bar{I}_h - \gamma y_3y_4 - \mu_2 y_4\\
\frac{dy_5}{dt} &= \gamma y_3\bar{S}_v + \gamma y_4\bar{I}_h - \gamma y_3y_4 - \mu_2 y_5
\end{aligned}$$

Now, consider the Lyapunov function as:

$$V_2 = \frac{1}{2}\left(c_1y_1^2 + c_2y_2^2 + c_3y_3^2 + c_4y_4^2 + c_5y_5^2\right)$$

we have

$$\begin{aligned}
\frac{dV_2}{dt} =& c_1\left[-\lambda y_1y_3\left(\bar{S}_v + y_1\right) - \lambda y_1^2\bar{I}_h - \beta y_1y_5\left(\bar{S}_v + y_1\right) - \beta y_1^2\bar{I}_h - \mu_1 y_1^2\right] + c_2\left[\lambda y_2y_3\left(\bar{S}_h + y_1\right)\right.\\
&\left.+\beta y_1y_2\left(\bar{I}_v + y_5\right) + \lambda y_1y_2\bar{I}_h + \beta y_2y_5\bar{S}_h - (k+\mu_1)y_2^2\right] + c_3\left[ky_2y_3 - (d+\delta+\mu_1)y_3^2\right]\\
&+ c_4\left[-\gamma y_3y_4\left(\bar{S}_v + y_4\right) - \gamma y_4^2\bar{I}_h - \mu_2 y_4^2\right] + c_5\left[\gamma y_3y_5\left(\bar{S}_v + y_4\right) + \gamma y_4y_5\bar{I}_h - \mu_2 y_5^2\right]
\end{aligned}$$

Now using the inequality,$\pm 2ab \leqslant \left(a^2+b^2\right)$ on the right hand side of $\frac{dV_2}{dt}$, we find that

$$\begin{aligned}\frac{dV_2}{dt} =& c_1\left[\frac{1}{2}\lambda y_1^2\left(\bar{S}_v+y_1\right)+\frac{1}{2}\lambda y_3^2\left(\bar{S}_v+y_1\right)-\lambda y_1^2\bar{I}_h+\frac{1}{2}\beta y_1^2\left(\bar{S}_v+y_1\right)+\frac{1}{2}\beta y_5^2\left(\bar{S}_v+y_1\right)-\beta y_1^2\bar{I}_h-\mu_1 y_1^2\right]\\ &+c_2\left[\frac{1}{2}\lambda y_2^2\left(\bar{S}_h+y_1\right)+\frac{1}{2}\lambda y_3^2\left(\bar{S}_h+y_1\right)+\frac{1}{2}\beta y_1^2\left(\bar{I}_v+y_5\right)+\frac{1}{2}\beta y_2^2\left(\bar{I}_v+y_5\right)+\lambda y_1y_2\bar{I}_h+\beta y_2y_5\bar{S}_h\right.\\ &\left.-\left(k+\mu_1\right)y_2^2\right]+c_3\left[ky_2y_3-\left(d+\delta+\mu_1\right)y_3^2\right]+c_4\left[\frac{1}{2}\gamma y_3^2\left(\bar{S}_v+y_4\right)+\frac{1}{2}\gamma y_4^2\left(\bar{S}_v+y_4\right)-\gamma y_4^2\bar{I}_h-\mu_2 y_4^2\right]\\ &+c_5\left[\frac{1}{2}\gamma y_3^2\left(\bar{S}_v+y_4\right)+\frac{1}{2}\gamma y_5^2\left(\bar{S}_v+y_4\right)+\gamma y_4y_5\bar{I}_h-\mu_2 y_5^2\right]\end{aligned}$$

Again using the region Ω_0 on the right hand side of the above inequality, we get

$$\begin{aligned}\frac{dV_2}{dt} =& c_1\left[\frac{1}{2}\lambda y_1^2\frac{b_1}{\mu_1}+\frac{1}{2}\lambda y_3^2\frac{b_1}{\mu_1}-\lambda y_1^2\bar{I}_h+\frac{1}{2}\beta y_1^2\frac{b_1}{\mu_1}+\frac{1}{2}\beta y_5^2\frac{b_1}{\mu_1}-\beta y_1^2\bar{I}_h-\mu_1 y_1^2\right]\\ &+c_2\left[\frac{1}{2}\lambda y_2^2\frac{b_1}{\mu_1}+\frac{1}{2}\lambda y_3^2\frac{b_1}{\mu_1}+\frac{1}{2}\beta y_1^2\frac{b_2}{\mu_2}+\frac{1}{2}\beta y_2^2\frac{b_2}{\mu_2}+\lambda y_1y_2\bar{I}_h+\beta y_2y_5\bar{S}_h-\left(k+\mu_1\right)y_2^2\right]\\ &+c_3\left[ky_2y_3-\left(d+\delta+\mu_1\right)y_3^2\right]+c_4\left[\frac{1}{2}\gamma y_3^2\frac{b_2}{\mu_2}+\frac{1}{2}\gamma y_4^2\frac{b_2}{\mu_2}-\gamma y_4^2\bar{I}_h-\mu_2 y_4^2\right]\\ &+c_5\left[\frac{1}{2}\gamma y_3^2\frac{b_2}{\mu_2}+\frac{1}{2}\gamma y_5^2\frac{b_2}{\mu_2}+\gamma y_4y_5\bar{I}_h-\mu_2 y_5^2\right]\\ =& -\left[\left(c_{11}y_1^2-c_{12}y_1y_2+\frac{1}{3}c_{22}y_2^2\right)+\left(\frac{1}{3}c_{22}y_2^2-c_{23}y_2y_3+c_{33}y_3^2\right)\right.\\ &\left.+\left(\frac{1}{3}c_{22}y_2^2-c_{25}y_2y_5+\frac{1}{2}c_{55}y_5^2\right)+\left(c_{44}y_4^2-c_{45}y_4y_5+\frac{1}{2}c_{55}y_5^2\right)\right]\end{aligned}$$

where

$$\begin{aligned}c_{11} =& c_1\left(\mu_1+\left(\lambda+\beta\right)\bar{I}_h-\frac{\lambda b_1}{2\mu_1}\right)-c_2\left(\frac{\beta b_2}{2\mu_1}\right) & c_{22} =& c_2\left(\left(k+\mu_1\right)-\frac{\lambda b_1}{2\mu_1}-\frac{\beta b_2}{2\mu_2}\right)\\ c_{33} =& c_3\left(d+\delta+\mu_1\right)-\left(c_1+c_2\right)\frac{\lambda b_1}{2\mu_1}-\left(c_4+c_5\right)\frac{\gamma b_2}{2\mu_1} & c_{44} =& c_4\left(\mu_2+\gamma\bar{I}_h-\frac{1}{2}\gamma y_4^2\frac{b_2}{\mu_2}\right)\\ c_{55} =& c_5\left(\mu_2-\frac{\lambda b_2}{2\mu_2}\right)-c_1\frac{\beta b_1}{2\mu_1} & c_{12} =& c_2\lambda\bar{I}_h\\ c_{23} =& c_3k, & c_{25} =& c_2\beta\bar{S}_h\\ c_{45} =& c_5\gamma\bar{I}_h.\end{aligned}$$

Now, using Sylvester's criteria, it can be observed that $\frac{dV_2}{dt}$ is negative definite under the conditions (5.4).

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